

Ethnicity, Family, and Social Networks:  
A Multiscalar Bioarchaeological Investigation of Tiwanaku Colonial

Organization in the Moquegua Valley, Peru

by

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## ABSTRACT

Many models of colonial interaction are built from cases of European colonialism among Native American and African peoples, and, as a result, they are often ill-suited to account for state expansion and decline in non-Western contexts. This dissertation investigates social organization and intraregional interaction in a non-western colonial context to broaden understanding of colonial interaction in diverse sociocultural settings. Drawing on social identity theory, population genetics, and social network analysis, patterns of social organization at the margins of the expansive pre-Hispanic Tiwanaku state (ca. AD 500-1100) are examined.

According to the dual diaspora model of Tiwanaku colonial organization in the Moquegua Valley of southern Peru, Chen Chen-style and Omo-style ethnic communities who colonized the valley maintained distinct ethnic identities in part through endogamous marriage practices. Biodistance analysis of cranial shape data is used to evaluate regional gene flow among Tiwanaku-affiliated communities in Moquegua. Overall, results of biodistance analysis are consistent with the dual diaspora model. Omo- and Chen Chen-style communities are distinct in mean cranial shape, and it appears that ethnic identity structured gene flow between ethnic groups. However, there are notable exceptions to the overall pattern, and it appears that marriage practices were structured by multiple factors, including ethnic affiliation, geographic proximity, and smaller scales of social organization, such as corporate kin groups.

Social network analysis of cranial shape data is used to implement a multi- and mesoscalar approach to social organization to assess family-based organization at a regional level. Results indicate the study sample constituted a social network comprised

of a dense main component and a number of isolated actors. Formal approaches for identifying potential family groups (i.e., subgroup analysis) proved more effective than informal approaches. While there is no clear partition of the network into distinct subgroups that could represent extended kin networks or biological lineages, there is a cluster of closely related individuals at the core of the network who integrate a web of less-closely related actors. Subgroup analysis yielded similar results as agglomerative hierarchical cluster analysis, which suggests there is potential for social network analysis to contribute to bioarchaeological studies of social organization and bioarchaeological research in general.

This dissertation is dedicated to my parents, Kent and Judy Johnson, and my wife,  
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## CHAPTER 1

### INTRODUCTION

The rise and fall of states as political institutions dramatically alters relationships within and between human communities, particularly in cases of political expansion and colonization. Many models of colonial interaction are derived from examples of European colonialism among Native American and African peoples and are often ill-suited to account for state expansion and decline in non-Western contexts (see Das and Poole, 2004; Ferguson and Whitehead, 1992a; Gosden, 2004; Hill, 1996; Voss, 2008). This dissertation investigates social organization and intraregional interaction in a non-western colonial context to broaden understanding of colonial interaction in diverse sociocultural settings and contribute to the development of general models of state expansion and colonization. Drawing on social identity theory, population genetics, and social network analysis I examine patterns of social organization at the margins of the pre-Hispanic expansive Tiwanaku state. I use phenotypic data to evaluate the ethnicity-based dual diaspora model of social organization within the Tiwanaku colonies in the Moquegua Valley of southern Peru. Additionally, I develop a mesoscale approach to social organization that uses social identity theory and social network analysis to explore family-based affiliations within Tiwanaku-affiliated communities in Moquegua. This multiscale approach to social organization considers how ethnic and kin identities created an interwoven fabric of affiliations that structured patterns of social interaction within the multiethnic Tiwanaku colonies in Moquegua.

Situated at an elevation of 3850 meters above sea level (masl) in the Andean *altiplano* (i.e., high-altitude plains) of northern Bolivia, the site of Tiwanaku developed

from a nondescript village into a complex urban center whose influence spanned the south central Andes (e.g., Bermann, 1994, 1997; Isbell and Vranich, 2004; Janusek, 1999, 2004a,b, 2005a,b, 2008; Kolata, 1982, 1985, 1986, 1993a,b, 1997, 2003; Posnansky, 1914, 1945, 1957; Stanish, 2002, 2003; Vranich, 1999). Over the course of the Middle Horizon (ca. AD 500-1100), Tiwanaku material culture, ideology, and rituals were exported by Tiwanaku colonists and adopted by diverse ethnic communities located in the coastal valleys in what are now southern Peru and northern Chile, the high desert inland oases of northern Chile, and the intermontane regions on the eastern slopes of the Andes in Bolivia (e.g., Anderson, 2013; Bennett, 1936; Berenguer and Dauelsberg, 1989; Browman, 1981, 1997; Céspedes Paz, 1993; Goldstein, 1985, 1996, 1989a, 2005; Knudson, 2004, 2007; Knudson et al., 2004; Knudson and Torres-Rouff, 2014; Kolata, 1992, 1993b; Oakland Rodman, 1992; Ponce Sanginés, 1980, 1981; Torres-Rouff, 2008; Torres-Rouff et al., 2013).

Tiwanaku scholars have long been interested in how Tiwanaku influence came to span such a large region of the Andes. Depictions of Tiwanaku's political economy and means of expansion and integration have changed dramatically over the past several decades. The Tiwanaku polity was initially thought to represent a centralized expansive state (Goldstein, 1989a,b, 1993b; Kolata, 1993a,b, 1997, 2003; Moseley et al., 1991; Stanish, 2002, 2003). This interpretation was based on the rapid growth of the city of Tiwanaku, including the unprecedented construction of monumental architecture (Escalante M., 1993; Kolata, 1993a; Manzanilla, 1992) during Tiwanaku IV (AD 400 – 800). Additionally, a four-tiered hierarchical settlement pattern emerged in the state



hinterland (Albarracín-Jordán, 1996; Bandy, 2001; Janusek and Kolata, 2003; McAndrews et al., 1997).

During Tiwanaku V (AD 800 – 1150), there is evidence of increasing bureaucratic centralization and consolidation. The city of Tiwanaku was reorganized into residential neighborhoods (Couture, 2003; Janusek, 1999, 2002, 2004a). Competition increased between elite factions as elite residences and elite-sponsored feasts became more ostentatious (Janusek, 2008). As a result, elites tightened control over agricultural production at hinterland and provincial sites (Goldstein, 1989b, 1993b, 2005, 2009; Janusek, 2004a, 2008; Janusek and Kolata, 2004).

As additional data have been amassed from the Tiwanaku heartland and periphery, interpretations of Tiwanaku sociopolitical orientation have shifted. It appears that Tiwanaku was not a classically imperial state like the contemporaneous Wari polity (e.g., Edwards et al., 2014; Lumbreras, 1974; Moseley et al., 2005; Nash and Williams, 2009; Schreiber, 1992, 2001, 2005; Tung, 2012; cf. Jennings, 2010) nor the more recent Inka empire (e.g., Alconini, 2008; Andrushko and Torres, 2011; Bauer and Covey, 2002; D’Altroy, 2001, 2003; Morris, 1982; Murra, 1986; Rostworowski de Diez Canseco, 1988). Instead, Tiwanaku is often portrayed as a loosely confederated segmentary state within which affiliated communities were linked through shared ideology and economic interaction (Albarracín-Jordán, 1996a,b; Bermann, 1994, 1997; Browman, 1978, 1980, 1984, 1997; Goldstein, 2005, 2009; Janusek, 1999, 2004a, 2008; Mathews, 1997; McAndrews et al., 1997).

The work of Juan Albarracín-Jordán has been influential among Tiwanaku scholars who favor a more heterarchical interpretation of Tiwanaku sociopolitical

organization. Albarracín-Jordán (2003) notes that the heterogeneous nature of buildings and diverse stone-carving styles at the site of Tiwanaku reflect the influence of multiple social groups within Tiwanaku society. Seeking an Andean-specific model for pre-Hispanic social organization, Albarracín-Jordán builds upon ethnographic and ethnohistoric accounts of Andean social organization (Bastien, 1978; Bouysse-Cassagne, 1987, 1988; Murra, 1975; Platt, 1982; Ponce Sanginés, 1983, 1985) and suggests the various social groups at Tiwanaku were *ayllus*. *Ayllus* are multiscale social groups in contemporary Andean highland societies composed of nested levels of affiliation ranging from household kin groups (minimal *ayllus*) to ethnic communities (maximal *ayllus*) (Abercrombie, 1998; Albarracín-Jordán, 1996a; Allen, 1988; Bastien, 1978; Isbell, 1978). Thus, Tiwanaku society is interpreted within a uniquely Andean framework and imagined as a confederation of autonomous settlements articulated through non-coercive, reciprocal relationships cemented through ritual and family ties (i.e., *ayllus*), rather than a state-level centralized bureaucracy (Albarracín-Jordán, 1996a,b, 2003).

Additional evidence from the Tiwanaku heartland supports interpretations of Tiwanaku society as comprised of diverse social groups thought to represent *ayllus*. Janusek (1999, 2002, 2003, 2004a,b, 2005a,b) argues that the production and use of distinct ceramic assemblages by different residential compounds was important in creating and reproducing social boundaries between households, ethnic communities, and Tiwanaku-affiliated regions. These distinct social groups simultaneously used Tiwanaku corporate styles and engaged in shared practices that signaled their membership in the Tiwanaku sphere and forged bonds across social boundaries (Bermann, 1994; Janusek, 1999, 2002, 2004a,b, 2005a,b). This pattern of social diversity has also been identified

within site groups in the Tiwanaku periphery (e.g., Goldstein, 2005, 2015; Hoshower et al., 1995; Knudson et al., 2014; Owen, 2005; Torres-Rouff et al., 2013).

Although recent interpretations have tended to favor heterarchical portrayals of Tiwanaku sociopolitical organization, evidence for Tiwanaku as a powerful, hierarchical state – from the urban core with its monumental architecture, status-differentiated residential sectors, hinterland settlement hierarchy, and increasingly centralized agriculture production – cannot be denied (Berryman, 2010; Goldstein, 2005; Janusek, 2004b; Kolata, 1986; Stanish, 2003). In fact, contrasts between Tiwanaku expansion and Wari and Inka expansion may have been overstated. Current depictions of Tiwanaku sociopolitical organization fall somewhere between the two extremes of heterarchy and hierarchy, blending aspects of each (Berryman, 2010; Goldstein, 2013; Stanish, 2013; Stanish et al., 2010).

### **Tiwanaku social organization in the Moquegua Valley colonies**

One of the best-documented Tiwanaku-affiliated peripheral regions is the Moquegua Valley of southern Peru, which lies approximately 300 km from the Tiwanaku capital in the Bolivian *altiplano*. The Moquegua Valley is part of the Osmore Drainage, a component of the Pacific Watershed on the western slopes of the Andes. The lower Osmore Drainage consists of three environmental zones: the lower, middle, and upper valleys (Williams, 1997). The middle valley, also called the Moquegua Valley, has a wide valley floor circumscribed by low hills that facilitate irrigation agriculture both in the past and today (Goldstein, 2005; Williams, 2002).

The Tiwanaku colonial enclave established in the Moquegua Valley between AD 600 and AD 1000 was comprised of two Tiwanaku-affiliated populations: camelid

agropastoralists who used Omo-style ceramics and maize agricultural specialists associated with Chen Chen-style ceramics (e.g., Blom et al., 1998; Buikstra, 1995; García Marquez, 1990; Goldstein, 1985, 1989a,b, 1993a,b, 2005; Goldstein and Owen, 2001; Knudson et al., 2004; Moseley et al., 1991; Owen, 1997; Owen and Goldstein, 2001; Vargas, 1994). Initially Omo and Chen Chen settlements were thought to represent temporally discrete Tiwanaku occupations (Goldstein, 1985), but subsequent survey, excavation, and radiocarbon data indicate Omo- and Chen Chen-style Tiwanaku communities were contemporaries in the Moquegua colony (Goldstein, 2005; Owen, 2005; Owen and Goldstein, 2001).

The Tiwanaku colonial enclave in the Moquegua Valley persisted for approximately three hundred years. Around the beginning of the eleventh century AD, incipient factionalism in the Tiwanaku homeland contributed to the diminished influence of the Tiwanaku state in the *altiplano* and peripheral regions (Goldstein, 1993b, 2005; Janusek, 2004b, 2005a; Owen and Goldstein, 2001). In the lower Osmore Drainage, this decrease in Tiwanaku state influence, combined with local water shortages caused by upriver Wari irrigation systems, prompted Tiwanaku-affiliated communities to abandon their large middle Moquegua Valley settlements in favor of smaller, fortified or naturally-protected settlements in previously uninhabited regions of the upper Moquegua Valley and the coastal Ilo Valley (Bawden, 1989, 1993; Goldstein, 2005; Owen, 1993, 2005; Owen and Goldstein, 2001; Sharratt, 2011; Sims, 2006; Stanish, 1992; Umire and Miranda, 2001; Williams, 2002).

Decades of research in the lower Osmore Drainage have contributed greatly to our understanding of the Tiwanaku colonial presence in Moquegua. Early systematic

archaeological research in the Moquegua Valley strongly supported the centralized state model of Tiwanaku political organization and expansion (Goldstein, 1989a,b, 1993a,b; Moseley et al., 1991). Goldstein (2005) has recently reinterpreted the nature of the Tiwanaku presence in Moquegua. Building on Murra's (1964, 1968, 1972, 1975, 1985) multi-ethnic vertical archipelago model of Andean sociopolitical organization, Goldstein (2005) argues the Tiwanaku colony did not begin as a state-driven project, but instead resulted from the expansion of Tiwanaku corporate groups who established diasporic archipelago settlements in the valley. These kin-based groups belonged to two different maximal *ayllus*, Chen Chen- and Omo-style ethnic communities, and members of these "dual diasporas" likely saw themselves as part of an imagined Tiwanaku corporate identity, not a centralized *altiplano* state (Goldstein, 2005).

Consistent with data from the *altiplano* sites of Tiwanaku and Lukurmata (e.g., Janusek, 2002, 2004a,b, 2005a,b), Tiwanaku communities in Moquegua shared practices and ideologies that connected them to the broader Tiwanaku sphere, while they simultaneously asserted their differences through material culture styles and practices brought with them from their respective homelands (Goldstein, 2005; see also Korpisaari, 2006). Chen Chen- and Omo-style communities differed across a variety of cultural domains including ceramic styles, subsistence strategies, settlement patterns, residential architecture, and funerary practices (Baitzel, 2008; Goldstein, 1989a,b, 1993a, 2000b, 2005, 2009; Goldstein and Owen, 2001; Hoshower et al., 1995; Knudson and Blom, 2009; Owen and Goldstein, 2001; Sharratt, 2011). It is also suggested that Omo and Chen Chen communities maintained separate group identities for several centuries in part

through endogamous marriage practices (Goldstein, 2005, 2009; see also Goldstein and Owen, 2001; Owen and Goldstein, 2001).

The dual diaspora model proposed for Middle Horizon Tiwanaku colonists in the Moquegua Valley is supported by much of the current archaeological evidence from the region, and it has been applied effectively by other scholars (e.g., Knudson, 2011).

However, there is some evidence to suggest the social and cultural boundaries between Omo- and Chen Chen-style communities were permeable. Sharratt (2011: 148) describes a hybrid vessel excavated in 2002 that has a polished black-ware, Omo-style interior and a red-slipped Chen Chen-style exterior decorated with stair-step motifs. Additionally, an Omo-style jar was found associated with a burial from the site of Chen Chen-style site of Chen Chen M1 (Lewis, 2005: 142).

Evidence of cultural hybridity and cross-cultural interaction, although limited, highlights the need to evaluate endogamous marriage practices posited for Omo- and Chen Chen-style communities. This hypothesis has not been assessed previously, due in part to the lack of Omo-style Tiwanaku skeletal samples (Goldstein, 2005). The recent exhumation and curation of two Omo-style skeletal samples (see Baitzel, 2008; Goldstein, 2005; Knudson et al., 2014; Oquiche et al., 2003) make it possible for the first time to evaluate the biological implications of the dual diaspora model of Moquegua Tiwanaku social organization.

Evaluating the dual diaspora model using biological data represents a significant step in the process of refining interpretive models applied to archaeological data. Ethnographic and ethnohistoric studies of Andean communities emphasize the fluidity of *ayllu* membership and the degree of inter-community variation in marriage practices,

rules of descent, and post-marital residence practices (e.g., Abercrombie, 1998; Bastien, 1978; Harris, 1978; Murra, 1972; Platt, 1982; Rasnake, 1988), and multiple investigations of Andean archaeological contexts have found that mate exchange was not as strictly governed as suggested by ethnohistoric accounts (Lozada Cerna and Buikstra, 2002; Nystrom and Malcom, 2010; Sutter, 2005). Thus, the assumption of *ayllu*-based group endogamy among pre-Hispanic ethnic groups requires formal evaluation.

Among contemporary Andean highland Aymara and Quechua communities *ayllu* is a salient axis of social organization. *Ayllu* can be difficult to define because it describes a flexible and multiscalar social identity, much like the English word “group” (Rasnake, 1988; see also Abercrombie, 1986, 1998; Urton, 1990). For example, the term *ayllu* is used to refer to one’s family, a network of families, a neighborhood, or a village depending on the context (e.g., Abercrombie, 1986; Isbell, 1997; Urton, 1990; Valderrama Fernandez and Escalante Guitierrez, 1996). As a result, *ayllu* is sometimes defined in a scale-free, functional way as any group of social, political, economic, and ritual cohesion or action (Urton, 1990: 22). *Ayllus* organize and sponsor ritual events, prepare feasts and drinking bouts, and enact ceremonies that map social relationships, reinforce member affiliation, and reify group solidarity (Abercrombie, 1998; Bastien, 1978; Platt, 1986).

Although the concept of *ayllu* is variable (Isbell, 1997; Rasnake, 1988), there is a core notion of what constitutes an *ayllu*. In its most basic form an *ayllu* is a group of households bound together in part through descent from a common ancestor and through ties to a particular landscape (Albó et al., 1972; Allen, 1988; Bandelier, 1911; Bastien, 1978; Harris, 1978; Isbell, 1978; Izko, 1986; LaBarre, 1948; Platt, 1987; Rasnake, 1988).

It is this level of *ayllu* organization, referred to as the minimal *ayllu* or *microayllu*, that is comparable to a corporate kin group and therefore is likely to represent a fundamental axis of individual affiliation and identity. Minimal *ayllus* are often exogamous, largely because of taboos regarding sexual and marital relations with close kin (Bastien, 1978; Isbell, 1977; Rasnake, 1988).

The most inclusive form of *ayllu* organization is variously termed ‘unitary *ayllu*’, ‘maximal *ayllu*’, or ‘macro*ayllu*’. Such large scale *ayllus* are comparable to ethnic groups (Izko, 1986; Platt, 1982). Larger *ayllu* collectives, such as maximal *ayllus* or *sayas* (a meso-level of *ayllu* organization between minimal and maximal that is comparable to moiety) are generally endogamous, as these are typically perceived more as administrative- or ritual-based collectives that envelop multiple kin groups rather than representing a kin-based collectivity themselves (Hickman and Stuart, 1977).

Archaeological and bioarchaeological investigations of social organization among Osmore Drainage Tiwanaku-affiliated communities emphasize ethnic-level group affiliations (Blom, 1999; Blom et al., 1998; Goldstein, 2005; Owen, 2005; Sutter and Sharratt, 2010). In fact, the only formal model of Moquegua Tiwanaku social organization, the dual diaspora model (Goldstein, 2005), is based upon ethnic-level affiliations (see also Owen, 2005). While this approach has yielded important insights, the emphasis on ethnic level patterns of organization inadvertently may neglect the role of smaller scales of social affiliation in the daily lives of individuals in the past.

Archaeologists and ethnographers recognize the critical role of family relationships and obligations in structuring present-day Andean social organization (e.g., Goldstein, 2005, 2013; Van Vleet, 2008). Tiwanaku scholars report settlement and



economic activity patterns that seemingly highlight the importance of kin-based social organization in the heartland and the periphery. Residential neighborhoods at the site of Tiwanaku were organized around spatially discrete compounds (Janusek, 2003, 2004a,b, 2005a,b). Each residential compound had its own kitchen, patio space, storage facilities, and space for domestic animals, and it is believed each compound was inhabited by a household (i.e., social house). Janusek (2002, 2003, 2004a,b, 2005a,b) suggests this repeated pattern of nested residential space reflects the centrality of kin-based affiliations to Tiwanaku social organization.

Diasporic communities reproduced the homeland social system in the peripheral colonies, including the recursive social hierarchy into maximal (ethnic), moiety, and minimal *ayllu* units (Goldstein, 2005). Omo-style settlements in the Moquegua Valley exhibit segmentary organization with “numerous insular communities, each arrayed around its own common plaza for assembly or ritual” (Goldstein, 2009: 284). Goldstein (2005, 2009) hypothesizes that Omo-style plaza-centered neighborhoods are comparable to present-day minimal *ayllus* (i.e., corporate kin groups) whose distinct identities were maintained in part through their spatial separation in residence and ritual activities. However, the dual diaspora model of Moquegua Valley Tiwanaku social organization emphasizes ethnic-level (maximal *ayllu*) affiliations over corporate kin group (minimal *ayllu*) affiliations (see Goldstein, 2005; Owen, 2005; cf. Lewis, 2005).

Previous studies have investigated smaller scales of affiliation among Middle Horizon (ca. AD 500-1100) Tiwanaku-affiliated communities in the Moquegua Valley, including corporate kin-based organization, but still we know little about how smaller scales of social organization influenced patterns of interaction and affiliation within these

communities. This is because prior efforts evaluated data from different sites independently and because previous investigations of kin-structuring within Middle Horizon Chen Chen-style Tiwanaku mortuary contexts have produced mixed results. Correlations between different cranial modification techniques and spatially discrete cemeteries at the Omo site group (M10 and M11) suggest a scenario in which different corporate groups, perhaps similar to minimal *ayllus*, maintained their own cemeteries (Buikstra, 1995; Hoshower et al., 1995). In contrast, spatial distributions of cranial modification, mortuary, genotypic, and phenotypic data suggest a larger, ethnic scale of social affiliation, perhaps similar to a maximal *ayllu*, was emphasized at the site of Chen Chen M1 (Blom, 1999, 2005b; Blom et al., 1998; Sharratt, 2011; see also Lewis, 2005). Notably, Blom (1999, 2005b; Blom et al., 1998) did not find evidence of corporate kin-based cemetery use at the M1 site.

Thus, it appears that social organization within Middle Horizon Tiwanaku communities in the Moquegua Valley was influenced by diverse affiliations that cut across multiple scales of social groups (i.e., corporate, ethnic, and regional level affiliations), and these different aspects of social identity were variably expressed within and between sites through cultural practices including, for example, mortuary rituals and cranial modification techniques. Yet few studies of Moquegua Tiwanaku social organization have incorporated a multiscale framework. Blom (1999, 2005a,b; Blom et al., 1998) investigated patterns of social affiliation using bioarchaeological data, but her research combined an intrasite analysis of Chen Chen M1 with an interregional analysis of Tiwanaku-affiliated samples from the *altiplano* and the Moquegua Valley. As such,

her project was not designed to identify patterns of variation within the Moquegua Valley in the sense of an intraregional analysis.

In contrast, a recent study by Sharratt (2011) highlights the value of implementing a multiscalar research design for investigating social organization among Tiwanaku-affiliated communities. Sharratt reports that intracommunity affiliations were more important among the residents of the post-collapse site of Tumilaca la Chimba than they were among the Middle Horizon inhabitants of the middle valley site of Chen Chen M1, where expressions of community-wide ethnic affiliation were predominant (Sharratt, 2011; see also Blom, 1999; Blom et al., 1998). However, Sharratt's investigation included only two sites, and its focus was temporal rather than spatial: an intrasite analysis of a site (Chen Chen M1) occupied primarily prior to the decline of Tiwanaku state influence compared with an intrasite analysis of a site (Tumilaca la Chimba) occupied primarily after the decline of Tiwanaku state influence. To investigate the ways diverse social affiliations (e.g., family, residential group, ethnic community) intersected to form the fabric of social organization that structured the lives of Middle Horizon Moquegua Tiwanaku peoples, a regional-level, multiscalar analysis of social organization using bioarchaeological data from multiple Tiwanaku-affiliated sites, including samples from Omo-style mortuary contexts, from the Moquegua Valley is needed.

### **Research orientation**

This dissertation complements previous research on Moquegua Tiwanaku social organization by implementing a multiscalar approach to social affiliation grounded in social identity theory that applies biodistance and social network analytical methods to bioarchaeological data from Tiwanaku-affiliated Middle Horizon (AD 500-1100)

contexts from the Moquegua Valley. The use of social identity theory to evaluate social organization is not new to bioarchaeological studies of lower Osmore Drainage contexts (e.g., Blom, 1999, 2005b; Blom et al., 1998; Buikstra et al., 2005; Hoshower et al., 1995; Knudson et al., 2004; Lewis, 2005; Lozada Cerna, 1998; Sharratt, 2011; Sutter, 2005, 2009a; Sutter and Sharratt, 2010), but the majority of this research has focused on ethnic-level or greater scales of social organization (cf. Blom, 1999, 2005b; Hoshower et al., 1995; Lewis, 2005; Sharratt, 2011). A multiscale approach to Andean social organization that does not reduce *ayllu* organization to a single aspect of social affiliation but is flexible enough to address multiple scales of *ayllu* affiliation, specifically kinship and ethnicity, is needed to reconstruct the complex sociality that structured interactions within pre-Hispanic communities.

Bioarchaeology is a theoretically-oriented field that incorporates data from human skeletal remains and associated mortuary settings into highly contextualized, smaller scale regional-, and site-based archaeological investigations (see Agarwal and Glencross, 2011; Buikstra and Beck, 2006; Larsen, 2015; Martin et al., 2013). However, bioarchaeological approaches to kinship remain largely rooted in outdated, predominantly Western notions of what constitutes kinship (Johnson and Paul, 2016; cf. Meyer et al., 2012; Pilloud and Larsen, 2011). This study draws from recent developments in sociocultural theory on kinship and the bioarchaeology of identities literature to develop a theoretical framework of family organization that can be used to investigate multiple

scales of social organization among Tiwanaku-affiliated communities in the Moquegua Valley.

Herein kinship is conceptualized more broadly as social relatedness, which may or may not include biological relationships as a salient aspect of relatedness (Bamford, 2009; Carsten, 2004; Franklin and McKinnon, 2001; Leach, 2009; McKinnon and Cannell, 2013; Sahlins, 2013; Viveiros de Castro, 2009). A broader conception of kinship as relatedness expands the criteria (e.g., cultural practices, concepts, perspectives, etc.) upon which family relationships can be based and make kinship (as relatedness) amenable to investigation as a multi-scale form of social identity (see Buikstra and Scott, 2009; Díaz-Andreu et al., 2005; Gowland and Knüsel, 2006; Insoll, 2007; Jones, 1997; Knudson and Stojanowski, 2008, 2009; Meskell, 2001). An identity-based analytical framework combined with biodistance analysis and the flexible analytical techniques afforded by social network analysis is used to explore connections between individual-, small group-, and community-level affiliations and thus provide a more complex and nuanced investigation of social organization in the past.

Analysis of phenotypic variation is used to investigate social organization within Middle Horizon Tiwanaku communities of the lower Osmore Drainage in southern Peru. Biodistance and exploratory data analysis of basicranial and temporal bone landmarks are used to evaluate patterns of gene flow among samples of human skeletal remains from five archaeological sites in the middle Moquegua Valley. Results are used to evaluate the dual diaspora model of multiethnic social organization within the Moquegua Tiwanaku colonies. In addition, social network analysis of basicranial and temporal bone landmarks is used to develop a family-based approach to social organization within the Tiwanaku

colonial enclave in the Moquegua Valley. Together these approaches provide a more nuanced and multiscalar model of *ayllu* organization for evaluating the influence of ethnic- and family-based social affiliation on patterns of social interaction within a non-Western colonial context.

### **Organization of the dissertation**

This dissertation is organized into five chapters. Chapter 2 presents the theoretical orientation for the dissertation, focusing on anthropological kinship research and social identity theory. Theoretical developments in sociocultural anthropology are reviewed, emphasizing the conceptual changes precipitated by the work of David Schneider, specifically the overall shift from viewing kinship as genealogical to kinship as social relatedness. Quantitative and qualitative literature reviews are used to assess the extent to which these developments have influenced bioarchaeological kinship research. A framework for approaching kinship as a mid- or multiscalar form of social identity is presented, and future areas of research are discussed.

Chapter 3 introduces the cultural context and background of recent work on social organization within the Tiwanaku colonies in the Moquegua Valley. The dual diaspora model of Moquegua Tiwanaku social organization is presented, including one of its secondary tenets or hypotheses: maximal *ayllu* communities maintained separate ethnic identities over 300 plus years of close contact in part through endogamous marriage practices. Phenotypic data are analyzed to evaluate this hypothesis in contrast with a model of isolation by distance. Results suggest that although maximal *ayllu* affiliations influenced or somewhat structured gene flow within the Moquegua Tiwanaku colonies, Omo- and Chen Chen-style communities were not strictly endogamous. Nor do the

results fit a pattern of isolation by distance. Instead, it appears that a mosaic of factors influenced marriage patterns. It is suggested that extended family networks along with ethnic affiliations likely structured marriage practices, gene flow, and phenotypic variation within Moquegua Tiwanaku communities.

Chapter 4 presents an initial attempt to apply social network analysis to phenotypic data collected from human skeletal remains. Social network analytical techniques are amenable to multiscalar analyses and provide a flexible alternative to traditional biodistance methods. The goal is to use social network analysis to scale up kinship analysis beyond the intracemetery and intrasite levels to investigate kin-based social relations at a regional scale. The basic tenets and concepts of social network analysis are introduced, and its applications within several subfields of anthropology (e.g., sociocultural, primatology, and archaeology) are reviewed. The appropriateness, benefits, and challenges of applying social network analysis to bioarchaeological data are considered, with special attention paid to the use of phenotypic data to identify potential kin networks comprised of close and extended biological relatives. Results of social network analysis are compared with those of other analytical methods (e.g., cluster analysis and multidimensional scaling) to evaluate the effectiveness at identifying kin-based social networks and the potential for applying social network analysis more broadly within bioarchaeology.

Chapter 5 presents a summary of the dissertation and its conclusions. This includes an evaluation of whether the dissertation successfully achieved its stated aims of developing an effective multiscalar framework for investigating social organization in archaeological contexts. The dissertation closes with a consideration of how future

research can contribute to increasingly nuanced research into family-based social organization in the past.



## CHAPTER 2

### BIOARCHAEOLOGY AND KINSHIP: INTEGRATING THEORY, SOCIAL RELATEDNESS, AND BIOLOGY IN ANCIENT FAMILY RESEARCH

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Family is a fundamental human institution that forms the basic social units of collective action beyond the individual agent. Families instill social roles and values in children, influence mate choices, and organize subsistence activities. Whereas family relationships are a near universal aspect of the human experience, conceptions of relatedness vary among societies past and present. In an era where the definition of “family” grows increasingly flexible and biosocial in nature, it is important that we place current conceptions of kinship within an expansive temporal perspective. The variable nature of family composition through time and space has important social and legal implications in our society in terms of who has the right to marry, to raise children, or to inherit material wealth. Investigating family-based social organization and social relatedness in the past helps highlight their fluid natures and, in turn, can help educate against general misperceptions and discrimination based on ideas about the naturalness of the nuclear family within human evolutionary history.

Why kinship? At a time when funding for the social sciences faces the constant threat of dissolution, it is imperative that social scientists communicate the relevance of their work. Why is it that we “care” about kinship? What are the practical applications of ancient family research? In Western academia, the resurgence of kinship studies, in part, reflects increasing politicization and popularization of “the family” as projected through public media (Carsten, 2000, 2004; Farber, 1981; Stone, 2001). In recent years,

legislation, news outlets, and even television programs have dedicated their attention to the “crisis of the family.” This is not surprising considering that the past several decades have witnessed scientific advances in reproductive technologies and sociopolitical movements that have challenged the “typical” Western family structure (see Blackwood, 2005; Butler, 2002; Edwards et al., 1999; Franklin, 2001; Hayden, 1995; Levine, 2003, 2008; Ragoné, 1996; Strathern, 1992c; Thompson, 2001; Weston, 1991).

The public’s fascination with ancient “family” burials and the importance of engaging broader audiences in (bio)archaeological research must also be acknowledged (Stojanowski and Duncan, 2015). Images of small group burials containing individuals interpreted as family members tend to capture the public imagination due to their propensity to invoke sentiments of empathy and commonality between modern and past peoples (e.g., Cohen, 2015: 35). It is for this reason, too, that we must continue to develop methods and theory aimed at more nuanced understandings of relatedness.

The study of kinship was a staple of ethnographic research for much of anthropology’s history as a discipline (e.g., Evans-Pritchard, 1951; Lévi-Strauss, 1969; Malinowski, 1913; Morgan, 1871; Radcliffe-Brown, 1952; Radcliffe-Brown and Forde, 1950; Rivers, 1914). Rivers’ (1910) genealogical method of fieldwork was a cornerstone of British social anthropology for decades (Bouquet, 1993). Envisioned as a “natural” system for recording relationships, genealogies have a complicated history within Western society (Bamford and Leach, 2009; Bouquet, 1993; Klapish-Zuber, 1991, 2000). Genealogical models of relatedness based on inheritance of shared biogenetic substance have served as the normative paradigm for conceptualizing kinship in Western society as far back as the Middle Ages. Drawing from traditions dating to classic antiquity, 11th-

century Christian scholars formalized the genealogy depicted as a family tree in order to represent Jesus Christ's ancestors (Klapish-Zuber, 1991, 2000), and by the 16th century family genealogies were popular across Europe (Connerton, 1989). Although Euro-Americans tend to take the language and symbols of genealogies as naturally constitutive aspects of kinship, genealogies were produced through experiments with different visual tools and organizing metaphors (Klapish-Zuber, 2000). Thus, the normative Western conception of relatedness emerged around the same time as Western conceptions of the body (Burkitt, 1999; Giddens, 1991), two critical components of modern Euro-American ontology.

Beginning in the 1960s, kinship research met considerable resistance from scholars who identified the concept as “biologistic” and at the root of anthropology's Eurocentric perspectives on social structure, broadly, and gender and “relatedness,” specifically (see Collier and Yanagisako, 1987; MacCormack and Strathern, 1980; Schneider, 1968, 1972, 1984). In response, kinship within sociocultural anthropology has largely been reconceptualized as a social process, and studies of kinship increasingly embrace more complex and culturally relativistic conceptions of relatedness (e.g., Carsten, 2000, 2004; Franklin and McKinnon, 2000, 2001). For example, Lévi-Strauss' “house society” model – in which social relatedness is primarily organized around shared space, practice, and (im)material property – emphasizes affinal relations over genealogical relations and has been applied as an alternative to biologically-structured kin systems in anthropological research over the past four decades (Lévi-Strauss, 1983a,b, 1984, 1987, 1991). More recently, Sahlins (2013: 2) has defined kinship as “mutuality of being”: people who are intrinsic to one another's existence....” a definition

that may prioritize social aspects of relatedness but accommodates genealogical or biological aspects of kinship relevant in many cultural contexts past and present, even though Sahlins ultimately considers these fundamentally social as well.

As sociocultural anthropologists began turning away from biological and genealogical approaches to kinship, biological anthropologists seized on genealogical kinship as a viable approach to understanding human origins and humankind's relationship with other primates. Since the mid-20th century, evolutionary scholarship has cited genetic relatedness as a vehicle for the rise of "behavioral modernism" and various human social behaviors (e.g., Hewlett, 2001; Salter, 2008; Silk, 1987; Silk and House, 2011). Most famously, Hamilton's Rule outlines a potential explanation for the practice of altruistic behavior among social organisms (Hamilton, 1964). This rule claims that altruism (i.e., an act that enhances another's fitness at the expense of the actor's) is selected for when the cost of performance is eclipsed by the benefit to the other individual, as weighted by their degree of genetic affinity to the actor (i.e., coefficient of relatedness) (Hamilton, 1964; Salter, 2002, 2008). Thus, biological affinity is thought to drive the behaviors of social actors (Hamilton, 1964; Silk, 1987; Trivers, 1971). Some have examined Hamilton's Rule as a means of understanding individual versus collective fitness within primate communities and evolutionary settings (e.g., Silk, 2002); other scholars have explored how genetic relatedness influences the actions of humans across various contexts (e.g., Hewlett, 2001).

Building on this theoretical framework, empirical ethnographic research on modern foraging societies also provides insights into the role of kinship in structuring social group composition and interaction (e.g., Bailey et al., 2014; Hill et al., 2011). Kin

co-residence, for example, has been found to have strong impacts on reproductive success and/or parenting investment (Ellsworth et al., 2014; Sear and Mace, 2008), marriage practices (Walker et al., 2013), social inequality or distribution of material wealth (Smith et al., 2010), and cooperative foraging and group size (Smith, 1985). Additional developments within evolutionary and/or biological anthropological approaches to kinship include kin recognition (e.g., Langergraber et al., 2007b; Lieberman et al., 2007; Pfeifferle et al., 2014), the origins of human and non-human primate kin formations and the social and environmental landscapes in which they emerged (e.g., Chapais, 2008, 2013, 2014; Hill et al., 2014; Jones, 2003, 2011; Wood and Marlowe, 2011), and relationships between kin-based social organization and other adaptive collective behaviors (e.g., altruism, cooperation, and the evolution of language) (e.g., Boyd et al., 2014; Langergraber et al., 2007a, 2011; Milicic, 2013; Shenk and Mattison, 2011).

Within anthropology there have been recent attempts to bridge the rift between sociocultural and biological approaches to kinship. For example, Chapais (2014) uses a comparative phylogenetic approach to demonstrate that the suite of complex social traits relating to kinship, what Chapais refers to as the “human kinship configuration”, has a deep evolutionary history and, thus, a biological foundation. Although Chapais (2014: 754) makes a compelling case for the dual nature of human kinship as “biological and cultural,” the comments made by kinship scholars on Chapais’ article demonstrate the extent to which Chapais’ approach unfortunately characterizes social aspects of kinship as secondary byproducts of a set of universal behaviors and reflect the extent to which evolutionary and sociocultural approaches to kinship continue to diverge. Developing an holistic approach to kinship that incorporates biological and cultural aspects requires

capturing the complexities of biocultural behaviors without reducing either the biological or social factors (McKinnon and Silverman, 2005).

As a synthetic field championing “biocultural” and problem-oriented research, bioarchaeology is well positioned to embrace novel conceptions of kinship and use diverse sets of data (i.e., biological and cultural) to undertake the challenge of reconstructing ancient kin relations (Meyer et al., 2012). Yet, intracemetery biodistance methods commonly employed in bioarchaeological investigations of “relatedness” are often focused on methodological improvement or generate inferences that are quite narrow in scope: reconstructing site formation processes, identifying kin-structured cemeteries, or assessing relatedness among skeletons interred within a collective grave, for example (Stojanowski and Schillaci, 2006). Although bioarchaeologists recognize the potential of kinship studies for addressing scales of sociopolitical organization relevant to broader anthropological questions (e.g., Alt and Vach, 1998; Case, 2003; Stojanowski and Schillaci, 2006), this potential remains relatively undeveloped, presenting a challenging but fruitful direction for future research (Meyer et al., 2012; Stojanowski and Schillaci, 2006). Of special promise is the use of social identity frameworks to address broader questions of human social organization in the past through kin-based social identity. To date, bioarchaeological studies of identity have concentrated on individual (e.g., osteobiographies) and community/population (e.g., age, gender, status, and ethnic identities) levels of analysis, while mid-or multiscale kin-based identity remains underexplored.

In this chapter, I critically review recent developments among anthropological approaches to kinship, emphasizing consideration of relatedness as “mutuality of being”

following Sahlins (2013) and how this perspective can be applied to the bioarchaeological record. Next, I present a brief historical overview of bioarchaeological kinship research. Results from a formal literature review of kinship studies in bioarchaeology are used to assess overall trends with regard to data types and conceptualizations of kinship. Then I present a broader review of bioarchaeological kinship literature and discuss how kinship is being defined and reconstructed from complex datasets, focusing on developments over the past 10 years. I highlight studies that consider non-biological forms of kinship, go beyond the mere identification of relatives within mortuary contexts, and make broader inferences about social organization and the ways in which family relations were constituted. I identify important methodological developments but note the overall lack of theoretical development compared to ethnographic considerations of social relatedness.

In the second half of the chapter, I present a new vision for bioarchaeological approaches to relatedness that builds on social identity theory, and I consider the strengths and limitations of its utility as a conceptual framework for interpreting bioarchaeological data. This approach to kinship diverges from recent archaeological efforts to revitalize the investigation of kinship in past societies (Ensor, 2011, 2013a, b) and is a unique and timely contribution to anthropological discussions of relatedness. Finally, I highlight potentially fruitful directions for future research by identifying critical issues to be addressed in order to establish kinship and family as vibrant topics of inquiry within bioarchaeology.

## **Recent developments in sociocultural approaches to kinship**

The title of Sahlins' recent book *What Kinship Is – And Is Not* (2013) captures one of the fundamental questions addressed by anthropological kinship research: to what extent does biology influence kin structure and family-centered behaviors? Biological relatedness is a universal reality – every person is a progeny of other human beings (Godelier, 2011) – but its social significance varies widely, and thus kinship cannot be equated with biological affinity. Durkheim (1898) was among the first social theorists to take this stance, claiming that kinship is dynamic and malleable and requires participation beyond biological reproduction. He cited acts of marriage, adoption, and parent-offspring emancipation as evidence of the schism between predetermined relatedness and social affinity (Durkheim, 1898).

In this section, I review recent developments in anthropological kinship research of greatest relevance to bioarchaeological approaches to kinship. I briefly trace currents of theoretical development that arose amid the initial wave of responses to Schneider's critiques; in doing so, I contextualize developments over the past 10 years. Due to constraints of space and the dense nature of this literature, I omit from this discussion recent developments in formal (i.e., quantitative) kinship analysis (e.g., Leaf, 2013; Read, 2007, 2011, 2012), historical linguistics (e.g., Ehret, 2011; Fortunato, 2011a, b; Jones, 2010; Jones and Milicic, 2011), and isonymy (e.g., Darlu et al., 2012; King and Jobling, 2009; Larmuseau et al., 2012). Readers interested in developments within these approaches to kinship should consult the preceding citations.

The 1960s and 1970s marked a transitional phase in kinship research. As evolutionary anthropologists and primatologists embraced kinship as a subject for



comparative investigation, sociocultural anthropologists began questioning the genealogical method and the presumptive biological nature of kin relatedness prevalent in kinship studies from their inception (e.g., Beattie, 1964; Leach, 1961, 1971; Needham, 1971; Southwold, 1971). David Schneider (1968, 1972) published several critiques during this period, denouncing kinship as a cross-cultural system. He insisted that previous research reinforced Western preoccupation with “natural kinship” and prioritized classification of kin systems over consideration of social experience. Schneider’s critique focused on the genealogical model as a Western cultural construct. Schneider (1968, 1972, 1984) argued that seemingly biological objects such as blood are social constructs that convey biological affinity (see also Carsten, 2001, 2011, 2013; Marks, 2002; Strong and Van Winkle, 1996; Tallbear, 2013). Kin are ultimately connected by an ‘enduring solidarity’ produced and maintained through social interactions and expressed as ‘blood ties’ (Schneider, 1968; see also Baumann, 1995). Thus, rather than reflecting a naturalistic human universal (i.e., a “biological fact”), the genealogical basis underlying Euro-American conceptions of kinship – and therefore anthropological kinship theory – is a culturally constituted symbolic system unique to Western societies (Schneider, 1968). In other words, the cross-cultural study of kinship, which had been one of anthropology’s major contributions to the social sciences, was invalid (Schneider, 1984). Several in depth explorations of Schneider’s lasting contributions to the field and critiques of his approach are available to readers looking for additional details of his work and its impact (e.g., Carsten, 1995; Feinberg and Ottenheimer, 2001; Holy, 1996; Leaf, 2001; McKinley, 2001; Ottenheimer, 1995; Peletz, 1995; Yanagisako, 1978).

Instead of signaling the end of kinship studies, Schneider's deconstruction of kinship research precipitated a variety of reactions and responses, including explorations of alternatives to heteronormative models of kinship and family (Borneman, 1992, 2001; Collier and Yanagisako, 1987; Franklin and Ragoné, 1998; Hayden, 1995; Lewin, 1993; Modell, 1994; Strathern, 1992a, 2001; Weston, 1991), new emphasis on previously unchallenged assumptions about gender relations that permeate earlier models of kinship (e.g., Blackwood, 1995, 2000; Collier et al., 1982; Collier and Yanagisako, 1987; Leacock, 1981; MacCormack and Strathern, 1980; Rosaldo, 1974; Rubin, 1975; Scheffler, 1991; Yanagisako, 1979; Yanagisako and Delaney, 1995), and development of constructivist approaches to kinship within a variety of cultural contexts (e.g., Bodenhorn, 2000; Carsten, 1995, 1997; Leach, 2003; Rival, 1998).

To emphasize the shift away from genealogical approaches to kinship, researchers began framing kinship as "relatedness." An effort was made to disentangle biological relationships based on reproduction (i.e., genitrix and genitor) from kinship as social relationships (i.e., mother and father) (e.g., Ottenheimer, 1995). Constructivists argued that there is no pretheoretical, prediscursive "intractable core" to human relatedness (Astuti, 2009: 229). Rather than a universal "biological fact," relatedness is a "process of becoming" generated and maintained by purposeful action (Carsten, 1995: 223). Viewed in this light, kinship as social relatedness can be based on any number of shared experiences, practices, and commonalities – including commensality, co-residence, shared knowledge, shared status, shared labor, shared connections to "place" and landscape, and naming rituals or name sharing – that establish a "mutuality of being" between people who see themselves as "intrinsic to one another's existence" (Sahlins,

2013: 2; see also Bodenhorn, 2000; Carsten, 1997; Merlan and Rumsey, 1991; Nuttall, 2000; Strathern, 1973; Weismantel, 1995).

Kinship manifested as “household” or “residence” emerged as yet another productive area of post-Schneiderian scholarship (see Carsten and Hugh-Jones, 1995; Joyce and Gillespie, 2000). Drawn from and expanding the concept of “house societies” developed by Lévi-Strauss (1983a,b, 1984, 1987, 1991), the social house was developed as a non-biological manifestation of relatedness. The house is considered a meaningful space that serves as a nexus for social memory formation and the transgenerational regulation of resources particular to domestic collectives (or kin) (Chesson, 2001; Gillespie, 2000b, 2001, 2002; Hodder and Cessford, 2004; Joyce, 2000, 2001a, 2008). One advantage of this model is that the material correlates of the social group (social house) can be readily identified in the archaeological record (e.g., the material remains of the physical house and objects that symbolize the house), thus facilitating considerations of kinship and relatedness in prehistory (Gillespie, 2000a; Joyce, 2000; Marshall, 2000; cf. Carleton et al., 2013; Ensor, 2011, 2013a,b). House society approaches to kinship have been used to explore small-scale, kin-based social organization within a variety of archaeological and ethnographic contexts (e.g., Carsten, 1997; Carsten and Hugh-Jones, 1995; Joyce and Gillespie, 2000; McKinnon, 1991).

Within the past 10 years, another wave of kinship research has emerged in sociocultural anthropology. Many of the research foci developed following Schneider’s critiques – including gender inequality within families, kinship and power, non-normative family formations, and non-biological bases of relatedness – persist as vibrant areas of research (e.g., Bamford, 2009; Howell, 2009; Lamphere, 2001, 2005; Lancaster, 2005;

Van Vleet, 2008; see also Kakaliouras, 2006). Additionally, scholars continue to explore how kinship intersects with broader social issues. Kinship is no longer conceptually isolated as a separate “domain” of human behavior (Collier and Yanagisako, 1987); it is considered interrelated with – and critical to understanding – human impact on the environment, interpersonal violence, socioeconomic behavior, political organization, patient care, and ideology (e.g., Bodenhorn, 2013; Kelly, 2011; Lambek, 2013; McKinnon and Cannell, 2013; Rutherford, 2013; Shever, 2013; Yanagisako, 2013).

A growing number of scholars have directed critical focus at constructivist approaches to family. The constructivist model has been described as a “reactive inversion” of the genealogical model, but it has had little effect in terms of displacing biological relatedness as the basis of kinship in anthropology (Sahlins, 2013; Viveiros de Castro, 2009). This is, in part, because the influence of genealogical discourse permeates Western worldview (e.g., Bamford, 2009; Bamford and Leach, 2009; Holmes, 2009; Ingold, 2009; Leach, 2009). Although shared biological substances are less valued within constructivist approaches, biology is still present – often implicitly – as what is given or immutable within constructions of relatedness (Astuti, 2009; Bamford and Leach, 2009; Ingold, 2009; Sahlins, 2013; Viveiros de Castro, 2009). The genealogical model continues to play a prominent role in anthropological kinship studies in general (see Ensor, 2013a,b; Godelier, 2011; Holy, 1996; Shenk and Mattison, 2011; Trautman and Whitley, 2012) and implicitly underlies and informs constructivist approaches to relatedness (Astuti, 2009; Leach, 2009; Viveiros de Castro, 2009). Thus, despite appearances or claims otherwise, “the outcome of the focus on kinship as Western cultural construction has perversely resulted in a reinscription of the notion that human

beings are everywhere biological beings with the capacity for culture.... People may share culture, but it never makes them *kin*” (Leach, 2009: 185, emphasis original).

There also is increased awareness that other aspects of Western worldview permeate constructivist approaches to kinship. A view of kinship in which individuals create their own kin connections using potentially flexible forms of relatedness may represent “the final hegemony of consumptive individualism” (Viveiros de Castro, 2009: 261; see also Leach, 2009; Strathern, 1992a,b). Therefore, even recent anthropological approaches to kinship are ill-suited for analyzing social relatedness in non-Western contexts where their application can obscure differences in the way family relatedness is understood and experienced (Astuti, 2009; Holmes, 2009; Lambek, 2011; Schneider, 1984; Viveiros de Castro, 2009). To apply Western notions of kinship – genealogical or constructivist – to non-Western contexts is to impose “alien ontological categories” on non-Western peoples (Astuti, 2009: 216).

A key to moving beyond Western understandings of kinship is to adopt conceptions of relatedness suitable to different contexts. Ethnographers are attempting to convey non-Western ontologies of relatedness and truly explore what kinship means in different cultural contexts (Bamford, 2004, 2009; Kelly, 2011; Leach, 2003, 2009; Viveiros de Castro, 2009). For example, according to Viveiros de Castro (2009: 241), Amazonian kinship is based on a “nonbiological theory of life.” Within Amazonian worldview, the soul or spirit is a shared substance that connects all persons (human or non-human), whereas a person’s body is constructed through interactions with others. Those interactions with other bodies form the basis of Amazonian kinship and reveal that within Amazonian ontology, affinity is “given, internal and constitutive,” whereas

consanguinity is “constructed, external and regulative” (Viveiros de Castro, 2009: 258–259). In Papua New Guinea, the Kamea conceptualize the parent–child bond as an “inherently disembodied one”; social relatedness is based on relationships formed through interactions with other persons within an engaged landscape (Bamford, 2009: 160). Similarly, the Reite of Papua New Guinea have a non-genealogical understanding of relatedness wherein knowledge of and interaction with an engaged landscape is a shared substance that forms the basis of relatedness (Leach, 2009). The Vezo in Madagascar make an ontological distinction between biological inheritance/genealogical relatedness and social relatedness, but they emphasize non-biological parent-child relationships as critical to family life (Astuti, 2009).

These ethnographic examples represent fundamentally different ways of conceptualizing personhood, family, and relatedness compared to the normative ontologies found in Western sociocultural contexts (Descola, 2013; Ingold, 2000, 2009, 2013; Oliver, 2009; Palsson, 2013; Robertson, 2011; Viveiros de Castro, 2009). Conveying non-Western forms of relatedness requires consideration of non-Western ontologies of gender, personhood, and human/non-human animal/landscape interactions (Descola, 2013; Ingold, 2000, 2009, 2013). However, one must exercise caution when drawing distinctions between Western and non-Western ideologies, as preconceived notions of innate differences can result in over-simplistic and “othering” representations of non-Western forms of kinship.

More generally, researchers are trying to develop alternatives to genealogical thinking. Genealogies are a particular way of thinking about and establishing the parameters of possible relationships within a very narrow perspective (Ingold, 2000;

Klapish-Zuber, 1991, 2000). Depictions of genealogies (i.e., family trees or kinship diagrams) restrict the potential to recognize other conceptualizations of relatedness and forms of kin-based organization (Bamford and Leach, 2009; Bouquet, 1996, 2001; Ingold, 2009; Leach, 2009). Researchers have employed alternative models to the tree analogy for genealogical relationships, with many favoring a rhizome model, a web, or an interwoven “meshwork” of relatedness in which “everything is potentially interconnected with everything else” (Pálsson, 2009: 107; see also Deleuze and Guattari, 1988; Holmes, 2009; Ingold, 2009). In sum, kinship remains a flourishing field of study in sociocultural anthropology. Ongoing theoretical debates have produced new insights into relatedness in Western and non-Western contexts, many of which involve non-biological or non-genetic conceptions of kinship.

### **Bioarchaeological kinship research**

In this section, I provide a brief historical overview of bioarchaeological kinship research, focusing on approaches used to explore family organization in the past, conceptions of kinship and relatedness applied to ancient contexts, and the types of inferences or observations drawn from data on kinship. Because the focus is on theoretical developments, I only briefly discuss data and analytical methods. The diverse types of data and analytical methods used to investigate postmarital residence practices and to identify closely related individuals in archaeological contexts are reviewed in detail elsewhere (see Alt and Vach, 1998; Hauser and DeStefano, 1989; Konigsberg, 1987, 1988; Stojanowski and Schillaci, 2006). I also present the results of a formal literature review to evaluate publishing trends for bioarchaeological kinship studies.

The origins of bioarchaeological kinship research are difficult to pinpoint (Stojanowski and Schillaci, 2006), but by the 1970s two distinct areas of inquiry emerged in bioarchaeological family research: (1) the identification of kin or family groups within mortuary contexts, and (2) the investigation of postmarital residence patterns. In the bioarchaeological literature, the former is referred to as “kinship analysis” (Stojanowski and Schillaci, 2006). Rather than place a singular emphasis on consanguineal relationships accessed via kinship analysis, I discuss both kinship and postmarital residence analysis; each uniquely contributes to more holistic understandings of relatedness in the past, providing greater opportunities to generate broad inferences about social organization and sociocultural practices.

The study of postmarital residence practices using skeletal and dental data from archaeological samples began in earnest in the 1970s (e.g., Corruccini, 1972; Lane, 1977; Lane and Sublett, 1972; Spence, 1974a,b). Collectively, scholars established methods for identifying postmarital residence practices using biodistance analysis of within-group and between-group biological distance and variance. The assumption is that the more mobile sex will exhibit greater intrasite skeletal/dental variation, and the non-mobile sex will exhibit greater intersite variation and biodistance. Konigsberg (1987, 1988) provided formal justification of postmarital residence studies by using population genetics models to demonstrate that the differential movement of females or males into a settlement results in measurable distinctions in phenotypes that persist through time as long as the predominant pattern remains stable. Drawing on socioeconomic and political correlates of particular postmarital residence patterns documented in ethnographic contexts (e.g., Divale, 1977; Ember and Ember, 1971; Korotayev, 2003; Murdock, 1967; Porčić, 2010;



cf. Allen and Richardson, 1971), bioarchaeologists use postmarital residence practices to make inferences about changes in subsistence, the formation of descent groups, gendered divisions of labor, resource control, and the nature and extent of intergroup hostility or warfare (e.g., Schillaci and Stojanowski, 2002, 2003; Tomczak and Powell, 2003).

Kinship analyses use phenotypic (e.g., skeletal and dental discrete trait frequencies or metric values) or genetic data to identify close biological relatives in mortuary contexts. Alt and Vach (1998) describe three types of research contexts that affect the methodology used and the expected outcome in kinship analyses: small grave analyses, structured spatial analyses, and unstructured spatial analyses. In small grave analyses, the objective is to infer whether a group of individuals within a clearly delimited mortuary context (e.g., a tomb, a cave, or under a house floor) are close biological relatives (e.g., Alt and Vach, 1998; Bondioli et al., 1986; Sjøvold, 1976/1977). Structured kinship analysis quantifies (non)correspondence of cemetery spatial structure (e.g., distinct sectors or “family plots” within a cemetery), cultural attributes (e.g., grave structure, body treatment), and patterns of biological variability in order to identify mortuary behavior with potential familial bases (e.g., Bondioli et al., 1986; Howell and Kintigh, 1996; Jacobi, 1997, 2000; Shimada et al., 2004; Strouhal and Jungwirth, 1979). Unstructured spatial analysis attempts to identify members of kin groups without a priori reference to spatial structure or cultural attributes within larger cemeteries. A non-random distribution of phenotypic (e.g., Alt and Vach, 1995a,b; Vach and Alt, 1993) or genetic (Dudar et al., 2003; Stone, 1996; Stone and Stoneking, 1993) data suggests some underlying factor(s) influenced the burial program. Alt and Vach (1995b) refer to identified clusters as “hypothetical families” and recommend verifying these groupings

with additional data including archaeological and demographic evidence (i.e., skeletal age and sex).

Identification of close biological relatives in mortuary contexts and the development and refining of research methodologies for doing so are often the primary goals of bioarchaeological kinship analysis (Alt and Vach, 1998; Case, 2003; Stojanowski and Schillaci, 2006). Some studies have evaluated the probability of familial relationship using phenotypic data (e.g., Alt and Vach, 1995a,b; Alt et al., 1997; Doi et al., 1986; Hanihara et al., 1983; Matsumura and Nishimoto, 1996) and genetic data (e.g., Gerstenberger et al., 1999; Hummel and Herrmann, 1996; Keyser-Tracqui et al., 2003; Scholz et al., 2001; Shinoda and Kanai, 1999; Shinoda and Kunisada, 1994), while others have attempted to reconstruct pedigrees among individuals (e.g., Rösing, 1986; Spence, 1996). Studies also have explored the goodness of fit between results obtained from genetic and phenotypic data and the relative effectiveness of different types of phenotypic traits in reconstructing biological relatedness (e.g., Adachi et al., 2003; Corruccini and Shimada, 2002; Shimada et al., 2004; Shinoda et al., 1998).

By drawing on ethnographic data suggestive of broad patterns of correlation between kin-based mortuary practices and other sociocultural phenomena (see Carr, 1995; Goldstein, 1976, 1980; Parker Pearson, 1999; Saxe, 1970), bioarchaeologists can use the identification of kin groups within mortuary contexts to make inferences regarding the inheritance of wealth, social status, and sociopolitical organization. Unfortunately, many studies remain focused on methodological improvement and do not attempt to use kinship data to make inferences about broader anthropological issues (Alt and Vach, 1998; Case, 2003; Stojanowski and Schillaci, 2006). Alt and Vach (1998) note

the potential for kinship studies to contribute to reconstructions of higher scale issues regarding social organization, including the “constitution of social families” and the role of heredity in ascribed social inequality. Case (2003) comments on the potential for kinship studies to elucidate the development of multigenerational political and economic inequality within communities (see also Stager, 1985).

This broader potential remains unrealized, a tendency that may be linked to underlying Western notions of relatedness that influence the ways in which kinship is studied. Indeed, throughout the first three decades of bioarchaeological research, kinship was almost ubiquitously reduced to close biological affinity. It remains unclear, though, whether recent theoretical developments in sociocultural approaches to relatedness have influenced contemporary bioarchaeological studies of kinship and family. To address this unknown I conducted a formal literature review to empirically assess theoretical and analytical trends in bioarchaeological kinship research.

## **MATERIALS AND METHODS**

### **Quantitative literature review**

The goals for the quantitative literature review were to assess broad temporal patterns in the terminology and types of anthropological data employed in bioarchaeological kinship studies, as well as the dimensions or forms of relatedness that these studies considered. I administered keyword searches of nine terms relevant to kinship or family-centered research using the digital archives of 13 English-language academic journals in which bioarchaeological studies are commonly published (Table 1). I included only studies set within bioarchaeological contexts; that is to say, I counted

only those studies that included, at a minimum, data generated from non-contemporary human remains or their surrounding mortuary contexts.

Results were tallied as decadal publication counts of relevant keyword hits between 1950 and 2013. Counts from 2010–2013 were used to project trends throughout the current decade; the same was done to obtain decadal counts for journals that were first published after 1950 and whose inaugural issue fell between the first and tenth year of a decade. As a requirement for generating keyword-based counts, terms of interest were always identified (at a minimum) within the body of the text of a publication. Decadal counts also were recorded for types of anthropological data employed in bioarchaeological kinship/family studies (i.e., archaeological, bioarchaeological, linguistic, sociocultural). Finally, I noted whether individual articles addressed biological relatedness, social relatedness, or some combination of the two. To examine trends over time, counts were standardized by the number of journals monitored per decade. I made no adjustment for overall increase in the number of issues and/or articles published by journals through time; I have considered this limitation in the interpretation of the results. Ultimately, the *International Journal of Paleopathology* yielded a zero count for publications containing any of the monitored keywords during the period surveyed; thus, I do not present results for this journal.

Table 1. Journals and variables included in the formal literature review monitoring trends in bioarchaeological kinship research.

Journals <sup>a</sup> (Years Monitored)	Key Words <sup>b</sup>	Data Types	Kinship “Type” <sup>c</sup>
American Anthropologist (1950-2013)	Affine/Affinal	Archaeological	Biological
American Antiquity (1950-2013)	Family	Biological	Biological and Social
American Journal of Physical Anthropology (1950-2013)	House/household Intracemetery	Linguistic Sociocultural	Social
Anthropological Science (1993-2013)			
Archaeological Papers of the American Anthropological Association (1989-2013)	Kin/Kinship Mate Exchange		
Current Anthropology (1950-2013)	Matrilocal/Matrilineal		
HOMO- Journal of Comparative Human Biology (2000-2013 <sup>d</sup> )	Patrilocal/Patrilineal Postmarital Residence		
Human Biology (1950-2013)			
International Journal of Osteoarchaeology (1991-2013)			
International Journal of Paleopathology (2011-2013)			
Journal of Archaeological Sciences (1974-2013)			
Journal of Human Evolution (1972-2013)			
Latin American Antiquity (1990-2013)			

<sup>a</sup>Only bioarchaeological publications (i.e., those involving archaeological skeletal/dental or mortuary data) were included.

<sup>b</sup>Publications were only included in keyword counts if the keyword appeared in the body of the article.

<sup>c</sup>Kinship “type” was categorized as follows: biological, biological, and social, or social.

<sup>d</sup>Search dates reflect limitations to journal access, not publication duration.

Though informative, journal-based literature reviews have limitations. They may unintentionally exclude those sources most likely to report research that incorporates emerging data or theoretical models: dissertations. Single author books and edited volumes have also emerged as important media for presenting bioarchaeological research, and their contribution is not measured by the quantitative review. Additionally, the quantitative literature review was limited to English-language journals.

### **Qualitative literature review**

To address the limitations of the quantitative literature review, a more inclusive, qualitative review of bioarchaeological literature from the past 10 years was performed. This review is designed to assess whether developments identified in the quantitative literature review reflect meaningful changes in the way kinship and relatedness are conceptualized in bioarchaeology. The qualitative literature review facilitated the identification of general topical, methodological, and interpretive trends in recent bioarchaeological kinship research. Although English-language publications are emphasized, a sampling of non-English sources is cited below.

## **RESULTS**

### **Quantitative literature review**

The quantitative literature review revealed increasing variability in published family/kin terminology through time (Fig. 1). There are zero articles from the 1950s referencing any of the nine monitored terms, but the 2000s and 2010s (projected) boast bodies of bioarchaeological kinship literature that reference all nine keywords (Table 2).

This pattern underscores the growing diversity of contexts, questions, and theoretical frameworks with which bioarchaeologists are engaging during the 21st century.

Across the last six decades, diversity in the lines of evidence utilized to examine kinship increased. In the 1960s, bioarchaeological family research drew heavily on ethnohistoric and ethnographic data; biological and archaeological data grew more prevalent in the following decades (Table 3). The 2000s and 2010s (projected) have been marked by almost equal prevalence of sociocultural, biological, and archaeological data, whereas the use of linguistic (surname) data was minimal during the same period.

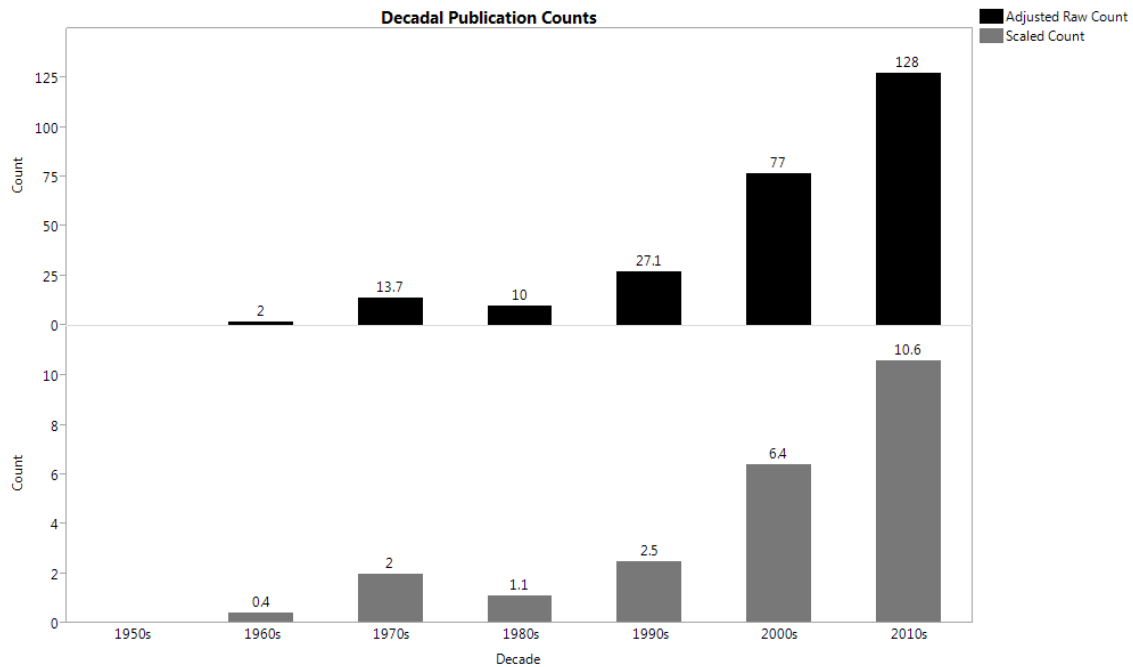


Figure 1. Counts of bioarchaeological kinship studies published across decades. Adjusted raw counts incorporate projected counts for those journals whose inaugural issues were published mid-decade, as well as projections for the 2010s as based on raw counts from 2010–2013. Scaled decadal counts are equivalent to the adjusted raw counts divided by the number of journals monitored during each 10-year span.

Table 2. Raw and adjusted keyword count values<sup>a</sup> and keyword percentage values<sup>b</sup> across monitored decades.

	Affine/ Affinal	Family	House/ Household	Intra- cemetery	Kin/ Kinship	Mate Exchange	Matrilocal/ local/-lineal	Patrilocal/ Patrilineal	Post- marital
1950s	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>
1960s	0.0 <i>0.0</i>	2.0 <i>50.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	2.0 <i>50.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>
1970s	1.0 <i>3.6</i>	8.0(8.5) <i>28.6</i>	5.0 <i>17.9</i>	1.0 <i>3.6</i>	4.0 <i>14.3</i>	0.0 <i>0.0</i>	4.0 <i>14.3</i>	4.0 <i>14.3</i>	1.0 <i>3.6</i>
1980s	0.0 <i>0.0</i>	9.0 <i>33.3</i>	4.0 <i>14.8</i>	1.0 <i>3.7</i>	7.0 <i>25.9</i>	1.0 <i>3.7</i>	1.0 <i>3.7</i>	2.0 <i>7.4</i>	2.0 <i>7.4</i>
1990s	0.0 <i>0.0</i>	21.0(22.1) <i>33.3</i>	11.0 <i>17.5</i>	2.0(2.4) <i>3.2</i>	20.0(20.8) <i>31.7</i>	0.0 <i>0.0</i>	4.0(4.1) <i>6.3</i>	2.0 <i>3.2</i>	3.0 <i>4.8</i>
2000s	4.0 <i>1.8</i>	55.0 <i>25.3</i>	36.0 <i>16.6</i>	6.0 <i>2.8</i>	54.0 <i>24.9</i>	8.0 <i>3.7</i>	14.0 <i>6.5</i>	21.0 <i>9.7</i>	19.0 <i>8.8</i>
2010s <sup>a</sup>	3.0(7.5) <i>2.1</i>	40.0(100.0) <i>27.8</i>	26.0(65.0) <i>18.1</i>	5.0(12.5) <i>3.5</i>	41.0(102.5) <i>28.5</i>	2.0(5.0) <i>1.4</i>	9.0(22.5) <i>6.3</i>	11.0(27.5) <i>7.6</i>	7.0(17.5) <i>4.9</i>

<sup>a</sup>Raw counts were adjusted to incorporate projections for those decades in which a journal was not in print throughout all 10 years. Where raw and adjusted counts do not correspond, the adjusted count is enclosed by parentheses. Raw counts for 2010-2013 were adjusted for all journals in order to project trends for the current decade (2010s).

<sup>b</sup>Percentages of total raw counts are italicized.



Table 3. Data types used in published bioarchaeology kinship studies by decade<sup>a</sup>.

	Biological	Archaeological	Sociocultural	Linguistic
1950s	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>
1960s	1.0 <i>25.0</i>	1.0 <i>25.0</i>	2.0 <i>50.0</i>	0.0 <i>0.0</i>
1970s	13.7 <i>48.2</i>	12.7 <i>44.7</i>	2.0 <i>7.1</i>	0.0 <i>0.0</i>
1980s	9.0 <i>64.3</i>	3.0 <i>21.4</i>	2.0 <i>14.3</i>	0.0 <i>0.0</i>
1990s	15.1 <i>36.7</i>	21.0 <i>51.1</i>	5.0 <i>12.2</i>	0.0 <i>0.0</i>
2000s	51.0 <i>34.9</i>	64.0 <i>43.9</i>	30.0 <i>20.5</i>	1.0 <i>0.7</i>
2010s	95.0 <i>42.7</i>	92.5 <i>41.6</i>	35.0 <i>15.7</i>	0.0 <i>0.0</i>

<sup>a</sup>Percentages of total raw counts are italicized.

A concordant temporal trend was identified in the form(s) of relatedness considered. Throughout the 1960s, publications featuring bioarchaeological explorations of kinship primarily dealt with issues of biological or biosocial relatedness (Table 4). The 2000s were the first to approach a balance between the volume of bioarchaeological papers discussing biological relatedness, social relatedness, and both biological and social relatedness within the same paper (Table 4). Since the start of the 21st century, the field has witnessed considerable intensification in the publication of bioarchaeological studies of all kinship types, with biosocial kinship investigations enjoying the greatest relative

increase in publication frequency. This trend may reflect the progressively interdisciplinary nature of bioarchaeological research in recent years, or possibly a greater integration of contemporary social theory into what would otherwise be more biologically oriented considerations of affinity.

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Table 4. Kinship “types” considered in published bioarchaeological studies by decade<sup>a</sup>.

	Biological	Social	Biological and Social
1950s	0.0 <i>0.0</i>	0.0 <i>0.0</i>	0.0 <i>0.0</i>
1960s	1.0 <i>50.0</i>	0.0 <i>0.0</i>	1.0 <i>50.0</i>
1970s	10.7 <i>78.1</i>	0.0 <i>0.0</i>	3.0 <i>21.9</i>
1980s	6.0 <i>60.0</i>	2.0 <i>20.0</i>	2.0 <i>20.0</i>
1990s	14.1 <i>52.0</i>	5.0 <i>18.5</i>	8.0 <i>29.5</i>
2000s	31.0 <i>40.4</i>	13.0 <i>16.9</i>	33.0 <i>42.9</i>
2010s	47.5 <i>37.3</i>	20.0 <i>15.7</i>	60.0 <i>47.0</i>

<sup>a</sup>Percentages of total raw counts are italicized.

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In sum, the volume of published bioarchaeological research focusing on kinship has increased over the last several decades, especially since the start of the 21st century, and this trend is projected to continue throughout the near future (Fig. 1). These results highlight sustained growth in academic curiosity surrounding relatedness and family in

the past. These trends also are likely influenced, in part, by the emergence of bioarchaeology as a distinct subdiscipline during the late 20th century and the (variably) expanding volume of articles published within journals annually, often associated with the increased prevalence of online publishing, both generally and for bioarchaeology specifically.

### **Qualitative literature review**

The types of inferences generated in recent bioarchaeological kinship research exhibit a similar pattern as seen in theoretical developments in kinship studies – a mixture of “business as usual” and novel efforts. Scholars continue to make important methodological contributions to the study of kinship by identifying traits potentially useful as indicators of genetic relatedness within skeletal samples (e.g., Offenbecker and Case, 2012; Paul and Stojanowski, 2015; Villotte et al., 2011), comparing the effectiveness of different types of data for identifying biological relatedness (e.g., Adachi et al., 2006; Ricaut et al., 2010; Velemínský and Dobisíková, 2005), and incorporating new analytical techniques (e.g., Gamba et al., 2011; Ricaut et al., 2006; Usher and Allen, 2005; Usher and Weets, 2014).

Identification of close biological relatives in small grave and cemetery contexts continues to be the primary objective of many studies (e.g., Baca et al., 2012; Deguilloux et al., 2014; Gamba et al., 2011; Lee et al., 2014; Lull et al., 2013; Perego, 2012). Criteria for positively identifying probable nuclear families vary widely between studies; the most effective efforts establish (and sometimes meet) rigorous criteria that yield more nuanced interpretations of social aspects of family organization in the past (e.g., Bentley, 2013;

Grumbkow et al., 2013; Mata-Míguez et al., 2014; Meyer et al., 2012; Simón et al., 2011). Initial excitement about the potential of ancient DNA (aDNA) to directly test hypotheses regarding systems of inheritance, postmarital residence patterns, and kinship systems (Kaestle and Horsburgh, 2002; Shinoda and Kanai, 1999; Stoneking, 1995; Usher et al., 2003; Williams et al., 2002) have been tempered in recent years. The more precise identification of genetically related individuals afforded by analysis of autosomal, mitochondrial, and Y-chromosomal genetic markers, or some combination of the three, has contributed inferential power to studies of kin-based social organization in the past (e.g., Haak et al., 2008). However, inferences made using aDNA data are subject to the same conceptual issues as other indicators of biological or genetic relatedness (Deguilloux et al., 2011; Meyer et al., 2012).

Analysis of postmarital residence practices in archaeological contexts continues to yield important insights into sociopolitical organization, population migrations, and subsistence practices (e.g., Bentley, 2013; Bentley et al., 2012). In their diachronic analysis of postmarital residence practices in the Middle Ohio Valley, Cook and Aubry (2014) identify matrilineal, patrilineal, and “multilocal” residential patterns. They suggest that people likely connected with kin on either side of the family in an opportunistic fashion (see Ember and Ember, 1972). In another example, Nystrom and Malcom (2010) identify two different postmarital residence patterns within the Chiribaya polity on the south coast of Peru: non-elite patrilocality combined with elite male mobility.

Methodological refinements are welcome and necessary contributions to the field, but it is important that bioarchaeological kinship research connects understandings of

family organization with issues of broader anthropological (and societal) interest. Bioarchaeologists have recently begun to consider non-biological forms of relatedness in archaeological contexts (e.g., Gregoricka, 2013; Lozada, 2011b; Pilloud and Larsen, 2011). Interpretive work of this kind creates space for alternative family structures such as fictive kin, households, residence groups, or *ayllus* within bioarchaeological kinship research. *Ayllus* are multiscale social groups in contemporary Andean highland societies (and described in ethnohistoric sources) as based on nested levels of affiliation ranging from household kin groups (minimal *ayllu*) to the ethnic community (maximal *ayllu*) (Abercrombie, 1998; Albarracín-Jordán, 1996b; Allen, 1988; Bastien, 1978; Isbell, 1978). Through careful application of *ayllu* organization to archaeological contexts, bioarchaeological research in the Andes has used more flexible, non-biological conceptions of relatedness to interpret data and make inferences regarding social organization and social identity (e.g., Blom, 1999; Knudson and Blom, 2009; Torres-Rouff et al., 2013).

Bioarchaeologists often cite interment with symbolic “inalienable possessions” or within residence areas as behaviors tied to the direct or indirect generation of social memory; such acts are often viewed as ancestor veneration or as reflecting traditional or “alternative” forms of relatedness (Christensen, 1998a,c; González-Ruibal, 2006; Hutchinson and Aragon, 2002; King, 2006, 2010; Laneri, 2010). The house model and ancestor veneration have been discussed in detail by Mesoamericanists, particularly for the Maya (e.g., Duncan and Hageman, 2015; Gillespie, 2000b, 2001, 2002; Joyce, 2001b;

Miller, 2015; Novotny, 2013; Watanabe, 2004), and by archaeologists working in Southeast Asia (e.g., White and Eyre, 2010).

A critical aspect of implementing broader conceptions (i.e., non-Western, non-biological) of kin relatedness is establishing criteria for identifying families in archaeological contexts when there is little or no biological evidence of distinct genealogical groupings (Duncan, 2005). Thus, studies that operationalize alternative (i.e., non-genealogical) conceptions of relatedness are required. Researchers in the Near East have explored the role of fictive kinship in socioeconomic organization. Pilloud and Larsen (2011) borrow the concept of “practical” kin from Bourdieu (1977) to interpret data patterns that indicate biological affinity did not influence residential burial practices at the Neolithic site of Çatalhöyük. Pilloud and Larsen suggest that practical kin relationships were established to facilitate large-scale economic activities requiring cooperative labor or were potentially related to issues of inheritance or religious practices. Gregoricka (2013) uses strontium isotope signatures to identify three non-local individuals buried in six monumental Umm an-Nar tombs. These “non-local” individuals are otherwise indistinguishable from burials of local individuals based on mortuary practices. Gregoricka suggests this pattern may reflect possible fictive kinship relations established to foster economic exchange as interregional economic activity became more important. These considerations of flexible kin identities make a valuable contribution to the literature and underscore the importance of rigorous hypothesis testing or evaluation of alternative explanatory models before inferring fictive kinship in archaeological contexts.

Overall, there is a marked lack of precision in the use of the term “kinship.” Sometimes kinship is used – explicitly or implicitly – to mean biological, genetic, or molecular relatedness, and other times (even within the same study) kinship is differentiated from biological affinity and used more broadly to incorporate social aspects of relatedness (e.g., Česnys and Tutkuvienė, 2007; Gamba et al., 2011; Kurin, 2012; Miller, 2013; Scott, 2006). Even studies that implement broader conceptualizations of relatedness can reduce kinship to biology either through data analysis or interpretations of results (e.g., Harper and Tung, 2012; Matney et al., 2012; Ricaut et al., 2006; Scott, 2006). This may reflect the complexity of kinship and its manifold nature and perhaps indicate disciplinary growing pains as scholars attempt to push conceptual boundaries (e.g., Gregoricka, 2013; Paul et al., 2013; Pilloud and Larsen, 2011).

Bioarchaeologists are using investigations of family-based social organization to make inferences about major subsistence transitions (i.e., foraging to agriculture), differential access to land, and health (e.g., Alt et al., 2013; Alzualde et al., 2007; Bentley et al., 2009, 2012; Harper and Tung, 2012). Expanding on a strong European tradition of methodological and interpretive intracemetery kinship research (e.g. Alt et al., 1997, 2005; Haak et al., 2008), Meyer et al. (2012) use molecular genetic data to determine whether past peoples structured mortuary contexts based on biological lineage, but they integrate this information with archaeological and osteological data, including information on paleopathology and trauma, to examine intra-familial relationships and their manifestation within the funerary space. This approach yields highly detailed kinship reconstruction, exposing potential sibships, parent–offspring relationships, and

marital partnerships. Here, genetic relationships reveal dimensions of personhood and kinship at the individual scale but also “scale up” to inform understandings of mortuary practice, exogamy, and postmarital residence systems at the community level.

In a holistic research program that marks a productive direction for spatially structured kinship research, Stojanowski (2013) integrates data from mortuary practices, age-structured phenotypic variation, and paleopathology to access hidden heterogeneity and differential frailty of a familial nature. Building on the identification – using archaeological data – of distinct kin-based burial programs in two different mission period cemeteries in La Florida, Stojanowski suggests that the Native American communities associated with the cemeteries had different experiences within the sociopolitical climate of the Spanish colony (Stojanowski, 2005c, 2013b). Stojanowski’s (2013b) novel integration of family, community, and environmental factors in the exploration of differential stress and frailty provides a fruitful avenue for engaging with the Osteological Paradox, a fundamentally important, yet often overlooked conceptual issue that affects interpretations of health in past populations (DeWitte and Stojanowski, 2015; Wood et al., 1992; Wright and Yoder, 2003). Furthermore, this study realizes the potential for bioarchaeological research to elucidate interrelations between family social organization and intergenerational socioeconomic inequality (Alt and Vach, 1998; Case, 2003; Stojanowski and Schillaci, 2006).

In sum, bioarchaeological kinship research continues to have a methodological focus. Although methodological improvements are critical to advancing the field, the identification of genetically related individuals in archaeological contexts is merely one



component of what should be a multifaceted effort to understand how kin-based relations were established and maintained within specific cultural contexts in the past. It appears that progress in the ethnographic and theoretical realms are, to some extent, influencing the ways in which bioarchaeologists are tackling the ancient family experience. The use of multiple lines of evidence – including molecular, phenotypic, body modification, isotopic, and myriad types of archaeological data – is becoming more common. Analysis of complex datasets and subsequent interpretation of results can be complicated, but such approaches can produce more nuanced reconstructions of relatedness in the past (e.g., Alt et al., 2013; Haak et al., 2008; Meyer et al., 2012; Paul et al., 2013; Stojanowski, 2013b). In some cases, kinship is incorporated as a post hoc interpretation (e.g., Scott, 2006; Zvelebil and Pettitt, 2013), rather than included as an integral component of the research design (e.g., Harper and Tung, 2012; Huffer, 2012; Miller, 2013; Stojanowski, 2013b). Although there are exceptions, it appears that Stojanowski and Schillaci's (2006) assessment stands: the potential of bioarchaeological kinship studies to contribute to broader anthropological questions remains unrealized.

Part of the problem is an imbalance between the incorporation of diverse types of data used to investigate kinship within the past. Many bioarchaeological studies are not fully integrating archaeological data or theory into their research design but instead do so in an ad hoc or post hoc fashion. Rather than prioritizing one line of evidence over another, different kinds of data should be brought to bear on a question either simultaneously through advanced modeling methods or separately but within a framework where each is equally weighted and not granted greater value a priori. I am

not suggesting a devaluing of biological evidence in lieu of other data. Biological data will continue to play an integral role in past explorations of relatedness. As Geller (2008: 130) notes, the balance of sociocultural and biological data in bioarchaeology offers a “welcome counterpoint to social constructivists’ scholarship” not only in terms of conceptualizing the body “strictly in terms of the late modern individual” but also with regard to the nature of relatedness.

## **DISCUSSION**

Bioarchaeology has developed into a theoretically-oriented field that incorporates data from human skeletal remains and associated mortuary settings into highly contextualized, smaller scale regional- and site-based archaeological investigations (see Agarwal and Glencross, 2011; Buikstra and Beck, 2006; Larsen, 2015; Martin et al., 2013). I agree with Geller’s (2008: 129) assessment that bioarchaeologists, in general, have “exercised caution with respect to their theoretical engagement” and support her call for a more theoretically informed bioarchaeology. One way to develop a more theoretically oriented bioarchaeological approach to family is to consider kinship using social identity theory. Kinship has been identified in the bioarchaeological literature as a potentially informative aspect of social identity in the lives of past peoples (e.g., Gregoricka, 2013; Scott, 2006; Temple et al., 2011), but it has not been fully developed within a social identity framework (cf. Paul et al., 2013).

### **Kinship as social identity**

The concept of identity describes a universal experience of human sociality. Social identity marks an integration of an individual’s diverse statuses, roles, and

experiences into a coherent image of self (Epstein, 1978; Holland et al., 1998) and involves the negotiation of self-identification(s) with and external ascriptions to multiple social groups (e.g., Jenkins, 2008; Shennan, 1989). Social identities can be individual or collective; collective identities, specifically, are founded on an individual's sentiments of belonging within a broader group and others' recognition of the individual's affiliation with that collective (Jenkins, 2008).

Social identities are dynamic and continuously altered or reaffirmed through signifying behaviors and practices (Díaz-Andreu et al., 2005; Insoll, 2007; Jones, 1997). Of importance to archaeologists, these behaviors often involve recognizable, physical correlates rendering social identities materially substantiated (Díaz-Andreu and Lucy, 2005; Giddens, 1979; Jenkins, 2008; Sofaer, 2006; Stein, 1999a; Voss, 2008).

Expressions of identity can be visible in the archaeological record in various forms: material remnants of funerary ritual and habitual practices, body modification, and patterns of mate exchange genetically and phenotypically encoded within individual bodies, to name a few (e.g., Blom et al., 1998; Hamilakis et al., 2002; Joyce, 2005; Sharratt, 2011; Sofaer, 2006; Stojanowski, 2010).

In concert with these lines of physical evidence, the application of social identity theory to bioarchaeological research has provided a means for examining dimensions of the lived experience in ancient contexts. Indeed, over the past decade, "bioarchaeology of identities" has grown in popularity as an area of research and as a topic of numerous edited volumes (e.g., Agarwal and Glencross, 2011; Amundsen-Meyer et al., 2011; Baadsgaard et al., 2011; Knudson and Stojanowski, 2008, 2009). Since their advent,

bioarchaeological investigations of social identity have focused on broad-scale collective identities such as ethnicity, gender, social or socioeconomic status, religion, and age (Buikstra and Scott, 2009; Gowland and Knüsel, 2006; Hollimon, 2011; Meskell, 2001). Another subset of identities research has focused on the individual, using social theory and osteobiographical data to access facets of personhood and to examine a single life course (e.g., Boutin, 2011, 2012; Gilchrist, 2000; Hawkey, 1998; Knudson et al., 2012; Robb, 2002; Stodder and Palkovich, 2012). Studies of the individual tend to invert analytical approaches that use population or sample averages to understand individuals to instead start from individuals and thereby emphasize variation rather than some postulated norm (Zvelebil and Weber, 2013). By comparison, mid-scale (e.g., neighborhoods, parishes, sodalities, etc.) and multiscalar collective identities (e.g., kin groups) remain largely underinvestigated despite representing key spheres of social interaction and identification (cf. Paul et al., 2013; Pilloud and Larsen, 2011).

Kin identity is both personal and interpersonal, but it is ultimately based on commonality and shared experience (e.g., ancestry, domestic space) and, therefore, is collective in nature (McKinnon, 1991). Kinship/family represents a critical multiscalar collective identity for which bioarchaeology can offer deep time perspectives. Approaching kinship as a multilevel form of social identity provides a yet undeveloped scale of analysis to explore connections between individual-, small group-, and community-level identities to address broader questions of human social organization in the past (Meyer et al., 2012).

Operationalizing this approach will be challenging. Limited to often incomplete ethnohistoric records and/or material manifestations of identity that survive taphonomic processes, bioarchaeologists must fully engage archaeological and biological data to make informed inferences on past social behaviors and practices. Traditional practice has been to employ mortuary analysis in combination with complementary biological methods. By acknowledging that burial reflects social memory of the deceased and that it is the living who bury the dead, the contextualized extrapolation of social information from mortuary contexts is often an essential aspect of bioarchaeological identities research (Goodenough, 1965, 1968; Hodder, 1980, 1982, 1987; Hodder and Cessford, 2004; Parker Pearson, 1982, 1999; Thomas et al., 2006). More recently, the physical body has emerged as an essential source of data on identity, one integrated into the overall funerary context (see Duncan and Hofling, 2011; Duncan and Schwarz, 2014; Geller, 2009b; Parker Pearson, 1999; Rakita et al., 2005; Sofaer, 2006).

Bioarchaeological work that examines the corporeal correlates of social relatedness (e.g., isotopic patterning, body modifications, patterned activity markers, or stress indicators) permits inferences regarding kin practices and principles of social organization, both in cases of biological kinship as well as those of “alternative” or “fictive” kin (Gregoricka, 2013; Meyer et al., 2012; Pilloud and Larsen, 2011). In fact, in an effort to avoid biologically deterministic or primordialist interpretations of relatedness, archaeologists have grown increasingly cognizant that genotypic/phenotypic variability and behavioral/cultural variability are not directly related (Díaz-Andreu, 2005; Stojanowski, 2005a,b; see also Barth, 1969). Collective identities are often founded on

non-biological factors; notions of relatedness – like ethnic identity – can be borne out of fictive ancestry or fictive notions of shared origin (Barth, 1969; Jones, 1997; see also Bourdieu (1977) and Pilloud and Larsen (2011) for a discussion of “official” versus “practical” kin). Additionally, genetic relatives do not always affiliate with a bounded social collective (i.e., families) (Stojanowski, 2005b). Thus, biological and mortuary evidence are mutually informative but not inherently linked. For example, renegotiation of corporate membership and kin/residence identity need not preclude the possibility for reactive exclusion (Barth, 1969; Bawden, 2005)

In addition to further developing conceptions of what constitutes relatedness and identifying types of data that can be used to evaluate kin identity in different contexts, it is equally important to think about ways to differentiate kinship from other forms of social identity within archaeological contexts. What distinguishes kin-based identities from other social identities? Specifically, without reference to small-scale biological relationships, how is kinship to be disentangled from community and ethnicity? What are the material correlates of each? What lines of evidence might be effective in distinguishing between them? There is unlikely to be an analytical panacea or highly diagnostic line of evidence for isolating kinship identity in the past. Rather, effective interpretations will rely on attenuated readings of patterns (along with consideration of multiple analytical scales) within different archaeological contexts combined with analogic reasoning (e.g., incorporation of ethnographic and ethnohistoric data and cross-cultural comparisons) when appropriate.

## **Future directions**

Approaching relatedness as a multiscalar form of social identity provides a holistic approach to family organization that is flexible enough to be sensitive to salient aspects of relatedness in diverse archaeological contexts and sufficiently generalizable to permit cross-cultural explorations of family life. There are a number of conceptual lacunae that need to be addressed as bioarchaeologists explore aspects of relatedness in the past. These include expanding conceptions of relatedness associated with Western-derived models of kinship by focusing more attention on sibling relationships and non-normative (i.e., non-genealogical, non-biological) family models. Bioarchaeological investigations of family organization and kin-based social identity can both draw on and inform considerations of other aspects of social organization and worldview, including relatedness and power, and how family relations structure and are structured by locally-salient conceptions of gender, age, and the life course, for example.

*Alternative models of families and conceptions of relatedness.* Anthropology has struggled with the study of kinship in part because it “deals with a biological process culturally defined and a cultural process with biological consequences” (Ottenthaler, 1995: 65). Kin-based relations are universal (Godelier, 2011; Lancaster, 2005), but the content of kinship – the way that people marry or raise children, whatever it is that establishes a mutuality of being – is “multivocal,” meaning it varies between and within societies (Lancaster, 2005; Ottenthaler, 1995; Sahlins, 2013). Further, what constitutes kinship, what kinship does, and what kinship means are not static but have certainly varied over the vast temporal spans subject to anthropological investigation. Therefore,

perhaps the only flawed approach to investigating kinship is a monistic one (Ottenheimer, 1995). There is room for many different conceptions of kinship and different (bio)archaeological approaches to kinship (e.g., Ensor, 2013a,b). To effectively explore the biocultural underpinnings of kin-based behavior, theoretical approaches to kinship, whether rooted in evolutionary or sociocultural perspectives, should be able to accommodate – or at a minimum not preclude – approaches from either subdiscipline (Chapais, 2014).

Undeniably, human reproduction is necessary for the perpetuation of the species. This does not mean that physical relationships that produce offspring necessarily form the basis of social relatedness in the present or in the past (Sahlins, 2013). Surrogacy and adoption could have enabled same-sex spouses the opportunity to raise children in the past just as they do today. The notion that husband-wife and parent-child relationships – cornerstones of “nuclear” or “conjugal” family units – are paramount to understanding kinship is flawed, biased, and prohibits a more complete understanding of relatedness (Blackwood, 2005; Dowson, 2006; Geller, 2009a; Hayden, 1995; Weston, 1991). Even within biological or consanguineal models of kinship, the focus on genealogical (i.e., intergenerational) relationships marginalizes siblingship, a potentially significant aspect of relatedness in many contexts (see Carsten, 1995; Gibson, 1995; Marshall, 1983; Paul and Stojanowski, 2015). Alternative, non-heteronormative models of family units are needed to foster different considerations of relatedness.

Bioarchaeologists are attempting to accommodate non-biological forms of relatedness in their studies of family-based social organization in the past. These



contributions are noteworthy for expanding beyond genealogical conceptions of relatedness, but they are still predominantly situated within a Western conception of kinship wherein biology is the de facto characteristic that defines family relations and alternative forms of relations are supplemental (Viveiros de Castro, 2009). To truly develop alternative (i.e., non-biological or non-Western) forms of relatedness, bioarchaeologists will need to develop conceptual models for evaluating non-biological forms of social relatedness in the archaeological record. Although this will be challenging in application – with or without ethnographic and/or ethnohistoric analogs – it is critical to consider alternative models of relatedness when reconstructing kinship in the past (Watanabe, 2004).

This is not to suggest a post-biological era of kinship research. Cross-culturally, a common aspect of mutuality of being is sharing common biogenetic substance (Sahlins, 2013), and in many contexts performative or process-based kin relations are modeled on procreative ones (Holy, 1996; Shapiro, 2014). Although kinship is not simply reducible to genealogy, consideration of genetic relatedness will continue to play an important role in the future of kinship studies. The use of biodistance and genetic analysis in combination with contextually relevant cultural indicators of relatedness can help disentangle kin-based affiliations from other mid-level and larger scales of social identities including neighborhood, community, and ethnic affiliations.

There is a need, for example, to develop and evaluate alternative interpretive models when individuals buried in close spatial proximity within a cemetery are not close genetic relatives (Deguilloux et al., 2011; Rudbeck et al., 2005). Additionally, the

absence of evidence of genetic relatedness in cases where other types of data (e.g., mortuary, isotopic, etc.) are suggestive of a family-based relationship could be an indication of kinship based at least in part on social relatedness or, minimally, a non-genealogical conception of kinship (Deguilloux et al., 2011). Alternatively, these data could be indicators of a shared social identity based on something other than kinship (e.g., community, status, etc.).

***Postmarital residence patterns.*** Postmarital residence analyses involve several (often implicit) assumptions (Nystrom and Malcom, 2010; Stojanowski and Schillaci, 2006) that must be carefully considered in terms of potential limitations on the inferences drawn from such studies as currently configured. First, for studies using skeletal samples, it is assumed that skeletons are correctly sexed. This is treated as primarily a methodological concern, although greater consideration of the influence of heteronormative bias in sexing techniques should be considered (Geller, 2005, 2008, 2009b; Hollimon, 1997). In some contexts, it may be more appropriate to group individuals for analysis using culturally salient gendered identities, including any potential “third gender” categories (e.g., Geller, 2005; Hollimon, 1997) rather than using biological sex estimated from the skeleton.

Second, there is an implicit assumption that postmarital residence practices in life are correlated with burial location at death or “postmortem residence” (Ensor, 2013b: 63). Ethnographic (Matney et al., 2012) and archaeological (Keegan, 2009) examples describe mortuary practices wherein individuals who were mobile during life were returned to their natal family for burial. Such practices create “interpretational problems” for

investigations of postmarital residence practices using biological data from archaeological contexts (Ensor, 2013b: 62). Bioarchaeologists need to explicitly state the assumptions underlying their analyses and interpretations and actively build on current conceptual frameworks to address these issues.

To the extent to which contemporary horticulturalist and foraging groups provide acceptable models of social group interaction and behavior in the past, bioarchaeologists might draw on ethnographic evidence to formulate both expectations and inferences about kinship in ancient contexts. Information on postmarital residence and social group composition in modern hunter-gatherer societies (e.g., Bailey et al., 2014; Hill et al., 2011; Walker et al., 2013) might inform expectations of intracemetery analyses, where the proportion of co-residing (and co-interred) kin is otherwise indeterminable. These studies also might shed light on complex kin dynamics of which archaeologists must be cognizant while reconstructing past social relationships; for example, co-parenting and partible paternity, in which more than one male is thought to be essential to offspring conception (see Ellsworth et al., 2014).

In some archaeological contexts social relatedness may have been more significant in determining burial location within cemeteries than genetic relatedness, rendering biologically-based interpretations of postmarital residence problematic. The modeling and simulation research of Usher and colleagues marks a promising avenue for explicitly testing the correspondence of conscious mortuary behavior (i.e., cemetery composition) and kin/community structure observable in the archaeological record (see Usher and Allen, 2005; Usher and Weets, 2014; Usher et al., 2003). Related endeavors

referencing simulated data or conducted in highly controlled archaeological contexts will shed light on the life and death manifestation of kinship identity, as well as our ability to recover dimensions of relatedness from mortuary data.

*Family, childhood, and life course.* Developments in life-course theory highlight the influence of age-dependent facets of social identity and status in structuring social interactions (e.g., Gilchrist, 2000, 2004; Prowse, 2011; Robb, 2002; Zvelebil and Weber, 2013). Bioarchaeological investigations of family and relatedness will benefit from incorporating life-course and life-history perspectives. For example, Robb (2002) describes the ways in which individuals' life histories influence social group histories. As posited by Robb (2002: 159), "'linear biographies' are interwoven via age-status identity and interage relations to form a cyclical history of the group as a whole." As cyclical histories are dependent on reproduction and regeneration of the collective, it is reasonable to consider families and children essential to this circuit. Bioarchaeologists may, for example, identify mortuary treatments corresponding to interwoven patterns of skeletal age and relatedness, indicating socially meaningful transitions in the life course that correspond to shifts in kin identity.

Explorations of childhood, in particular, might be effectively conducted within a research framework centered on collective kin identity. For most individuals, their earliest and most formative social interactions are shared with relatives (Carsten, 2000; Jenkins, 2008). And, relevant to Robb's (2002) conception of time and the life course, children both physically and symbolically perpetuate and eternalize family identities (Carsten, 2000; Stafford, 2000). The intersection of childhood and family represents a

potentially rewarding direction for theoretical bioarchaeological research.

Bioarchaeological approaches to childhood already constitute a developing sector of social identities research (e.g., Lewis, 2007; Perry, 2005; Sofaer, 2006). Yet to date, these research programs are rarely integrated into more comprehensive investigations of archaeological kinship.

King's (2006) study of age-centered mortuary behavior at Early Postclassic Río Viejo, Oaxaca, provides an example of bioarchaeology's potential to access the intersection of childhood and kinship. King's research centers on mortuary contexts and asks why subadults were excluded from burials beneath house floors, a common mortuary context for adults at Early Postclassic Río Viejo (King, 2006, 2010). Instead of interpreting the absence of child burials as evidence for the exclusion of children from household or kin collectives, King references childhood imagery in ceramic figurines to construct an alternative interpretation. Children were not simply "nonmembers" of houses; they occupied fluid social positions (King, 2006). Affiliation with specific households (and/or biological kin collectives) remained fluid until an individual passed through a socially significant stage of the life course. In this way, the experiential time of the individual child was "interwoven via age-status identity" into the non-linear history of the corporate residence (family) (King, 2006, 2010; Robb, 2002: 159). Studies of this kind, especially if both biological and social models of relatedness are integrated, would make a strong addition to bioarchaeological approaches to kinship.

***Kinship and power.*** Kinship conceptualized as mutuality of being does not imply that relationships are inherently beneficent practices (cf. Fortes, 1949). Kinship relations

are as likely to be characterized by enmity as by amity (e.g., Franklin and McKinnon, 2001; Freeman, 1973; Peletz, 2001; Strong, 2001, 2002; Van Vleet, 2008). Family dynamics can include acts of violence and establish relationships enmeshed with power hierarchies, what Van Vleet (2008: 195) calls the “micropolitics of interactions.” Skeletal evidence of trauma consistent with familial or “domestic” violence is well documented in the bioarchaeological literature (e.g., Martin, 1997; Martin et al., 2012; Novak, 2006; Walker, 1997; Wilkenson, 1997). However, despite an increase in theoretical approaches to violence in the past (e.g., Martin et al., 2012; Tung, 2012), a disconnect between bioarchaeological investigations of domestic trauma and family-based social organization remains. The integration of evidence for familial violence with social relatedness, gender relations, and embodiment theory could generate new insights on individual experience and social organization in past societies. In addition, the antiquity of modern behavioral phenomena like interpersonal (or kin-structured) violence is a topic of contemporary social importance and public interest.

### **Conclusions**

Kinship is currently a vibrant topic of research across the humanities, social sciences, and life sciences, with applications to diverse fields including modern human origins (e.g., Chapais, 2014), social inequality (e.g., Cohen, 2015; Smith et al., 2010), and genetic counseling (e.g., Atkinson et al., 2013). Kinship remains an active area of research within all anthropological subdisciplines. In particular, Ensor (2011, 2013a,b) has recently pushed to make kinship a focus within archaeological research. Bioarchaeology, too, has witnessed an amplification of published kinship studies that

have grown increasingly dependent on diverse lines of evidence and engagement with sociocultural theory. Consideration of kin-based social organization can complement a wide array of research topics about the past. Furthermore, I believe that bioarchaeology has the potential to offer significant contributions to the study of kinship.

I have reviewed bioarchaeological approaches to kinship in light of recent theoretical developments in sociocultural kinship studies to provide both historical foundation and theoretical orientation for a new model of bioarchaeological kinship research. Results of quantitative and qualitative literature reviews suggest bioarchaeologists realize that Western conceptions of biogenetic relatedness are unlikely to capture the diversity of family organization that likely existed in the past (e.g., Deguilloux et al., 2011; Pilloud and Larsen, 2011). Notably, there is growing recognition that conceptions of family common among modern Western societies (i.e., nuclear families based on consanguineal and affinal relations) may not be “suitable to the people of antiquity” (Simón et al., 2011: 10; see also Deguilloux et al., 2011; Gilbert et al., 2007; Haak et al., 2008). Scholars are beginning to use broader, more flexible conceptions of relatedness to access that diversity and postulate examples of non-biological forms of kinship (e.g., fictive and practical kin) in archaeological contexts (e.g., Gregoricka, 2013; Lozada, 2011b; Paul et al., 2013; Pilloud and Larsen, 2011). The careful combination of diverse types of data and consideration of both biological and social aspects of relatedness demonstrated by Meyer et al. (2012) provides a model of research design and conceptual clarity on which future efforts should build. Stojanowski’s (2013) examination of the role of kinship in the structuring and/or institutionalization of

intergenerational social inequality illustrates the potential of bioarchaeological research to link kinship to broader social issues that have real consequences on the lives of individuals in the present.

These advances are laudable, but conceptual challenges must be addressed if the field is to realize its potential. There continues to be a lack of precision in key terms. Within discussions of kinship and family, it is helpful to identify whether one is referring to genetic relatedness (e.g., Alt et al., 2013), social relatedness (e.g., Gregoricka, 2013; Pilloud and Larsen, 2011), or some combination of these (e.g., Meyer et al., 2012). Even when scholars embrace non-biological forms of relatedness, there persists a reliance on Western modes of relatedness in non-Western contexts (cf. Lozada, 2011b), including approaches that frame kinship as social identity, as I propose here. Efforts to apply our own epistemology to understand other ontologies will always struggle (Viveiros de Castro, 2009), but unless we are able to develop and operationalize theoretical frameworks for investigating kinship in ancient contexts using non-Western ontologies (a challenging goal), a social identity framework seems well adapted to incorporate both biological and cultural data without inherently prioritizing one over the other.

There is room for the incorporation of recent theoretical developments into all phases of bioarchaeological kinship research. Contextually relevant conceptions of relatedness are essential to bioarchaeological family research; they should inform not only the interpretations generated but also the hypotheses formulated, the data collected, and the analyses performed in the course of these studies. Clear expectations of data patterns consistent with non-biological forms of relatedness combined with either



rigorous hypothesis testing or evaluation of alternative explanatory models will help scholars avoid the “just so” stories that accompany ad hoc or post hoc applications of social theory to one’s data. At present, nuanced reconstructions of kinship and relatedness in the past may only be possible in contexts with clearly established chronology and availability of diverse data, including ethnohistoric, epigraphic, or ethnographic evidence of kinship organization to aid inferential precision. Notwithstanding, much can be learned about the past through the study of kinship, even in contexts where these criteria are not met. Bioarchaeologists can contribute to an understanding of the fluctuating biological and social realities of kinship experienced throughout the history of our species. Such an understanding might, in turn, inform sociocultural theory, which often assumes that the range of human experiences observed today encompasses all of the forms of human experiences that existed in the past, a biased and likely untenable assumption.

In addition to providing a fruitful course of future research, a bioarchaeology of kinship as multiscalar social identity has the potential to build bridges within the academy and provide a conduit for anthropological scholarship to reach a wider audience. Bioarchaeology is well suited to incorporate both biological and social perspectives into holistic understandings of kinship (Meyer et al., 2012), as well as to provide the time-depth that sociocultural approaches are lacking and that most evolutionary approaches fail to directly access. Bioarchaeological kinship research should provide a common ground that facilitates collaborative research among archaeological, sociocultural, and evolutionary anthropologists specifically and contribute to cross-disciplinary research initiatives in general.

Within academia, a bioarchaeology of kinship as social identity would be ideally positioned to contribute to one of the 25 most important scientific challenges for archaeology presented by Kintigh et al. (2014). One of their 25 challenges (Challenge D2) concerns how people form social identities; specifically, the authors state that a critical aspect of future research will be understanding “how human identities (vs. the modes of affiliation among other species) form with respect to biological and emotional bonds” (Kintigh et al., 2014: 14-15). By exploring the ways in which multiscale family identities are formed, modified, and interact with other forms of social identities, bioarchaeologists can provide important insights into the long-term and large-scale effects of the processes of identity formation and transformation.

Stojanowski and Duncan (2015) note that for the field of bioarchaeology to remain relevant in contemporary public discourse, bioarchaeologists must develop research projects of general interest and disseminate findings among broad audiences. The investigation of families in the ancient and recent past has the potential to attract widespread interest via major media outlets and science news aggregators. Today, as North American media attention centers on the “crisis of the [Western] family,” scientific/technological endeavors (e.g., genetic counseling, in vitro fertilization, prenatal medicine) intersect with social endeavors (e.g., same-sex marriage and adoption legislation, foster parenting systems, an increasing number of stay-at-home fathers) in both complementary and conflicting ways (e.g., Carsten, 2004, 2011; McKinnon, 1991; McKinnon and Cannell, 2013; Stone, 2001). Holistic bioarchaeological perspectives on

relatedness can inform popular imaginations of kinship and, perhaps, influence the ways in which we advocate, legislate, and approach changes to current social structure.

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## CHAPTER 3

### MULTIETHNIC COMMUNITIES AND ENDOGAMY: EVALUATING THE BIOLOGICAL IMPLICATIONS OF THE DUAL DIASPORA MODEL OF MOQUEGUA TIWANAKU COLONIAL SOCIAL ORGANIZATION

Target Journal: Latin American Antiquity

The emergence of expansive states as political institutions dramatically altered relationships among human communities. State expansion and colonialism disrupted marriage practices and restructured economic activities as new economic, ideological, and political systems took hold. Most theoretical models of colonialism are based on cases of European colonial incursions among Native American and African peoples and are often ill-suited to account for state expansion in exclusively non-Western contexts (see Das and Poole, 2004; Ferguson and Whitehead, 1992; Gosden, 2004; Hill, 1996; Voss, 2008; cf. Goldstein, 2005; Smith, 2003; Stein, 2005). Colonial interactions between European and indigenous peoples were structured in part by Western conceptions of race, religion, and sexuality as well as capitalist motivations, thereby confounding inferences about impacts of state expansion on the social organization of incorporated peoples.

The prototypical example of state society expansion is influenced by Western European colonial incursions in Africa, Asia, and North and South America during the 15<sup>th</sup>-19<sup>th</sup> centuries and involves members of a dominant society “imposing conditions of inequality and assimilation over subordinate groups” (Goldstein, 2015: 9202). Taking this as a pervasive model of colonialism throughout time unduly limits our characterizations of colonial interactions in the past and the present. As Stojanowski (in press) notes, it is

necessary to move beyond simplistic models based on dichotomies of “European/non-European” or “the colonized and the colonizer” to develop alternative models of colonial interactions. The study of colonial interactions in non-Western contexts, where factors such as race may be absent from the colonial experience, provides opportunities to investigate the diversity of ideologies, cultural practices, and social formations that structure colonial relationships and develop alternative models of colonialism.

The analysis of indigenous instances of state expansion and colonialism from pre-Hispanic South America can contribute to the formulation of general frameworks for investigating colonialism within contexts in which Western conceptions of race, sex, and religion were absent. The pre-Hispanic Tiwanaku state (ca. AD 500-1000) provides an example of colonial expansion and interaction within an ancient non-Western setting (Goldstein, 2000b, 2005, 2009, 2013, 2015; see also Goldstein and Owen, 2001; Owen and Goldstein, 2001). The present study investigates biosocial interactions within the Tiwanaku colonies in the Moquegua Valley of southern Peru to evaluate and extend current interpretations of Tiwanaku colonial organization.

Goldstein’s (2000, 2005, 2009, 2013, 2015) dual diaspora model characterizes the Moquegua Valley Tiwanaku colonies as multiethnic, with most major Tiwanaku-affiliated settlements in the valley comprised of Chen Chen-style and Omo-style communities. Members of Chen Chen- and Omo-style communities were united in their shared use of corporate Tiwanaku material culture and ritual practices, but they maintained distinct social identities through differences in settlement practices, residential architecture, economic production, mortuary practices, and material culture

styles. Goldstein interprets Chen Chen- and Omo-style communities as separate diasporic communities who maintained strong ties with their respective maximal *ayllus* based in their ancestral homelands (Goldstein, 2005, 2015). He posits that Chen Chen- and Omo-style communities in Moquegua also maintained distinct social identities through endogamous marriage practices, but this hypothesis has yet to be evaluated.

In this chapter, biodistance and exploratory data analysis of phenotypic data are used to evaluate the biological implications of the dual diaspora model of Tiwanaku colonial organization in the Moquegua Valley. Coordinate data of basicranial and temporal bone landmarks are subjected to analytical techniques including R-matrix analysis, discriminant function analysis, and canonical variates analysis to evaluate marital migration (i.e., mate exchange) between Chen Chen- and Omo-style Tiwanaku-affiliated communities to assess whether they were endogamous social groups. Reconstructing patterns of biosocial interactions within the Moquegua colonies is important for understanding the processes of Tiwanaku state expansion, which in turn allows for the development of alternative models of colonial interaction that are more broadly relevant at the global scale.

### **Biodistance, biosocial interaction, and social identity**

Biological distance (i.e., biodistance) analysis uses observable phenotypic variation among polygenic traits as a proxy for the degree of genetic relatedness among samples. Biodistance is a measure of similarity or distance among samples or individuals based on the amount of phenotypic variation they share in polygenic morphological traits. The phenotypic expression of polygenic traits is governed by multiple alleles; hence,

their expression varies within and between populations (Hartl and Clark, 2007).

Bioarchaeological applications of biodistance analysis use skeletal and dental metric and morphoscopic traits from samples of human skeletal remains to evaluate patterns of genetic variation and reconstruct microevolutionary processes among (sub)populations in the past (Buikstra et al., 1990; Larsen, 2015; Relethford, 2016).

Microevolutionary theory suggests that populations that exchange mates (or otherwise experience gene flow) become more phenotypically similar, while those that do not exchange mates are likely to become more dissimilar due to the stochastic vagaries of genetic drift (Hartl and Clark, 2007). Therefore, results of biodistance analysis can be used to make inferences regarding population structure and population history (e.g., Cheverud, 1988; Konigsberg and Ousley, 1995; Relethford, 2003, 2016; Smith, 2009; Williams-Blangero and Blangero, 1989, 1990). Population structure is a nonrandom distribution of genetic variation within a population (Hedrick, 2011). In other words, in a population there are localized subpopulations with different allele frequencies. The study of population structure involves the identification of the factors that influence a nonrandom pattern of genetic microdifferentiation within populations or subpopulations, especially mate choice and patterns of marital migration (i.e., gene flow) (Mielke et al., 2011; Relethford, 2012). Population history is similar to population structure, but it generally involves the exploration of the genetic impact of historical factors (e.g., invasions, migrations, and population bottlenecks) that affect patterns of genetic variation (and genetic distances) among (sub)populations (Hedrick, 2011; Mielke et al., 2011; Relethford, 2012).

A fundamental assumption of biodistance studies is that phenotypic variation corresponds with genetic microdifferentiation (Corruccini, 1976; Larsen, 2015; Pietrusewsky, 2008; Relethford, 2016; Rightmire, 1999). However, dental and skeletal traits are influenced by non-genetic (i.e., developmental, environmental, and epigenetic) factors as well as by one's genotype (Berry and Berry, 1967; Brook, 2009; Buikstra et al., 1990; Larsen, 2015; Parsons et al., 2015; Townsend et al., 2012). Because of the multifactorial nature of the phenotypic traits typically used for biodistance analysis, some have questioned the reliability of morphological features for assessing biological relatedness among past populations (Tyrrell, 2000). These concerns include the lack of singular correlations between a metric or nonmetric trait and an individual's genome (see Larsen, 2015) and imprecise understanding of trait heritability within different populations (see Carson, 2006a,b; Vitzthum, 2003).

Various lines of evidence support the continued use of phenotypic traits as proxies for genetic variation. For instance, quantitative traits, even though not strictly heritable, have been successfully used with some living populations to document aspects of population structure (e.g., Williams-Blangero and Blangero, 1989, 1990). The appearance of certain non-metric traits prior to birth (El-Najjar and Dawson, 1977) and agreements in trait frequencies among related groups (Pietrusewsky and Douglas, 1993) provide direct evidence for the genetic basis of some non-metric traits. Additional support for the use of morphological characteristics as proxies for genetic variation comes from archaeological and historical evidence (Brace et al., 1990), from familial studies of modern humans (e.g., Paul and Stojanowski, 2015; Saunders and Popovich, 1978; Townsend et al., 2009,

2015), from studies of rhesus monkeys (Cheverud and Buikstra, 1981a,b, 1982), and from meta-analyses of published data (Cheverud, 1988). Finally, a number of studies have found a correlation between results from analyses of phenotypic data (e.g., anthropometric and craniometric) and results of quantitative genetic analyses (Konigsberg and Ousley, 1995; Smith, 2009; Smith et al., 2007; Smith and von Cramon-Taubadel, 2015; von Cramon-Taubadel and Smith, 2012).

### **Bioarchaeological applications of biodistance analysis**

Within bioarchaeology biodistance analysis uses phenotypic data from samples of human skeletal remains to reconstruct population history and investigate population structure (see Buikstra et al., 1990; Cheverud, 1988; Konigsberg, 2006; Larsen, 2015; Stojanowski and Schillaci, 2006). Aspects of social organization and patterns of social interaction associated with socially prescribed marriage practices (e.g., social group endogamy) or post-marital residence patterns (e.g., matrilocality and patrilocality) may result in distinct patterns of genetic variation which can be assessed using biodistance analysis. Historically, population-based analyses have received the most attention in bioarchaeology, whereas individual-based applications of biodistance analysis have been more prevalent in paleoanthropology (e.g., Gordon et al., 2008; Stojanowski, 2014; White et al., 2003) and forensic anthropology (e.g., Pilloud and Hefner, 2016; Stojanowski and Duncan, 2009; Stojanowski and Duncan, in press). Bioarchaeological applications range from exploratory analyses with post hoc interpretations to formal hypothesis testing of models of social organization and interaction.



Biodistance analysis is used to investigate population history and population structure at a range of analytical scales: intercontinental, interpopulation, intraregional, and intrasite (Buikstra et al., 1990: 3). Of these four scales, intraregional (or simply regional) analyses are most relevant to exploring patterns of Tiwanaku colonial organization in the middle Moquegua Valley. Regional biodistance analyses examine patterns of phenotypic variation to make inferences regarding socially prescribed marriage practices, postmarital residence practices, and population replacement, dispersal, or aggregation (e.g., Aubry, 2009; Buikstra, 1976; Corruccini, 1972; Droessler, 1981; Galland et al., 2016; Irish, 2005; Konigsberg and Buikstra, 1995; Lozada Cerna, 1998; Rightmire, 1970, 1976; Spence, 1974a,b; Steadman, 2001; Stojanowski, 2010; Sutter, 2009a; Sutter and Sharratt, 2010; Tomczak, 2001). Interpretations of results typically consider the effects of local demographic variables, environmental factors, biocultural developments (e.g., economic transitions and technological innovation), and sociopolitical processes (e.g., inter- or intra-group conflict) on regional phenotypic variation. Given the emphasis on research questions involving population movements, population aggregation, and marital migration, regional biodistance studies have focused on exploring the effects of gene flow and genetic drift on patterns of phenotypic variation, although some have investigated the effects of natural selection on phenotypic traits (e.g., Christensen, 1998b; Sciulli et al., 1988; Sciulli and Mahaney, 1991). Gene flow is of particular interest in the present study, as the central question explored in this chapter concerns the occurrence of marital migration between Chen Chen- and Omo-style Tiwanaku communities in the Moquegua Valley.

Although evolutionary geneticists sometimes treat gene flow and migration interchangeably (Merrell, 1981: 9), it is important to distinguish between them. Migration refers to the movement of an organism (i.e., individual) across the landscape to a new environment or to a new population (see Cabana and Clark, 2011: 5; Tsuda et al., 2015: 19), whereas gene flow involves the movement of alleles between subpopulations (Endler, 1977; Fix, 1999; Mielke et al., 2011). Migration is often contrasted with mobility, which refers to movements within a given territory or environment (Adams et al., 1978; Cabana and Clark, 2011; Tsuda et al., 2015). Migration can occur without gene flow, but gene flow cannot occur without migration. Gene flow has the effect of increasing genetic variation within subpopulations and decreasing genetic variation between subpopulations (Fix, 1999; Hedrick, 2011), unless the migrating individuals represent a non-random sampling of the source population (e.g., kin-structured migration), in which case the opposite effects may be observed (Fix, 1978, 1999; Rogers, 1987).

Past migrations are typically studied by identifying changes in the spatial distributions of biological, cultural, and/or linguistic traits (e.g., Adams et al., 1978; Anthony, 1990, 2007; Burmeister, 2000; Clark, 2001, 2011; Ehret et al., 2004; Ehret and Posnansky, 1983; Greenberg et al., 1986; Kirch and Green, 2001; Ortman, 2009; Renfrew, 1987; Rouse, 1986). However, material culture, patterned behaviors, and aspects of language can disperse through means other than migration, making biological evidence collected directly from the bodies of past individuals the strongest evidence of past migrations (Cowgill, 2015). Biological data include phenotypic traits (e.g., Blom et

al., 1998; Cucina, 2015; Jantz, 1972, 1973, 1977; Jantz et al., 1981; Konigsberg, 1988; Sutter, 2000, 2009a,b; Zakrzewski, 2007), genetic markers (e.g., Bolnick and Smith, 2007; Lewis et al., 2007; Moraga et al., 2005), as well as biogeochemical data to assess paleomobility (e.g., Bentley, 2006; Bentley et al., 2004; Buzon and Simonetti, 2013; Dupras and Schwarcz, 2001; Haak et al., 2008; Knudson, 2008; Knudson and Price, 2007; Price et al., 1994; Stantis et al., 2016). Also useful for inferring past migrations are changes in demographic structure (e.g., Ortega Muñoz, 2015; Paine and Boldsen, 2002), diet (e.g., King et al., 2013; Müldner et al., 2011; Schroeder et al., 2009), patterns of disease and generalized stress (e.g., Conlee et al., 2009; Harrod et al., 2012; Lewis, 2016), and body modifications that affect the teeth and skeleton (e.g., Blom et al., 1998; Tiesler, 2014, 2015). Marital migration (i.e., gene flow), is typically studied using the same types of data, perhaps with greater evidence on genetic (e.g., Krings et al., 1999) and/or phenotypic data (e.g., Aubry, 2009; Steadman, 2001; Stojanowski, 2005a,b,c,d, 2009, 2013a,b; Tatarek and Sciuli, 2000) to assess population structure and population history.

Bioarchaeological investigation of gene flow and genetic drift are built upon the foundational work on migration and gene flow in anthropological genetics in the 1970s (e.g., Friedlaender, 1971a,b, 1975; Harpending and Jenkins, 1973; Malcolm et al., 1971; Morton, 1977; Neel and Ward, 1970; Ward and Neel, 1970, 1976; Workman and Niswander, 1970). This early research was focused on understanding how migration, especially marital migration, affects levels of genetic microdifferentiation among subpopulations and adapting general models of migration and gene flow (e.g., Bodmer

and Cavalli-Sforza, 1968; Kimura and Weiss, 1964; Malécot, 1969; Wright, 1943, 1951) to human populations. One of the difficulties in modeling marital migration and gene flow among human populations is that in addition to geographic proximity, a key component of genetic microdifferentiation in human and nonhuman populations, there are a variety of sociocultural factors that structure mate choice and marital migration among human societies (e.g., Cannings and Skolnick, 1975; Fix, 1979; Workman et al., 1976). In the 1980s biological anthropologists and bioarchaeologists began applying approaches to and models of human migration, gene flow, and population structure developed using data from polymorphic genetic systems to phenotypic data from contemporary populations and archaeological samples (e.g., Blangero, 1990; Konigsberg, 1988, 1990; Relethford, 1988; Relethford and Blangero, 1990; Relethford et al., 1980, 1997; Williams-Blangero, 1989a,b, 1990; Williams-Blangero and Blangero, 1989, 1990).

Because social boundaries can influence patterns of gene flow through socially prescribed parameters for mate selection (Cannings and Skolnick, 1975; Chapman, 1993; Fix, 1979; Relethford, 2010; Stojanowski, 2010; Wright, 1946; Workman et al., 1976), mate exchange (i.e., marital migration) has a very powerful social component (Sahlins, 2013). Therefore, patterns of gene flow reflect human behavior (e.g., mate choice) both at the level of the individual and at the community or subpopulation level that can reflect emic conceptions of 'self,' 'us,' and 'other' (Stojanowski, 2005a, 2010: 51-52; see also Blom et al., 1998; Macbeth, 1993; Sutter, 2005, 2009a). As marital migration and gene flow influence patterns of genetic variation, biodistance analysis of phenotypic traits can

be used to investigate patterns of affiliation and interaction and make inferences about broader structures of social organization and social interaction in the past.

Although social boundaries often influence patterns of gene flow, this does not guarantee that social boundaries necessarily restrict or prohibit gene flow. Numerous studies have documented examples of marked social boundaries that do not inhibit mate exchange and gene flow (e.g., Buikstra, 2005; Lozada Cerna, 1998; Lozada Cerna and Buikstra, 2002, 2005; Moore, 1994a; Morton et al., 1971; Pilloud and Larsen, 2011; Sutter, 2005; Tomczak, 2001; Williams, 2005). Therefore, despite diverse lines of evidence suggestive of pronounced social boundaries between Chen Chen-style and Omo-style Tiwanaku-affiliated communities, it is critical to formally evaluate whether these communities were endogamous.

Biodistance analysis can contribute to study of Moquegua Tiwanaku social organization in a way that analysis of cultural data cannot. Certain material culture indicators of social identity and affiliation (e.g., styles of clothing or ceramics) can be rather easily manipulated and can communicate different signatures of social identities throughout the lifecourse (e.g., Bourdieu, 1990; Conkey and Hastorf, 1990; Dietler and Herbich, 1998; Hegmon, 1998; Sackett, 1977; Wells, 1998; Wiessner, 1983). Marital migration, along with presumptive gene flow, may have occurred among Chen Chen- and Omo-style communities, and it could be quite difficult to detect if the mobile spouse aligned his or her social identity with and/or adopted the cultural attributes of the maximal *ayllu* into which he or she married. Importantly, the genetic affiliation of an

individual is less easily manipulated than artifactual expressions of social identities (Knudson and Blom, 2009; Stojanowski, 2010; Sutter, 2005, 2009a).

The unique insight biodistance analysis can provide into patterns of affiliation and interaction in the Moquegua Valley Tiwanaku colonies has the potential to inform our understanding of Tiwanaku state expansion. State ingressions in peripheral areas often induce new principles of social organization (Ferguson and Whitehead, 1992; Hechter, 2000; Hill, 1996; Jennings, 2003; Stojanowski, 2005a,b, 2009; Whitehead, 1992) that can disrupt or transform existing social and biological networks and lead to new patterns of gene flow and/or genetic drift in peripheral areas (Klaus and Tam, 2009a; Nystrom, 2009; Stojanowski, 2005a, 2009). Analysis of population structure among peripheral communities using patterns of phenotypic variation can aid investigations of changes in colonial social organization and core-periphery relations, and it can lead to new inferences about Tiwanaku sociopolitical organization and Tiwanaku state expansion.

#### **The site of Tiwanaku and emergence of the Tiwanaku state**

The site of Tiwanaku developed from one of many unremarkable villages in the Lake Titicaca Basin into a complex urban center (e.g., Bermann, 1994, 1997; Isbell and Vranich, 2004; Janusek, 1999, 2004a,b, 2005a,b; Kolata, 1993a, 1997; Posnansky, 1914, 1945, 1957; Vranich, 1999; Stanish, 2003). During the Early Formative period (2000-1300 BC), inhabitants of the Lake Titicaca Basin lived in small communities along the lake shore. Pottery first appears in the archaeological record of the Basin during this period, in the form of cooking, storage, and serving ware (Stanish, 2003).

Major social transformations began during the Middle Formative period (1300-500 BC). The region's first non-residential corporate architecture was created, and sunken courts were constructed at sites including Chiripa, Pajchiri, Qaluyu, and Tiwanaku. Stanish (2003) suggests that these sites were regional centers formed through the activities of emergent elites and linked by a shared religious ideology materialized in the sunken courts and the Yaya-Mama iconographic style (Chavez, 2004; Chavez and Chavez, 1975). Hastorf (2005) argues that these shared religious beliefs not only brought disparate communities together but also spurred competition between families and communities.

The Upper Formative period (500 BC-AD 400) in the Lake Titicaca Basin was marked by population growth, agricultural intensification, incipient craft production, and long-distance trade (Bandy, 2001). Within this context, the centers of Pukara and Tiwanaku became considerably larger than the other population centers and competed for primary influence in the region (Stanish, 2003). Stanish (2003) argues that Tiwanaku and Pukara elites expanded their influence by creating alliances based on competitive feasting, marriage, and fictive kinship rather than coercion. However, the depiction of trophy heads in Pukara and Early Tiwanaku iconography (see Hastorf, 2005) and recent bioarchaeological evidence of trophy-head taking and political violence from the site of Wata Wata (Becker and Alconini, 2015), located east of the Titicaca Basin, may be suggestive of intergroup conflict or warfare during the transition from the Late Formative period to the Tiwanaku period. With the decline of Pukara around AD 200-300,

Tiwanaku emerged as the primary cultural and political influence in the Lake Titicaca Basin (Augustyniak, 2004; Janusek, 2004a, 2008; Stanish, 2003).

During Tiwanaku IV (AD 400-800), correlates of hierarchical sociopolitical organization are evident at the site of Tiwanaku and beyond. The city grew to 4-6 square kilometers in size (Kolata, 2003), and the construction of monumental architecture progressed at an unprecedented scale. Monumental constructions such as the Akapana pyramid and Pumapunku temple made the site a symbolically potent center that subsequently was referenced by nearby and peripheral communities in the creation of their own ritual spaces (Escalante M., 1993; Goldstein, 1993a; Kolata, 1993a; Manzanilla, 1992). Additionally, a four-tiered hierarchical settlement pattern emerged in the state hinterland (Albarracín-Jordán, 1996; Bandy, 2001; Janusek and Kolata, 2003; McAndrews et al., 1997).

The burgeoning population of the capitol and hinterland was provisioned with high altitude crops such as quinoa (*Chenopodium quinoa*), potatoes (*Solanum tuberosum*), oca (*Oxalis tuberosa*), and ulluco (*Ullucus tuberosus*) grown in the numerous raised field agricultural systems as well as through the exploitation of lacustrine resources (Berryman, 2010; Kolata, 1986, 1991, 2003; Kolata and Ponce Sanginés, 1992). Agricultural production intensified, as extensive land reclamation projects allowed farmers to expand the raised field system into marshy areas of the southern basin (Janusek, 2008). These *altiplano* resources were supplemented with agricultural resources from warmer, lower altitude ecozones (Berryman, 2010; Kolata, 1992). Communities of pastoralists in the outer districts of the city of Tiwanaku tended



large camelid herds which were critical to maintaining the long-distance trade networks linking the heartland and distant provinces throughout the south central Andes and provided an important source of animal protein to pastoralist groups (Berryman, 2010).

In Tiwanaku V (AD 800 – 1150), data support an interpretation of increasing bureaucratic centralization and consolidation. The city, inhabited by as many as twenty thousand people during this period (Kolata, 2003), was reorganized into residential neighborhoods (Couture, 2003; Janusek, 1999, 2002, 2004a). Competition increased between factions at the site of Tiwanaku as elite residences and elite-sponsored feasts became more ostentatious (Janusek, 2008). As elites sought to provide for their increasingly elaborate competitive feasts, they tightened control over agricultural production at hinterland and provincial sites (Goldstein, 2005; Janusek, 2004a, 2008). For example, as control of maize (*Zea mays*) and coca (*Erythroxylum coca*) production became increasingly centralized, settlements in Moquegua shifted from a loosely-integrated diaspora-based enclave to a colony fully integrated into a hierarchical, tightly-controlled political economy (Goldstein, 2005, 2009).

### **Tiwanaku expansion**

Over the course of the Middle Horizon (ca. AD 500-1100) Tiwanaku influence spread across a large region of the south central Andes, including coastal valleys in southern Peru and northern Chile, the high desert inland oases of northern Chile, and the intermontane regions on the eastern slopes of the Andes in Bolivia (Anderson, 2013; Browman, 1997; Céspedes Paz, 2000; Goldstein, 2005; Ibarra Grasso and Querejazu Lewis, 1986; Janusek, 2008; Knudson, 2004, 2007; Knudson et al., 2004; Knudson and

Torres-Rouff, 2014; Knudson et al., 2015; Stovel, 2002, 2008; Torres-Rouff, 2008; Torres-Rouff et al., 2013). Communities in different areas of the south central Andes were selectively incorporated and/or engaged in exchange relationships for strategic and economic purposes (Erickson, 1988; Goldstein, 2009; Janusek, 2008; Luque and Canahua, 1997; Stanish, 2002, 2003, 2009; Stanish et al., 1997). Colonies and trading partners at lower elevations were critical to Tiwanaku's political economy (Goldstein, 2000, 2005; Janusek, 2008; Stanish et al., 2010). For example, surplus maize grown in peripheral regions was sent to the *altiplano* and used to make the fermented beverage *chicha* that was critical for elite-sponsored feasts (Berryman, 2010).

In the Azapa Valley of northern Chile, a variety of Tiwanaku artifacts has been found at cemetery and habitation sites, but Tiwanaku artifacts are present in such limited numbers in these contexts that it suggests they were imported from the *altiplano* rather than produced locally (Goldstein, 2005). According to Goldstein (1996, 2005), the Azapa Valley's Tiwanaku occupation most likely reflects the presence of small enclaves of colonists – perhaps a trade diaspora community – from the Tiwanaku core region who coexisted with a larger local population.

A similar pattern is emerging from the intermontane Cochabamba Valley, located on the eastern slopes of the Bolivian Andes. Based on the high volume of Tiwanaku-style ceramics, Cochabamba was initially thought to reflect the presence of a Tiwanaku colony (Bennett, 1936; Browman, 1981; Caballero, 1984; Céspedes Paz, 1993; Kolata, 1992, 1993b; Ponce Sanginés, 1980, 1981). However, two separate lines of evidence have led to a reevaluation of the inference of a Tiwanaku colonial presence in Cochabamba. First,

data indicate that many of the Tiwanaku-style ceramics recovered from Cochabamba contexts were produced locally (Anderson, 2013; Browman, 1997; Céspedes Paz, 2000; Ibarra Grasso and Querejazu Lewis, 1986). Second, settlement data provide no evidence of shifts in site locations or settlement patterns from pre-Tiwanaku- to Tiwanaku-period sites (Higueras-Hare, 1996). Thus, it seems Tiwanaku influence in the Cochabamba region was based primarily on long-distance trade, elite clientage, and stylistic emulation rather than direct colonization by highland populations (Anderson, 2013; Browman, 1997; Céspedes Paz, 2000; Higueras-Hare, 1996; O'Brien, 2003).

Archaeological data from the oases of San Pedro de Atacama in the Atacama Desert of northern Chile present a more complex picture of interaction compared to Azapa and Cochabamba. Situated roughly 800 kilometers south of Tiwanaku at an elevation of 2,430 masl, the oases of San Pedro de Atacama are strategically located relative to valuable mineral resources and represent an important waystation for accessing food and water in the hyperarid Atacama Desert on the thoroughfares between the *altiplano*, coastal Chile, and northwestern Argentina (Berenguer and Dauelsberg, 1989; Lechtman and Macfarlane, 2005, 2006; Llagostera, 1996; Nielsen, 2006; Nuñez, 1992; Pimentel, 2009). The presence of Tiwanaku-style material culture in the oases of San Pedro de Atacama was initially interpreted as evidence of Tiwanaku colonies (e.g., Berenguer and Dauelsberg, 1989; Kolata, 1993a; Oakland Rodman, 1992). However, the distribution of mortuary artifacts (Oakland Rodman, 1992), cranial modification data (Torres-Rouff, 2008), biogeochemical data (Knudson, 2004, 2007; Knudson et al., 2004; Knudson and Torres-Rouff, 2014; Knudson et al., 2015) and results of biodistance

analysis (Torres-Rouff et al., 2013) suggest a scenario of non-colonial Tiwanaku interaction. Though it appears San Pedro de Atacama was heavily influenced by Tiwanaku, current interpretations suggest Atacameños retained some degree of political autonomy and regional identity (Janusek, 2008; Knudson and Torres-Rouff, 2009; Stovel, 2002, 2008; Torres-Rouff, 2008). Furthermore, their interactions with Tiwanaku were merely one component of a broader pattern of interregional interaction (Knudson et al., 2015; Torres-Rouff et al., 2013). There is evidence that individuals interred in cemeteries at the oases of San Pedro de Atacama came from or spent part of their lives in regions outside of the Tiwanaku sphere, suggesting a far more cosmopolitan system of relationships and interregional interactions (Knudson et al., 2015; Torres-Rouff et al., 2013; Varela et al., 2013).

Situated approximately 300 km southwest of the capital of Tiwanaku in the *altiplano* of Bolivia, the Moquegua Valley, Peru, was home to the most substantial Tiwanaku colonial presence in the Andes (Goldstein, 2005, 2009). The Moquegua Valley is part of the Osmore River drainage in southern Peru. The valley's lower elevation (from 900 to 2,000 masl) and warmer climate compared to the *altiplano* combined with the potential for riverine irrigation make it a productive agricultural setting (Goldstein, 2003, 2005; Goldstein and Magilligan, 2011; Williams, 2002). Evidence for a Tiwanaku colonial enclave in Moquegua comes from multiple lines of archaeological and bioarchaeological data, including settlement patterns, mortuary practices, residential and monumental architecture, ceramics, textiles, cranial modification style, biogeochemical analyses, and biodistance analyses (e.g., Blom, 1999, 2005a,b; Blom et al., 1998;

Buikstra, 1995; García Marquez, 1990; Goldstein, 1989a,b, 1993a,b; Goldstein and Owen, 2001; Knudson, 2004; Knudson et al., 2014; Knudson et al., 2004; Moseley et al., 1991; Owen, 1997; Owen and Goldstein, 2001; Plunger, 2009; Vargas, 1994).

In sum, Tiwanaku influence in its peripheries was heterogeneous and noncontiguous (Goldstein, 1989a,b, 1993a,b, 2000a, 2005, 2009; Kolata, 1993a; Moseley et al., 1991). This variability was shaped by preexisting local sociopolitical conditions as well as Tiwanaku interests in a given region (Janusek, 2008: 235; see also Schreiber, 1992, 2005; Smith, 2003; Stein, 1999a,b, 2002). Overall, data suggest highland-lowland interactions were mutual and interactive; lowland populations were interested in acquiring Tiwanaku-crafted items and establishing cosmopolitan connections (Janusek, 2008). People and goods did not just flow out from the capital and heartland to the peripheries, but from the peripheries to the capital as well as between different peripheral regions (Baitzel and Goldstein, 2016; Knudson et al., 2014; Marsteller et al., 2011; Torres-Rouff et al., 2013; Varela et al., 2013).

### **Tiwanaku sociopolitical organization**

Andean archaeologists have long sought to explain the wide geographic distribution of Tiwanaku-style material culture across the south central Andes. In light of the monumental architecture at Tiwanaku, early scholars attribute the large-scale distribution of Tiwanaku-style artifacts to an expansive Tiwanaku empire (e.g., Posnansky, 1914, 1945). Reconstructions that depict Tiwanaku as an expansive conquest state envision it as a smaller-scaled version of the Inka Empire (e.g., Kolata, 1982, 1985,

1986, 1993a,b, 1997; Ponce Sanginés, 1976, 1991; see also Bermann, 2003; Moseley et al., 1991; Stanish, 1989, 2002, 2003; Stanish et al., 1996).

The large urban scale of and the monumental public works at the site of Tiwanaku, the sophistication of Tiwanaku craft production, and the scale of agrarian and settlement systems in the *altiplano* core region were initially interpreted as evidence that Tiwanaku was a strong centralized state (Bennett, 1936; Goldstein, 1989a,b, 1993b; Kolata, 1993a,b, 1997, 2003; Moseley et al., 1991; Ponce Sanginés, 1972; Stanish, 2002, 2003). Kolata (1993a) describes Tiwanaku as a highly centralized political economy in which urban elites controlled the production and movement of resources between the heartland, hinterland, and provinces. Arguing that the construction of raised agricultural fields on the margins of Lake Titicaca occurred at a scale which only could have been organized and managed by a centralized state, Kolata (1986, 1991) suggests that urban elites controlled both land and labor. Thus, state expansion was driven by elites who established proprietary agricultural estates in the hinterland and low-altitude provincial colonies to control desired agricultural commodities such as coca and maize and to generate personal wealth and influence via competitive feasting (Kolata, 1986, 1993a,b).

More recently, multiple lines of evidence undermine portrayals of Tiwanaku as a strong centralized state. Field experimentation by Erickson (1993) indicates that raised field systems do not require large-scale corporate organization; they can be constructed and maintained by households. Research in the Pampa Koani, an important area for raised field agriculture in the basin, suggests raised fields continued to be constructed after the “collapse” of the Tiwanaku state, implying state-level administration was not

requisite for their construction (Graffam, 1992; cf. Janusek and Kolata, 2004). Despite marked social stratification within Tiwanaku society, there is no evidence of elaborately rich, “royal” tombs from the Tiwanaku heartland in the Bolivian *altiplano* (Korpisaari, 2006). Additionally, the lack of significant iconographic, bioarchaeological, and settlement pattern evidence of warfare or military force (Goldstein, 2015; cf. Becker and Alconini, 2015) undermines depictions of Tiwanaku colonialism as a state sanctioned project for expansion.

More heterarchical interpretations of Tiwanaku sociopolitical organization suggest Tiwanaku was not a bureaucratic expansive state but a social phenomenon structured by kinship and integrated through ritual and economic exchange. These reconstructions place greater emphasis on archaeological data that support the continuing importance of local community autonomy. Systematic settlement pattern data for the Tiwanaku core region suggest a more complicated picture of regional sociopolitical organization, one that may indicate autonomous but federated settlements throughout the Titicaca Basin (Albarracín-Jordán, 1996a,b; Browman, 1978, 1984, 1997; Mathews, 1997; McAndrews et al., 1997). Likewise, settlement pattern data from the four best known peripheral regions (Azapa, Cochabamba, Moquegua, and the oases of San Pedro de Atacama) have failed to show a shift to settlement systems indicative of a centralized tributary system (Berenguer and Dauelsberg, 1989; Goldstein, 1996; Higuera-Hare, 1996, 2001; Muñoz, 1996; Rivera, 1991).

Albarracín-Jordán (1996a,b, 2003) argues that the fundamental system of organization in Tiwanaku society was the *ayllu*, not the state. He interprets the diversity

in raised-field agrotechnology in different areas of the Tiwanaku Valley as evidence that autonomous local groups, not elite bureaucrats, oversaw agricultural production (Albarracín-Jordán, 1996a; see also Erickson, 1985, 1993, 1999; cf. Janusek and Kolata, 2004; Stanish, 2003). While it is clear that rural agrarian and household craft production increased as a result of Tiwanaku vertical integration, these changes may have been a relatively superficial overlay on long-standing local patterns (Bermann, 1994). Additionally, the heterogeneous nature of buildings and diverse stone-carving styles at the site of Tiwanaku reflect the influence of multiple influential social groups (Albarracín-Jordán, 2003). Thus, for Albarracín-Jordán (1996a,b, 2003), Tiwanaku is imagined as a confederation of autonomous settlements articulated through non-coercive, reciprocal relationships cemented through ritual and family ties, rather than a state-level centralized bureaucracy.

Although there is strong evidence to suggest aspects of Tiwanaku sociopolitical organization was heterarchical, evidence for Tiwanaku as a powerful, hierarchical state – from the urban core with its monumental architecture and status-differentiated residential sectors, hinterland settlement hierarchy, and increasingly centralized agriculture production – cannot be denied (Berryman, 2010; Goldstein, 2005; Janusek, 2004b; Kolata, 1986; Stanish, 2003). Current interpretations of Tiwanaku political economy tend to incorporate aspects of hierarchy and heterarchy (Berryman, 2010; Goldstein, 2013, 2015; Janusek, 2008; Stanish, 2013; Stanish et al., 2010). It appears that Tiwanaku society was segmentary in nature (*sensu* Southall, 1974; see also Stein, 1999) and organized into a nested hierarchy similar to ethnohistorically-derived models of



indigenous Andean sociopolitical structure (Albarracín-Jordán, 1996a,b, 2003; Goldstein, 2005; McAndrews et al., 1997).

Archaeological data from the Tiwanaku colonies in the Moquegua Valley of southern Peru has been critical to the ongoing development and evaluation of models of Tiwanaku sociopolitical organization. The Moquegua Valley offers a unique case study for investigating Tiwanaku sociopolitical organization as it is the only region in the Andes known to date that has substantial settlements affiliated with Tiwanaku and Wari, a Middle Horizon expansive state based in the central highlands of Peru (e.g., Goldstein, 2013; Moseley et al., 1991, 2005). The next section presents a detailed discussion of Tiwanaku Moquegua colonial organization.

### **Tiwanaku colonial organization in Moquegua**

Decades of archaeological research in the lower Osmore Drainage inform current interpretations of the Tiwanaku colonial presence in Moquegua. Between AD 525 and AD 700 Omo-style Tiwanaku camelid agropastoralists established “opportunistic” settlements at the Moquegua Valley Omo site group (Goldstein, 1989a,b, 2005, 2009; Owen, 2005; Owen and Goldstein, 2001). Most Omo-style settlements were located in the middle Moquegua Valley in open areas away from the river plain near natural springs and caravan routes (Goldstein, 2005). Omo-style colonial settlements were clustered in large residential sectors at the four major site groups of Omo, Chen Chen/Los Cerrillos, Cerro Echenique, and Rio Muerto.

Beginning around AD 785, a second wave of *altiplano* colonists associated with Chen Chen-style material culture is evident in the archaeological record of the lower

Osmore Drainage (Goldstein, 2005; Goldstein and Owen, 2001; Owen, 2005; Owen and Goldstein, 2001). Chen Chen-style immigrants settled alongside Omo-style communities within several of the largest Tiwanaku site groups in the middle valley but in distinct and independent settlements (Goldstein, 2005, 2009). Chen Chen-style settlements were typically situated near large artificially irrigated *pampas* or productive natural springs suitable for intensive agriculture (Goldstein, 2000b, 2005; Goldstein and Owen, 2001; Williams, 2002).

The designations Omo- and Chen Chen-styles were originally based on differences in ceramic assemblages (Goldstein, 1985). While Omo- and Chen Chen-style ceramics are functionally similar, there are noticeable variations in ceramic technology, form, and decoration. Omo-style pottery is characterized by red-slipped and black polished fine serving wares, but polished blackware serving vessels are absent from Chen Chen-style assemblages (Goldstein, 1985, 2005). Chen Chen redware includes several forms not found among Omo-style assemblages, including the *tazón*, a flaring-sided bowl, and the less common *fuelle*, a thick serving platter (Goldstein, 1985, 2005). Omo-style pottery has been dated to cal AD 538-1030, whereas Chen Chen-style ceramics date to cal AD 785-1000 (Goldstein, 2005).

Despite their close spatial proximity, Omo and Chen Chen communities maintained distinct ethnic identities for several centuries. In addition to the different ceramic styles from which their names are derived and different subsistence strategies described above, Omo- and Chen Chen-style communities differed across a variety of cultural domains including settlement patterns, residential architecture, and funerary

practices (Baitzel, 2008; Goldstein, 1989a,b, 1993a, 2000b, 2005, 2009; Goldstein and Owen, 2001; Hoshower et al., 1995; Knudson and Blom, 2009; Owen and Goldstein, 2001; Sharratt, 2011). Goldstein (2005) interprets these data as evidence that Omo- and Chen Chen-style Tiwanaku colonists represent two separate but interconnected diasporas, comparable to maximal *ayllus* and analytically equivalent to dispersed ethnic groups, whose members maintained their affiliations with their ancestral homelands.

Tiwanaku communities in Moquegua also maintained social distance from communities affiliated with other polities. The Moquegua Valley was already occupied by the Huaracane, an autochthonous population that practiced floodplain agriculture (Goldstein, 2000a, 2005), and there is presently little evidence to suggest interaction between the indigenous Huaracane and Tiwanaku colonists (Costion, 2009; Goldstein, 2000a, 2005). Similarly, there is limited evidence of Tiwanaku interaction with the Wari-affiliated settlements centered around the Wari colonial outpost of Cerro Baul (Goldstein, 2005, 2013; Moseley et al., 1991; Nash and Williams, 2004; Sims, 2006; Williams, 2001). Thus, peripheral organization in the Moquegua Valley is inherently different from other Tiwanaku peripheries, where local populations far outnumber Tiwanaku immigrants from the *altiplano* (e.g., Goldstein, 1996, 2005; Knudson, 2007; O'Brien, 2003; Sutter, 1997; 2000).

Recent attempts to characterize Moquegua Tiwanaku colonial organization have shifted away from core-periphery models drawn from world systems theory, which was initially developed to model exploitative interactions between state and non-state societies within modern global capitalist systems (Wallerstein, 1974; see also Dietler,

1998; Doyle, 1986; Kardulias, 2007; Schreiber, 1992, 2005; Stein, 1998a,b, 1999a,b, 2002), and instead have drawn heavily from social identity theory (e.g., Goldstein, 2005, 2009). Social identity theory provides a dynamic framework for investigating social organization and intergroup interaction (Giddens, 1979; Jenkins, 2008). Aspects of group membership salient within local and regional contexts are signaled through patterned behaviors (i.e., habitus), styles of dress and personal adornment, material culture, and culturally modified lived spaces or landscapes which may be detectable in the archaeological record (e.g., Bell, 2005; Díaz-Andreu et al., 2005; Goldstein, 2005; Insoll, 2007; Jones, 1997; Smith, 2005; Sofaer, 2006; Stein, 1999a; Voss, 2005, 2008). As the recent literature on the body as material culture has demonstrated, signals of social identities and expressions of social affiliations can be encoded in individual bodies through habitual practices, body modification, and patterns of mate exchange in the form of one's DNA and/or phenotypic traits (e.g., Agarwal and Glencross, 2011; Hamilakis et al., 2002; Knudson and Stojanowski, 2008, 2009; Sofaer, 2006; Stojanowski, 2005a, 2010; see also Blom et al., 1998; Geller, 2004; Gowland and Knüsel, 2006; Joyce, 2005; Lozada, 2011a; Meskell, 1998; Sutter, 2005, 2009a; Tiesler, 2014; Torres-Rouff, 2009).

Some of the more effective studies of identity and social organization in the pre-Hispanic Andes have applied ethnicity-based approaches to historically- and ethnographically-derived models of Andean socio-political organization including *señoríos*, a polity composed of loosely integrated communities of economic specialists (e.g., Buikstra, 1995; Lozada 2011a, Lozada Cerna and Buikstra, 2002, 2005; Lozada et al., 2009; Rostworowski, 1977a,b, 1978; Tomczak, 1995, 2001), and *ayllus* (e.g., Blom,

1999, 2005b; Blom et al., 1998; Goldstein, 2000b, 2005; Janusek, 2004a, 2008). Among contemporary Andean highland Aymara and Quechua communities *ayllu* is a salient axis of social organization, with the *ayllu* serving as a kin group with corporate interests in land (e.g., Abercrombie, 1986; Isbell, 1997; Urton, 1990). *Ayllu* can be difficult to define, partly because it describes a flexible and multi-layered social identity (Abercrombie, 1986, 1998; Rasnake, 1988; Urton, 1990). Urton (1990: 22) characterizes the *ayllu* broadly as any group of social, political, economic, and ritual cohesion or action. *Ayllus* organize and sponsor ritual events, prepare feasts and drinking bouts, and enact ceremonies that map social relationships, reinforce member affiliation, and reify group solidarity (Abercrombie, 1998; Bastien, 1978; Platt, 1986).

Goldstein (2005, 2009, 2013, 2015; see also Goldstein and Owen, 2001; Owen and Goldstein, 2001) has recently reinterpreted the nature of the Tiwanaku presence in Moquegua. Goldstein integrates Murra's (1964, 1968, 1972, 1975, 1985) multiethnic vertical archipelago with Clifford's (1994) conception of diaspora to describe the particular types of dispersed Tiwanaku communities that colonized the Moquegua Valley. In Murra's model, a single core population (i.e., an ethnic community) based in the highlands controls "several geographically dispersed ecological tiers" through permanent colonies which ensure access to resources unique to those regions (Murra, 1985a: 3). By exploiting a variety of complementary resources, such mixed elevation agricultural systems maximize seasonal procurement, serve as risk-averaging mechanisms, and facilitate self-sufficiency (Goldstein, 2000b).

Despite spatial separation from their homeland, these ethnic ‘islands’ actively participated in the homeland community’s system of socio-economic organization through continuous social contact and trade (Murra, 1985b [1978]). Archipelago communities are multiethnic; immigrant colonies of a particular sociocultural group are interspersed with similar colonial settlements from other sociocultural groups seeking to diversify their productive strategies (Murra, 1985b [1978]). Rather than attempting to integrate or assimilate with members of host or other colonial communities, diaspora communities maintain their homeland affiliations and identities over time (Goldstein, 2015).

Goldstein (2000b, 2005, 2015) suggests Omo- and Chen Chen-style Tiwanaku groups represent “dual diasporas” of maximal *ayllus* (i.e., ethnic communities) that colonized the Moquegua Valley. Tiwanaku communities in Moquegua shared practices and ideologies that connected them to the broader Tiwanaku sphere, while they simultaneously asserted and maintained distinct social identities through different cultural traditions brought with them from their respective homelands, including different ceramic styles, residential architecture, and funerary practices (Goldstein, 1989b, 2005; see also Bermann, 1994; Blom et al., 1998; Janusek, 1999, 2002, 2003, 2004a,b, 2005a,b; Knudson et al., 2014; Korpisaari, 2006; Torres-Rouff et al., 2013). Thus, Tiwanaku expansion in the south central Andes was fueled by strong corporate or *ayllu* groups who saw themselves as part of an imagined Tiwanaku corporate identity, not at the direction of a strong, centralized *altiplano* state (Goldstein, 2005).

Goldstein (2005) suggests that the two Tiwanaku diasporic communities may have maintained separate group identities in part through endogamous marriage practices. However, this supposition has not been tested due to a lack of Omo-style Tiwanaku skeletal samples (Goldstein, 2005). The recent exhumation and curation of human skeletal remains from Omo-style cemeteries at Omo Alto M16 and Rio Muerto M70 (see Baitzel, 2008; Goldstein, 2005; Oquiche et al., 2003) make it possible for the first time to use biological data to evaluate whether Omo- and Chen Chen-style communities were endogamous, as speculated by Goldstein. Biological distance measures can be used to assess phenotypic similarity and make inferences regarding microevolutionary processes including gene flow and genetic drift among past communities and can therefore provide an independent line of evidence to evaluate the dual diaspora model, which is based on interpretations of material culture and settlement patterns (Goldstein, 2005, 2015; Stovel, 2013).

## **MATERIALS AND METHODS**

To investigate social organization within Tiwanaku Moquegua communities, phenotypic and cranial modification data were collected from human skeletal remains from five Tiwanaku-affiliated sites (ca. AD 600 – 1000) from the Osmore Drainage: Chen Chen M1, Omo Alto M16, Omo M10, Rio Muerto M43, and Rio Muerto M70B (Fig. 2). Three samples (M1, M10, and M43) are from Chen Chen-affiliated contexts and M16 and M70 are from Omo-affiliated contexts (Table 5). Study collections are curated in the repositories of the Museo Contisuyo in Moquegua, Peru. These sites and the skeletal samples are described below.



Figure 2. Map of the lower Osmore Drainage.



Table 5. Study samples and number of skeletons observed by site.

Site	Calibrated Dates	Cultural Affiliation	Observed	Included in Study <sup>a</sup>
Chen Chen M1	AD 656-1155 <sup>b</sup>	Chen Chen	446	45
Omo M10	AD 705-1005 <sup>c</sup> AD 765-1025 <sup>d</sup>	Chen Chen	223	35
Omo Alto M16	AD 635-890 <sup>e</sup>	Omo	22	3
Rio Muerto M43	AD 780-1017 <sup>f</sup>	Chen Chen	65	7
Rio Muerto M70	AD 705-1005 <sup>g</sup> AD 780-997 <sup>g</sup>	Omo	78	12
Total			834	102

<sup>a</sup>This represents the number of intact and undamaged adult crania suitable for collection of basicranial and temporal bone landmarks.

<sup>b</sup>The dates listed here represent the maximum range derived from 12 calibrated radiocarbon dates (2 sigma) reported by Sharratt (2011:156, Table 5).

<sup>c</sup>Calibrated radiocarbon date (2 sigma) reported by Goldstein (1993).

<sup>d</sup>Calibrated radiocarbon date (2 sigma) reported by Goldstein (1989a).

<sup>e</sup>Calibrated radiocarbon date (1 sigma) reported by Goldstein (2005: 128-131, Table 5.2).

<sup>f</sup>Calibrated radiocarbon date (2 sigma) reported by Goldstein (2005: 128-131, Table 5.2).

<sup>g</sup>Calibrated radiocarbon dates (2 sigma) reported by Magilligan and Goldstein (2000).

### Chen Chen M1

The type-site for the Chen Chen ceramic style, M1 is an approximately 30 ha, multicomponent site located northeast of the modern city of Moquegua in the middle valley (Goldstein, 1985, 2005; Williams, 1997, 2002). Chen Chen served as a major center of agricultural production for export to the Tiwanaku heartland, especially maize (Goldstein, 2000b, 2005; Goldstein and Owen, 2001). The mortuary component covered over 10 ha and was comprised of 29 independent cemeteries estimated to have once held approximately 12,800 individuals, making it the largest known Tiwanaku necropolis (Goldstein, 2005; Owen, 1997; Sharratt, 2011; Vargas, 1988). The majority of habitation

and mortuary contexts are associated with Chen Chen-style material culture and date to between cal AD 780-1100, although there is also a much smaller Tumilaca phase occupation at the site (Goldstein, 1985, 2005; Owen, 1997, 2005; Sharratt, 2011; Williams, 2002).

Systematic excavations of the Chen Chen cemeteries have been conducted intermittently over a three-decade span in response to urban development (Owen, 1997; Palacios, 2008; Pari Flores et al., 2002; Vargas, 1988, 1994). Over 5,500 tombs at Chen Chen have been excavated, but the vast majority of these were disturbed, with less than 10% of excavated tombs considered intact (Owen, 1997; Pari Flores et al., 2002; Vargas, 1994). Most tombs contained single interments, with the deceased typically placed in a seated, flexed position facing east. The sample from Chen Chen M1 analyzed in this study is drawn from cemetery excavations directed by Vargas, Owen, and Pari Flores.

### **Omo M10**

Omo M10 is the largest and most intensive occupation among the five distinct bluff top settlements (along with M11, M12, M13, and M16), which make up the Omo site group (Goldstein, 2005). Located approximately ten km downriver from Chen Chen M1, Omo M10 consists of a residential component, nineteen spatially distinct cemeteries, and a temple complex that likely served as a ritual and administrative center for the Moquegua Tiwanaku colony (Goldstein, 1989a, 1993a, 2005). Omo M10 has been dated to AD 785-1000 using a combination of radiocarbon dates from test excavations and analysis of surface collections (Goldstein, 1993). Thirteen of the preserved cemeteries at

M10 are associated with Chen Chen-style Tiwanaku material culture (Baitzel and Goldstein, 2014; Goldstein, 2000a, 2005).

### **Omo Alto M16**

Omo Alto (M16) is one of several sites within the Omo site group associated with Omo-style assemblages (Goldstein, 2005). M16 is located on a plateau and includes three elongated residential groups separated from one another by *quebradas* (Goldstein, 2000b: 199) and a cemetery located on an isolated hillside between Omo M12 and M16. The cemetery was completely excavated in 1999 during salvage work directed by Paul Goldstein (Oquiche et al., 2003; Goldstein, 2005). Nineteen tombs were excavated, and a total of 22 individuals were exhumed, including three adults and nineteen subadults (Oquiche et al., 2003:51). A wood post from Tomb 15 returned a 2 sigma calibrated radiocarbon date of AD 635-890 (Goldstein, 2005: 128-131, Table 5.2).

### **Rio Muerto M43**

Rio Muerto M43 is a Chen Chen-style Tiwanaku site with domestic and cemetery components. M43 is part of the Río Muerto site complex, the third-largest Tiwanaku settlement group in the middle Moquegua Valley after Omo and Chen Chen (Goldstein, 2005). The Rio Muerto settlements date to approximately AD 700–1050 and include three Chen Chen-style sites (M43, M48, and M52), one Omo-style site (M70), and one site of Tumilaca affiliation (M44) (Goldstein, 2005). At M43 there are at least five distinct groups of tombs arranged around a small hill overlooking the habitation sector, as well as some heavily disturbed, isolated tombs around and on top of the hill (Plunger,

2009). A total of 63 tombs have been excavated at M43, and 98 whole or partial individuals were exhumed (Goldstein and Palacios F., 2007, 2008).

### **Rio Muerto M70**

Approximately 200 m to the northeast of the domestic area of M43 lies the Omo-style M70 site. M70 consists of two domestic areas (M70A and M70C) and a separate cemetery (M70B) (Goldstein and Palacios F., 2007; Palacios F., 2006). M70B is only the second Omo-style cemetery excavated in the Moquegua Valley, after Omo M16D, and it is one of the few Moquegua Tiwanaku cemeteries to be excavated in its entirety (Baitzel, 2008). The M70B cemetery contained 73 single-individual burials, the majority of which were intact (Baitzel and Goldstein, 2011).

### **Models**

***Dual diaspora model.*** If the diasporic Tiwanaku communities who established colonies in the Moquegua Valley were endogamous social groups, as has been posited by Goldstein (2005), then samples affiliated with the same ethnic community/maximal *ayllu* are expected to exhibit smaller biodistances from each other, signaling greater phenotypic similarity corresponding with greater genetic similarity due to higher levels of gene flow and/or descent from a common ancestral population. If, as is hypothesized as part of the dual diaspora model, maximal *ayllus* were endogamous social groups, individuals from the same maximal *ayllu* are expected to be more similar genetically and phenotypically because closely-related individuals are more likely to share genes that are identical by descent than are distant relatives or nonrelatives (Blouin, 2003; Konigsberg, 2000; Thompson, 1986). At the same time, samples affiliated with different maximal *ayllus* are

expected to exhibit greater phenotypic difference and greater biodistances because they share a more distant common ancestor due to limited gene flow between maximal *ayllu* communities. For example, the Chen Chen-style sample from Chen Chen M1 is expected to have smaller biodistances with samples from other Chen Chen-style contexts (Omo M10 and Rio Muerto M43) and greater biodistances with samples from Omo-style contexts (Omo Alto M16 and Rio Muerto M70).

***Isolation by distance.*** An alternative to the dual diaspora model is an isolation-by-distance model (see Kimura and Weiss, 1964; Konigsberg, 1990; Malécot, 1969; Morton, 1977; Relethford, 2004; Relethford et al., 1981; Wright, 1943; Yasuda and Morton, 1967). According to this model, rates of gene flow between samples are structured by spatial proximity. Humans and nonhuman organisms that are farther apart are less likely to mate. Thus, under isolation by distance there is a positive correlation between spatial distance and biological distance; as one increases the other also increases and vice versa. As a result, communities who live near one another are expected to be more similar in genotype and phenotype than communities who live farther apart.

Under an isolation-by-distance model, phenotypic similarity in basicranial and temporal bone shape and biodistances between Moquegua Tiwanaku skeletal samples is structured by spatial proximity, regardless of *ayllu* affiliation. For example, samples from the same site group (e.g., Rio Muerto M43 and M70 or Omo M10 and Omo Alto M16) are expected to have smaller biodistances with one another than they are with samples from different site groups. Likewise, samples from sites that are farthest from one another

geographically (e.g., Chen Chen M1 and Rio Muerto M43) are expected to have the greatest biodistance values among the study samples.

### **Data recording methods**

Cranial shape is used here to assess phenotypic similarity between samples to evaluate models of biosocial interaction. These data are suitable for estimating biological relatedness, reconstructing population history and modeling population structure (e.g., Howells, 1973; Harvati and Weaver, 2006b; Smith, 2009). Previous studies suggest the basicranium and temporal bone are biologically informative and phylogenetically conservative regions of the skull and are suitable for biodistance analysis at a variety of analytical scales (e.g., Enlow, 1990; Harvati, 2001; Harvati and Weaver, 2006a,b; Houghton, 1996; Lieberman et al., 1996, 2000; Lockwood et al., 2004; MacPhee and Cartmill, 1986; McHenry, 1994, 1996; Olson, 1981; Smith, 2009; cf. Roseman et al., 2010; von Cramon-Taubadel, 2009, 2011).

Cranial geomorphometric data collection followed standard methodology (e.g., Adams et al., 2004; McKeown and Jantz, 2005; Slice, 2005). Seventeen landmarks from the basicranium and temporal bone were mechanically registered in three-dimensional space using a Microscribe digitizer MX and uploaded to an Excel spreadsheet. Table 6 and Figure 3 identify the cranial base and temporal bone landmarks collected (see Howells, 1973; Smith, 2009). Traits are midline or from the left side of the cranium only.

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Table 6. Geomorphometric cranial landmarks.

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<u>Landmark</u>	<u>Description</u>
1. Basion	Midline point on the anterior margin of the foramen magnum
2. Opisthion	Midline point at the posterior margin of the foramen magnum
3. Inferior nuchal	Midline point on the inferior nuchal line
4. Condylar foramen	The posterior point on the margin of the condylar foramen
5. Condyle posterior	The most posterior point on the occipital condyle
6. Condyle anterior	The most anterior point on the occipital condyle
7. Jugular	Most lateral point of the jugular fossa
8. Mastoidale	The most inferior point on the mastoid process
9. Postglenoid	Most inferior point on the postglenoid process
10. Lateral eminence	Point on the center of the lateral margin of the articular surface of the articular eminence
11. Anterior articular	Most anterior point on the articular surface of the articular eminence
12. Entoglenoid	Most inferior point on the entoglenoid process
13. Lateral ovale	Most lateral point on the margin of the foramen ovale
14. Petrous apex	Apex of petrous part of the temporal bone
15. Tympanic	Most inferolateral point on the tympanic element of the temporal
16. Porion	Most superior point of the external auditory meatus
17. Auriculare	Point of deepest incurvature on the lateral aspect of the root of the zygomatic process

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Figure 3. Basicranial and temporal bone landmarks. Image adapted from White et al. (2012).

Cranial measurements have not previously been used to analyze biological distances, assess population structure, and reconstruct population histories among



Moquegua Valley samples due to concerns about the effects of cranial modification on these measurements (see Cocilovo, 1975; Cocilovo et al., 2011; Rhode and Arriaza, 2006). Most types of cranial modification affect the face and cranial base in addition to the vault (Cocilovo et al., 2011; Frieß and Baylac, 2003), but there is little agreement over which areas of the skull are adversely affected by modification and therefore ill-suited for biodistance analysis (see Antón, 1989; Bjork and Bjork, 1964; Blackwood and Danby, 1955; Boston, 2012; Brown, 1981; Cheverud et al., 1992; Cocilovo, 1975; Cybulski, 1975; Ewing, 1950; Frieß and Baylac, 2003; Hrdlička, 1914; Kohn et al., 1993; Manríquez et al., 2006; Moss, 1958; Pomeroy et al., 2010; Rhode and Arriaza, 2006; Ross and Ubelaker, 2009; Rothhammer et al., 1982; Schendel et al., 1980; Verano, 1987; cf. Cocilovo, 1975). The effects of modification on craniometric data must be evaluated within each sample and can be treated as a source of non-genetic variation that can be removed prior to analysis if necessary (e.g., Nystrom and Malcom, 2010; Varela et al., 1993).

Crania were observed for artificial cranial modification following a scoring protocol used in previous studies of samples from the Moquegua Valley (Blom, 1999; Blom et al., 1998; Hoshower et al., 1995). For the present study crania were observed for modification presence/absence and modification type – annular and fronto-occipital – to assess the effects of cranial modification on cranial base and temporal bone shape.

A total of 834 burials were examined for the present study (Table 4). Crania were evaluated for completeness and preservation to remove individuals with damaged and weathered crania and to mitigate the amount of missing landmarks in the dataset. Only

102 of the 834 individuals observed have crania suitable for geometric morphometric data collection of basicranial and temporal bone landmarks (Table 4). For some sites the number of adult individuals with complete/intact crania was limited, resulting in small sample sizes, particularly for Omo Alto M16 and Rio Muerto M43.

Interpretation of biodistance analysis results requires consideration of how age and sex structure patterns of phenotypic variation. Assessments of skeletal age and sex were obtained from previous research involving the study samples (Baitzel and Goldstein, 2016; Becker, 2013; Goldstein, 1989a; Sharratt, 2011) and confirmed by the author using standard methods (e.g., Buikstra and Ubelaker, 1994). Subadult age at death was estimated using standard indicators of skeletal and dental development, and a multifactorial approach was used for assessing skeletal age in adults, including cranial suture closure, auricular surface morphology, pubic symphyseal face morphology, and dental attrition scores (Buikstra and Ubelaker, 1994; Hillson, 1996; White and Folkens, 2000). To mitigate interobserver error in estimates of skeletal age at death, individuals were assigned to broad age categories according to the midpoint of their age ranges as derived from skeletal and dental indicators of physiological age at death: infant (0-3), child (3-12), adolescent (12-20), young adult (20-35), middle adult (35-50), older adult (50+). Adults who could not be assigned to a specific age category were designated adult indeterminate (21+).

### **Analytical Methods**

Prior to biodistance analysis basicranial and temporal bone shape data were subjected to several exploratory analyses and pre-analysis data treatments to screen for

the effects of measurement error and age, sex, and intertrait correlations. To evaluate intraobserver error, 26 individuals drawn from three sites (Chen Chen M1, Rio Muerto M43, and Rio Muerto M70) were digitized a second time, six weeks after the initial data collection. The initial and repeated digitizations were statistically compared in several ways.

Repeatability of specific landmarks was evaluated following methods outlined by von Cramon Taubadel and colleagues (2007). All specimens were registered via partial Procrustes superimposition in the Morphueus software package (Slice, 2013) by using three control landmarks: basion, lateral eminence, and porion. Partial Procrustes superimposition is a modification of generalized Procrustes analysis (GPA), a standard analytical procedure for geometric morphometric data that registers objects in a common morphospace by rescaling objects to a standard size, translating (i.e., shifting) them to a standard position, and rotating them to a standard orientation. This serves to standardize (and thus remove) the other components of variation (i.e., size, position, and orientation) within the raw coordinate data, effectively isolating information on shape. The resulting values are termed Procrustes coordinates. The use of three control landmarks as part of a partial Procrustes superimposition permits the repeated digitizations of the nonreference landmarks for each individual to be registered in a common morphospace despite the fact that crania were moved between digitization sessions (see Corner et al., 1992).

Inter-landmark linear distances were then calculated using PAST v. 3.11 (Hammer et al., 2001) for each landmark (i.e., reference and nonreference) between the original and repeated digitizations (Ross and Williams, 2008; Terhune, 2010). For

example, after the partial Procrustes superimposition, the linear distance between landmark 1 for a given specimen from the initial digitization and landmark 1 from the repeat digitization of the same specimen was calculated. This was done for all landmarks, allowing the error for each landmark to be quantified and evaluated. The average error is the average of the intra-landmark linear distances for a given landmark across all individuals in the measurement error study. In the present study, the average error for landmarks ranged from 0.018 mm (porion) to 0.28 mm (inferior nuchal crest). The average error for inferior nuchal crest (0.28) and posterior condyle (0.25) exceed acceptable levels of error (i.e., average error greater than 0.20 mm), and these landmarks were removed from the dataset.

Overall levels of measurement error were evaluated following Lockwood et al. (2002). Forty-one principal components (PCs) were generated using principal components analysis (PCA) of Procrustes coordinates in the software program MorphoJ (Klingenberg, 2011). PC scores for individuals were used to generate a Euclidean distance matrix in XLSTAT, from which intra-individual and inter-individual Euclidean distances were extracted. Intra-individual distances represent measurement error, whereas inter-individual distances should reflect phenotypic variation.

Samples of intra-individual and inter-individual Euclidean distances were compared using a two-sample t-test. The mean intra-individual distance is 0.201 (sd = 0.046) compared to the mean inter-individual distance of 0.236 (sd = 0.053) (Fig. 3). Results of the two-sample t-test indicate intra-individual distances are significantly smaller than inter-individual distances ( $t = 3.243$ ,  $df = 349$ ,  $P \text{ value} = 0.0013$ ). This

suggests that measurement error is sufficiently low to allow detection of phenotypic differences in cranial shape within the study sample.

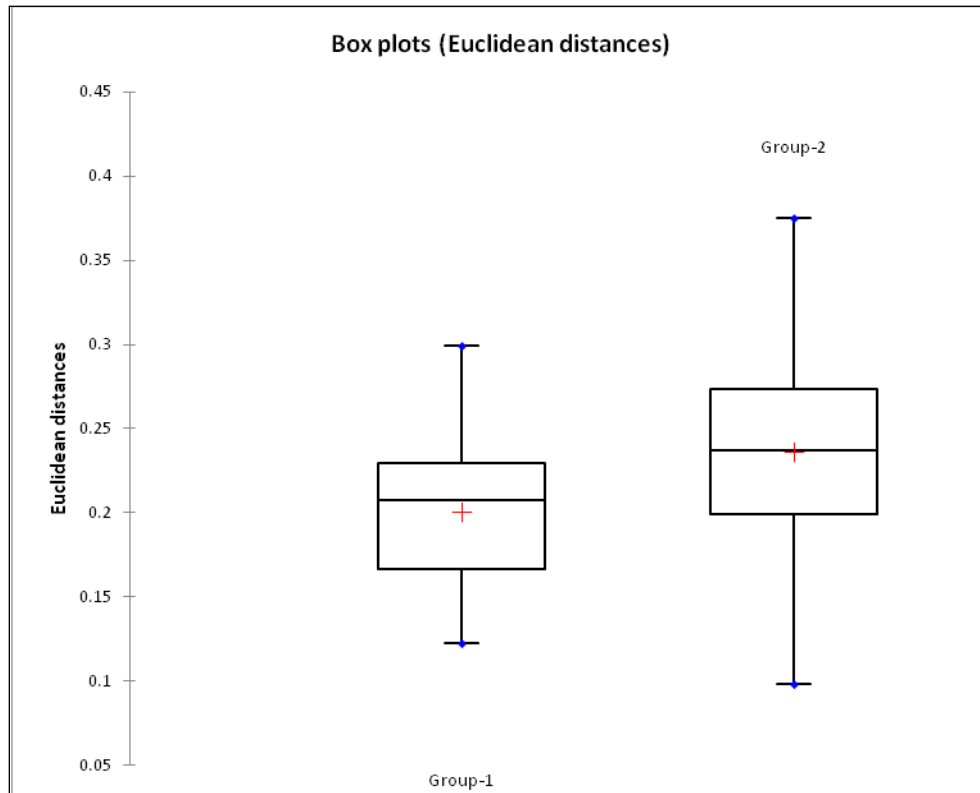


Figure 4. Box plots of intra-individual (Group 1) and inter-individual (Group 2) distances.

Cranial shape data were informally assessed for age effects in MorphoJ using PCA of Procrustes coordinates with within-group covariances pooled by the age cohorts described above. Visual analysis of scatter plots of the first three PCs indicates that age is not structuring variation in cranial shape (Appendix B). Age effects on cranial shape data were also formally assessed using Wilks' Lambda test in XLSTAT. This method provides an observed F-statistic, a critical value for the F-statistic, and a P value for lambda which facilitate decision making regarding whether to accept or reject the null hypothesis: variability among mean landmark coordinates (mean shapes) among age

cohorts exceeds that expected due to chance (XLSTAT). Results confirm the results of the PCA; variability in mean cranial shape does not differ between age cohorts ( $\lambda = 0.226$ ,  $F_{\text{observed}} = 0.781$ ,  $F_{\text{critical}} = 1.572$ ,  $df_1 = 68$ ,  $df_2 = 48$ ,  $P \text{ value} = 0.828$ ).

Metric data are known to be sexually dimorphic with males tending to be larger than females (Kimmerle et al., 2008; Rosas and Bastir, 2002; Wood et al., 1991). Size is automatically removed as a confounding factor from raw landmark data via generalized Procrustes analysis (Bookstein, 1996; Dryden and Mardia, 1998; Gower, 1975; McKeown and Jantz, 2005; Rohlf and Slice, 1990; Slice, 1996, 2005). To ensure that GPA effectively removed sex-specific size effects on cranial shape data, a PCA was performed on Procrustes coordinates with the within-group covariances pooled by sex. Visual analysis of scatter plots of the first three PCs indicates that sex is not structuring variation in cranial shape (Appendix E). Results of Wilks' Lambda tests for sex effects on multivariate data confirm that GPA effectively removed effects of sexual dimorphism from the cranial landmark data set as variability in mean cranial shape does not differ significantly between males and females ( $\lambda = 0.449$ ,  $F_{\text{observed}} = 1.588$ ,  $F_{\text{critical}} = 1.694$ ,  $df_1 = 34$ ,  $df_2 = 44$ ,  $P \text{ value} = 0.074$ ).

Of the 102 individuals in the sample, 92 are modified and 10 are unmodified. All of the 92 modified crania exhibit fronto-occipital modification. Cranial shape data were informally assessed for effects of cranial modification on basicranial and temporal bone shape in MorphoJ using PCA of Procrustes coordinates with within-group covariances pooled by modification presence/absence. Visual analysis of scatter plots of the first three PCs indicates that cranial modification is not structuring variation in cranial shape.

Effects of cranial modification on cranial shape data were formally assessed using Wilks' Lambda test in XLSTAT. Results are consistent with the results of the PCA; variability in mean basicranial and temporal bone shape does not significantly differ between modified and unmodified crania ( $\lambda = 0.639$ ,  $F_{\text{observed}} = 1.081$ ,  $F_{\text{critical}} = 1.609$ ,  $df_1 = 34$ ,  $df_2 = 65$ ,  $P \text{ value} = 0.385$ ).

Missing data prohibit certain multivariate analyses useful for assessing biological distances between samples and modeling microevolutionary processes. The cranial landmark data set was assessed to identify cases and variables with high levels of missing data for removal to produce a nearly complete data matrix (Adams et al., 2004; Slice, 2005). No individuals exhibited levels of missing data sufficiently high to warrant removal from the data set, but one variable, condylar foramen, was removed. This produced a data matrix that was 97.8% complete, with a total of 102 empty cells out of 4578 total cells in the cranial landmark data set. This equates to a total of 34 missing landmarks out of a possible 1526 landmarks.

Missing landmark coordinates were estimated using the GPA mean substitution method in Morpheus (Slice, 2013). First a GPA is performed on the dataset with missing values to align the objects within a common morphospace. Then grand-mean coordinate values are computed for each landmark using the non-missing data points, and those values are used as estimates for the coordinates of missing landmarks. Finally, the inverse of the scale, rotation, and translation applied during the GPA are used to restore the data to their original size, location, and orientation (Slice, 2013).

A generalized Procrustes analysis was performed on the complete dataset of raw landmark coordinates in MorphoJ to extract the shape variation from the coordinates. Principal components analysis of Procrustes coordinates was then used to extract non-correlated cranial shape variables. The first eleven principal components were extracted, representing 89.8% of the variation in the original cranial landmark data matrix. None of the factor loadings for the PCs are easy to interpret with respect to cranial shape.

The first 11 principal components from PCA of the cranial shape data were imported to RMET 5.0 (Relethford, 2003; Relethford et al., 1997) to characterize the degree of genetic differentiation and evaluate patterns of similarity between study samples using a relationship (R) matrix (Harpending and Ward, 1982; see Relethford and Blangero, 1990). RMET requires estimation of population genetic parameters, including narrow-sense heritability ( $h^2$ ) values for the phenotypic traits analyzed and the relative population sizes of the study samples. A narrow-sense heritability value of 0.55 was used for this study. Relative population sizes of the once-living populations from which the samples were drawn were estimated by summing the total area of the domestic and mortuary sectors for each site, and then dividing each summed area by the value for the smallest site. This resulted in the following relative population estimates: Chen Chen M1: 12.7, Omo M10: 3.1, Omo Alto M16: 1.3, Rio Muerto M43: 2.3, and Rio Muerto M70: 1.0.

R-matrix analysis generates statistics that can be used to make inferences about the microevolutionary processes (e.g., gene flow and genetic drift) that contributed to the population histories and population structures of the samples. For example, RMET



generates a bias-corrected estimate of Mahalanobis distance ( $D^2$ ) between samples, an unbiased estimate of overall regional genetic variability ( $F_{ST}$ ), and Relethford-Blangero residuals, which can be used to make inferences regarding relative levels of extra-local gene flow for each sample (Relethford, 2003; Relethford and Blangero, 1990; Relethford et al., 1997; Williams-Blangero, 1989; Williams-Blangero and Blangero, 1989). The P value for the unbiased  $F_{ST}$  can be obtained by dividing the value by its standard error to generate a t-statistic, which can be compared to a t-distribution with degrees of freedom of  $n-1$  to generate the P value for the unbiased  $F_{ST}$ . The same process can be used to obtain P values for the  $D^2$  distances generated from the scaled R-matrix, which weights the samples according to estimates of population size (Relethford et al., 1997). To obtain P values for Relethford-Blangero residuals the standard error for observed residuals can be obtained by first jackknifing the residuals and then calculating the standard deviation of the jackknifed residuals; the standard deviation of the jackknifed residuals is the standard error for the observed residuals.

Isolation by distance is formally evaluated using a Mantel test (Mantel, 1967; Smouse et al., 1986) in XLSTAT to compare a matrix of spatial distances between the sites from which the study samples were drawn with a matrix of biodistances (e.g., Mahalanobis  $D^2$  distances) between samples. The  $D^2$  matrix based on the scaled R-matrix generated using RMET was used as the biodistance matrix in the Mantel test. A two-step procedure was used to produce the geographic distance matrix. First, intersite distances were derived from UTM East and North coordinates for the cemeteries at each site included in the study (Goldstein, 2005). For sites with multiple cemeteries, the UTM East

and North coordinates were averaged to produce a single set of coordinates per site.

Second, these coordinates were used to create a Euclidean distance dissimilarity matrix for the samples in XLSTAT.

Matrices were formally compared using both Pearson ( $r$ ) and Spearman ( $r_s$ ) correlations, and exact P values were generated using 10,000 permutations. A strong ( $r / r_s > 0.66$ ) or moderate ( $0.33 \leq r / r_s \leq 0.66$ ) positive correlation is considered support for marriage practices consistent with an isolation-by-distance model. Such a pattern would suggest that phenotypic similarity decreases as spatial distance increases. A weak positive correlation ( $r / r_s < 0.33$ ) could suggest that either there is little support for isolation by distance or that genetic microdifferentiation was structured by other factors in addition to isolation by distance (see Workman et al., 1976). A strong ( $r / r_s > -0.66$ ) or moderate ( $-0.33 \leq r / r_s \leq -0.66$ ) negative correlation would suggest that individuals preferentially sought marriage partners from communities located far from their own. In this case, factors other than spatial proximity, including ethnic community affiliation, likely were critical to choice of marriage partners.

The dual diaspora model of Moquegua Tiwanaku social organization is evaluated using several techniques to assess multivariate phenotypic similarity and difference within a general comparative analytical framework. Discriminant function analysis (DFA) is used to distinguish between two groups and to predict group membership by generating a discriminant function (i.e., a new variable representing a single canonical axis) that is a linear combination of the original variables that produces the maximal separation between the groups of interest (Hammer, 2015), in this case individuals from

Omo-style contexts compared to individuals from Chen Chen-style contexts. Canonical variates analysis (CVA) is a type of discriminant analysis for differentiating between more than two groups, and it is used here to distinguish between the five study samples. Canonical variates analysis produces a set of new variables, the canonical variates (CVs), which successively account for the maximum amount of among-group variance relative to within-group variance. The CVs are uncorrelated within and among groups, but the assumption is that the groups all share the same covariance matrix.

Both DFA and CVA emphasize between-group variation in order to maximize separation between groups. Like PCA, DFA and CVA produce eigenvalues that indicate the amount of variation explained by the canonical axes (i.e., the discriminant function and the canonical variates, respectively). DFA and CVA also generate classification/misclassification tables by assigning each observation (i.e., individual) to the (pre-defined) group that produces the minimal Mahalanobis distance to the group mean. These group assignments are cross-validated by a jackknifing procedure (Hammer, 2015). The cross-validation of the classification-misclassification table provides an assessment of how the discriminant function/canonical variates would perform with new data (i.e., new skeletons of unknown affiliation). Both DFA and CVA were performed using MorphoJ and PAST. The two programs were used for these analyses because MorphoJ produces inferential statistics (such as Hotelling's T-test, the multivariate version of Student's t-test) and estimates of significance (i.e., estimated P values) whereas PAST produces graphics which allow visualization of nearest neighbor trees.

To assess the degree of similarity within and between maximal *ayllu* communities, inter-individual Euclidean distances were calculated for the entire study sample, and intra-*ayllu* pairwise distances were compared to inter-*ayllu* pairwise distances. Inter-individual distances were averaged across all individuals within the same maximal *ayllu*, across all individuals from different maximal *ayllus*, and across all individuals in the study sample. Inferential statistics are not directly applicable to distance statistics; instead, bootstrap resampling in Excel's Resampling Stat add-in was used to generate P values to assess whether intra-*ayllu* pairwise distances are significantly smaller than inter-*ayllu* distances (Microsoft, 1999, 2003).

Bootstrap resampling was used to generate P values for the observed average intra-*ayllu* inter-individual distances. Two pools of pseudo-distances were resampled for comparison with the intra-*ayllu* pairwise distances: 1) the observed inter-*ayllu* inter-individual distances and 2) the observed inter-individual distances for all individuals in the data set. The average inter-individual distance was calculated for each pool of resampled pseudo-distances, and this process was repeated 9999 times for both pools of inter-individual Euclidean distances (inter-*ayllu* and all). The replicates were seriated along with the observed average intra-*ayllu* inter-individual distance. To generate a two-sided P value, the rank of the actual average value for each test was divided by the total number of samples. P value 1 is derived from resampling inter-*ayllu* inter-individual distances, and P value 2 is derived from resampling inter-individual distances from the sample of all individuals. For P value 1, the number of pseudo-distances sampled was equivalent to the number of inter-*ayllu* inter-individual biodistances in the data set (i.e.,

1305). For P value 2, the number of pseudo-distances sampled was equivalent to the number of intra-*ayllu* inter-individual distances within the data set (i.e., 3846).

## RESULTS

### R-Matrix analysis

The cranial shape data set was subjected to R-Matrix analysis using RMET 5.0. The unbiased  $F_{ST}$  of 0.081715, significant at alpha 0.05 (P value = 0.0025), suggests there is a moderate amount of regional variation in basicranial and temporal bone shape (see Stojanowski, 2010). Relethford-Blangero residuals are presented in Table 7. Chen Chen M1 and Rio Muerto M43 have negative residuals, but this is significant at alpha 0.05 only for Chen Chen M1. Omo M10, Omo Alto M16, and Rio Muerto M70 have positive residuals, but these are significant only for Omo Alto M16 and Rio Muerto M70. The residuals for Omo M10, while positive, are very small and not significantly different from zero, suggesting the observed level of extra-local gene flow is close to the expected level. These results suggest that the communities at Chen Chen M1 experienced slightly lower than expected levels of extra-local gene flow, whereas the Chen Chen-style communities at Omo M10 and Rio Muerto M43 had levels of extra-local gene flow consistent with expectations given their estimated population sizes. In contrast the two Omo-style samples, Omo Alto M16 and Rio Muerto M70, experienced greater than expected levels of extra-local gene flow.

Table 7. Relethford-Blangero residuals.

	Residuals	P value <sup>a</sup>
Chen Chen M1	-0.105	<b>0.0006</b>
Omo M10	0.038	0.3692
Omo Alto M16	0.719	<b>0.0031</b>
Rio Muerto M43	-0.007	0.9252
Rio Muerto M70	0.292	<b>0.0249</b>

<sup>a</sup>Values in bold are significant at alpha of 0.05.

The  $D^2$  distances derived from the scaled R-matrix (Table 8) are not as readily interpretable as the Relethford-Blangero residuals, but several observations can be made. For the Chen Chen-style sample from Chen Chen M1, the smallest biodistance is with the Omo-style sample from Rio Muerto M70 and the greatest biodistance is with the Omo-style sample from Omo Alto M16. However, neither of these biodistances are statistically significant. The small, non-significant  $D^2$  value for the distance between Chen Chen M1 and Rio Muerto M70 may indicate these samples represent a single population. In contrast, the large, non-significant  $D^2$  value for the distance between Chen Chen M1 and Omo Alto M16 simply may reflect the small sample size for M16 ( $n=3$ ). The Chen Chen-style sample from Omo M10 shows the same pattern as the sample from Chen Chen M1. Its greatest biodistance is with the Omo-style sample from Omo Alto M16 and its smallest is with the Omo-style sample from Rio Muerto M70, but neither of these distances are statistically significant. The Chen Chen-style sample from Rio Muerto M43 is most similar to (i.e., has the smallest biodistance with) the Omo-style sample from Rio Muerto M70, while the latter sample has its smallest biodistance with the Chen Chen-

style sample from Chen Chen M1. Overall, the  $D^2$  matrix does not provide clear support for regional gene flow structured by the dual diaspora model.

Table 8. Matrix of intersample  $D^2$  distances based on the scaled R-matrix of the cranial shape data set derived from the first 11 principal components.

	Chen Chen	Omo M10	Omo Alto	RM M43	RM M70
Chen Chen	0	<b>0.153132</b> <sup>a</sup> (2) <sup>b</sup>	0.334601 (4)	<b>0.279686</b> (4)	0.081192 (1)
Omo M10	<b>0.153132</b> (2)	0	0.202609 (1)	0.183351 (2)	0.151346 (3)
Omo Alto	0.334601 (4)	0.202609 (4)	0	0.233894 (3)	0.250151 (4)
RM M43	<b>0.279686</b> (3)	0.183351 (3)	0.233894 (2)	0	0.143982 (2)
RM M70	0.081192 (1)	0.151346 (1)	0.250151 (3)	0.143982 (1)	0

<sup>a</sup>Values in bold are significant at alpha of 0.05.

<sup>b</sup>Values in parentheses represent the rank of distances within columns, from smallest (1) to greatest (4) biodistance for each sample.

### Mantel test of isolation by distance

An isolation-by-distance model was formally evaluated using Mantel tests of the matrix of geographic distances among sites (Table 9) and the biodistance matrix (Table 8). There is a weak positive correlation between the spatial distance and biodistance matrices that is not statistically significant for either Pearson's  $r$  (0.035,  $P$  value = 0.925) or Spearman's  $r$  (0.115,  $P$  value = 0.735). The positive correlations suggest that gene flow among the Moquegua Tiwanaku communities is consistent with a model of isolation by distance. However, the fact that the correlations are weak and non-significant suggests that isolation by distance only partially explains patterns of mate exchange and suggests that other factors likely influenced gene flow in addition to spatial proximity.

Closer scrutiny of the  $D^2$  matrix (Table 8) provides additional detail for the lack of strong positive correlations between the spatial and biodistance matrices. I focus here

on the Chen Chen M1 sample as it is the only sample that produced multiple statistically-significant biodistances. Under isolation by distance the Chen Chen M1 sample is expected to be most similar to one of the samples from the Omo site group, as these are closest in spatial proximity to the site of M1. According to the dual diaspora model, the sample from Chen Chen M1 should be most similar to the other Chen Chen-style samples and most different from the Omo-style samples. As discussed above, the smallest biodistance for the Chen Chen-style sample from Chen Chen M1 is with the Omo-style sample from Rio Muerto M70, which is the second furthest site from Chen Chen in terms of geographic distance (Table 9). Additionally, the Chen Chen-style sample from M1 has statistically significant biodistances with the Chen Chen-style samples from Omo M10 and Rio Muerto M43. Thus far, the results do not provide clear evidence to support or reject either isolation by distance or the dual diaspora model.

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Table 9. Matrix of geographic (Euclidean) distances between Moquegua Valley Tiwanaku-affiliated sites from which study samples are drawn.

	Chen Chen	Omo M10	Omo Alto	RM M43	RM M70
Chen Chen	0	8088.33	6715.07	14439.64	13678.26
Omo M10	8088.33	0	1419.88	7519.50	7032.25
Omo Alto	6715.07	1419.88	0	8358.49	7760.88
RM M43	14439.64	7519.50	8358.49	0	897.56
RM M70	13678.26	7032.25	7760.88	897.56	0

### **Evidence for endogamous maximal *ayllus***

To further evaluate whether patterns of gene flow and marriage practices among Moquegua Tiwanaku colonial communities are consistent with a dual diaspora model of biosocial organization discriminant function analysis and canonical variates analysis were



performed. DFA and CVA were conducted in MorphoJ using Procrustes coordinates for the 14 basicranial and temporal bone landmarks. DFA yielded a Procrustes distance of 0.0567 (permutation P value = 0.0650), a Mahalanobis distance of 3.01, and a  $T^2$  statistic of 116.05 (parametric P value = 0.0031, permutation P value = 0.004). The discriminant function correctly allocated 81 of 87 individuals (93.1%) from Chen Chen-style cemeteries and 13 of 15 individuals (86.7%) from Omo-style cemeteries (Fig. 5).

Cross-validation suggests the discriminant function would perform moderately well with new data, correctly allocating 83.9% of individuals (or 73 of 87) from Chen Chen-style contexts and 66.7% of individuals (or 10 of 15) from Omo-style contexts (Fig. 6). The poorer performance of the cross-validation of the discriminant function for the Omo-style sample likely reflects the small sample size of individuals from Omo-style contexts and the large proportion of variation within this sample. Removing one individual likely causes a noticeable shift in the average shape, complicating allocation.

A lollipop graph of the discriminant function (i.e., CV1) illustrates the average shape differences between individuals from Chen Chen- and Omo-style contexts (Fig. 7). The most notable differences are in the position of landmarks 2 (opisthion) and 4 (jugular), and to a lesser extent shifts in landmarks 6 (postglenoid), 9 (entoglenoid), and 10 (lateral ovale). This suggests the primary anatomical differences in cranial shape between Chen Chen- and Omo-style samples are in the shape of the foramen magnum and the glenoid fossa.

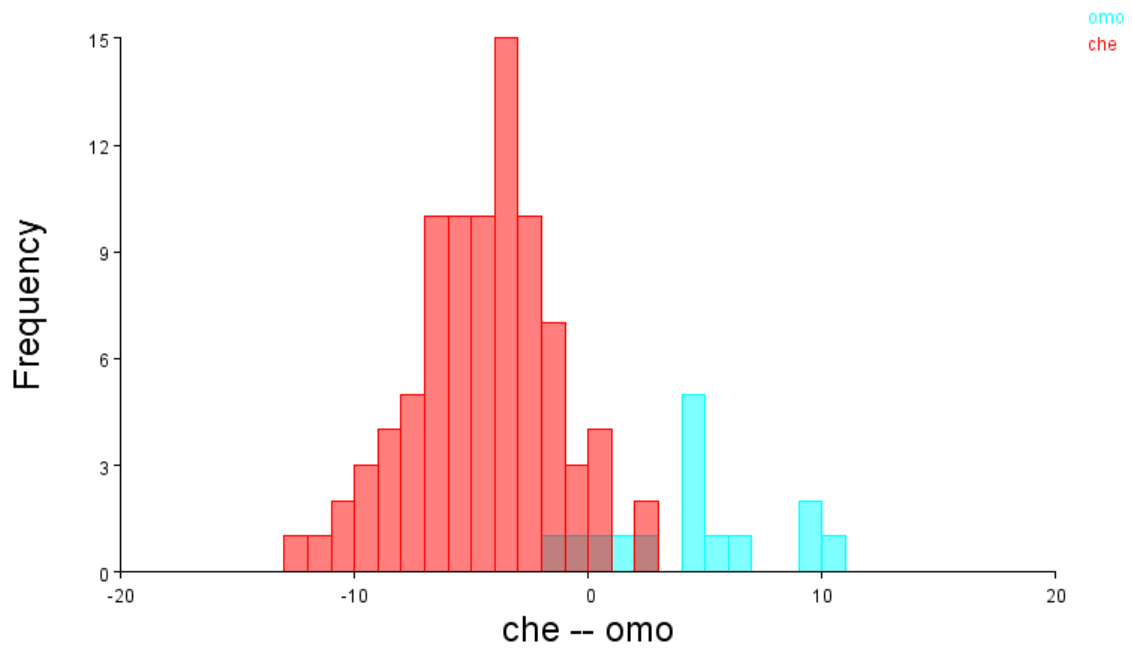


Figure 5. Histogram of discriminant scores.

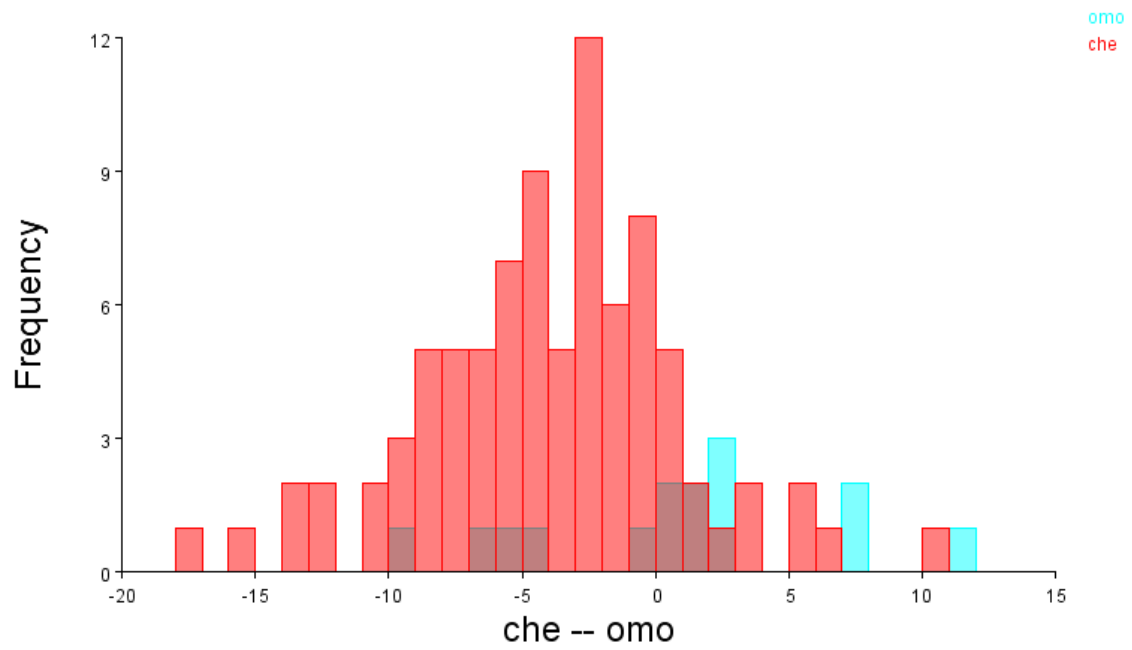


Figure 6. Histogram of cross-validated discriminant scores.

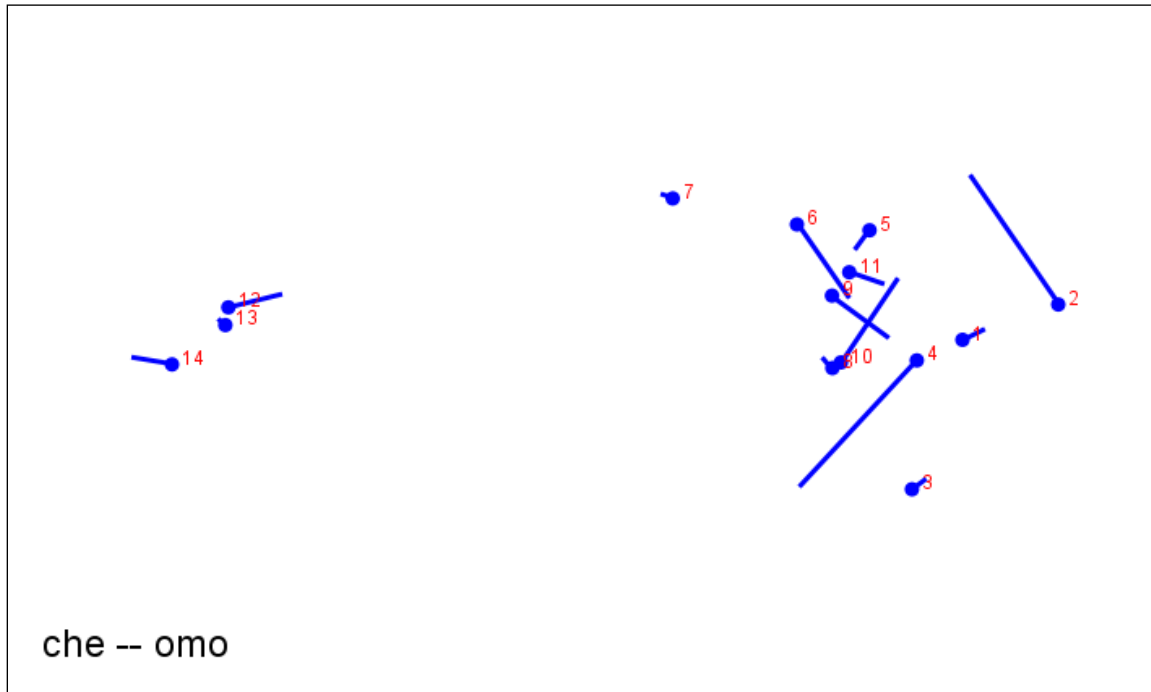


Figure 7. Lollipop graph of the average basicranial and temporal bone shape difference between individuals from Chen Chen- and Omo-style contexts (scale factor 5.0).

Canonical variates analysis of Procrustes coordinates for the 14 cranial landmarks produced four canonical variates (CVs). The first three CVs have eigenvalues greater than one and account for 87.23% of the cumulative variance. A scatter plot of CV1 (43.5%) and CV2 (25.0%) indicates CVA is able to partially differentiate individuals from contexts associated with Chen Chen-style and Omo-style communities according to basicranial and temporal bone shape, but members of these communities are not sufficiently differentiated to form distinct clusters (Fig. 8).

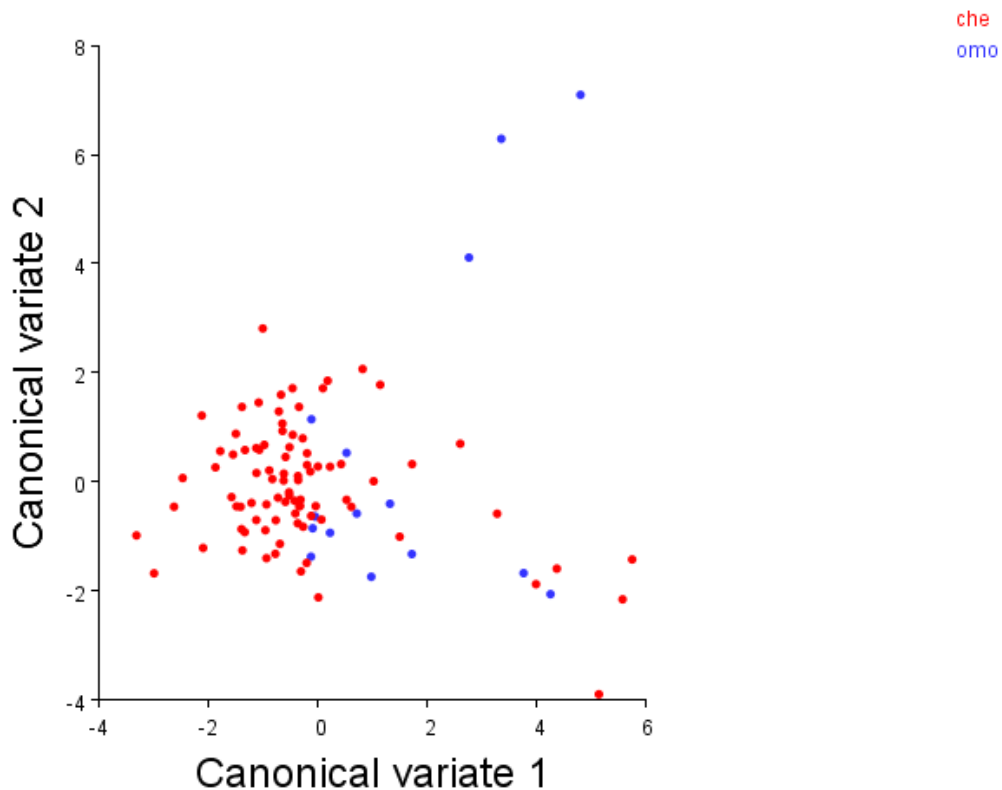


Figure 8. Scatter plot of the first and second canonical variates of cranial shape, coded by maximal *ayllu* affiliation.

Looking at the same scatter plot with individuals indicated by site (Fig. 9), an interesting pattern emerges. Individuals from the Omo-style cemetery at Omo Alto M16 form a distinct cluster, whereas individuals from the Omo-style cemetery at Rio Muerto M70 overlap with individuals from Chen Chen-style contexts at Chen Chen M1, Omo M10, and Rio Muerto M43. The two Omo-style samples, Omo Alto M16 and Rio Muerto M70, are entirely distinct, suggesting different patterns of social interaction for the Omo-style communities who inhabited these sites. The Omo-style community at Rio Muerto M70 likely did not practice maximal *ayllu* endogamy but instead probably exchanged mates with three different Chen Chen-style communities. The sample representing the Omo-style community at Omo Alto M16 appears to represent a biologically distinct

population among the five Moquegua Valley Tiwanaku samples, although the possibility that the small sample size for M16 is skewing these results must be considered.

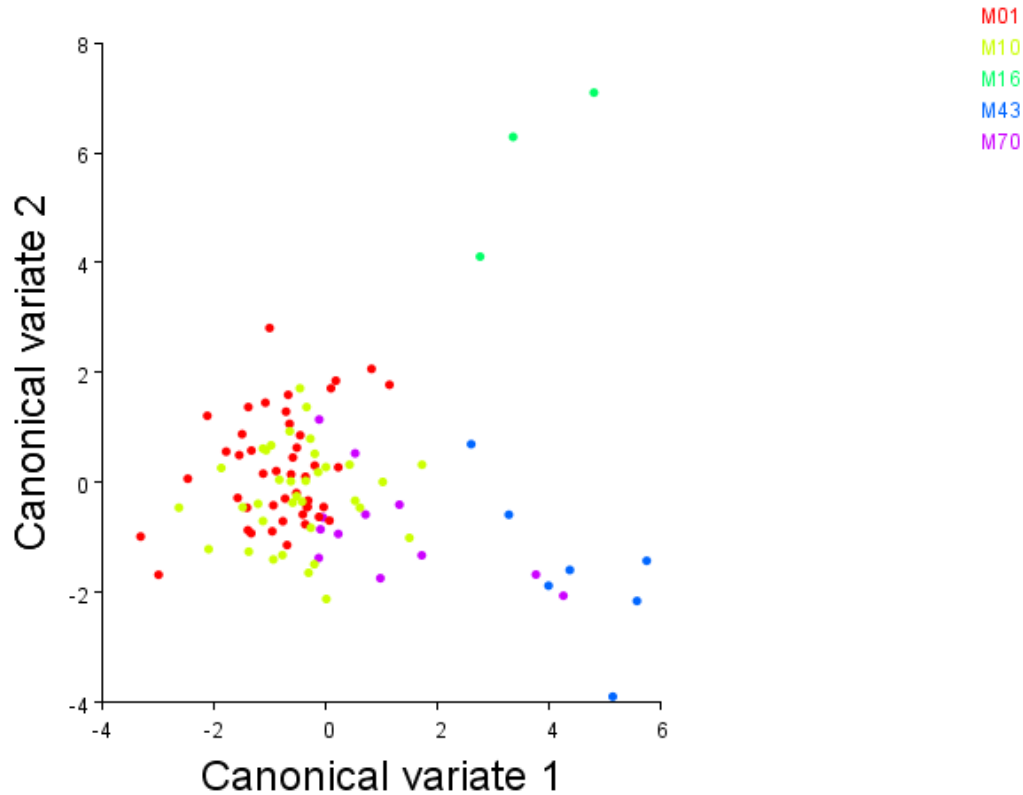


Figure 9. Scatter plot of the first and second canonical variates of cranial shape, coded by site.

The plot of PCo1 and PCo2 with the nearest-neighbor tree provides additional evidence against strict maximal *ayllu* endogamy (Fig. 10). Looking only at the fifteen individuals from Omo-style contexts (three from Omo Alto M16 and 12 from Rio Muerto M70) demonstrates this point. Five of the fifteen individuals have nearest-neighbors who are also from an Omo-style context, while the other 10 individuals have nearest neighbors from Chen Chen-style contexts. That two-thirds of individuals from Omo-style contexts have nearest neighbors who are from Chen Chen-style contexts is compelling evidence for inter-*ayllu* mate exchange.

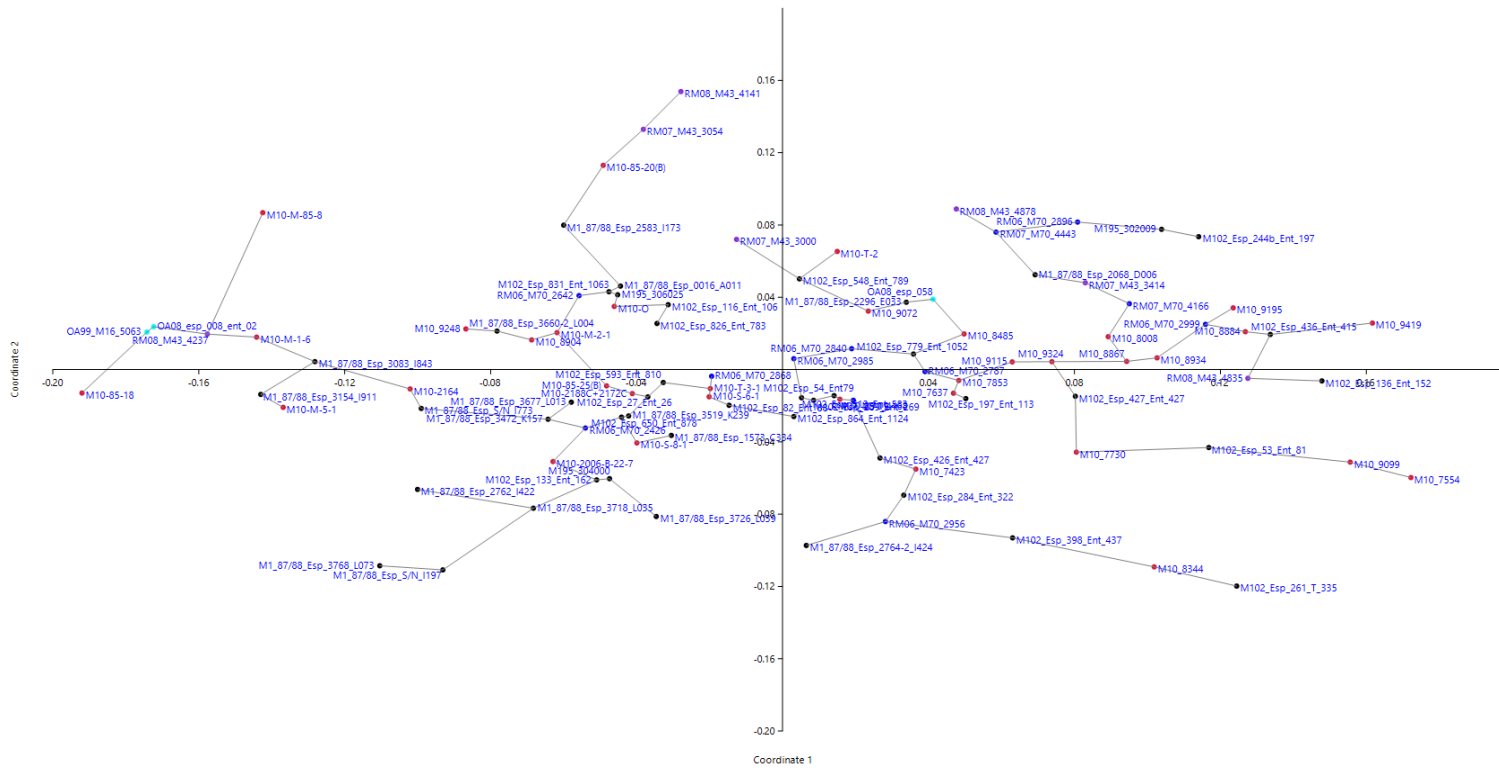


Figure 10. Plot of PCo1 and PCo2 with nearest neighbor tree.

Results of inter-individual Euclidean distances are presented in Table 10. The average intra-*ayllu* inter-individual distance (.206) is smaller than the average inter-*ayllu* inter-individual distance (.210), and bootstrap resampling indicates this difference is statistically significant (P value 1 =0.009). The average intra-*ayllu* inter-individual distance is also smaller than the average of all inter-individual Euclidean distances (.207), but this difference is not statistically significant (P value 2 = 0.140). Although intra-*ayllu* distances are smaller on average compared to inter-*ayllu* distances, the ranges of inter-individual Euclidean distances overlap between the two groups. This suggests that while the overall pattern is consistent with maximal *ayllu* endogamy, the examples where inter-*ayllu* distances are smaller than intra-*ayllu* distances indicate there are exceptions to the overall pattern.

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Table 10. Inter-individual Euclidean distances generated from the cranial shape data set.

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Comparison	Average Inter-individual			Range (min – max)
	Euclidean Distance	P value 1	P value 2	
Intra- <i>ayllu</i> (n=3846)	.206	<b>0.009</b>	0.140	0.072 – 0.405
Omo (n=105)	.207			0.086 – 0.323
Chen Chen (n=3741)	.206			0.072 – 0.405
Inter- <i>ayllu</i> (n=1305)	.210			0.068 – 0.378
All (n=5151)	.207			0.068 – 0.405

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The inter-individual distances for the 15 individuals from Omo-style contexts are presented in Table 11. Only two individuals from Omo-style contexts have their least pairwise distance with another individual from an Omo-style context; individuals RM07 M70 2787 and RM07 M70 4468 form a dyad with a pairwise distance of 0.089. The other 13 individuals have their least pairwise distance with an individual from a Chen Chen-

style context. Interestingly, all of the greatest pairwise distances for the individuals from Omo-style contexts are with individuals from Chen Chen-style contexts. These results indicate that overall, Chen Chen- and Omo-style communities are differentiated from each other, but many individuals from Omo-style contexts are phenotypically most similar to individuals from Chen Chen-style contexts, which suggests that community boundaries were permeable and/or maximal *ayllu* affiliations were flexible to some degree.



Table 11. Summary of inter-individual Euclidean distances for individuals from Omo-style contexts.

	<u>Minimum</u>		<u>Maximum</u>		<u>Average</u>		Smallest pairwise		Context		
	<u>Individual</u>	Omo	Chen	Chen	Omo	Chen	Omo	Chen		Chen	distance with
	M16 008	0.136	0.095		0.312	0.343	0.215	0.214		M10 M-5	Chen Chen style
	M16 058	0.177	0.119		0.323	0.327	0.238	0.239		M1 2296	Chen Chen style
	M16 5063	0.136	0.115		0.322	0.371	0.239	0.234		M1 S/N I773	Chen Chen style
	M70 2426	0.115	0.097		0.243	0.285	0.181	0.186		M1 3677	Chen Chen style
	M70 2868	0.086	0.068		0.234	0.260	0.162	0.157		M10 85-25(B)	Chen Chen style
	M70 2985	0.115	0.094		0.275	0.333	0.192	0.192		M10 S-6	Chen Chen style
	M70 2840	0.086	0.079		0.249	0.270	0.158	0.160		M1 513	Chen Chen style
	M70 2642	0.132	0.131		0.297	0.353	0.218	0.204		M10 T-3	Chen Chen style
153	M70 2956	0.226	0.195		0.323	0.378	0.278	0.273		M1 284	Chen Chen style
	M70 2787	0.089	0.108		0.267	0.284	0.183	0.192		M70 4468	Omo style
	M70 2999	0.204	0.183		0.284	0.365	0.241	0.252		M10 85-18	Chen Chen style
	M70 2896	0.158	0.154		0.312	0.357	0.217	0.234		M43 4878	Chen Chen style
	M70 4166	0.146	0.129		0.278	0.316	0.207	0.203		M1 427	Chen Chen style
	M70 4443	0.126	0.108		0.301	0.320	0.196	0.210		M1 302009	Chen Chen style
	M70 4468	0.089	0.092		0.258	0.322	0.183	0.199		M70 2787	Omo style

## DISCUSSION

Overall the biodistance results are suggestive of a complex pattern of biosocial interaction among Tiwanaku colonial communities in the Moquegua Valley. The negative Relethford-Blangero residuals for Chen Chen M1 are statistically significant and indicate this community experienced lower than expected levels of extra-local gene flow. This could simply reflect the fact that Chen Chen M1 has the largest estimated population size among the Moquegua Valley Tiwanaku colonies and, as a result, residents of M1 did not have to seek marriage partners from other sites to avoid taboos against marrying close relatives (such as minimal *ayllu* co-members). This is consistent with findings that indicate exogamy tends to decrease as population size increases (e.g., Fix, 1999; Malcolm et al., 1971; McCullough, 1989; cf. Relethford, 1986; Workman and Jorde, 1980).

The positive residuals for Omo Alto M16 and Rio Muerto M70 are statistically significant and suggest these communities experienced greater than expected levels of extra-local gene flow. This is consistent with interpretations of Omo-style communities as smaller settlements comprised of more mobile camelid agropastoralists whose livelihood likely depended on seasonal transhumance (Goldstein, 2005; see also Fix, 1999). Additionally, the small population size estimated for Omo Alto M16 may have required residents of the site to seek marriage partners from other sites to avoid taboos against marrying close relatives (see Malcolm et al., 1971; McCulloch, 1989; Relethford, 1986; cf. Relethford, 1992).

The Mantel test of the geographic distance and biodistance matrices provides a straightforward method for evaluating whether gene flow among the study samples was

consistent with a model of isolation-by-distance. The weak positive Pearson's and Spearman's correlations suggest genetic microdifferentiation among the study samples, as assessed using cranial shape, is consistent with isolation by distance. However, the weak positive correlations are not statistically significant, and this may indicate that other factors were structuring gene flow within the Moquegua Valley Tiwanaku colonial enclave. For example, in some cases members of Tiwanaku-affiliated communities avoided marrying individuals from nearby communities affiliated with a different maximal *ayllu* (e.g., Omo M10 and Omo Alto M16), which would support the dual diaspora model. The Mahalanobis  $D^2$  matrix indicates some members of Tiwanaku-affiliated communities sought marriage partners from sites far away from their own *and* affiliated with a different maximal *ayllu* (e.g., Chen Chen M1 and Rio Muerto M70). Overall, results of the Mantel test provide some support for the isolation-by-distance model, but they do not indicate the dual diaspora model should be rejected outright.

Results of discriminant function analysis and canonical variates analysis produced moderate support for the dual diaspora model. DFA proved rather effective at differentiating between individuals from Chen Chen- and Omo-style contexts, and it identified statistically significant differences between the mean cranial shapes of individuals from Omo-style cemeteries compared with individuals from Chen Chen-style cemeteries. Although the overall differences in the mean cranial shapes are small, they do seem to reflect real differences in the shape of the foramen magnum and the glenoid fossa between Chen Chen- and Omo-style samples. The canonical variates analysis was also able to successfully differentiate between individuals from Omo-style and Chen Chen-

style contexts, but whether these results are a reflection of population structure (e.g., mate exchange and gene flow among Moquegua Valley Tiwanaku communities) or of population history (e.g., differences between the initial founding Chen Chen- and Omo-style immigrants or their ancestral populations) is unclear.

Patterns of phenotypic variation among Moquegua Tiwanaku-affiliated communities were undoubtedly influenced by the genetic variation present in the individuals who migrated from the Tiwanaku heartland and established colonial settlements in the middle Moquegua Valley. Unfortunately, little is known about the amount of genetic diversity present in the founding populations of the Moquegua Tiwanaku colonies or the ancestral populations of Chen Chen- and Omo-style communities, although they are thought to have originated in the *altiplano* (Goldstein, 2005). The effects of isolation by altitude may have influenced the genetic diversity within the ancestral populations of the Moquegua Tiwanaku colonists. Gómez-Pérez et al. (2011) found that heterozygosity was lower in samples from high-altitude regions of the Andes compared to lower altitude regions due to lower population density and lower levels of exogamy among high-altitude populations. There are insufficient radiocarbon data to permit a diachronic analysis of population structure to investigate whether genetic microdifferentiation changed through time within the Moquegua Tiwanaku colonies. Additionally, ongoing migration between the ancestral homeland and the Moquegua colonies (see Baitzel and Goldstein, 2016), and likely between the Moquegua colonies and other areas of the south central Andes, would also have influenced patterns of genetic

microdifferentiation among Tiwanaku-affiliated samples included in this study. However, this information is not currently available to aid interpretation of the present results.

Altogether, these results suggest that marriage practices and the resultant patterns of gene flow and genetic drift within the Moquegua Valley Tiwanaku colonies were influenced by multiple factors. In some cases spatial proximity seems to have structured gene flow, but maximal *ayllu* affiliation was also important as indicated by the results of discriminant function analysis and canonical variates analysis. If maximal *ayllus* in the Tiwanaku Moquegua colonies were endogamous social groups, then intra-*ayllu* inter-individual Euclidean distances should be significantly smaller than inter-*ayllu* inter-individual Euclidean distances. The fact that average intra-*ayllu* inter-individual distance (0.206) is smaller than the average inter-*ayllu* inter-individual distance (0.210), and this difference is significant ( $P$  value = 0.009) also supports an overall pattern of maximal *ayllu* endogamy. This suggests that members of Tiwanaku-affiliated ethnic communities may have tended to marry someone from the same maximal *ayllu*, but there were certainly exceptions to this general pattern, as indicated by the high proportion of individuals from Omo-style contexts who have their least pairwise Euclidean distance with an individual from Chen Chen-style contexts. In sum, marriage practices within the Tiwanaku-affiliated colonial enclave in the Moquegua Valley were structured by a mosaic of factors (see Fix, 1999; Workman et al., 1976) that included ethnic or maximal *ayllu* affiliation, spatial proximity, and perhaps smaller scales of social affiliation.

### **Multiscalar *ayllu* organization**

Archaeologists have effectively applied *ayllu*-based models of social organization to pre-Hispanic contexts, but typically only the maximal *ayllu* or ethnic-level aspect of *ayllu* organization is rigorously applied to the archaeological record as an interpretive framework. For example, the dual diaspora model (Goldstein, 2005, 2015), like many recent efforts to reconstruct social organization among Moquegua Tiwanaku communities, emphasizes ethnic-level group affiliations (e.g., Baitzel and Goldstein, 2011; Blom, 1999; Blom et al., 1998; Owen, 2005; Sutter and Sharratt, 2010; cf. Hoshower et al., 1995; Lewis, 2005; Lewis and Stone, 2005; Sharratt, 2011). While this approach has yielded important insights regarding social organization in the Tiwanaku colonies, results from the present study suggest that an analytical framework that emphasizes ethnic-level affiliations is insufficient to elucidate the multifaceted nature of social life within these ancient communities. A continued emphasis on ethnic level organization inadvertently contributes to the neglect of the role of smaller scales of social affiliation and their influence on patterns of biosocial interactions.

Among contemporary and historic Andean communities, *ayllus* tend to be segmented into nested hierarchies of subunits at different levels of scale within a ‘recursive hierarchy’ (Platt, 1986; Urton, 1993). Platt (1986) describes such a nested system of *ayllu* identities among the present-day Macha of Potosí, Bolivia. The entire Macha ethnic community can be considered a maximal *ayllu*, which is primarily an imagined community that only forms a coherent group during political confrontations or major rituals (Allen, 1988; Abercrombie, 1998; Wachtel, 1994). The maximal *ayllu* is

divided into two moiety divisions, each of which is comprised of ten minor *ayllus*. Each minor *ayllu* includes several minimal or micro *ayllus*, corporate groups that may include a cluster of several household compounds and their resident descent groups who worship a common ancestor and sometimes engage in economic specialization (Abercrombie, 1986, 1998; Izko, 1992; Platt, 1986; Wachtel, 1994).

Efforts to incorporate smaller scales of *ayllu* affiliation into models of past social organization remain underdeveloped, despite archaeological evidence suggestive of recursive, hierarchical social organization at settlements in the Tiwanaku *altiplano* homeland and in Tiwanaku-affiliated peripheral communities. Social groups of different scales of organization (e.g., households, communities, ethnic groups, and regions) used Tiwanaku corporate styles and engaged in common practices (e.g., rituals) that signaled their shared Tiwanaku identity (Bermann, 1994; Blom et al., 1998; Goldstein, 1989b, 2005; Janusek, 1999, 2002, 2003, 2004a,b, 2005a,b; Knudson et al., 2014; Torres-Rouff et al., 2013). At the same time, members of these social groups signaled their differences from one another at regional, maximal *ayllu*, and corporate levels through distinctions in their habitual practices and material culture styles (Blom, 1999, 2005; Buikstra, 1995; Hoshower et al., 1995; Goldstein, 2005; Janusek, 2003, 2004a,b, 2005a,b, 2008; Owen, 2005; Sharratt, 2011; Torres-Rouff et al., 2013).

Bioarchaeological evidence from the Moquegua Valley illustrates not only the multiscale nature of social organization among Tiwanaku communities, but suggests different scales of affiliation were emphasized at different sites within the middle valley. Spatial distributions of phenotypic, mortuary, and cranial modification data suggest

different levels of social affiliation were emphasized at different Chen Chen-style cemeteries. Previous research at Omo M10 has interpreted spatial distributions of cranial modification practices as evidence that cemeteries were associated with distinct lineages or social groups similar to *ayllus* (Buikstra, 1995; Goldstein, 2005; Hoshower et al., 1995). In contrast, larger scales of social affiliation were emphasized at the site of Chen Chen M1 (Blom, 1999, 2005; Blom et al., 1998; Sharratt, 2011). Blom found that among the members of residential descent groups who buried their dead at Chen Chen M1, “there were few social boundaries to reproduction or movement between groups” (Blom, 1999: 182). As a result, commonalities among individuals buried at the site, such as their shared maximal *ayllu* affiliation, were emphasized (Blom, 1999, 2005; Sharratt, 2011). Similarly, Lewis (2005) concludes that the overall level of homogeneity in mitochondrial DNA haplogroups from burials sampled from Chen Chen M1 is consistent with the presence of a single matrilineal *ayllu* at the site rather than multiple matrilineal *ayllus*.

Thus, it appears that social organization within Middle Horizon Tiwanaku communities in the Moquegua Valley was influenced by diverse affiliations that cut across social groups of varying scale (i.e., corporate, ethnic, and regional level affiliations), and it seems these different aspects of social identity were variably expressed within and between sites through cultural practices including mortuary rituals and cranial modification techniques. It seems likely that one or more of the smaller scales of *ayllu* organization, such as the moiety or corporate (i.e., minimal *ayllu*) level, could have influenced decisions regarding suitable marriage partners. Thus, a multiscale approach (Read and van der Leeuw, 2015) to social organization is needed to more



effectively illuminate interaction patterns within and among sites and within and across ethnic community boundaries. An analytical framework that can operationalize *ayllu* organization as multiscalar will likely provide a more nuanced reconstruction of Moquegua Tiwanaku social organization.

### **Variability in *ayllu* organization**

Ethnographic and ethnohistoric studies emphasize not only the multiscalar quality of *ayllu* organization but also the fluidity of *ayllu* membership and the degree of inter-community variation in marriage practices, rules of descent, and post-marital residence practices (Abercrombie, 1986, 1998; Bastien, 1978; Harris, 1978; Isbell, 1978; Murra, 1972; Platt, 1982; Rasnake, 1988; Urton, 1990). *Ayllu* composition is flexible; membership can be based on literal or fictive descent, adoption, political negotiation, marriage, alliance, or other criteria (Abercrombie, 1986, 1998; Bastien, 1978; Platt, 1982; Rasnake, 1988; Urton, 1990). *Ayllu* members are linked through shared ascribed origins from specific ancestral origin places, such as *huacas* or *mallkus* (Albarracín-Jordán, 1996a; Arriaga, 1968[1621]; Allen, 1988; Abercrombie, 1998; Bastien, 1978; Bauer and Stanish, 2001). Thus, contemporary *ayllus* are “defined more by social solidarity than either geography or genealogy” (Goldstein, 2015: 9203). However, the extent to which similar practices characterized earlier Andean communities is not well known.

Although it is problematic to assume that modern *ayllus* are similar to sixteenth-century *ayllus* (Isbell, 1997; Stanish, 2003) in light of the demographic, sociocultural, and political transformations that resulted from European colonization of South America (e.g., Gaither and Murphy, 2012; Klaus, 2008, 2013; Klaus and Tam, 2009a,b, 2010;

Larsen, 1994; Liebmann and Murphy, 2011; Livi-Bacci, 2006; Murphy et al. 2010; O'Fallon and Fehren-Schmitz, 2011), there is evidence to suggest that similar flexibility or variability in social group composition and marriage practices characterized pre-Hispanic Andean communities. Multiple archaeological investigations have found that mate exchange was not governed as strictly as suggested by ethnohistoric accounts (e.g., Lozada Cerna, 1998; Lozada Cerna and Buikstra, 2002; Nystrom and Malcom, 2010; Sutter, 2005). Therefore, archaeological approaches to social organization would be well served to incorporate those flexible and fluid aspects of recent and contemporary *ayllu* organization, regardless of whether one focuses on ethnic-like maximal *ayllu* affiliation or smaller scales or affiliation such as family.

It is difficult to interpret the significance of the numerous examples of individuals from Omo-style contexts that have their smallest inter-individual Euclidean distance with an individual from a Chen Chen-style context in terms of social group (i.e., *ayllu*) composition. It is unclear how an individual's *ayllu* membership was determined (e.g., via matrilineal, patrilineal, or bilateral descent) and how marriage impacted *ayllu* membership, post-marital residence patterns, and burial location. If maximal *ayllus* were endogamous, and mate exchange was largely consistent with the normative social rules for marriage, then this issue is irrelevant because each individual's maximal *ayllu* affiliation would have been the same as both of his or her parents and each individual's maximal *ayllu* identity would have been the same as his or her spouse's. Thus, if *ayllus* were endogamous social groups, one's *ayllu* affiliation would not change following marriage, as one's spouse's *ayllu* affiliation would be the same as one's natal *ayllu*

affiliation. Results presented above indicate that while Chen Chen- and Omo-style communities were not endogamous social groups, maximal *ayllu* identity was part of a suite of factors, including spatial proximity and perhaps corporate kin and regional trade networks, that influenced marriage practices within these communities.

Further complicating interpretations of biodistance analysis and post-marital practices is the possibility that post-mortem burial location does not reflect post-marital residence location (Ensor, 2013b). Individuals could have been returned to their natal minimal *ayllu* or corporate group for burial (see Keegan, 2009; Matney et al., 2012). These issues highlight the need for analytical and interpretive models that incorporate more flexible notions of relatedness as a basis of affiliation, not simply biological relatedness (Johnson and Paul, 2016; Lozada, 2011b).

### ***Ayllu* organization as family organization**

Archaeological evidence from Tiwanaku sites in the *altiplano* homeland and its periphery reflect the central role of family in Tiwanaku-affiliated communities. Residential neighborhoods at the site of Tiwanaku were organized around spatially discrete, walled compounds (Janusek, 1999, 2002, 2003, 2004a,b, 2005b). Janusek (2002, 2003, 2004a,b) suggests the social groups who resided within compounds were composed of multiple domestic units or households, similar to minimal or micro *ayllus* in the present-day Andes, and were the fundamental unit of Tiwanaku social life. In Moquegua, Omo-style settlements exhibit segmentary organization with “numerous insular communities, each arrayed around its own common plaza for assembly or ritual” (Goldstein, 2009: 284). Goldstein (2005, 2009) suggests these plaza-centered residential

communities are comparable to present-day minimal *ayllus*, and he hypothesizes that their spatial segregation reinforced salient social boundaries between them.

Investigations of social organization in pre-Hispanic Andean contexts that use *ayllu* organization to model social interaction in the past would benefit from incorporating family-based aspects of *ayllu* organization in their research design. Emerging trends within bioarchaeological research (see Johnson and Paul, 2016) suggest that a family-based approach would complement existing models of social organization emphasizing ethnic affiliations. As proposed by Johnson and Paul (2016), a bioarchaeological approach to family-based organization is multiscalar and can accommodate diverse criteria as the basis for affiliation.

Approaching kinship as a multiscalar form of social identity provides an analytical framework that can explore connections between individual-, small group-, and community-level identities to address broader questions of human social organization in the past (Johnson and Paul, 2016; see Meyer et al., 2012; Stojanowski, 2013b). Kinship manifests as a collective social identity (McKinnon, 1991), but its experience is both personal and interpersonal (Carsten, 1995; Van Vleet, 2008). By using multiple lines of evidence, including data amenable to intra-individual and inter-individual analyses (e.g., radiogenic isotopes and molecular genetic data), a family-based approach can scale down to examine relationships among individuals (e.g., Baca et al., 2012; Haak et al., 2008; Meyer et al., 2012) and also scale up to assess family organization within and across communities (e.g., Meyer et al., 2012; Stojanowski, 2013b).

As noted above, *ayllu* membership among contemporary and historic Andean communities is not based on strict rules of descent. It could be that biological relatedness is not the most contextually appropriate conception for assessing aspects of *ayllu* membership. Again, recent developments within bioarchaeological studies of kinship can inform efforts to reconstruct smaller scales of social organization in the pre-Hispanic Andes. To disassociate from reductive biological conceptions of relatedness common to Western culture and anthropological kinship research (e.g., Sahlins, 2013; Schneider, 1968, 1972, 1984), bioarchaeologists are developing broader conceptions of relatedness and incorporating non-biological aspects of kinship into investigations of socioeconomic organization in archaeological contexts (e.g., Česnys and Tutkuvienė, 2007; Gamba et al., 2011; Gregoricka, 2011, 2013; Lozada, 2011b; Paul et al., 2013; Pilloud and Larsen, 2011; see also Hutchinson and Aragon, 2002). Considerations of non-genealogical forms of kinship such as practical kin (Pilloud and Larsen, 2011), fictive kin (Gregoricka, 2011, 2013), and social houses or households (e.g., Duncan and Hageman, 2015; Hutchinson and Aragon, 2002; King, 2006, 2010; Miller, 2015; Novotny, 2013) have made valuable contributions to the literature, and they can inform efforts to develop alternative family structures within pre-Hispanic communities in the Andes.

### **Conclusions**

The dual diaspora model of Tiwanaku colonial organization in the Moquegua Valley of southern Peru is supported by much of the current archaeological data from the region. Consistent with predictions made by Goldstein (2005), results from the present study suggest maximal *ayllu* affiliation influenced marriage practices among Moquegua

Tiwanaku colonial communities. However, it does not appear that Chen Chen- and Omo-style communities were entirely endogamous social groups. This does not invalidate the dual diaspora model, but it suggests the model would benefit from a slight repositioning or reconceptualization. Results of the present study suggest ethnic community boundaries were permeable and/or that *ayllu* affiliation was fluid. These findings are consistent with studies of ethnic communities in a variety of cultural contexts (e.g., Barth, 1969; Bell, 2005; Haley and Wilcoxon, 2005; Moore, 1994, 2001; Sattler, 1996; Voss, 2005).

As currently conceived, the dual diaspora model perhaps overemphasizes the maintenance of distinct, diaspora identities (see Goldstein, 2015). Clearly, the archaeological evidence supports the presence of two Tiwanaku ethnic communities within the Tiwanaku colonies, but ethnic group boundaries can be flexible and permeable (Barth, 1969). Social identities are dynamic and reflect on-going processes of negotiation between self and others in relation to the changing nature of social networks (Andolina et al., 2005; Bourdieu, 1977; Díaz-Andreu and Lucy, 2005; Insoll, 2007; Jones, 1997). Individuals potentially can shift identities from one moment to the next, embracing a homeland identity while also developing hybrid frontier identities (Lightfoot, 1994; Lightfoot and Martinez, 1995).

It is not unreasonable to expect that members of Moquegua Tiwanaku-affiliated communities had shifting, multiplex social affiliations, with maximal *ayllus* maintaining distinct residential and mortuary sectors within sites and intermarried households interspersed across different sectors. Indeed, recent material culture evidence from a pre-Tiwanaku state decline context in the middle Moquegua Valley is suggestive of a hybrid

maximal *ayllu* identity. Sharratt (2011: 149) describes a ceramic vessel with an Omo-style polished black-ware interior and a Chen Chen-style red-slipped exterior. This hybrid Chen Chen-/Omo-style vessel may provide material evidence, however limited, that cultural boundaries between Tiwanaku-affiliated maximal *ayllus* were permeable or fluid. Alternatively, it could represent the complementary and mutually-interdependent relationship between the two maximal *ayllu* communities in the Moquegua Valley colonies.

Individuals' and small social groups' behavior and actions were certainly constrained – but not necessarily determined – by ethnic affiliations. Social organization in the Tiwanaku Moquegua colonial enclave likely was based on the complex dynamics of multi-layered and cross-cutting aspects of social affiliation, with smaller scales of affiliation – minimal or micro *ayllu* organization or households, for instance – playing important roles in the daily lives of members of Chen Chen and Omo-style communities. Members of Tiwanaku-affiliated communities in the Moquegua Valley likely simultaneously embodied affiliations with the Tiwanaku state or a general Tiwanaku corporate identity (vís a vís Wari or Huaracane), their maximal *ayllu*, their residential community (i.e., neighborhood district), and their family or corporate group, emphasizing one or multiple aspects in a given moment depending on the circumstances (i.e., vís a vís the 'other(s)' with whom they were interacting). A multiscalar approach to social organization that incorporates family-based aspects of affiliation may contribute a more nuanced understanding of colonial interactions not only in the Tiwanaku-affiliated

settlements in the Moquegua Valley, and such an approach could inform investigations of social organization in a wide array of colonial settings past and present.



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## CHAPTER 4

### SOCIAL NETWORK ANALYSIS OF MOQUEGUA TIWANAKU BIOSOCIAL ORGANIZATION: A MULTISCALAR BIOARCHAEOLOGICAL KINSHIP ANALYSIS

Target Journal – American Journal of Physical Anthropology

Understanding how, why, and with whom individuals form and maintain relationships is critical to the analysis of political organization, economic interaction, and religious movements, both in the present and in the past (Borgatti et al., 2013; Collar, 2013; Scott, 2013). Bioarchaeologists have embraced social identity theory as a flexible framework for investigating social interaction and affiliation at the interpersonal level and in terms of broader aspects of social organization. These conceptual developments have been mirrored in methodological advancements in data collection practices and technologies (e.g., next-generation sequencing, 3D scanning and printing technology, and tablet-based applications for scoring protocols and data entry), but similar advancements in analytical methods for investigating social organization in the past have not followed suit. Flexible analytical methods for investigating patterns of affiliation and interaction that are grounded in social theory are needed to more effectively evaluate the practice of interpersonal relationships and its effects on large scales of social organization.

Social network analysis has emerged as a powerful approach to investigating social organization in the biological (Borgatti et al., 2002; Flack et al., 2006; Krause et al., 2009; Lusseau, 2003; Whitehead, 2008) and social sciences (Carrington et al., 2005; Newman et al., 2006; Scott, 2013; Wasserman and Faust, 1994). Social network analysis

provides a rigorous corpus of techniques and theory for investigating how individuals create effective social groups and the ways in which those groups transform over time (Borgatti et al., 2013; Scott, 2013). Although early- to mid-20th century anthropological studies of kinship and socioeconomic organization contributed to social network theory's basic principles (see Freeman, 2004; Scott, 2013), formal social network analysis is less widely developed in anthropology compared to other disciplines (McCarty and Molina, 2015; cf. Terrell, 2010).

Over the past two decades applications of social network analysis in anthropological research have increased, especially within cultural anthropology, primatology, and archaeology. Ethnographic studies have used social network analysis to investigate organizational structure within businesses, nonprofits, and nongovernmental organizations (e.g., Provan and Milward, 2001), the role of social networks in managing social-ecological systems (Bodin and Crona, 2009; Schneider et al., 2003), and gift exchange (Schweitzer, 1996, 1997). Among studies of non-human primates, social network analysis is used to study factors that influence social group composition and dispersal (Langergraber et al., 2009; Wikberg et al., 2014), infectious disease risks across wild primate communities (Rushmore et al., 2013), management of captive chimp communities (Clark, 2011), social transmission of tool use (Hobaiter et al., 2014), and social power and dominance hierarchies (Beisner et al., 2016). Archaeologists use social network analysis to investigate patterns of material culture production and exchange to better understand broader sociopolitical processes in the past (e.g., Brughmans et al., 2016; Golitko and Feinman, 2015; Knappett, 2013; Mills et al., 2013; Peeples, 2011;

White, 2012). To date efforts to incorporate social network analysis methods and theory in bioarchaeological research have been extremely limited.

The present study explores the utility of social network analysis as an analytical methodology for investigating social organization among past peoples. Social network analysis of phenotypic data is used to explore small-scale social affiliations within the Tiwanaku colonies of the Moquegua Valley of southern Peru. Previous research has emphasized the role of ethnic-level affiliations in structuring biosocial interactions among Middle Horizon (ca. AD 500-1100) Moquegua Tiwanaku communities (e.g., Blom, 1999; Blom et al., 1998; Goldstein, 2005, 2015; Lewis, 2005; cf. Hoshower et al., 1995). Results presented in Chapter 3 suggest that in addition to ethnicity, smaller scales of affiliation – possibly kin based – influenced patterns of biosocial interactions in these communities. Prior attempts to identify corporate-like kin groups within Chen Chen-style Moquegua Tiwanaku contexts using intrasite biodistance analysis have had little success (Blom, 1999; Blom et al., 1998; Lewis, 2005). This chapter uses social network visualization techniques, analysis of network and node properties, and analysis of network structure, including subgroup analysis, in addition to standard biodistance techniques to identify potential (extended) biological relatives among archaeological samples of human skeletal remains from five sites within the middle Moquegua Valley.

### **Social network analysis**

Social network analysis is simply the study of relationships among units. Those units can be households within a village, and the relationships between them could be based on marriage or friendship ties. Or the units could be archaeological sites within a

region, and the links between them could be based on shared use of a particular style of ceramics or obsidian sourced from the same quarry. A comprehensive review of social network theory and analytical techniques is beyond the scope of this paper. Instead, the following is a brief discussion of basic concepts of social networks and of particular network measures that are typically applied within archaeology. Readers interested in a more detailed overview of social network analysis should consult Borgatti et al. (2013), Scott (2013), and Scott and Carrington (2011).

Any data that can be presented as an adjacency matrix is suitable for network analysis. An adjacency matrix consists of rows and columns defining specific actors (e.g., individuals, organizations, communities, populations, or species), and the cells of the matrix contain data that describe the relationship or attribute(s) shared by the actors. Graph theory is then used to represent the matrix as a network. A graph is a mathematical object that consists of a set of vertices (nodes or points) and a set of edges (links or ties) that connect pairs of vertices. Nodes can be directly connected (i.e., adjacent) or indirectly connected through other nodes. As a representation of a *social* network the nodes in the graph represent the actors in the adjacency matrix and the edges that connect them represent their relationship or shared attribute(s) (Borgatti et al., 2013; Scott, 2013).

Using this basic approach, a variety of different aspects of social life can be investigated. These include how individuals interact to maintain existing networks and under what circumstances individuals create new social networks. Additionally, social network analysis provides insights into the social, economic, and practical consequences of one's position within a network or the composition of one's network or subgroup



(Borgatti et al., 2013). Individual outcomes affected by network position include one's performance (e.g., a student's grades or which employee gets promoted), one's behavior (e.g., risk of suicide or likelihood of joining a particular club), and one's beliefs (e.g., likelihood of following a particular religious ideology or political philosophy) (Borgatti et al., 2013; Scott, 2013).

In social network analysis these aspects of social life are formally investigated as structure, cohesion, and centrality. Network structure is any pattern of connections within a network that deviates from one of random connections. Cohesion can be thought of as the extent of connectedness throughout a network. A maximally cohesive network is one in which every actor is directly connected (i.e., adjacent) to every other actor in the network. Centrality refers to the structural importance of a node to the network, and it can be measured in several ways, including degree centrality, which is simply the number of ties a node has, betweenness, and eigenvector centrality (Borgatti et al., 2013; Scott, 2013). Eigenvector centrality is a variation of degree centrality that incorporates the degree centralities of adjacent nodes (Bonacich, 1972; Newman, 2004). Related to centrality is the idea of centralization. Centralization is a property of a network rather than a node, and it reflects the degree of separation (i.e., difference in centrality) between the most central node and the other nodes in the network. A maximally centralized graph looks like a star, with the most central node in the center.

An important aspect of social network analysis is the identification and analysis of cohesive subgraphs. A subgraph is any set of nodes selected from the whole graph of a network, together with the lines connecting those nodes (Scott, 2013: 99). The aim of

subgraph analysis is to discover subgraphs that have sociological meaning and therefore represent a subgroup, a portion of the network in which actors interact more with (or are more similar to) one another than they are with actors who are not in the group. Such groups, also called cliques or clusters, often share common ideals, goals, and attributes and are therefore of particular interest to studies of social organization (Borgatti et al., 2013; Scott, 2013).

Archaeologists have embraced social network analysis as a flexible yet rigorous set of exploratory analytical techniques for visualizing data patterns and validating results obtained by other means (Isaksen, 2013; Knappett, 2013; Sindbæk, 2013; Terrell, 2013). Although social networks, in the general sense, are often implicated in bioarchaeological research, (e.g., McGrath, 1988), formal social network analysis of bioarchaeological data are almost non-existent. John Terrell's (2010) application of social network analytical techniques to molecular data from Pacific Island populations is currently the only published study that uses social network analysis in what loosely can be considered bioarchaeological research. Terrell applied social network analysis to multilocus genotype data and pairwise  $F_{ST}$  co-ancestry values published by Friedlaender and colleagues (2008) to evaluate hypotheses for the peopling of the Pacific. Terrell found that the use of social network techniques to visualize autosomal variation and explore genetic relationships among south-western Pacific Islanders produced results of greater clarity and resolution than Friedlaender and colleagues' results generated using more standard analytical methods, including clustering techniques.

Friedlaender and colleagues (2008) analyzed autosomal markers (687 microsatellite and 203 insertion/deletion polymorphisms) from 952 individuals sampled from 41 Pacific populations and found that genetic divergence among island Melanesian populations is structured by a suite of factors including island, island size, topographic complexity, and position (coastal vs. inland), but Melanesian population genetic structure is only weakly correlated with an isolation-by-distance model. Using a subset of 751 autosomal microsatellite loci from the same genetic dataset, Hunley et al. (2008) also find little support for a model of isolation-by-distance among Melanesian samples. Terrell (2010) applies social network analytical techniques to the mean population subgroup assignments and  $F_{ST}$  values for populations reported by Friedlaender et al. (2008), and he finds that isolation by distance constrained by social networks, along with coastal vs. inland position, best explain the observed population structure in island Melanesia (Terrell, 2010). Furthermore, the results generated using social network analysis are consistent with other lines of evidence on the biogeographical transformations associated with the peopling of Oceania. Building on Terrell's research, the present study explores how social network analysis of phenotypic data from samples of human skeletal remains can contribute to studies of social organization within pre-Hispanic Andean communities.

### **Social organization in the Moquegua Tiwanaku colonies**

Between the 7th and 11th centuries A.D. Tiwanaku-affiliated communities from the Bolivian *altiplano* established a series of colonial settlements in the Moquegua Valley of southern Peru (Blom et al., 1998; Goldstein, 2005; Knudson et al., 2014; Moseley et al., 1991). These colonial settlements were inhabited by two Tiwanaku-affiliated ethnic

communities: “Omo-style” camelid agropastoralists and “Chen Chen-style” intensive agriculturalists (Goldstein, 2005, 2009, 2015; Goldstein and Owen, 2001; Owen, 2005; Owen and Goldstein, 2001). Chen Chen- and Omo-style communities maintained distinct ethnic identities despite living in close spatial proximity for several hundred years (Baitzel, 2008; Goldstein, 1989a,b, 1993a, 2000b, 2005, 2009, 2015; Goldstein and Owen, 2001; Knudson and Blom, 2009; Owen and Goldstein, 2001). At the same time, members of Omo- and Chen Chen-style communities in the Moquegua Valley maintained strong ties with their ancestral or source communities in the *altiplano* (Goldstein, 2005, 2009). Isotopic evidence of paleomobility suggests there were continuing streams of migrants into the Tiwanaku colonies (Knudson et al., 2014), and paleodemographic data are interpreted as evidence of return migration from Moquegua to the *altiplano* (Baitzel and Goldstein, 2016).

Goldstein (2005, 2009, 2013) suggests Chen Chen- and Omo-style communities maintained distinct ethnic identities in part through endogamous marriage practices, but recent findings (see Chapter 3) indicate that while ethnic affiliation did influence marriage practices among Moquegua Tiwanaku colonists, Omo- and Chen Chen-style communities were not completely endogamous. Evidence for gene flow between individuals from Omo- and Chen Chen-style mortuary contexts suggests ethnic boundaries were permeable. Additionally, these findings may indicate that smaller scales of social affiliation, possibly family-based groups, were critical to structuring social interactions among residents of the Tiwanaku Moquegua colonies. Although archaeological, biodistance, and cranial modification data from the middle Moquegua

Valley indicate that corporate kin or family-level affiliations were an important axis of social identity in these communities (Hoshower et al., 1995; cf. Blom, 1999; Lewis, 2005), formal investigation of family organization among Tiwanaku contexts is underdeveloped.

Results presented in Chapter 3 show that some of the smallest inter-individual biodistances are between individuals from different sites in the middle Moquegua Valley. This may reflect the presence of kin networks whose members were spread across different sites as well as ethnic group boundaries within the region and possibly beyond. To verify the presence of extended kin networks at Tiwanaku-affiliated sites in the Moquegua Valley, flexible analytical methods for identifying kin at an intraregional scale are needed. Unfortunately, bioarchaeological kinship analysis is typically applied to cemetery or small grave contexts (see Alt and Vach, 1998; Stojanowski and Schillaci, 2006), and it is unclear whether standard methods can be applied at a regional scale.

### **Bioarchaeological kinship research**

Bioarchaeological kinship analysis evaluates patterns of phenotypic (e.g., skeletal and dental discrete trait frequencies or metric values) or genetic variability to identify close biological relatives. A full review of the different types of data and their application in kinship analysis is beyond the scope of this chapter; Stojanowski and Schillaci (2006) and Johnson and Paul (2016) provide recent overviews of types of data used for bioarchaeological kinship analysis. Among phenotypic data, rare discrete cranial, post-cranial, and dental traits are often preferred to metric data for reconstructing familial relationships (Rösing, 1986b; see Alt, 1991, 1997; Alt and Vach, 1991, 1992, 1995a,b,

1998; Alt et al., 1995, 1997; Corruccini and Shimada, 2002; Corruccini et al., 2002; Howell and Kintigh, 1996; Jacobi, 1996, 1997, 2000; Pietrusewsky and Douglas, 1992; Rösing, 1982, 1986a,c, 1995; Sjøvold, 1975, 1976/77; Spence, 1996; Strouhal, 1992), but metric data are used for kinship analysis (e.g., Adachi et al., 2003; Bondioli et al., 1984, 1986; Byrd and Jantz, 1994; Corruccini and Shimada, 2002; Doi et al., 1986; Hanihara et al., 1983; Stojanowski, 2003, 2005; Strouhal, 1992).

Bioarchaeological kinship studies are predominantly, if not exclusively, intracemetery or intrasite analyses. There are three basic types of kinship analysis: small grave, structured cemetery, and nonstructured cemetery (Alt and Vach, 1998; Stojanowski and Schillaci, 2006). Small grave analysis includes isolated multiple burials and spatially restricted burial contexts with limited interments such as caves, tumuli, and wells (e.g., Adachi et al., 2003, 2006; Bondioli et al., 1986; Corruccini and Shimada, 2002; Corruccini et al., 2002; Deguilloux et al., 2014; Doi et al., 1985, 1986; Hanihara et al., 1983; Matsumura and Nishimoto, 1996; Perego, 2012; Shimada et al., 2004; Sjøvold, 1976/1977). Structured kinship analysis is used to identify kin within large cemeteries that contain discrete burial areas (e.g., Bondioli et al., 1986; Howell and Kintigh, 1996; Jacobi, 1997, 2000; Meyer et al., 2012; Paul et al., 2013; Stojanowski, 2005c, 2013b; Stojanowski and Schillaci, 2006; Strouhal and Jungwirth, 1979). Nonstructured kinship analysis refers to efforts to identify biological kin within large cemeteries in which there are no distinct burial sectors and the burials have a relatively homogeneous spatial distribution (e.g., Alt and Vach, 1991, 1995a, b; Dudar et al., 2003; Stojanowski, 2003; Stone, 1996; Stone and Stoneking, 1993; Usher and Allen, 2005; Usher and Weets, 2014;

Usher et al., 2003; Vach and Alt, 1993). Nonstructured kinship analyses typically attempt to first identify non-random spatial patterns of burials with a high degree of phenotypic similarity compared to the other burials in the cemetery. These clusters of biologically similar individuals are considered a hypothesized family, and demographic and archaeological data (e.g., grave structure, body treatment) are used to support or reject the inference of kin-structured mortuary practices (Alt and Vach, 1995a,b).

Stojanowski and Schillaci (2006: 56) identified nonstructured kinship analysis as having the most potential for generating “important bioarchaeological inferences,” and it is this type of kinship analysis that is most similar (in design, objective, and analytical techniques) to the type of suprasite (i.e., intraregional) kinship analysis proposed here. Several of the analytical techniques used for intrasite and intracemetery kinship analysis, including cluster analysis and multidimensional scaling (MDS) (e.g., Howell and Kintigh, 1996; Paul et al., 2013; Stojanowski, 2013b; Stojanowski and Schillaci, 2006; Usher and Allen, 2005; Usher and Weets, 2014; Usher et al., 2003), are scale free and can be used to conduct an intraregional kinship analysis. Additionally, hierarchical clustering techniques and MDS do not require a priori knowledge about individual identification or group affiliation to structure the analysis; instead they identify potential kin groups based solely on the variable(s) of interest. Social network analysis is also scale free and does not require a priori identifications, but it has not previously been applied to bioarchaeological data for kinship analysis.

Stojanowski and Schillaci (2006) note that standard bioarchaeological kinship analysis, unlike postmarital residence analysis, does not engage social theory directly (cf.,

Dudar et al., 2003; Usher and Allen, 2005; Usher and Weets, 2014; Usher et al., 2003). However, recent theoretical and methodological developments may allow kinship analysis to engage directly with social theory. For example, kinship research can maintain a genealogical (e.g., biological and to a lesser extent affinal) focus and try to identify burial programs that conform to expectations of kin-based cemetery structure consistent with specific anthropological kinship systems (e.g., Crow and Omaha) defined in part through descent (e.g., patrilineal, matrilineal, or bilateral) and post-marital residence systems (patrilocal, matrilocal, etc.). However, it is unclear how successful such an approach could be even in the best of circumstances, given the diverse types of contextualized data that would be required to infer a particular kinship system from the (inherently biased and incomplete) archaeological record with any degree of confidence (cf., Ensor, 2013a,b). Furthermore, this type of approach is overly typological and designed to address macro aspects of sociopolitical organization in the past. As a result, it is unclear what insights such an approach might provide regarding sociality and the lived experiences of individuals in the past.

There is another potential avenue for kinship research to engage social theory. Kinship can be approached more broadly as social relatedness within a social identity theoretical framework (Johnson and Paul, 2016; see Chapter 2), and social network analysis method and theory can be used as an analytical, interpretive, and even predictive framework. For bioarchaeological data a general social network approach is preferable to specialized kinship network analysis (e.g., Hamberger et al., 2011), as the latter is based on the identification of specific kin relationships (e.g., parent-child, siblings), an



expectation that is difficult to meet under the best circumstances within archaeological contexts (Blouin, 2003; Meyer et al., 2012; Thompson, 1986).

Approaching family organization within Andean archaeological contexts using a broader conceptual framework of social relatedness rather than biological kinship may prove enlightening given that it is unclear how important biological relatedness was to family organization within pre-Hispanic societies (Lozada, 2011b). Andean ethnographic and ethnohistoric research suggests the criteria for kin group membership are flexible (Abercrombie, 1986, 1998; Bastien, 1978; Harris, 1978; Isbell, 1978; Murra, 1972; Platt, 1982; Rasnake, 1988; Urton, 1990; Van Vleet, 2008). Although it is problematic to assume long-term continuity in family organization given the widespread upheaval of indigenous Andean social organization, demography, and worldviews wrought by European colonization of South America (e.g., Gaither and Murphy, 2012; Klaus, 2008, 2013; Klaus and Tam, 2009a,b, 2010; Larsen, 1994; Liebmann and Murphy, 2011; Livi-Bacci, 2006; Murphy et al., 2010; O'Fallon and Fehren-Schmitz, 2011), a flexible, social identity-based approach to family organization is preferable to one rooted in Euro-American conceptions of relatedness (Schneider, 1968, 1972, 1984).

### **Social network analysis of kinship in archaeological contexts**

One of the critical challenges of applying social network analysis to (bio)archaeological data is that (bio)archaeologists are unable to directly observe the social network of interest. Instead, (bio)archaeologists have to first reconstruct a social network based on partial inputs and outputs (Knappett, 2013; Sindbæk, 2013). For this reason, before (bio)archaeological data are visualized or analyzed as network data

scholars must carefully consider whether their data justifiably can be conceptualized as network data (i.e., nodes and ties) (Brandes et al., 2013; Collar et al., 2015). For the present study, social network visualization and analytical techniques are applied to basicranial and temporal bone shape data to assess phenotypic similarity among individuals and to identify potential clusters of close biological relatives from Tiwanaku-affiliated sites in the middle Moquegua Valley. Phenotypic similarity, as measured by pairwise Mahalanobis ( $D^2$ ) distances, will serve as a relational index from which an adjacency matrix is constructed for the study sample.

The use of social network analysis to explore patterns of variation in basicranial and temporal bone shape among Tiwanaku-affiliated communities is based on the same assumption that underlies the majority of biodistance research: close relatives are more likely to be identical by descent than distant relatives and non-relatives (Thompson, 1986). Molecular genetic data are commonly analyzed as a source of network data among human and nonhuman populations, both past and present (e.g., Brohée et al., 2008; Kasper and Voelkl, 2009; McDonald, 2009; Proulx et al., 2005; Terrell, 2010; Wolf and Trillmich, 2008). As craniometric data are “reasonable proxies” for estimating biological relatedness among human skeletal samples (Algee-Hewitt, 2016: 2; see Carson, 2006; Cheverud, 1988; Harvati and Weaver, 2006b; Howells, 1973; Konigsberg and Ousley, 1995; Relethford, 1994, 2002, 2004; Relethford and Blangero, 1990; Roseman, 2004; Smith, 2009; Williams-Blangero and Blangero, 1989), it follows that phenotypic data generally – and cranial shape data specifically – are suitable proxies for evaluating genetic relatedness using social network analysis.

Although phenotypic traits are suitable proxies for genetic relatedness, they are also influenced by environmental effects. It is important to consider how environmental effects could affect regional patterns of phenotypic variation. For example, if environmental effects are family-based, they could contribute to similar within-family phenotypes and divergent between-family phenotypes that have a non-genetic basis (Stojanowski and Schillaci, 2006). Although it can be difficult to evaluate the effects of within-family versus between-family environmental variation on patterns of phenotypic data in archaeological samples, recent evidence from a Spanish mission cemetery in Florida provides suggestive evidence for family-based environmental effects. Stojanowski (2013) interprets the non-random spatial distributions of skeletal and dental pathological indicators associated with a kin-structured mortuary program as compelling evidence for multi-generational, family-based disparities in stress and disease experience, early childhood morbidity, and differential mortality. The higher prevalence of LEH among certain burial clusters combined with large sections of the cemetery with no LEH is suggestive of the potential for family-based environmental effects to influence phenotypic form. This example illustrates the importance of evaluating the extent to which environmental factors structure patterns of phenotypic variation in skeletal samples.

If phenotypic similarity is a reliable indicator of biological relatedness, then social network analysis of basicranial and temporal bone shape should identify clusters of close biological relatives. Importantly, social network analysis may provide a way to scale up kinship studies from an intrasite level of analysis to an inter-site or regional level of

analysis, similar to the way it has been used to scale up studies of social interaction among non-human primates, where the traditional emphasis (i.e., non-social network approach) has been on dyadic relationships (Sueur et al., 2011). Social network analysis provides a way to analyze all (potential) relationships linking all (potential) group members in a sample (Croft et al., 2005; Flack et al., 2006; Hinde, 1976; Wey et al., 2008; Whitehead, 2008). In essence this analytical approach has a similar objective as unstructured spatial kinship analysis (Alt and Vach, 1998), in that it attempts to identify members of kin groups without a priori reference to spatial structure or cultural attributes within larger cemeteries.

At this point it is useful to consider some similarities and differences between social network analysis and other exploratory data techniques more frequently used in biological anthropology and bioarchaeology. As described above, social network analysis uses graph theory to visualize and formally analyze configurations of real and potential social interactions and relationships. In archaeological applications it is generally used as an exploratory method intended to facilitate the identification and interpretation of underlying patterns of interaction and organization (Östborn and Gerding, 2014; Terrell, 2010). In this regard it is similar to other exploratory multivariate analytical methods used by biological anthropologists and archaeologists for visualization, ordination, and clustering, including principal component analysis (PCA), factor analysis, correspondence analysis, principal coordinates analysis (PCoA), and multidimensional scaling (MDS) (Baxter, 1994, 2003; Bølviken et al., 1982). The utility and popularity of analytical methods such as discriminant function analysis, PCA, and MDS lie in their

ability to reduce multivariate data to a more manageable (i.e., interpretable) number of uncorrelated variables (e.g., components, factors, canonical axes, discriminant functions, principal coordinates, etc.) underlying the original data. This in turn allows individuals or groups to be situated in a simplified representation of multidimensional space and facilitates the visualization of their interrelationships, which is often aided by the use of cluster analysis (Pietrusewsky, 2008). A complete review of analytical methods used in biodistance analysis generally and kinship analysis in particular is beyond the scope of this chapter, and reviews are provided elsewhere (see Konigsberg and Frankenberg, 2013; Larsen, 2015; Pietrusewsky, 2008; Stojanowski and Schillaci, 2006). The two techniques that serve similar purposes as social network analysis are clustering and multidimensional scaling, and the remainder of this brief review will focus on them.

Multidimensional scaling refers to a set of related ordination techniques (e.g., metric MDS and classical MDS or principal coordinates analysis) used to visualize the level of similarity among individual cases in a dataset or a distance matrix (Kruskal and Wish, 1978). MDS analyzes a matrix of dissimilarities between pairs of items and generates a coordinate matrix whose configuration attempts to minimize the loss of fidelity – measured as strain or stress – between the original data and the reduced dimensions produced (Kruskal, 1977; Kruskal and Wish, 1978). The closer the strain or stress is to zero, the better the representation of the original data.

Cluster analysis is not an ordination technique; it simply groups similar objects (individuals or groups) on the basis of the (multivariate) characteristics they possess (Aldenderfer and Blashfield, 1984; Everitt and Dunn, 2001; Kaufman and Rousseeuw,

1990). Objects are grouped in such a way that objects in the same group (or cluster) are more similar to each other than they are to objects in other groups. Results of cluster analysis are typically depicted as dendrograms.

Various clustering algorithms are based on different definitions of what constitutes a cluster and therefore use different protocols for identifying them (Everitt and Dunn, 2001; Kaufman and Rousseeuw, 1990). Partitioning methods (e.g., k-means) divide the data set into a number of groups pre-designated by the user and will not be discussed further. Hierarchical methods are not limited to a pre-determined number of clusters and are of greater relevance to the present study. Some hierarchical methods are divisive and progressively divide one large cluster containing all the samples into pairs of smaller clusters until all clusters have been divided into individual samples. Other hierarchical methods are agglomerative; they start with individual objects and form a cluster of the most similar objects, progressively joining objects and clusters until all have been joined into a single large cluster.

The order in which clusters are joined is determined by the linkage method used (Everitt and Dunn, 2001; Kaufman and Rousseeuw, 1990). The nearest-neighbor method is based on the elements of two clusters that are most similar, and it can be sensitive to outliers, which may not be desirable if the most similar objects are distant from the sample centroid. Group average methods are less sensitive to outliers, and they can be unweighted (e.g., unweighted pair-group method with arithmetic averaging or UPGMA) or weighted (e.g., weighted pair-group method with arithmetic averaging or WPGMA). The hierarchical clustering techniques described here are often used to

visualize and interpret data patterns as part of distance analysis, and they can aid in the evaluation of a novel analytical technique for exploring patterns of phenotypic variation, such as social network analysis.

The present study explores the utility of social network analysis for investigating social organization among past peoples using bioarchaeological data. Specifically, social network analytical techniques are applied to phenotypic data to identify potential biological kin networks among archaeological samples of human skeletal remains from five Tiwanaku-affiliated sites in the middle Moquegua Valley. Results of social network analysis are compared to results of MDS and agglomerative hierarchical clustering to evaluate the effectiveness of using social network analysis to explore patterns of genetic relatedness in the past, including as a method for conducting bioarchaeological kinship analysis.

## **MATERIALS AND METHODS**

Phenotypic and cranial modification data were collected from human skeletal remains from five Tiwanaku-affiliated sites (ca. AD 600 – 1000) from the middle Moquegua Valley: Chen Chen M1, Omo Alto M16, Omo M10, Rio Muerto M43, and Rio Muerto M70B. M1, M10, and M43 are Chen Chen-affiliated contexts whereas M16 and M70 are Omo-affiliated contexts (Goldstein, 2005). Study collections are curated in the Museo Contisuyo in Moquegua, Peru.

### **Data collection**

Cranial geomorphometric data were collected following standard methodology (e.g., Adams et al., 2004; McKeown and Jantz, 2005; Slice, 2005). Table 6 and Figure 3

in Chapter 3 present the seventeen basicranial and temporal bone landmarks (see Howells, 1973; Smith, 2009) that were registered in three-dimensional space using a Microscribe digitizer MX. Previous studies suggest that basicranial and temporal bone shape data are suitable for biodistance analysis at a variety of analytical scales (e.g., Enlow, 1990; Harvati, 2001; Harvati and Weaver, 2006a,b; Houghton, 1996; Lieberman et al., 1996, 2000; Lockwood et al., 2004; MacPhee and Cartmill, 1986; McHenry, 1994, 1996; Olson, 1981; Smith, 2009; cf. Roseman et al., 2010; von Cramon-Taubadel, 2009, 2011). Traits are midline or collected from the left side of the cranium only.

Crania were scored for artificial cranial modification using a protocol developed for previous studies of Moquegua Valley skeletal samples (Blom, 1999; Blom et al., 1998; Hoshower et al., 1995). For the present study crania were observed for modification presence/absence and modification type (e.g., annular and fronto-occipital) to assess the effects of cranial modification on cranial base and temporal bone shape.

Assessments of skeletal age and sex were obtained from previous research involving the samples used in the present study (Baitzel and Goldstein, 2015; Becker, 2013; Goldstein, 1989a; Sharratt, 2011). These assessments were confirmed by the author using standard methods (e.g., Buikstra and Ubelaker, 1994; Hillson, 1996; White and Folkens, 2000). To minimize the effects of interobserver error in estimates of skeletal age at death, individuals were assigned to broad age categories according to the midpoint of their age ranges as derived from skeletal and dental indicators of physiological age at death: infant (0-3), child (3-12), adolescent (12-20), young adult (20-35), middle adult



(35-50), and older adult (50+). Adults who could not be assigned to a specific age category were designated adult indeterminate (21+).

### **Pre-analysis data treatments**

Basicranial and temporal bone shape data were subjected to exploratory analyses and pre-analysis data treatments to screen for the effects of measurement error and cranial modification as well as age, sex, and intertrait correlations. As described in the previous chapter, overall measurement error is sufficiently small to allow for the detection of phenotypic differences in cranial shape within the study samples (see Lockwood et al., 2002). However, the average error (see von Cramon Taubadel et al., 2007) for two landmarks, inferior nuchal crest and posterior condyle, exceeded acceptable levels of error, and they were removed from the dataset. Informal evaluation and formal analysis of cranial shape data for effects due to age, sex, and cranial modification presence found that variation in basicranial and temporal bone shape within the study sample is not significantly structured by any of these factors. No individuals exhibited levels of missing data high enough to warrant removal from the data set, but condylar foramen was removed due to excessive missing values. After its removal the data matrix was 97.8% complete. Missing landmark coordinates were estimated using the GPA mean substitution method in Morpheus (Slice, 2013).

### **Preparing data for social network analysis**

To create an individual-level adjacency matrix the Procrustes coordinates of the 14 basicranial and temporal bone landmarks were used to generate an inter-individual Mahalanobis ( $D^2$ ) dissimilarity matrix (Defrise-Gussenhoven, 1967; Defrise-

Gussenhoven and Orban-Segebarth, 1984) in XLSTAT using the Moore-Penrose Generalized Inverse for multicollinearity (Rao and Mitra, 1972). The valued (i.e., continuous) adjacency matrix was dichotomized to simplify visual representations of networks and to aid interpretation of results; additionally, certain network analytical techniques such as cliques analysis require binary data. Given that the intent is to identify close biological relatives using phenotypic data, care was given in determination of the dichotomization threshold. The breakpoint used to dichotomize the valued adjacency matrix was selected by identifying the 5th percentile of pairwise Mahalanobis distances (6.386). The smallest 5% of pairwise  $D^2$  distances were coded as relationship present (1), and the remaining 95% of inter-individual pairwise distances were coded as relationship absent (0). Though conservative, the selected breakpoint is arbitrary; it is not known which level of pairwise Mahalanobis distance effectively approximates biological relatives from non-relatives, let alone different degrees of biological relatedness. However, the selection of a conservative breakpoint establishes ties between only the most phenotypically similar actors in the study sample.

Network structure and characteristics are sensitive to the breakpoints used to dichotomize valued data sets. The specific breakpoint used to dichotomize valued data and define binary ties can have a great impact on the resulting network (Peeples, 2011; Peeples and Roberts, 2013). To evaluate the sensitivity of the selected dichotomization breakpoint, the observed distribution of inter-individual  $D^2$  distances was compared to 10 pseudo distributions of inter-individual  $D^2$  distances generated using Monte Carlo simulation. Procrustes coordinates were shuffled within columns to randomize values of

x, y, and z coordinates for each landmark by individual. The shuffled Procrustes coordinates were then used to generate an inter-individual Mahalanobis  $D^2$  matrix in XLSTAT, and the pseudo matrix was converted to a vector to facilitate comparison with the observed  $D^2$  values. This process was repeated nine times to generate 10 distributions of pseudo  $D^2$  values, and descriptive statistics were used to compare the observed and randomized distributions of  $D^2$  distance values.

The observed distribution of pairwise Mahalanobis  $D^2$  distances is distinct from the average of the 10 pseudo distributions of pairwise Mahalanobis distances (Table 12). The observed  $D^2$  values has a wider range of minimum and maximum values (7.775 vs. 5.659), a lower average value (8.286 vs. 9.130), and a greater standard deviation (1.157 vs. 0.804) compared to the pseudo  $D^2$  distances. The differences between the observed and pseudo  $D^2$  distance distributions are also apparent in the different values for the percentiles listed in Table 12 and depicted in Figure 11. The 1st, 5th, 10th, 25th, 50th, and 75th percentiles of  $D^2$  values are lower in the observed distribution compared to the average of the 10 pseudo distributions, but the 95th and 99th percentiles are nearly equivalent between the observed and average pseudo distributions. In sum, the observed distribution of pairwise distances has a greater proportion of smaller distances compared to the pseudo distributions, and this suggests that individuals in the study sample tend to be more closely related (more similar) than what would be expected by chance alone.

Table 12. Pairwise Mahalanobis ( $D^2$ ) distances based on Procrustes coordinates for 14 basicranial and temporal bone landmarks.

	Observed	Randomized Average
Minimum	4.258	6.076
Maximum	12.033	11.735
Average	8.286	9.130
Standard Deviation	1.157	0.804
1st percentile	5.635	7.175
5th percentile	6.386	7.768
10th percentile	6.784	8.086
25th percentile	7.512	8.593
50th percentile	8.297	9.149
75th percentile	9.089	9.687
95th percentile	10.237	10.415
99th percentile	10.888	10.895

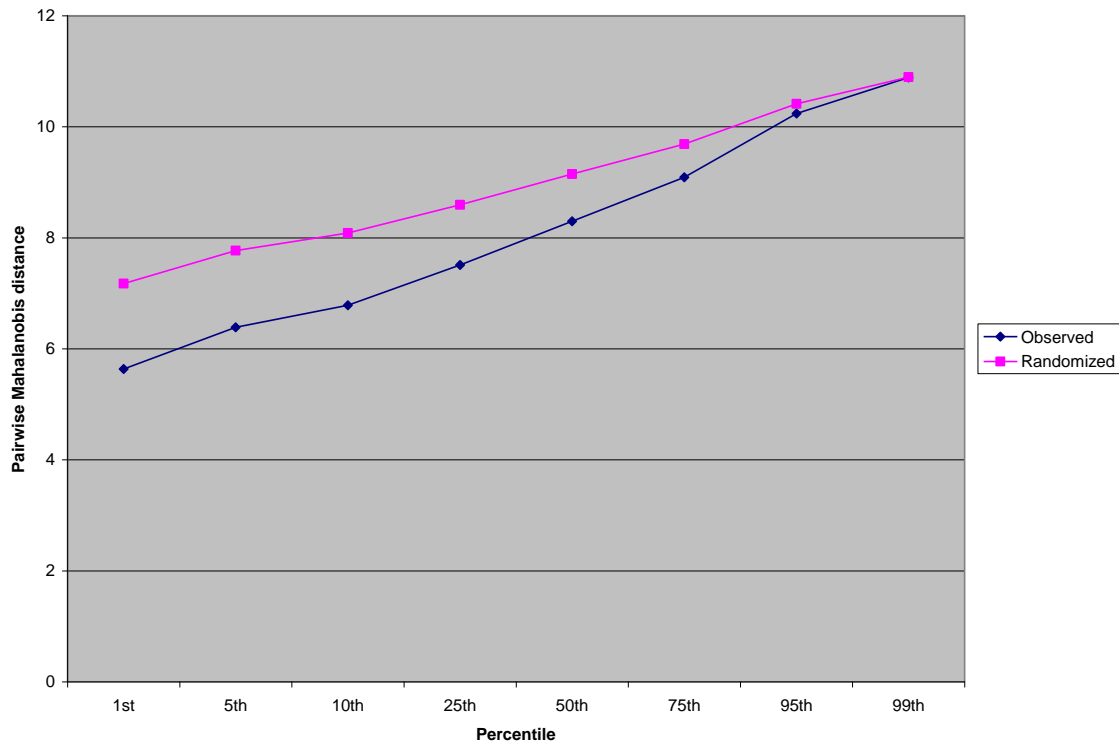


Figure 11. Observed and randomized pairwise Mahalanobis  $D^2$  distances.

Sensitivity of social network analysis results to the selected breakpoint is evaluated by repeating analytical techniques on networks created using different breakpoints to binarize the data and comparing the results. Comparative networks were created using several alternative breakpoints identified by using the 10th and 25th percentiles of observed Mahalanobis  $D^2$  values. Following Peeples (2011), an additional alternative breakpoint of 8.326 was generated by taking the average of the pseudo  $D^2$  distances minus one standard deviation of the distribution of the pseudo  $D^2$  distances. Similarities and differences in network and node properties, network structure, and subgroup analysis for the different breakpoints are presented and considered below (see RESULTS).

### **Social network analysis**

Social network analysis is applied to cranial base and temporal bone shape data for two objectives. First, SNA will provide a sense of overall connectedness (i.e., phenotypic similarity) in the study sample. This will be done using visualization, network measures of cohesion, and analysis of overall network structure (e.g., components). Second, SNA techniques are used to identify potential kin-groups (i.e., close biological relatives) based on phenotypic similarity. This will be done two ways: 1) using measures of node centrality to identify the most connected actors and visualizing the ego networks for these individuals, and 2) using formal subgroup analysis to identify clusters of nodes. All network analyses reported here were conducted using the UCINET 6.610 software package (Borgatti et al., 2002), while visualizations were completed using Netdraw version 2.158 (Borgatti, 2002).

*Network cohesion and structure.* Graph theoretic layout is used to visualize the dichotomized  $D^2$  matrix of individual pairwise distances. The graph theoretic layout algorithm in UCINET aids interpretability of network graphs by optimizing three criteria simultaneously: correspondence between point distance and path distance between nodes, maintaining sufficient space between nodes so they do not obscure one another, and a preference for equal-length lines (Hanneman and Riddle, 2005). The result produces a layout that tends to be more readable and aesthetically pleasing than one based on ordination or node attributes.

To evaluate the extent of connectedness within the network a number of measures of cohesion are calculated using UCINET. The simplest measure of cohesion is density; for binary data this is simply the number of ties in the network divided by the number of possible ties. Other measures of cohesion reported below include connectedness and clustering coefficient.

Connectedness is the proportion of pairs of nodes that can reach each other by a path of any length. It is calculated by subtracting the value of fragmentation, the proportion of pairs of vertices that are unreachable, from one. The higher the connectedness value, the more reachable pairs of vertices there are in the network.

Clustering coefficient provides a measure of the extent to which nodes form tightly knit groups characterized by a relatively high density of ties. UCINET calculates the clustering coefficient of every actor, the overall clustering coefficient of the network, and the weighted clustering coefficient of the network. The clustering coefficient of an actor is the density of its open neighborhood. The overall clustering coefficient is the

mean of all actors' clustering coefficients. The weighted overall clustering coefficient weights the neighborhood densities proportional to their size (Hanneman and Riddle, 2005). The weighted overall clustering coefficient is equivalent to the transitivity coefficient (Watts, 1999). Transitivity is the extent to which nodes that share a link also share links with a third node. Networks with high transitivity tend to have a clumpy structure as they contain knots of nodes that are all interrelated.

Overall network structure is evaluated by decomposing the network into components. In graph theory, a component of a graph is a maximally connected sub-graph (Borgatti et al., 2013; Scott, 2013). In other words, components are sections of a network within which every node can reach every other node but between these sections there are no connections. Two vertices are members of the same component if there is a path connecting them. Isolates within the network are considered components. The Components and Multiple cohesion measures routines in UCINET are used to identify the number of components in the network, the size of the largest (i.e., main) component, and the number of isolates.

***Kin group identification.*** Potential kin networks are identified using two different approaches. Centrality scores are assessed for all actors, and the ego-networks of those actors with the highest centrality scores are visualized. Centrality is a measure of how connected a node is. In sociological terms it is often interpreted as a measure of an actor's influence or power within a network (Scott, 2013). Degree centrality simply reflects the number of ties (connections) a given node has. If the network is comprised of kinship (or friendship) ties, then degree centrality indicates the number of relatives (or friends) a

node has (Hanneman and Riddle, 2005). However, degree centrality does not account for the centrality scores of the actors within ego's neighborhood. An actor connected to a number of other highly connected actors has greater potential influence within a social network compared to an actor connected to a number of actors with only a single or few ties. Eigenvector centrality is a variation of degree centrality that weights a node's centrality score by the degree centralities of the nodes to which it is connected (Bonacich, 1972; Newman, 2004; Whitehead, 2008). Thus, eigenvector centrality provides a sense of a node's connectedness relative to the overall pattern of connectedness in the network (Mizoguchi, 2013). These two measures of centrality are calculated using UCINET.

Individual actors with high centrality scores will have their ego-networks visualized using NetDraw (Borgatti, 2002) and evaluated as potential (biological) kin networks. Ego network graphs depict a specific actor (ego) embedded within the actor's one-step neighborhood, which refers to all nodes with whom ego has a direct connection. The ego network also depicts any ties between the nodes in ego's neighborhood (Hanneman and Riddle, 2005).

A more formal approach to identifying potential kin groups is performed using sub-group analysis. As stated above, a subgroup is a section of the network in which actors interact more often with (or are more similar to) one another than they do (or are) with actors who are not in the group. There are two different approaches to sub-group analysis. One can start with a formal definition of a subgroup and identify all examples of that type of subgroup in the network, or one can use an algorithm to identify subgroups based on certain network characteristics. Examples of the former include cliques, clans,



and k-plexes, whereas the Girvan-Newman algorithm and factions technique are examples of the latter (Borgatti et al., 2013; Scott, 2013).

The present study will use cliques and n-cliques for subgroup analysis because these are based on more conservative (restrictive) definitions of subgroups, and the intent here is to assess the utility of social network analysis for identifying clusters of close biological kin. A clique is defined as a “maximal complete subgraph” (Luce and Perry, 1949; Harary, 1969; Scott, 2013). Thus, a clique is a subset of nodes in which every possible pair of nodes is directly connected by an edge (i.e., line) and the clique is not contained in any other clique. Whereas a component is maximal and connected (i.e., all points are connected to one another through paths), a clique is maximal and complete - all points are adjacent (i.e., directly connected) to one another (Scott, 2013: 113). A clique is a suitable proxy for a kin group based on close biological relatedness because each member of a clique must be directly connected to every other member (Luce and Perry, 1949).

The Cliques routine in UCINET implements the Bron and Kerbosch (1973) algorithm to find all Luce and Perry (1949) cliques of a specified size and greater. Cliques of size 2 will identify every maximal subgraph including dyads, but cliques of such small size are unlikely to be helpful in the identification of extended family groups. For this reason cliques of size seven or greater will be used to identify potential kin groups.

In dense networks there are often multiple overlapping cliques, which complicates interpretation of meaningful subgroup structure. Clique composition is assessed to identify

whether there are central actors who appear in multiple cliques of the same size. UCINET provides secondary cliques analyses to facilitate interpretation. As part of its Cliques routine, UCINET generates actor and clique co-membership matrices that are submitted to hierarchical clustering procedures. These help reveal features of clique structure when there are numerous cohesive subgroups, and they should identify non-overlapping nested clusters of actors if these exist in the network (Borgatti et al., 2013; Hanneman and Riddle, 2005).

The concept of cliques has been characterized as an overly rigid and restrictive approach to subgroups in social network analysis, as groups in which every member is directly connected to every other member are uncommon in real world social networks (Borgatti et al., 2013; Scott, 2013). A number of more flexible definitions of subgroups have been proposed, including n-cliques (Mokken, 1979; Seidman and Foster, 1978a,b). With an n-clique an actor is identified as a member of a clique if he/she is connected to every other member of the group at a specified distance, where n stands for the length of the path allowed between all members (Mokken, 1979). Thus, n-cliques are subgroups comprised of members who share direct and indirect connections. Typically, a path distance of two is used (i.e., 2-cliques), which for a friendship network would correspond with a friend of a friend. For a network based on phenotypic similarity, the use of 2-cliques could allow for the identification of clique members who represent more distantly related kin (e.g., cousins) or affines. Other alternatives to cliques (e.g., plexes) may be excessively flexible for the purposes of the present study, as they loosen the criteria for

subgroup membership too much, so that potentially every connected node (i.e., non-isolate) in the network will be identified as a member of the subgroup.

N-cliques analysis is used in the present study to supplement the more conservative cliques analysis. The N-Cliques routine in UCINET identifies these subgroups within networks and performs over-lap analysis of n-cliques membership (Hanneman and Riddle, 2005). The effects of dichotomization breakpoint on clique and 2-clique number and composition are discussed.

### **Models**

To aid interpretation of results of social network analysis a set of hypothetical network configurations are presented. These heuristics are assumed to reflect different patterns of gene flow, population structure, and the presence and distribution of biological lineages.

***Null model.*** Within this scenario all actors are equidistant, reflecting a pattern of random interactions with no underlying network structure. This hypothetical network is comprised of one large, maximally dense (i.e., fully connected) component. There are no subgroups present as all actors are equally central and adjacent to all other actors.

***Site-based kin structuring model.*** This hypothetical network reflects kin structuring within sites. The overall network partitions into five or more components that represent the sites from which the study sample is drawn. Within these components subgroups suggestive of distinct biological lineages are present. Certain actors are likely to be more central than others given the degree of network structure and the presence of subgroups.

***Regional family networks model.*** This hypothetical network is comprised of one or more components that are not closely associated with the various sites in the study sample. Multiple subgroups are present, and these subgroups are comprised of actors from different sites and different ethnic communities. Thus, kin-based social networks are present, and these collectives cross site and ethnic boundaries. The subgroups (biological lineages) may be discrete, but it is likely they will be linked by one or several highly central individuals who serve to bridge different lineages.

### **Cluster analysis and multidimensional scaling**

To compare the results of social network analysis with those of analytical techniques more frequently used in bioarchaeological kinship analysis, cluster analysis and multidimensional scaling were applied to the inter-individual Mahalanobis  $D^2$  matrix calculated from the Procrustes coordinates of 14 basicranial and temporal bone landmarks. XLSTAT was used to perform an agglomerative hierarchical clustering analysis using unweighted pair-group average to generate clusters of close biological relatives. Metric MDS using 10 repetitions and 1000 iterations was performed using XLSTAT to provide an additional means of visualizing the data and identifying potential biological kin groups. MDS was performed from two to eleven dimensions to evaluate the distortion associated with the decrease in dimensions. XLSTAT generates a Shepard diagram to aid assessment of the reliability of the MDS map. This diagram plots the observed dissimilarities as the x-coordinates and the distance on the configuration generated by the MDS as the y-coordinates. The greater the spread is between the points, the less reliable the MDS.

## RESULTS

### Network structure and properties

The graph theoretic layout of the inter-individual Mahalanobis  $D^2$  matrix dichotomized at the 5th percentile of pairwise distances presents a network comprised of a rather densely interconnected core and a number of less well-connected nodes and isolates (Fig. 12). Overall, the network has low levels of cohesion (Table 13). Network density is quite low with only 5.1% of all possible ties actually present (0.0510,  $p=0.843$ ) and each node having an average of 5.06 ties (average degree=5.059). This is due in part to the 36 isolates, which represents a rather large proportion of the overall sample (Table 14).

The overall clustering coefficient of 0.530 reflects the presence of neighborhoods with comparatively high levels of density. The weighted overall clustering coefficient of 0.375 reflects how the large numbers of isolates and weakly connected nodes affect the overall network density. The connectedness value of 0.416 indicates there is a large proportion of node pairs that are not connected in the network, again reflecting the large number of isolates and minimally connected nodes.

The various network measures are sensitive to the particular breakpoint used to binarize the valued inter-individual Mahalanobis distance matrix. As the threshold for considering a tie as present is relaxed (i.e., the pairwise distance increases), all measures of network cohesion increase (Table 13). This pattern is consistent regardless of the dichotomization breakpoint used.

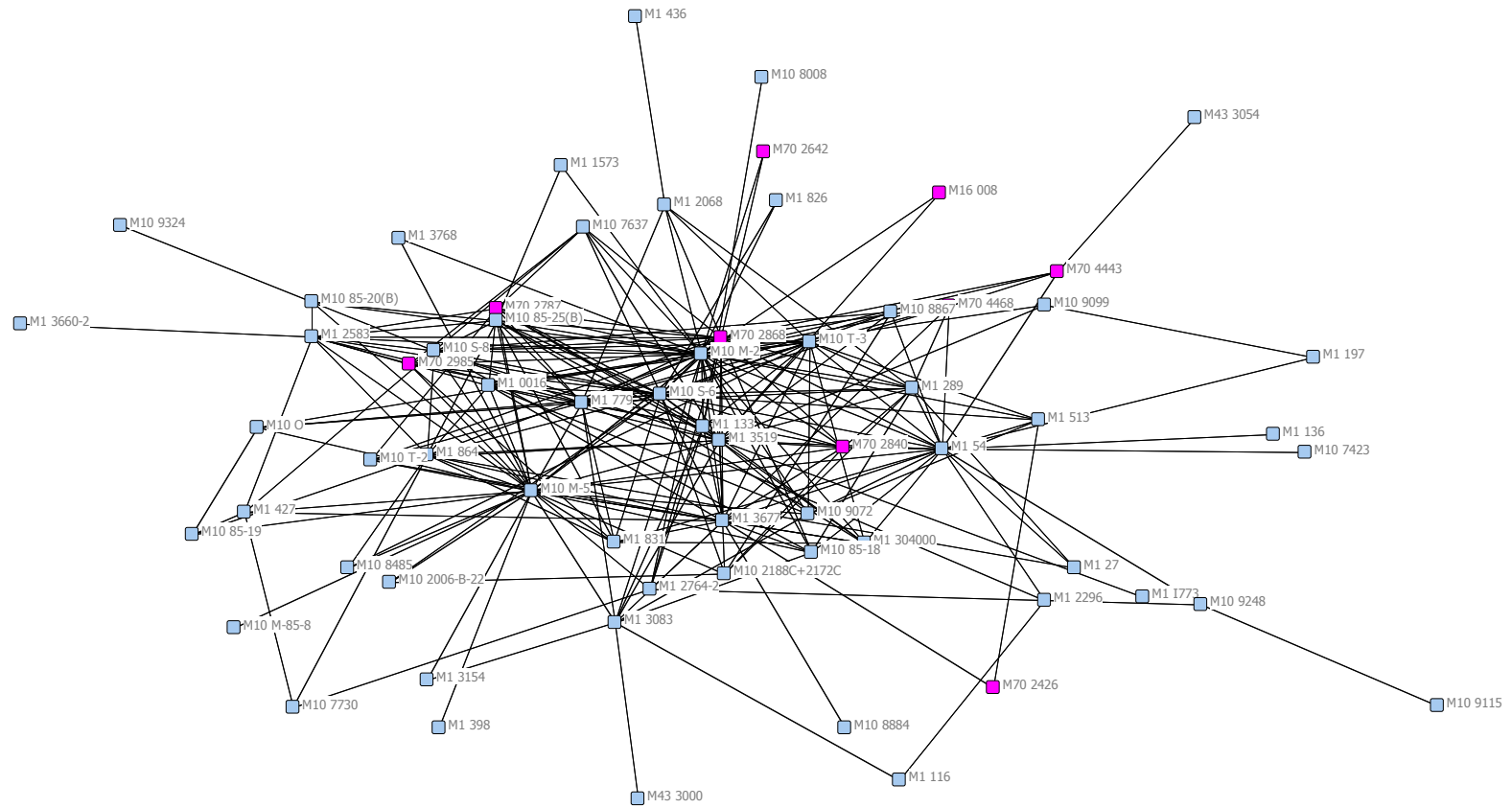


Figure 12. Graph theoretic layout of the dichotomized  $D^2$  distance matrix (isolates inactive). Pink indicates actors from Omo-style contexts, and blue represents actors from Chen Chen-style contexts.

Table 13. Measures of network cohesion at different dichotomization breakpoints.

Network measure	Mahalanobis D <sup>2</sup> distance dichotomization breakpoint			
	6.386 (5 <sup>th</sup> )	6.784 (10 <sup>th</sup> )	7.512 (25 <sup>th</sup> )	8.326 <sup>a</sup>
Density				
Value	0.050	0.100	0.250	0.511
No. ties	516	1030	2576	5266
SD	0.218	0.300	0.433	0.500
Average Degree	5.059	10.098	25.255	51.627
Alpha	0.843	0.919	0.971	0.991
Connectedness	0.416	0.629	0.904	0.961
Clustering coefficient				
Overall value	0.530	0.691	0.740	0.808
Weighted value	0.375	0.435	0.553	0.725

<sup>a</sup>Dichotomization breakpoint based on the average of the 10 pseudo distributions minus the average of the standard deviations of the 10 pseudo distributions.

Overall there is limited structure within the network. Components analysis identified a total of 37 components, with one main component comprised of 66 actors along with 36 isolates (Table 14). This type of structure is characteristic of relatively dense social networks (Scott, 2013). Analysis of network structure presents a pattern consistent with the character of the network obtained through visualization and measures of network cohesion.

This overall configuration of network structure is robust and maintained regardless of the breakpoint used to dichotomize the valued inter-individual Mahalanobis D<sup>2</sup> distance matrix (Table 14). With more inclusive dichotomization thresholds, the number of isolates – and therefore the number of components – decreases, and the size of the main component increases. At the most inclusive breakpoint (8.326), there are only

three components, with a main component consisting of 100 nodes and two isolates (M1 306025 and M70 2956).

Table 14. Network structure (components) at different dichotomization breakpoints.

Network structure	Mahalanobis $D^2$ distance dichotomization breakpoint			
	6.386 (5 <sup>th</sup> )	6.784 (10 <sup>th</sup> )	7.512 (25 <sup>th</sup> )	8.326
Components				
Number	37	22	6	3
Size of largest	66	81	97	100
Isolates	36	21	5	2

### Identification of potential kin groups

*Node centrality and ego networks.* Degree centrality and eigenvector centrality scores are presented in Appendix E. As indicated above, the average degree centrality is 5.059, with a range from 0 (isolates) to 36 for M10 M-2. The average eigenvector centrality score is 0.060, with a range from 0.000 to 0.328 (M10 M-2).

Measures of node centrality are robust to different dichotomization breakpoints (Table 15). The 10 actors with the greatest degree and eigenvector centrality scores are nearly identical regardless of the breakpoint used to binarize the adjacency matrix, although an actor's specific ranking within the top 10 varies depending on the dichotomization breakpoint used. Overall, as the threshold for establishing a tie between nodes becomes more inclusive, the distribution of degree and eigenvector centrality scores flattens out as more nodes are highly connected within the network.



Table 15. Centrality scores for select<sup>a</sup> actors at different dichotomization breakpoints.

ID	Mahalanobis D <sup>2</sup> distance dichotomization breakpoint			
	6.386 (5 <sup>th</sup> )	6.784 (10 <sup>th</sup> )	7.512 (25 <sup>th</sup> )	8.326 <sup>a</sup>
M10 M-2	36 (0.328) <sup>b</sup>	53 (0.272)	78 (0.197)	94 (0.144)
M10 M-5	33 (0.293)	48 (0.256)	72 (0.189)	95 (0.145)
M10 S-6	27 (0.287)	40 (0.233)	71 (0.188)	91 (0.142)
M1 3519	25 (0.263)	35 (0.213)	64 (0.178)	92 (0.143)
M70 2868	24 (0.267)	40 (0.238)	63 (0.181)	89 (0.140)
M1 54	23 (0.21)	46 (0.25)	70 (0.187)	90 (0.143)
M1 3677	21 (0.226)	31 (0.178)	63 (0.171)	86 (0.139)
M1 779	18 (0.191)	33 (0.209)	60 (0.177)	86 (0.139)
M10 T-3	15 (0.18)	32 (0.197)	58 (0.171)	85 (0.139)
M1 2583	14 (0.165)	22 (0.148)	47 (0.148)	80 (0.133)

<sup>a</sup>These 10 actors have the highest degree and eigenvector centrality scores for the adjacency matrix dichotomized at the 5th percentile.

<sup>b</sup>Eigenvector centrality scores are in parentheses.

The ego network graph for M10 M-2, the actor with the highest centrality scores, is presented in Figure 13. If the 5th percentile of pairwise Mahalanobis distances used to dichotomize the valued adjacency matrix effectively distinguishes close biological relatives from nonrelatives, then this graph depicts the kin network of M10 M-2. The majority of actors in this ego network are from M1, M10, and M70, with only a single individual from M16 and no actors from M43.

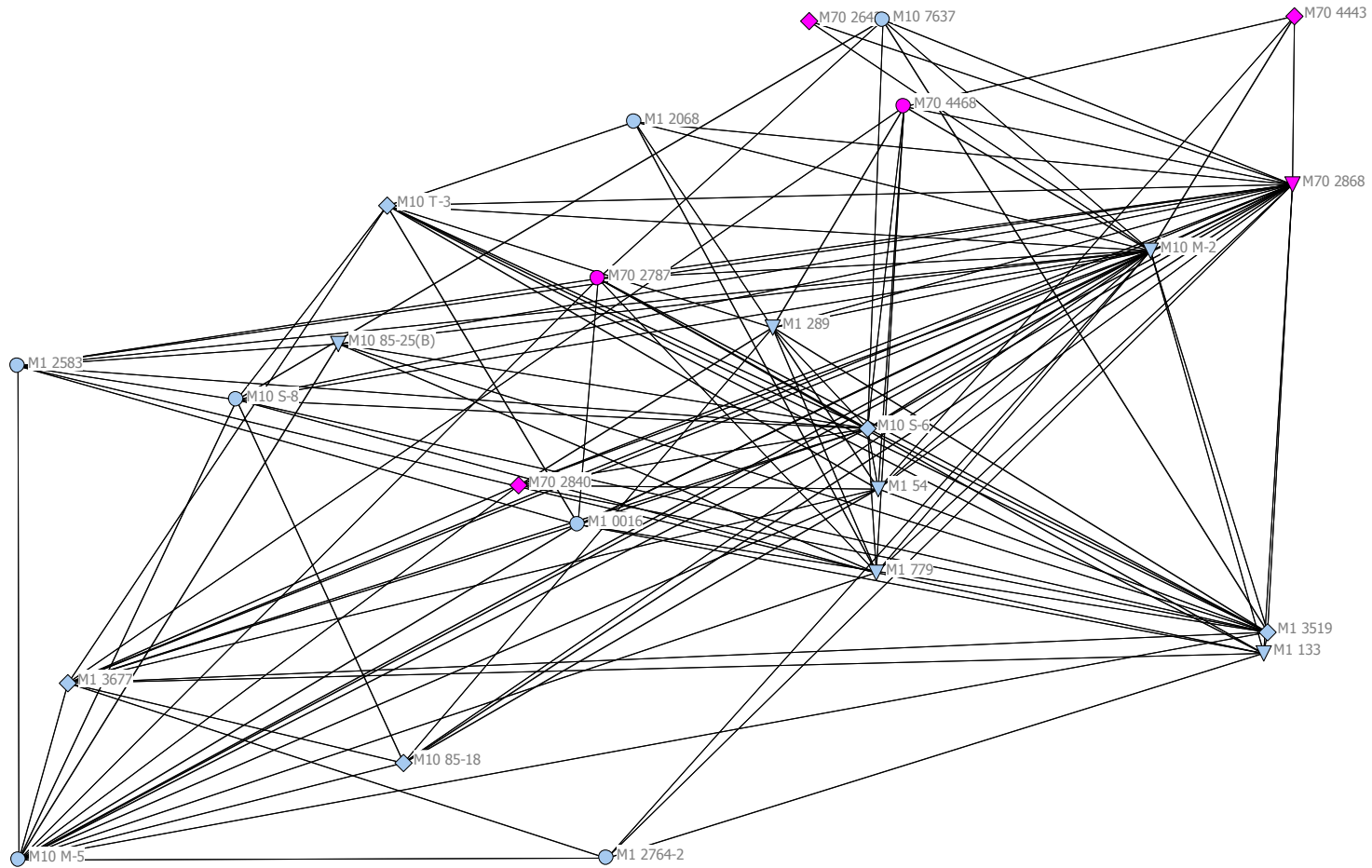


Figure 13. Ego network of M10 M-2. Node color reflects maximal *ayllu* affiliation of the mortuary context (blue – Chen Chen-style site, pink – Omo-style site), and node shape represents skeletal sex (circle – female, diamond – male, upside down triangle – sex undetermined).

Comparing this ego network to those for the next four actors with the greatest centrality scores (M10 M-5, M10 S-6, M1 3519, and M70 2868) reveals the extent of overlap among these actors' ties. Table 16 presents the number of actors who are co-members of these highly central actors' ego networks. The diagonal represents the total number of ties (or close biological relatives) an actor has (i.e., degree centrality). M10 M-2 has 22 actors (relatives) in common with M10 M-5, M10 S-6, and M70 2868 and 20 actors in common with M1 3519. M70 2868 has 22 of 23 possible actors in its kin network (95.7%) that are also in the kin network of M10 M-2.

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Table 16. Matrix of actor overlap among the ego networks of highly central actors.

	M10 M-2	M10 M-5	M10 S-6	M1 3519	M70 2868
M10 M-2	36	22	22	20	22
M10 M-5	22	33	19	16	15
M10 S-6	22	19	27	17	16
M1 3519	20	16	17	25	15
M70 2868	22	15	16	15	24

Informal appraisal of ego network graphs for each non-isolate actor in the study reveals how difficult it is to identify an ego network that does not include one of the top five central actors. There are several examples of ego networks comprised of a single dyad or triad, but activating the ego network for the other members of the dyad or triad reveals, without exception, that at least one of those actors is adjacent to one of the top five actors in centrality. For example, the ego network for M1 436 includes only M1 2068, but the ego network for M1 2068 includes M10 M-2 and M70 2868. Additionally, M1 116 is in a triad with M1 3083 and M1 2296, but M1 3083 is adjacent to M10 M-2,

M10 M-5, and M1 3519. The fact that nearly isolated nodes are a path distance of two from some of the most central nodes in the network reflects the high degree of cohesion within the main component and accounts for the extent of overlap among ego networks.

***Subgroup analysis.*** The number of cliques identified varies greatly depending upon the clique size specified (Appendix E). There is one clique of size eight and 14 cliques of size seven. The members of the maximum clique (M1 54, M1 3519, M1 3677, M10 M-2, M-10 M-5, M10 S-6, M70 2840, and M70 2868) are all adjacent to one another and therefore may represent a cluster of close biological relatives. Among these individuals are one female (M10 M-5), four males (M10 S-6, M1 3519, M1 3677, and M70 2840), and three individuals of undetermined skeletal sex (M10 M-2, M70 2868, and M1 54).

There is a considerable amount of overlap in clique membership at clique size seven, as the membership of these 15 cliques consists of only 19 different actors. Not surprisingly, these are 19 of the 20 individuals with the highest degree and eigenvector centrality scores (Appendix E). M10 M-2 is a member of all 15 cliques, while M10 S-6 is a member of 14 cliques. Rather than identifying several distinct cliques that might be interpreted as distinct lineages or kin groups, these results suggest there is a core group of biological relatives who function to connect the main component in the network. It is interesting to note that these actors are from only three sites (M1, M10, and M70), and they include five females, six males, and 8 individuals of undetermined skeletal sex.

Hierarchical clustering of the clique overlap matrix (Fig. 14) indicates two main divisions among the 15 cliques: cliques 3, 8, 9, 10, and 11 vs. cliques 1, 2, 4, 5, 6, 7, 12,

13, 14, and 15. However, even this partition of cliques is joined at level 3.360, which suggests these two clusters do not represent a clear separation into distinct groups of cliques (or actors). For example, clique 8 has at least two actors in common with each of the cliques in the other cluster.

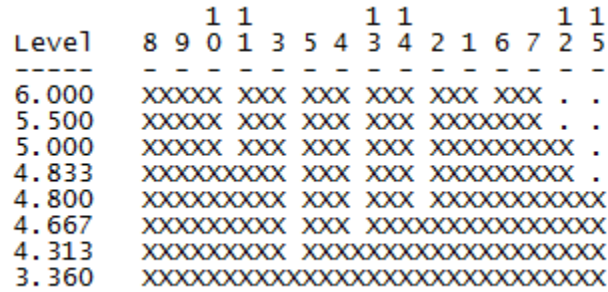


Figure 14. Hierarchical clustering of the clique overlap matrix, clique size seven.

The inclusion of nodes connected indirectly as part of n-cliques analysis (n=2) results in the identification of a greater number of cliques (Table 17). To simplify interpretation the minimum clique size was increased to reduce the number of identified cliques. At 2-cliques size 30, 32 2-cliques were identified. At 2-cliques size 37 a single 2-clique was found. Members of the 2-cliques identified for 2-cliques of sizes 30 and 37 are listed in Appendix E.

The number and size of cliques and 2-cliques are sensitive to the dichotomization breakpoint applied to the valued adjacency matrix (Table 17). Two trends are observable as more inclusive breakpoints are used to binarize the valued matrix. First, the number of ties identified among nodes increases and results in a greater number of identified cliques. For example, in the network created using the 5th percentile breakpoint there are 15 cliques at clique size seven compared to 118 cliques of size seven identified in the

network created using the 10th percentile as the dichotomization breakpoint. Second, as more inclusive breakpoints are used to dichotomize the valued adjacency matrix (e.g., 10th and 25th percentiles) cliques of greater size (i.e., number of members/actors) are identified. For example, the maximal clique found using the 5th percentile as the breakpoint is eight actors. The maximal clique found using the 10th percentile as the breakpoint is 12 actors, and the maximal clique found using the 25th percentile as the breakpoint is 20 actors. This trend is even more pronounced when subgroups of interest are n-cliques. As the dichotomization breakpoint becomes more inclusive, the number of n-cliques quickly becomes unwieldy making identification and interpretation of patterns difficult.

Table 17. Subgroups found at different clique sizes and dichotomization breakpoints.

Subgroup type	Mahalanobis D <sup>2</sup> distance dichotomization breakpoint		
	6.386 (5 <sup>th</sup> )	6.784 (10 <sup>th</sup> )	7.512 (25 <sup>th</sup> )
Cliques found			
Size 3	86	186	723
Size 5	64	161	714
Size 7	15	118	698
Size 8	1	*	*
Size 9	0	64	669
Size 10	-	22	*
Size 11	-	2	627
Size 12	-	1	*
Size 13	-	0	461
Size 15	-	-	266
Size 17	-	-	132
Size 19	-	-	22
Size 20	-	-	2
Size 21	-	-	0
2-cliques found			
Size 3	61	86	*
Size 5	60	86	*
Size 7	59	86	*
Size 9	58	85	*
Size 11	*	84	*
Size 13	*	*	*
Size 19	*	*	*
Size 30	32	82	*
Size 35	4	*	*
Size 36	1	*	*
Size 37	1	*	*
Size 50	0	13	*

\*Subgroup analysis was not run at the specified size.

### Cluster analysis and multidimensional scaling

Agglomerative hierarchical clustering (AHC) identified 57 clusters: 42 singletons, 11 dyads, two triads, one cluster of six, and one large cluster of 26 individuals (Fig. 15, Appendix E). This suggests there are 15 distinct potential kin groups within the study

sample, although 13 of these are dyads or triads. Nine of the 15 clusters (60%) are comprised of individuals from multiple sites, including three clusters comprised of individuals from sites associated with different ethnic communities. This pattern of multiethnic social groups is consistent with the results of social network analysis and with results presented in Chapter 3. The largest cluster, Cluster 1, includes individuals from M1, M10, and M70, while the second largest cluster, Cluster 2, includes only individuals from the Chen Chen-affiliated sites of M1 and M10.

These results are comparable to the overall structure of the social network, in terms of both the number and composition of components, created using the 5th percentile of  $D^2$  distances as the dichotomization breakpoint. The list of individuals in Cluster 1 (Appendix E) shares a high degree of overlap with the individual members of the various subgroups identified through cliques and n-cliques analysis. For example, all members of Cluster 1, the largest cluster, are also members of the maximal clique (i.e., clique of size eight), and 18 of the 19 core individuals identified in cliques analysis at clique size seven are members of Cluster 1. M1 133 is the only one of these 19 core actors who is not a member of Cluster 1, but this individual is a member of Cluster 2, the second-largest cluster. Only three of the 21 core individuals identified in 2-cliques analysis at clique size 30 are not members of Cluster 1: M1 3083 (Cluster 2), M10 O (Cluster 4), and M10 85-18 (Cluster 12). Of the 37 members of the single clique identified using 2-cliques analysis at 2-cliques of size 32, 22 (59.5%) are members of Cluster 1 and three (8.1%) are members of Cluster 2.



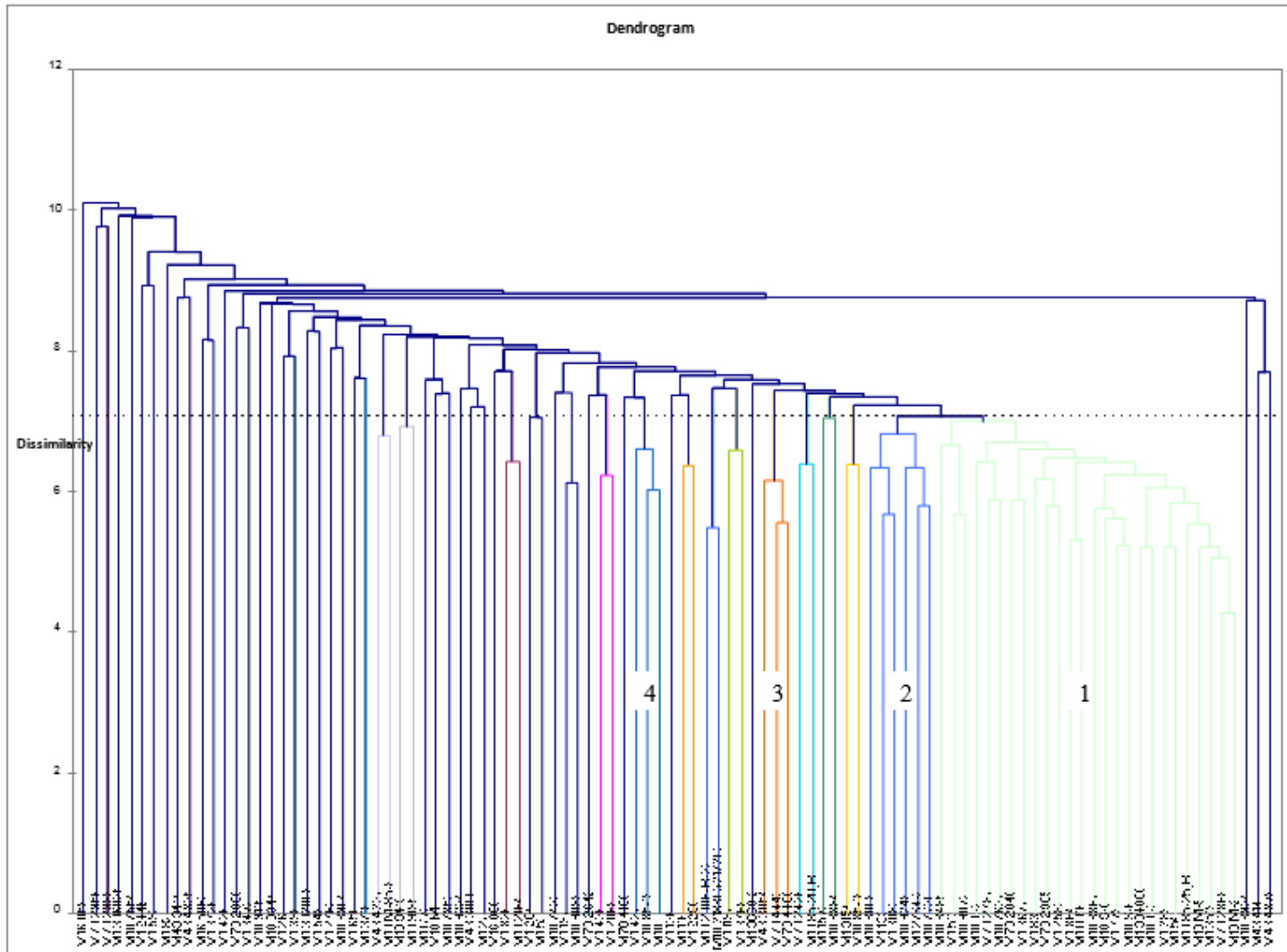


Figure 15. Dendrogram of hierarchical cluster analysis. Clusters of three or more individuals are indicated by Cluster number.

MDS was less successful at partitioning the sample into distinct clusters. A scatter plot of the first three dimensions of the MDS (Kruskal's stress = 0.305) depicts several clusters of two or three individuals, but no larger clusters are apparent at this scale of representation (Fig. 16). The Shepard diagram provides further evidence that the first three dimensions poorly represent the original data (Fig. 17). In fact, Kruskal stress scores for the MDS do not reach acceptable levels (i.e.,  $< 0.2$ ) until the first six dimensions are included (Fig. 18). While use of the first six dimensions from the MDS might facilitate the identification of large, discrete clusters of individuals, it is not possible to graphically visualize six dimensions. These results suggest both social network analysis and agglomerative hierarchical clustering are better equipped to identify subgroups of individuals within an archaeological sample drawn from a series of sites that likely experienced moderate levels of gene flow structured both by ethnic and kin-based affiliations.

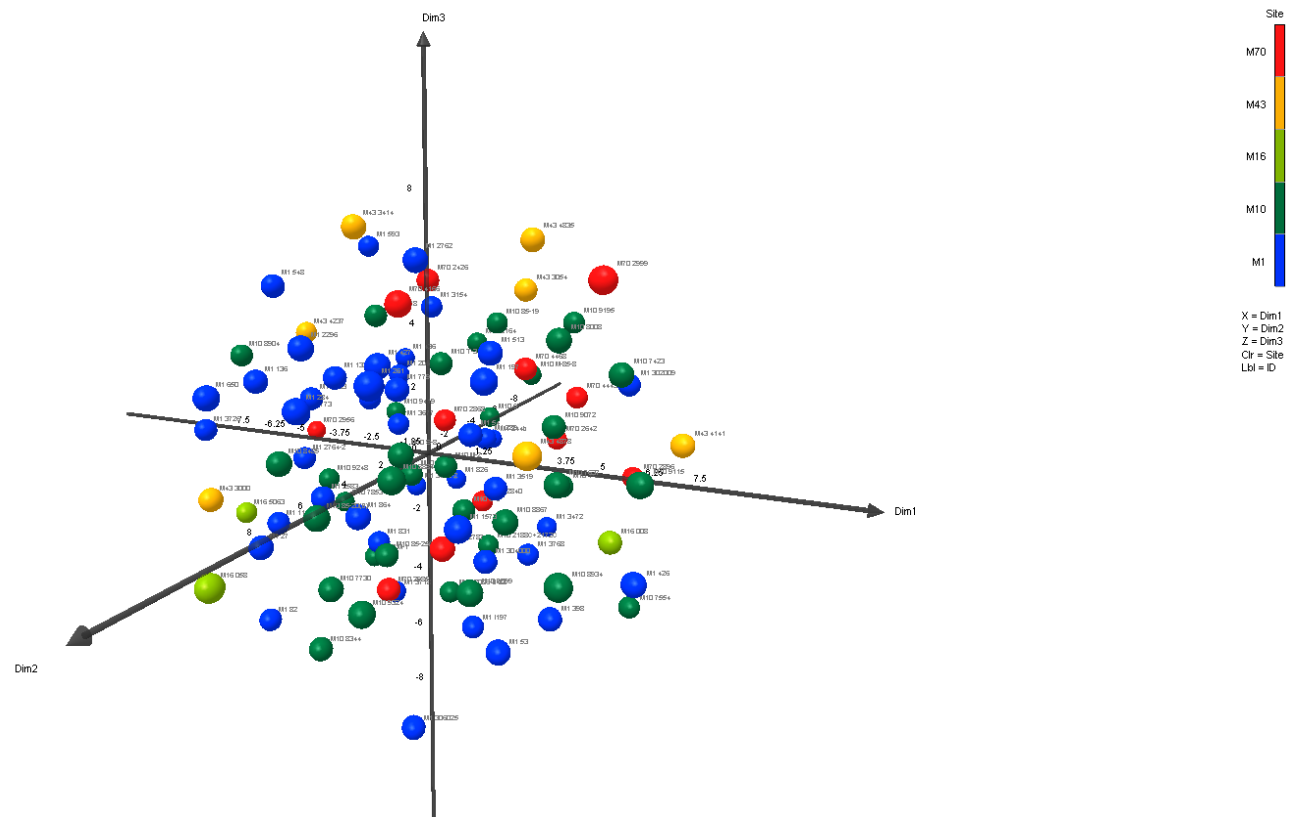


Figure 16. Scatter plot of MDS results in 3-dimensional representation space (Kruskal's stress = 0.305).

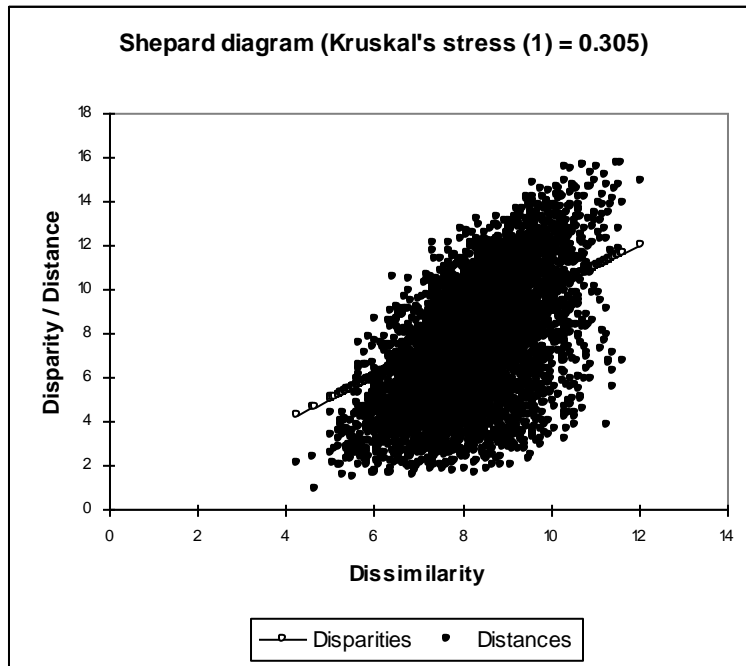


Figure 17. Shepard diagram of MDS at 3-dimensional representation space.

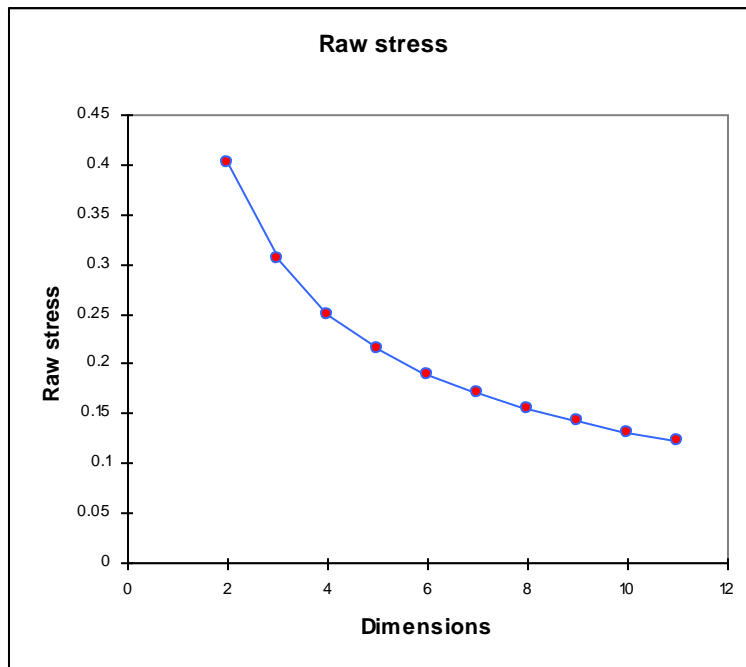


Figure 18. Kruskal's stress level of MDS by dimensions.

## DISCUSSION

Overall, the results of graph visualization, network measures, and network structure indicate the study sample from the Moquegua Tiwanaku colonies constituted a social network comprised of a dense main component and a number of isolated actors. In terms of the original data, this suggests there is a high degree of similarity in basicranial and temporal bone shape among a large proportion of the study sample and a number of individuals who are distinct in cranial shape. The large main component is likely attributable to high levels of gene flow among members of these communities, particularly M1, M10, and M70, while the underlying cause for the large number of isolates is less immediately clear.

Isolates could represent in-marrying spouses (or their offspring) from other Tiwanaku-affiliated communities in the Tiwanaku heartland or from other peripheral regions. Isolates could be individuals from other societies altogether, including the indigenous Huaracane communities who resided in the Moquegua Valley, communities from the coastal Ilo Valley, or the Wari colonial outposts in the middle and upper Moquegua Valley (see Blom et al., 2004; Costion, 2009; Goldstein, 2000a; Green and Goldstein, 2009; Moseley et al., 1991; Nash and Williams, 2004; Sims, 2006; Williams, 2001). Alternatively, actors could be identified as isolates simply due to sampling bias. Without further analysis the nature of the relationship, or lack thereof, between the isolates and the remainder of the study sample will remain speculative.

Informal and formal approaches used to identify potential family groups had mixed success. It was hoped that visualizing actors' ego networks would provide a

reliable, if informal, means of identifying distinct biological lineages within the network. However, comparing more than two ego networks at a time is an inefficient way to evaluate potential kin relationships within a densely connected network with a high degree of overlap. Although not effective here, visualization of ego networks to identify kin networks could prove useful in less dense social networks that feature more than a single large component.

The more formal method for identifying potential kin groups, subgroup analysis, proved more useful to an extent. While there is no clear partition of the network into distinct subgroups that could represent different extended kin networks or biological lineages, there appears to be a cluster of closely related individuals at the core of the network who anchor an interconnected web of less closely related actors. It is unclear whether the inability to partition the network into distinct biological family groups simply reflects the extent of gene flow within the Tiwanaku-affiliated communities of Moquegua or is a product of one or more confounding factors such as the social network methods used, the selected proxy for genetic relatedness (basiscranial and temporal bone shape), or the amount of time represented by the study sample.

The overall pattern of network and subgroup structure does not clearly fit any of the heuristic models described above. Instead, the observed pattern seems to combine aspects of the null model (a large, dense main – but not maximal – component) and the regional family networks model (one potential extended kin group that crosses site and ethnic boundaries). This core group of potential kin identified through subgroup analysis – and agglomerative hierarchical clustering – could be similar to what Hamberger and

colleagues (2011: 538) describe in formal kinship network terms as a consanguineous component: “a maximal set of individuals linked to each other by consanguineous paths.”

The demographic composition of this core group of potential kin reflects a fairly equivalent sex distribution with five females, six males, and eight individuals of undetermined skeletal sex. The presence of males and females from M1, M10, and M70 in this potential extended kin group suggests that post-marital residence practices could have been ambilocal or neolocal. Although ambilocal and neolocal post-marital residence patterns are less common than patrilocal and matrilocal practices, ethnographic accounts from the Andes describe flexible post-marital residence strategies consistent with ambilocality (e.g., Abercrombie, 1986; Allen, 1988; Bandelier, 1911; Cobo, 1979 [1653]; Isbell, 1978; Izko, 1986; Rasnake, 1988; Rowe, 1946).

### **Translating networks to families**

It is important to reiterate that the networks visualized and the subgroups identified in the present study do not reflect real social networks (Östborn and Gerding, 2014). The social networks depicted identify the potential for social relationships based on the selected criterion of similarity in basicranial and temporal bone shape as a proxy for genetic relatedness. Several issues limit the inferential power of the study results and complicate attempts to identify family groups using social network analysis. First, the time depth represented by the samples, a span of 300-400 years, means that individuals who are phenotypically quite similar and appear to have been close biological relatives may not have been contemporaries. However, recent considerations of postmortem agency (e.g., Crandall and Martin, 2014; Velasco, 2014) and the role of the ancestors in

Andean societies past and present (e.g., Buikstra, 1995; Lau, 2008; Shimada and Fitzsimmons, 2015) suggest noncontemporaneity does not preclude social relationships among actors.

Second, it is unclear how important biological relatedness was to pre-Hispanic conceptions of family and social relatedness (Lozada, 2011b). If biological relatedness was not positively correlated with social relatedness and social interaction, then actors identified as sharing an edge within the network may have had limited or zero social interactions during their lives. Similarly, individuals identified as isolates within a social network based on phenotypic data may have been highly central actors within Moquegua Tiwanaku communities according to other criteria. As the objective is to identify potential family groups, it is critical to consider how relatedness was conceptualized within the communities of interest.

Andean ethnographic and ethnohistoric research suggest a certain flexibility in the way kin groups are constituted through daily practices, marriage patterns, post-marital residence practices, and rules of descent and inheritance (Abercrombie, 1986, 1998; Bastien, 1978; Harris, 1978; Isbell, 1978; Murra, 1972; Platt, 1982; Rasnake, 1988; Urton, 1990; Van Vleet, 2008), but it is unclear to what extent similar practices characterized earlier Andean communities. Given the impact of Inka imperialism, Spanish colonization, and participation in the global marketplace, patterns of social organization among historical and recent Andean populations cannot be simplistically applied to archaeological contexts (e.g., Isbell, 1997; Stanish, 1989, 1992). Instead, their use within specific contexts must be carefully evaluated.



Using ethnographic data to predict the extent to which degree of biological relatedness corresponded with social closeness among Moquegua Tiwanaku colonial communities is complicated by the fact that Tiwanaku-affiliated settlements in Moquegua were comprised of communities of both Omo-style camelid agropastoralists and Chen Chen-style intensive agriculturalists. Among non-Western contemporary societies, agropastoralism and intensive agriculture are associated with different marriage, kinship, co-residence, and friendship patterns. Hill and colleagues (2011) found that modern hunter-gatherer bands are comprised of a large percentage of biologically unrelated individuals, contrary to long-standing assumptions that foraging bands (past and present) are composed of biological kin groups (Service, 1962). Such findings are consistent with the wide-ranging marriage, kinship, and friendship networks typical of many hunting-gathering societies (Mielke and Fix, 2007). Among more sedentary agricultural groups, the association between biological relatedness, social closeness, and co-residence is distinct. In contemporary Amazonian societies horticulturalists tend to live in larger settlements comprised of a higher proportion of genealogical kin (Walker, 2014). In general, agricultural populations have extremely localized patterns of marital migration (Fix, 1999).

There is yet another factor that complicates efforts to predict patterns of relatedness and co-residence within the Tiwanaku communities. Moquegua Tiwanaku colonists have been described as diasporic communities who maintained strong ties with homeland communities in the *altiplano* (Goldstein, 2005, 2009). Isotopic evidence of paleomobility suggests there were continuing streams of migrants into the Tiwanaku

colonies (Knudson et al., 2014). Paleodemographic evidence has been interpreted as evidence of return migration among elderly Tiwanaku Moqueguanos from the colonies to their ancestral homeland(s) (Baitzel and Goldstein, 2016). Although it is likely that patterns of paleomobility within Moquegua Tiwanaku-affiliated communities were structured by family networks, it is less clear how those patterns would have affected patterns of phenotypic variation within the study samples.

Although it is an imperfect proxy for social relatedness and social interaction, phenotypic data serve as a useful starting point for identifying potential extended family groups within archaeological contexts. Kinship is increasingly conceived of as first and foremost a social relationship within Western academia (Johnson and Paul, 2016; see Astuti, 2009; Sahlins, 2013; Viveiros de Castro, 2009), but, in many human societies kin-based social relationships closely parallel genealogical relationships (Hamberger et al., 2011; Schneider, 1968, 1972). A similar pattern is observed among non-human primates. Although there is variation across and within primate species in regard to the specific factors that influence the nature and strength of their social affiliations, close biological relatives often have higher rates of interaction than non-relatives (Clark, 2011; Sueur and Petit, 2008; Thierry et al., 2004). For ancient societies for which we cannot directly observe or question individuals about their family relationships, the identification of close biological relatives is a – but not necessarily *the only* - good place to begin to investigate family-based social networks in the past. Ideally, research should incorporate diverse lines of archaeological data, including mortuary practices and body modification practices, as well as demographic data (i.e., skeletal age and sex) to achieve a more

nuanced evaluation of potential kin networks based on social and biological relatedness (Alt and Vach, 1995b).

Third, it is not possible to verify whether social network analysis has correctly distinguished close biological relatives from non-relatives. Social network analysis has merely identified a cluster of actors who can be considered a “hypothetical” family (Alt and Vach, 1995b). However, the issue of the fidelity between hypothetical families identified through data analysis and actual families that existed in the distant past is one that plagues the majority of bioarchaeological kinship research, including studies that use molecular data (see Meyer et al., 2012; Thompson, 1986). The most effective way to evaluate the utility of social network analysis for investigating past biosocial interactions and identifying family networks would be to apply social network analytical techniques to phenotypic data from documented skeletal collections with genealogical data (see Doi et al., 1985, 1986; Hanihara et al., 1983; Paul and Stojanowski, 2015; Saunders and Popovich, 1978). In this way network cohesion, node centrality, and network structure, including subgroups, derived from social network analysis of phenotypic data could be compared directly to social networks constructed from genealogical data.

### **Social network analysis and (intra)regional biodistance analysis**

One objective of this chapter is to evaluate the utility of social network analysis as a method for investigating biosocial interactions in the past to see how it compares to traditional biodistance techniques. Over the past three decades regional studies have become a mainstay of bioarchaeological research. Regional analyses provide an opportunity for nuanced considerations of variation in data patterns, and they allow for

inferences that extend beyond a single site to address larger scale social, historical, and political processes. Regional biodistance approaches include matrix correlation method (e.g., Konigsberg, 1990; Steadman, 2001; Sutter 2009a,b; Sutter and Sharratt, 2010), wombling (Konigsberg and Buikstra, 1995), and the suite of analytical techniques based on R-matrix analysis and included in the RMET software program (e.g., Aubry, 2009; Steadman, 2001; Stojanowski, 2010). These regional-based approaches are, for the most part, sample- or group-based analyses, although the matrix method could be applied to a sample of individuals drawn from a regionally-based sampling strategy. As scale-free analytical methods for investigating biological relationships, social network analysis, cluster analysis, and MDS can contribute to broader applications of regional biodistance analysis, not only up-scaled kinship analysis.

Social network analysis performed well in an informal comparison with multidimensional scaling and agglomerative hierarchical clustering. Although MDS was uninformative at a level conducive to visualization and interpretation, agglomerative hierarchical clustering yielded similar results as social network analysis in terms of the overall structure of the data. Components analysis of the social network identified 37 components, 36 of which are isolates, and a main component of 66 individuals. Agglomerative hierarchical clustering identified 57 total clusters, 42 of which are singletons, and one large component of 26 individuals. As described above, there is a great deal of overlap in the memberships of the social network subgroups identified using cliques and n-cliques analysis and the cluster of 26 individuals identified using clustering.

Interestingly, social network analysis identified fewer isolates and a larger main component compared to hierarchical cluster analysis.

Social network analysis and agglomerative hierarchical clustering both prove useful at identifying patterns of phenotypic variation among individuals within a regional framework. Furthermore, neither of these approaches require a priori information on group affiliation nor involve assumptions about (dis)similarity or the potential for interaction based on spatial proximity (Ensor, 2013b; Keegan, 2009; Matney et al., 2012; Mills et al., 2013). As a result, they can accommodate an approach that builds up from individuals to address mid- or multi-scalar aspects of social organization such as extended family networks, which are the focus of the present study.

In addition to social network analysis, the methodological approach with the greatest potential for intraregional and intracemetery bioarchaeological kinship analysis is finite mixture analysis, a point made ten years ago by Stojanowski and Schillaci (2006). Finite mixture analysis is an unsupervised model-based clustering method for identifying substructure without a priori information on the number of subgroups or individual identity (Alexander et al., 2009; Algee-Hewitt, 2016; Dong, 1997; Everitt and Dunn, 2001; Li et al., 2008; McLachlan and Peel, 2000; Pearson et al., 1992; Pritchard et al., 2000; Rosenberg et al., 2002; Tang et al., 2005). Finite mixture analysis, like all forms of cluster analysis, is scale free, meaning it can be used to investigate the internal structure of cemetery samples or applied in an intraregional analysis to detect extended kin networks. However, social network analysis is the only one of these promising

methodologies whose analytical concepts are based on theoretical models of social interaction.

One limitation of certain social network analytic techniques, including those used in the present study, is the reliance on dichotomized data. This not only introduces a degree of uncertainty to the specific results generated through the selection of an arbitrary dichotomization breakpoint, but it also removes variability from the data set. In some cases this may facilitate visualization and interpretation, but it still involves discarding data from the analysis.

Despite this limitation, social network analysis offers a broad suite of techniques that can complement standard bioarchaeological methods for reconstructing social interaction in archaeological contexts. Stojanowski and Schillaci (2006: 60), comment that “archaeological kinship analyses must remain organic and flexible in practice.” Although their statement was made in regard to the data types most suitable for bioarchaeological kinship analysis, it is equally applicable to the analytical methods applied to different types of phenotypic and molecular data. Moving forward, best practice in biodistance research will likely involve the use of multiple analytical techniques, including social network analysis, hierarchical clustering techniques, and perhaps MDS.

## **Conclusions**

This chapter introduces social network analysis as a viable exploratory analytical technique for investigating biosocial interaction in the past. Social network analysis has several characteristics that make it well suited for bioarchaeological investigations of

social organization. First, social network techniques are scale free and easily accommodate a multiscale analytical framework. In the present study, social network analysis was able to scale up kinship analysis and identify a potential core group of close biological relatives from three different sites in the Tiwanaku colonial enclave in the Moquegua Valley. Second, social network analytical techniques are organic rather than classificatory; they do not require a priori information regarding an actor's affiliations or spatial (i.e., burial) location relative to other actors in the study sample. At the same time, additional variables such as ethnic affiliation or spatial location can be included in formal analyses by comparing social networks based on different adjacency matrices or performing bimodal analysis (Borgatti et al., 2013). Third, SNA techniques can accommodate diverse data types. Social network analysis can be performed on any data that can be presented as an adjacency matrix, an important characteristic for a field like bioarchaeology, that values the use of multiple lines of evidence to reconstruct past lifeways.

The present study has emphasized the potential contributions of social network analysis to bioarchaeological kinship research specifically and biodistance analysis generally. However, social network analysis has myriad potential applications to bioarchaeological research in general. For example, social network analysis can be used to investigate disease transmission using skeletal and dental indicators of stress and pathology. Isotopic data can be used to create an adjacency matrix, and social network techniques could be used to explore networks based on paleomobility and diet. Applying social network analysis to bioarchaeological data will not come without challenges, but

depending on one's data and research question(s), social network analysis should complement existing analytical methodologies and contribute new inferences about past.



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## CHAPTER 5

### CONCLUSION

#### **Problem orientation**

As illustrated in the previous chapters, several decades of intensive archaeological research in the Moquegua Valley of southern Peru has culminated in our current perspectives on Moquegua Tiwanaku social organization and contributed to our interpretations of Tiwanaku expansion. The dual diaspora model of Moquegua Tiwanaku colonial organization proposed by Goldstein (2005, 2015; see also Goldstein and Owen, 2001; Owen, 2005; Owen and Goldstein, 2001) has strong theoretical foundations and is supported by diverse lines of archaeological data. Thus it is both predictive and descriptive. By integrating diaspora theory with ethnohistoric models of Andean social organizations, Goldstein's (2005, 2015) depiction of Tiwanaku-affiliated ethnic communities as diasporic maximal *ayllus* explains why members of Chen Chen- and Omo-style communities colonized the Moquegua Valley and why they maintained distinct ethnic identities for several hundred years despite living in close proximity. Goldstein argues that Tiwanaku state expansion was a dynamic process propelled not only by the aims of ruling elites but also by diasporic communities that sought to diversify and stabilize their subsistence bases.

This emphasis on ethnic-level aspects of *ayllu* organization within models of Moquegua Tiwanaku social organization has proved informative, yet it neglects smaller scales of social organization such as corporate group affiliations (i.e., minimal *ayllus*) that likely structured the daily actions and interactions of the persons who comprised

Tiwanaku-affiliated communities in the Moquegua Valley. There have been several attempts to investigate corporate- or kin-based social organization within Moquegua Tiwanaku sites (e.g., Blom, 1999; Blom et al., 1998; Hoshower et al., 1995; Sharratt, 2011), but we still know very little about this scale of social organization within Middle Horizon (ca. AD 600-1000) Moquegua Tiwanaku communities. Knowledge of family organization is critical to understanding Moquegua Tiwanaku colonial organization. Additionally, to develop more nuanced models of state formation and expansion it is critical to explore how mesoscale levels of social organization, including families and communities, structure individual behaviors and shape broader patterns of social practices and cultural traditions (see Hechter, 2000; Read and van der Leeuw, 2015).

This dissertation seeks to complement existing research on Moquegua Tiwanaku social organization and Tiwanaku expansion by implementing a multiscale framework that investigates kin-based affiliations along with ethnic-based affiliations. There is no question that ethnic affiliations substantially influenced sociality within Tiwanaku-affiliated communities in the Moquegua Valley, yet kin-based collectivities (e.g., households, lineages, families, corporate groups, etc.) are more reasonably imbued with social agency than larger scale ethnic-based social collectives. As Read and Leaf (2015: 32) note, it is the “intervening levels of groups, networks, institutions, and organizations,” rather than the population level, that shapes our “behavior as individuals.” It is likely at smaller scales of affiliation within the social fabric of Tiwanaku-affiliated communities that decisions were made about whether to migrate from the ancestral homeland to the Moquegua Valley, where to settle, whom group members should marry,



with whom to engage in economic exchange, and when and where to relocate when Tiwanaku state influence began to decline sometime during the 11th century A.D.

This dissertation has three primary goals:

- 1) Develop a theoretical framework for investigating smaller scales of social organization. Bioarchaeological studies of social identity are effective at analyzing collective identities at larger scales (e.g., gender, ethnicity, religion, etc.) and at an individual level, but meso-scale investigations of social affiliations are few (cf. Stojanowski, 2013b).
- 2) Evaluate whether Chen Chen- and Omo-style communities were endogamous. Goldstein (2005) suggests that ethnic community boundaries may have been maintained in part through endogamous marriage practices. The biological implications of this corollary to the dual diaspora model are evaluated using standard biodistance analytical methods.
- 3) Implement a flexible analytical method suitable for multiscalar investigations of social organization using bioarchaeological data and social network analysis. Social network analysis is explored as a suite of flexible analytical techniques suitable for investigating multiple scales of social affiliation in an integrated framework.

### **Summary of results**

In Chapter 3 the biological implications of Tiwanaku-affiliated ethnic community endogamy, a corollary to the dual diaspora model, are evaluated using standard biodistance techniques applied to cranial shape data. A Mantel test was used to compare

the geographic distance matrix for intersite distances to a biodistance matrix based on Mahalanobis  $D^2$  values derived from 14 basicranial and temporal bone landmarks. This approach provides a straightforward method for evaluating whether biosocial interactions among the study samples were consistent with a model of isolation-by-distance, wherein marriage practices are expected to be influenced primarily by spatial proximity rather than ethnic affiliation. The positive Pearson's and Spearman's correlations between the matrices indicate patterns of phenotypic similarity in cranial shape are consistent with the expectations for a model of biosocial interaction according to isolation-by-distance. However the weak correlation values and lack of statistical significance suggest other factors also influenced patterns of mate exchange and gene flow within the Moquegua Tiwanaku colonies.

To more directly evaluate the dual diaspora model discriminant function analysis (DFA) and canonical variates analysis (CVA) were performed and inter-individual Euclidean distances were generated for all individuals in the sample. Results of DFA and CVA provide support for the dual diaspora model. DFA identified statistically significant differences between the mean cranial shape of individuals from Omo-style cemeteries and the mean cranial shape of individuals from Chen Chen-style cemeteries. Although the overall differences in the means are very small, the fact that differences are present is intriguing. The CVA was able to partially differentiate individuals from Omo-style and Chen Chen-style contexts, with individuals from the Omo-style cemetery of Omo Alto M16 forming a distinct cluster. The average intra-*ayllu* inter-individual distance (0.206) is smaller than the average inter-*ayllu* inter-individual distance (0.210), but of the 15

individuals from Omo-style contexts in the study sample, 13 have their smallest inter-individual Euclidean distance with an individual from a Chen Chen-style context. This suggests that members of these communities may have tended to marry someone from the same maximal *ayllu*, but there were certainly exceptions to this overall pattern. In sum, these results provide mixed support for the dual diaspora model. Although ethnic affiliation likely restricted gene flow between members of Omo- and Chen Chen-style communities, community boundaries were permeable and it is possible that *ayllu* affiliation was flexible.

Overall, the biodistance results suggest a complex pattern of biosocial interaction among the Tiwanaku-affiliated communities in the Moquegua Valley. Maximal *ayllu* identity structured gene flow, but ethnic-level affiliation was not the only relevant axis of social affiliation. Marriage practices appear structured by multiple considerations, including ethnic affiliations, spatial proximity, as well as corporate group (i.e., minimal *ayllu*) interests and relationships. These findings do not invalidate the dual diaspora model. However, they do suggest ethnic community boundaries were fluid and permeable, and they underscore the need for more nuanced, multiscale investigations of Moquegua Tiwanaku social organization.

Chapter 4 introduces social network analysis as a suite of analytical techniques sufficiently flexible enough to complement the multi- and mesoscale theoretical framework advocated in Chapter 2. A variety of social network analytical techniques are applied to cranial shape data from the study samples. Results of graph visualization, network measures, and network structure indicate the study sample from the Moquegua

Tiwanaku colonies constituted a social network comprised of a dense main component and a large proportion of isolated actors.

Informal approaches used to identify potential family groups (i.e., visualization of ego networks) proved less useful than formal approaches (i.e., subgroup analysis). While there is no clear partition of the network into distinct subgroups that could represent different extended kin networks or biological lineages, there is a cluster of closely related individuals at the core of the network that integrates a web of less-closely related actors. Interestingly, subgroup analysis yielded similar results as agglomerative hierarchical cluster analysis, which suggests there is potential for social network analysis to contribute to bioarchaeological studies of social organization and bioarchaeological research in general. Social network analysis not only provides a way to visualize data in a proximity matrix (like multidimensional scaling), it provides analytical techniques for exploring network structure at multiple scales (e.g., network, community, neighborhood, and individual). Thus, social network analysis provides an integrated suite of analytical methods that facilitate a truly multiscale analysis, rather than a scale free analytical method. For bioarchaeological investigations of social organization, social network analysis provides a flexible way to combine and shift between multiple scales of affiliation, and it facilitates efforts to scale up bioarchaeological kinship analysis from an intracemetery or intrasite level of analysis to a regional approach to family organization.

### **Future directions**

The findings of the present study demonstrate the potential of the theoretical framework and analytical techniques presented herein to contribute to bioarchaeological

research. At the same time, this dissertation has laid the groundwork for future research. Three different avenues for future research are considered.

First, social network analysis has the potential to make a significant contribution to bioarchaeological research in general. Examples of applications include the investigation of disease transmission using skeletal and dental indicators of stress and pathology and exploration of networks based on mortuary practices, body modification, or isotopic indicators of paleomobility and paleodiet. However, in terms of applying social network analytical procedures to biodistance analysis, including bioarchaeological kinship research, it is important that this approach be evaluated using documented skeletal collections with known genealogies.

Second, the findings presented here should be supplemented with additional analyses that incorporate multiple lines of bioarchaeological data. The incorporation of paleodietary, paleomobility, mortuary, and cranial modification data would provide a more robust evaluation of family organization in terms of social relatedness and may yield more nuanced results than those based solely on phenotypic data.

Third, this dissertation has focused on investigating social organization within the Moquegua Tiwanaku colonies during the Middle Horizon (ca. AD 500-1100), but Tiwanaku studies and Andean archaeology in general would be enriched by a more nuanced analysis of changes in sociopolitical organization among Tiwanaku-affiliated communities through time. After the decline of the Tiwanaku state around AD 1000, Tiwanaku-affiliated communities in the lower Osmore Drainage of southern Peru moved from large, multicultural settlements to smaller, isolated villages and turned to

household-centered economic production after the surplus-based export economy collapsed when long distance exchange networks disintegrated (Goldstein, 2005; Owen, 2005; Sutter and Sharratt, 2010). Recent findings from the Tiwanaku-affiliated site of Tumulaca la Chimba suggest that kin-based affiliations were expressed more strongly in post-collapse communities than they had been prior to state decline, when expressions of community-wide ethnic affiliation were prominent (Sharratt, 2011). At other sites, Tiwanaku social groups, perhaps corporate kin groups, seem to have responded to the socioeconomic turmoil that followed state decline by allying with communities affiliated with the neighboring Chiribaya polity (Owen, 2005; Sutter and Sharratt, 2010).

A diachronic, multiscalar approach to social organization can help us understand the roles that family organization played in the processes of ethnogenesis among lower Osmore Drainage communities following the decline of Tiwanaku state influence. For example, did larger communities split apart or come together along family-based affiliations? How did individuals and social groups decide when and where to migrate as middle valley Tiwanaku-affiliated communities were largely depopulated? More generally, a study of this nature is relevant to general models of state formation and “collapse”. Additionally, it would help us understand the range of variation in family-based responses to political decline and economic destabilization and the extent to which family-based responses to political and economic upheaval shape broader patterns of sociopolitical transformation. Teasing apart ethnic- and family-based aspects of social interaction in the past can help us not only reconstruct factors which shaped particular

historical processes and events, it can help us understand how communities and families adapt to changing circumstances in the present and in the future.

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APPENDIX A  
AUTHOR CONTRIBUTIONS



Chapter 2 of this dissertation was adapted from the article “Bioarchaeology and Kinship: Integrating Theory, Social Relatedness, and Biology in Ancient Family Research” previously published in the *Journal of Archaeological Research* (2016). This article was coauthored by the author of this dissertation and Kathleen S. Paul. Kathleen Paul has granted her permission for a modified version of this publication to be included in this dissertation.

APPENDIX B

ASSESSING AGE EFFECTS ON CRANIAL SHAPE

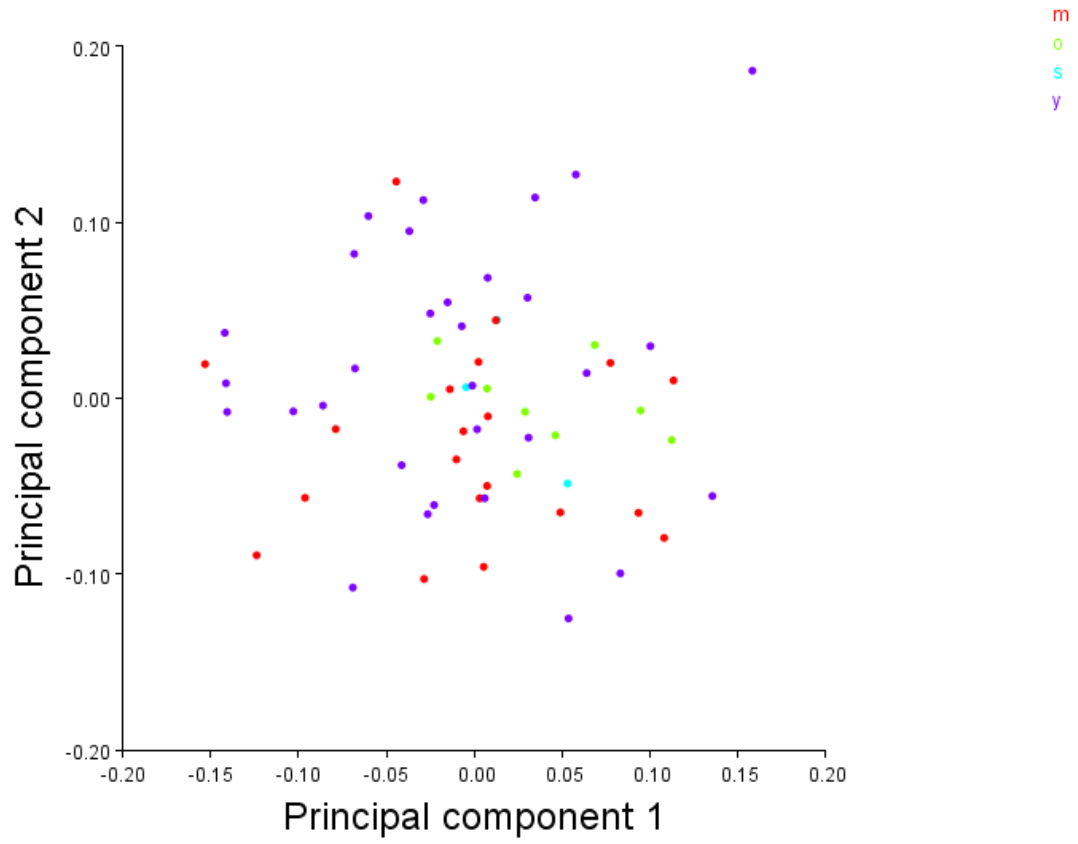


Fig. 1a. Scatter plot of PC1 and PC2 with individuals coded by age cohort (m – middle adult, o – older adult, s – subadult, y – young adult).

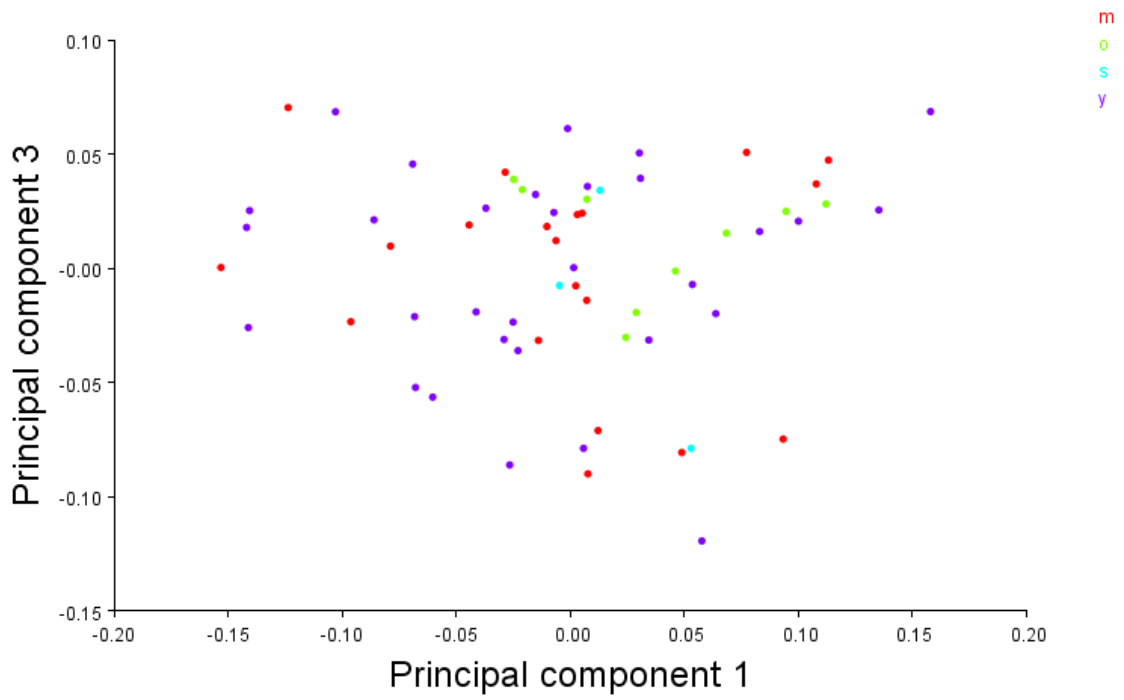


Fig. 1b. Scatter plot of PC1 and PC3 with individuals coded by age cohort (m – middle adult, o – older adult, s – subadult, y – young adult).

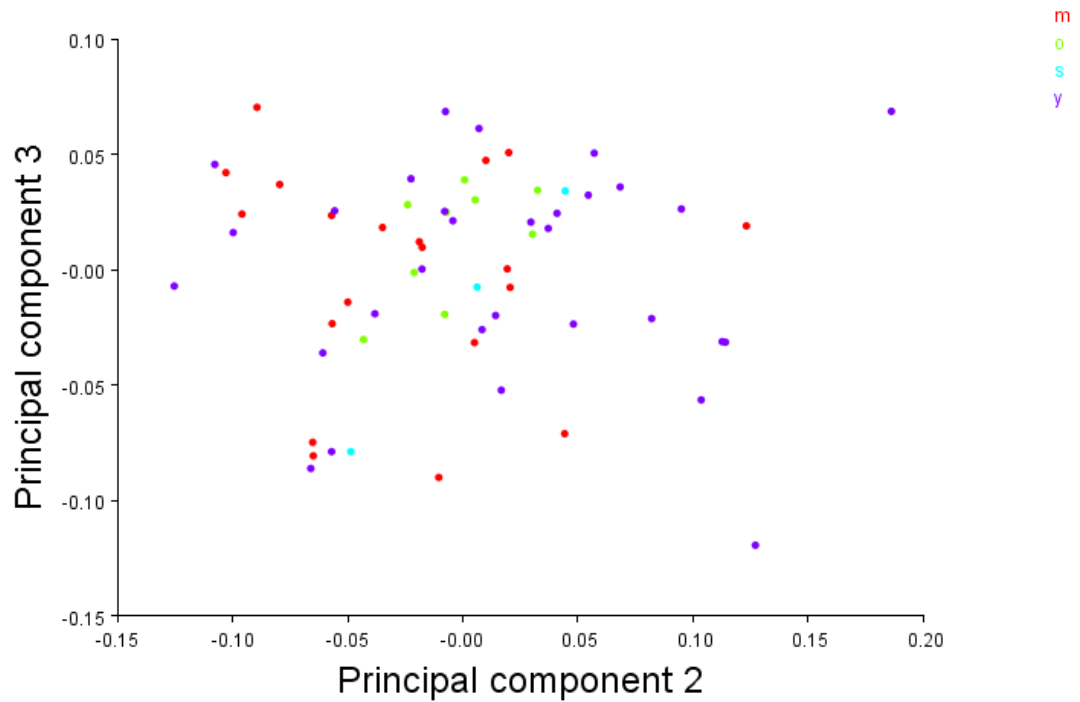


Fig. 1c. Scatter plot of PC2 and PC3 with individuals coded by age cohort (m – middle adult, o – older adult, s – subadult, y – young adult).

APPENDIX C

ASSESSING SEX EFFECTS ON CRANIAL SHAPE

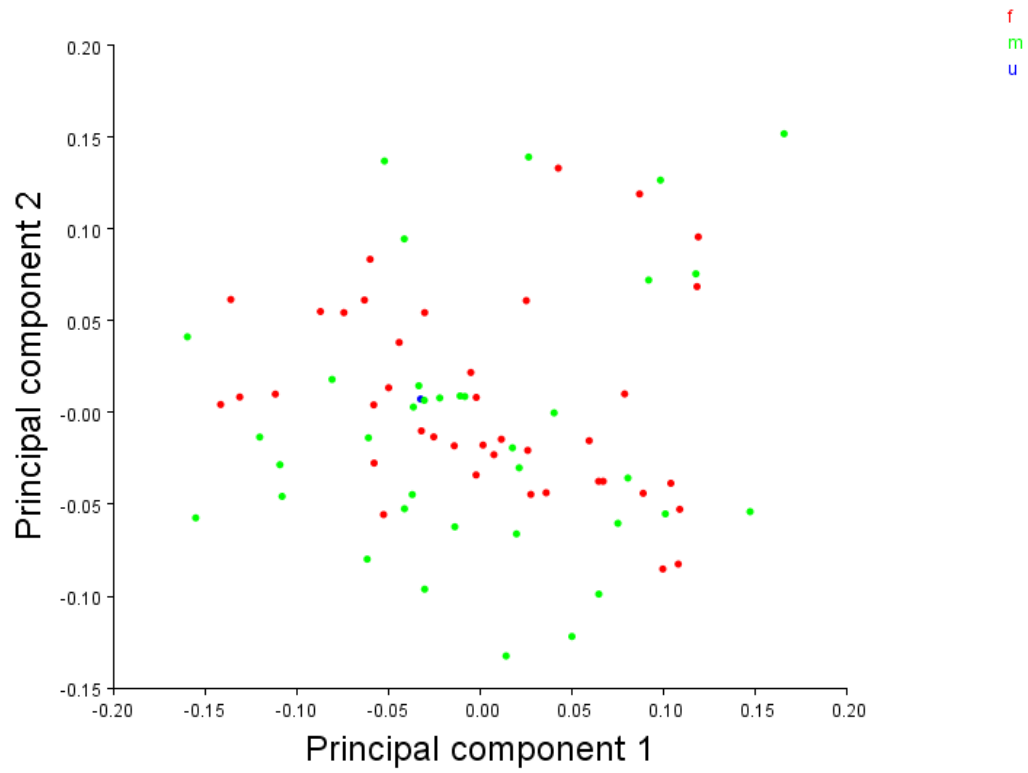


Fig. 1a. Scatter plot of PC1 and PC2 with individuals coded by sex (f – female, m – male, u – sex undetermined).

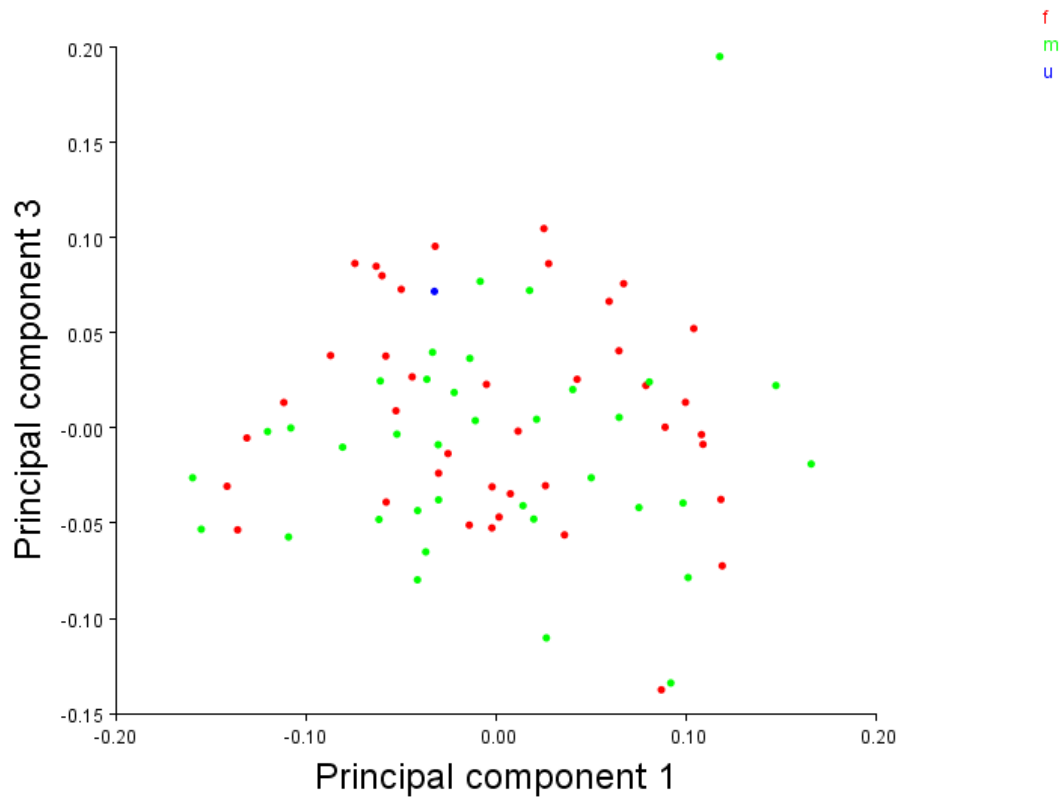


Fig. 1b. Scatter plot of PC1 and PC3 with individuals coded by sex (f – female, m – male, u – sex undetermined).

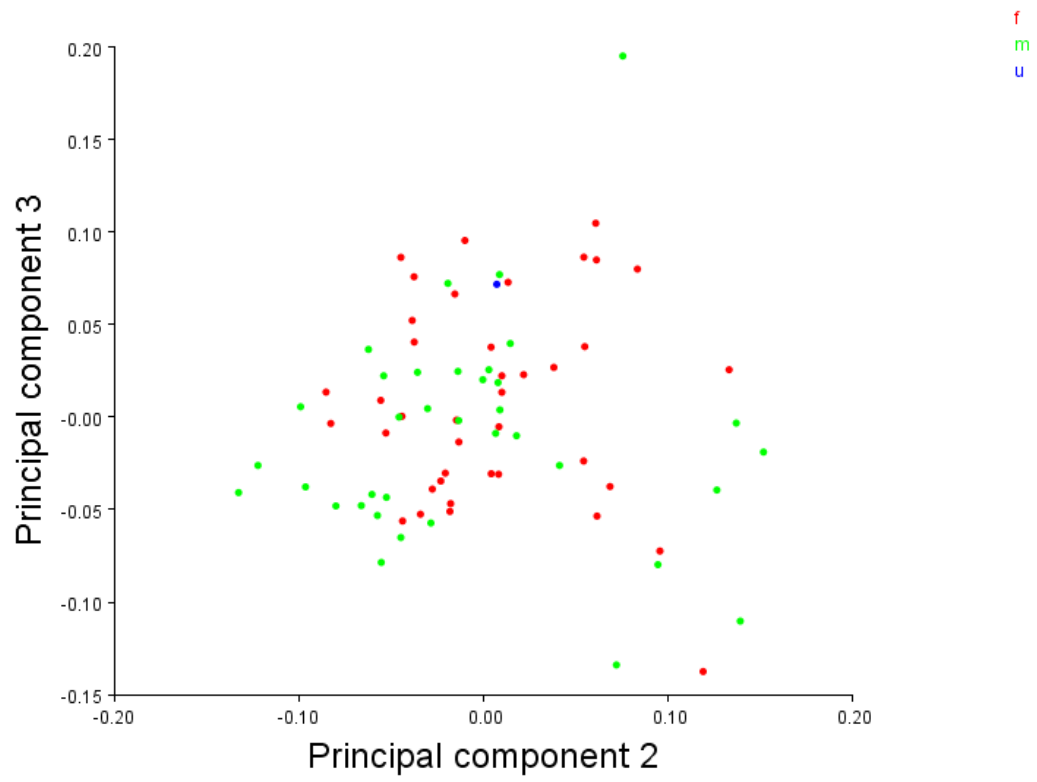


Fig. 1c. Scatter plot of PC2 and PC3 with individuals coded by sex (f – female, m – male, u – sex undetermined).



## APPENDIX D

### EFFECTS OF CRANIAL MODIFICATION ON CRANIAL SHAPE

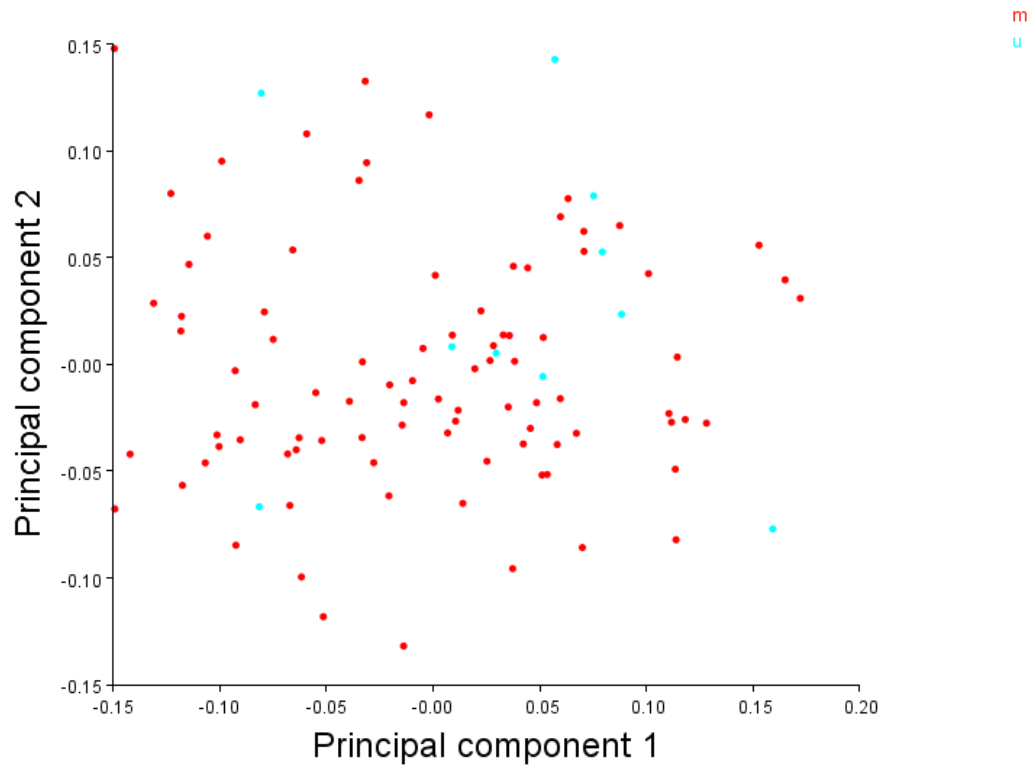


Fig. 1a. Scatter plot of PC1 and PC2 with individuals coded by modification presence (m – modified, u – unmodified).

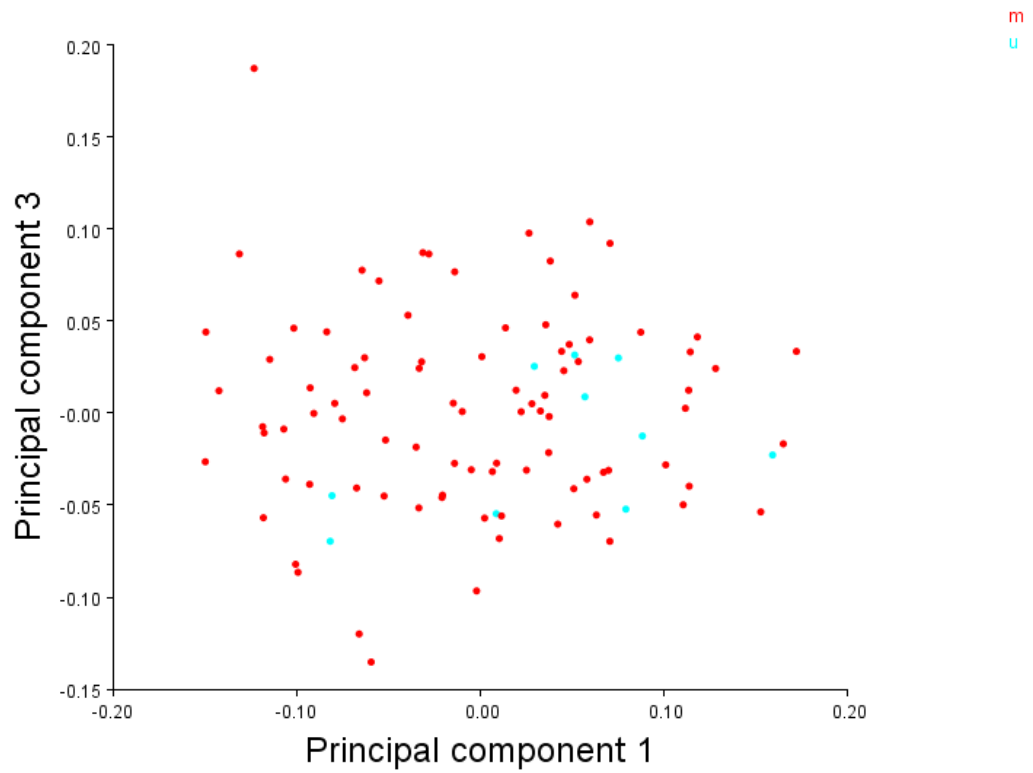


Fig. 1b. Scatter plot of PC1 and PC3 with individuals coded by modification presence (m – modified, u – unmodified).

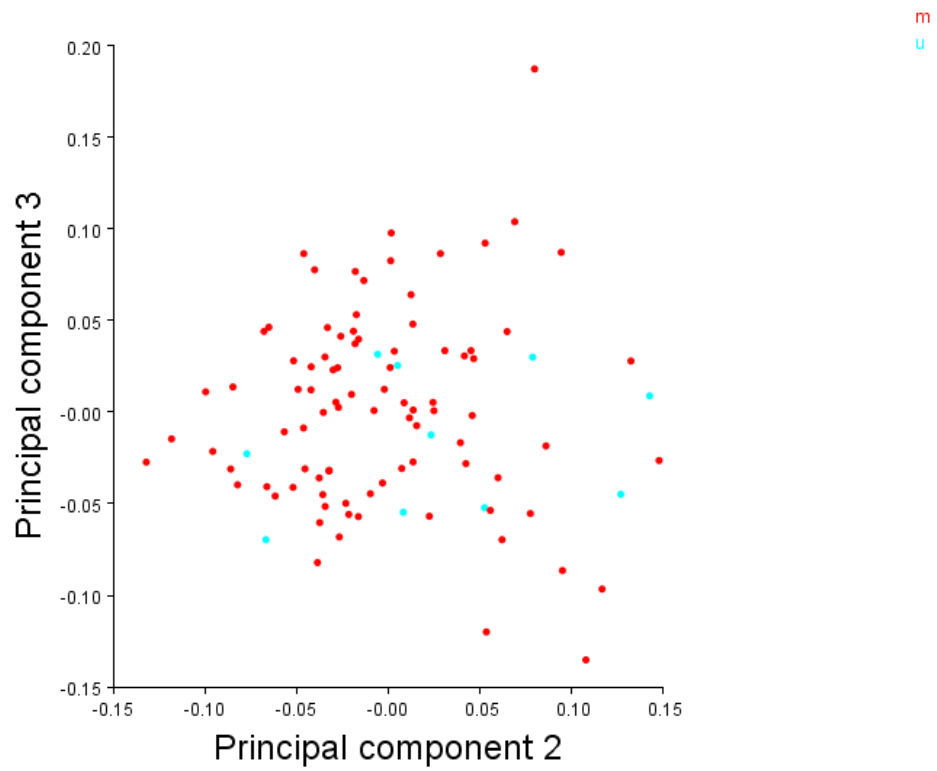


Fig. 1c. Scatter plot of PC2 and PC3 with individuals coded by modification presence (m – modified, u – unmodified).

APPENDIX E  
CENTRALITY VALUES AND SUBGROUP MEMBERSHIPS (NETWORK  
BINARIZED AT 5<sup>TH</sup> PERCENTILE)

ID	Degree centrality	Eigenvector centrality	Cliques (size 7) <sup>a</sup>	Cliques (size 8) <sup>b</sup>	2-cliques (size 30) <sup>c</sup>	2-cliques (size 37) <sup>d</sup>	Cluster <sup>e</sup>
M10 M-2	36	0.328	+	+	+	+	1
M10 M-5	33	0.293	+	+	+	+	1
M10 S-6	27	0.287	+	+	+	+	1
M1 3519	25	0.263	+	+	+	+	1
M70 2868	24	0.267	+	+	+	+	1
M1 54	23	0.21	+	+	+	+	1
M1 3677	21	0.226	+	+	+	+	1
M1 779	18	0.191	+		+	+	1
M10 T-3	15	0.18	+			+	1
M1 2583	14	0.165	+		+	+	1
M1 864	14	0.157	+		+	+	1
M10 S-8	14	0.17	+		+	+	1
M1 289	13	0.156	+			+	1
M10 85-25(B)	13	0.164	+		+	+	1
M1 0016	12	0.174	+		+	+	1
M1 133	11	0.135	+			+	2
M1 3083	11	0.116			+	+	2
M70 2787	11	0.156	+		+	+	1
M70 2840	10	0.15	+	+	+	+	1
M1 304000	9	0.14	+		+	+	1
M1 831	9	0.12					1
M10 85-18	8	0.119			+	+	12
M10 9072	8	0.111			+	+	1
M70 2985	8	0.109			+	+	1
M70 4468	8	0.117				+	3
M1 2764-2	7	0.087				+	2
M10 2188C	7	0.086					14
M10 7637	7	0.107				+	1

M1 2068	6	0.076		+	8
M1 427	6	0.062			4
M1 513	6	0.077		+	1
M10 8867	6	0.082			1
M10 T-2	6	0.094			1
M10 O	5	0.077	+	+	4
M70 4443	5	0.063		+	3
M10 85-19	4	0.04			4
M10 85-20(B)	4	0.064		+	5
M1 2296	3	0.028			9
M1 27	3	0.035			
M10 2006-B-22	3	0.045			14
M10 7730	3	0.021			2
M10 8485	3	0.043			1
M10 9099	3	0.041		+	7
M10 9248	3	0.02			2
M1 116	2	0.01			9
M1 1573	2	0.033		+	13
M1 197	2	0.017			7
M1 3154	2	0.028			12
M1 3768	2	0.042		+	11
M1 826	2	0.042		+	10
M16 008	2	0.04		+	
M70 2426	2	0.02			5
M70 2642	2	0.04		+	
M1 136	1	0.014			
M1 3660-2	1	0.011			
M1 398	1	0.02			
M1 436	1	0.005			8
M1 I773	1	0.018			
M10 7423	1	0.014			

	M10 8008	1	0.009	2
	M10 8884	1	0.015	13
	M10 9115	1	0.001	15
	M10 9324	1	0.011	
	M10 M-85-8	1	0.02	6
	M43 3000	1	0.008	
	M43 3054	1	0.004	3
	M1 244b	0	0	
	M1 261	0	0	
	M1 2762	0	0	
	M1 284	0	0	
	M1 302009	0	0	
	M1 306025	0	0	
	M1 3472	0	0	
	M1 3718	0	0	
394	M1 3726	0	0	
	M1 426	0	0	
	M1 53	0	0	
	M1 548	0	0	
	M1 593	0	0	
	M1 650	0	0	
	M1 82	0	0	
	M1 I197	0	0	11
	M10 2164	0	0	10
	M10 7554	0	0	
	M10 7853	0	0	
	M10 8344	0	0	
	M10 8904	0	0	
	M10 8934	0	0	
	M10 9195	0	0	
	M10 9419	0	0	15



M10 M-1	0	0
M16 058	0	0
M16 5063	0	0
M43 3414	0	0
M43 4141	0	0
M43 4237	0	0
M43 4835	0	0
M43 4878	0	0
M70 2896	0	0
M70 2956	0	0
M70 2999	0	0
M70 4166	0	0

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<sup>a</sup>The 19 actors who are members of at least one of the 15 cliques of size 7.

<sup>b</sup>The 8 actors who are the only members of the one clique of size 8.

<sup>c</sup>The 21 actors who are members of each of the 32 2-cliques of size 30.

<sup>d</sup>The 37 actors who are the only members of the 2-clique of size 37.

<sup>e</sup>The clusters are numbered lowest to highest from the largest to the smallest clusters. For example, the largest cluster (n=26) is designated Cluster 1, the second largest is Cluster 2 (n=6), and so one for each cluster with at least two individuals. The individuals without a cluster number reflect the 42 “clusters” comprised of a single individual.

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