

This study investigates how social organization and mobility changed during the Neolithic Demographic Transition (NDT) in northern Vietnam. Dental nonmetric traits were assessed for pre-Neolithic Con Co Ngua (early seventh millennium BP;  $n = 38$ ) and Neolithic Man Bac (c. 3800–3600 BP;  $n = 65$ ), along with cranial nonmetric data for the same Man Bac individuals. It identifies five putative kin lineages for Con Co Ngua and six for Man Bac, with little evidence for spatial organization by lineage in either cemetery. The mean  $^{87}\text{Sr}/^{86}\text{Sr}$  for Con Co Ngua was  $0.70947 \pm 0.00017$  ( $n = 40$ ), and for Man Bac  $0.70927 \pm 0.00055$  ( $n = 27$ ). Man Bac had more variance in overall  $^{87}\text{Sr}/^{86}\text{Sr}$ , but Man Bac females showed lower variance and a different mean than males within three of the putative lineages identified. While this may signal the presence of uxori-local postmarital residence at Man Bac, overall, we find no evidence for a marked change in social organization.

Keywords: cranial nonmetric trait, dental nonmetric trait, strontium isotope, kinship, Neolithic, Vietnam

## Chapter 11

# Community and Kinship during the Transition to Agriculture in Northern Vietnam

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## Introduction

The reconstruction of genetic kinship relations within prehistoric populations has become an important aspect of many bioarchaeological research programs (e.g., Stojanowski and Schillaci 2006; Pilloud and Larsen 2011; Paul et al. 2013). Recent molecular anthropological studies frequently report success in analyzing mitochondrial DNA (mtDNA) from archaeological remains (e.g., Kemp et al. 2009; Haak et al. 2008). As mtDNA only tracks

maternal inheritance, its value in defining prehistoric kinship structure greatly increases when results are viewed in light of those obtained from more traditional methods, such as craniometry and odontometry (e.g., Adachi et al. 2006; Corruccini et al. 2002; McClelland 2003). Although it will not specify the exact genealogical nature of the relationships, a bioarchaeological kinship analysis can identify individuals who are likely to be genetically related (Stojanowski and Schillaci 2006).

Nonmetric (discrete) traits have frequently been used to reconstruct kinship, especially for small samples already inferred from mortuary data to represent family units (e.g., Alt et al. 1997). Regardless of the size of the assemblage and complexity of the interment practices within a given cemetery, rare traits are more useful than commonly occurring traits for identifying closely related individuals (Alt and Vach 1998). Most of these rare traits are deformations or malocclusions of the dentition but include a range of osseous traits. The osteobiographic approach (e.g., Zvelebil and Weber 2012), which emphasizes that simply demonstrating that a given cemetery assemblage contained genetic kin, is of limited value. Instead, the determination of kinship should serve as a foundation on which other aspects of daily life and social identity can then be assessed (Stojanowski and Schillaci 2006; Alt and Vach 1998).

Deliberately maintained cemeteries of moderate to large size are best suited to a structured spatial analysis, regardless of the type of data (metric or nonmetric) employed. Although spatial organization is one of the many interacting dimensions of mortuary systems (Goldstein 1981), whose specific meanings to their users will never be fully understood to archaeologists (Ucko 1969), mortuary spatial patterning is likely to reflect kinship relations (Saxe 1970; Morris 1991). Structured analyses presume that the cemetery in question was laid out according to some sort of burial plan, corresponding to the deliberate arrangement of interments in order to display in death some aspect of social organization in life, be they

family plots, interment areas restricted to a specific lineage, moiety or sodality members, the segregation of children from adults, or division based on real or perceived ethnic or religious boundaries (Stojanowski and Schillaci 2006). Kinship analyses of individuals within structured cemeteries, then, seek “to examine patterns of within—and between-group variance and affinity . . . to investigate the degree of homogeneity within burial clusters” (Stojanowski et al. 2007:208).

Occasionally, contemporaneous individuals (Alt et al. 1997) or identified family members are observed buried in mutual embrace (Haak et al. 2008). However, for burials in cemeteries that accumulated over centuries, clustering based on isotopes and/or osteological traits is more conservatively interpreted as representative of multigenerational lineages. If osteological evidence for genetic relatedness shows significantly lower variability within than between spatially organized groups, the most parsimonious hypothesis would be that kinship was a factor in their spatial arrangement.

Combining dental and osteological observations with isotopic data makes it possible to assess diet and migration histories at the individual level (e.g., Montgomery 2010; Knudson et al. 2010) and potentially infer patterns of kinship, as increasingly demonstrated within Southeast Asia (e.g., Bentley et al. 2005, 2007, 2009; Cox et al. 2011). In larger samples, analysis of strontium isotope ratios,  $^{87}\text{Sr}/^{86}\text{Sr}$ , in archaeological tooth enamel may indicate sex-specific residential mobility reflective of kinship systems such as patrilocality (Bentley et al. 2012; Haak et al. 2008) or matrilocality (Bentley et al. 2005, 2007). The basic premise is that the  $^{87}\text{Sr}/^{86}\text{Sr}$  in tooth enamel reflects that of the cumulative geologic minerals that found their way into the adolescent enamel via the food chain. The simplicity of a  $^{87}\text{Sr}/^{86}\text{Sr}$  ratio measured in enamel may belie a complex history of diet, mobility, and geologic sources (Bentley 2006; Montgomery et al. 2010), but nevertheless one can still infer meaning from group-level differences in  $^{87}\text{Sr}/^{86}\text{Sr}$  (both mean and variance) and their

patterning by sex, burial position, funerary goods, and characteristics of the skeletal sample (Bentley 2013).

The principle aim of this chapter is to discuss what nonmetric trait and strontium isotopic data together reveal about how social organization changed before and during the mid-Holocene transition to agriculture in northern Vietnam.

## The Assemblages at Man Bac and Con Co Ngua

As case studies, we use skeletal assemblages from hunter-gatherer Con Co Ngua, dated to the early seventh millennium BP (Oxenham et al. 2019, and early Neolithic Man Bac, dated to circa 3800–3600 BP (Oxenham pers. comm.). The individuals of Man Bac and Con Co Ngua lived in similar estuarine environments with rich resource bases suitable for terrestrial, coastal, and in-shore maritime hunting, gathering, and fishing. Seasonal subsistence activities were practiced by both communities. In the case of Man Bac, this would have supplemented the rice agriculture, which the founding community lineages introduced into the region, and into neighboring indigenous populations in concert with human genetic exchange (Oxenham and Matsumura 2011). Both communities existed long enough to establish complex mortuary practices and, at least in the case of Man Bac, trade networks with inland and coastal neighbors, as was the case for other coastal regions of Southeast Asia (Higham et al. 2011) and other coastal locations in the world (Jerardino et al. 2009).

Con Co Ngua, a midden-cemetery located in Thanh Hoa province, northern Vietnam, was first excavated in late 1979 and early 1980 (see Oxenham 2001, 2006, 2016) and subsequently reexcavated by Oxenham in 2011 and 2013. The midden-cemetery at Con Co Ngua is attributed to the Da But culture, a pre-Neolithic hunter-gatherer culture that covers a wide region across northern Vietnam and southern China. Subsistence at Con Co Ngua appears to have focused on large-bodied terrestrial herbivores supplemented with riverine and marine resources (Oxenham 2001; Oxenham et al. 2018; Jones et al. 2019). Populations

associated with the Dan But culture are believed to represent the descendants of the original colonizers of Mainland Southeast Asia and can be craniofacially described as Australo-Melanesian or Australo-Papuan (Matsumura and Oxenham 2014; Oxenham and Buckley 2016).

Man Bac is an early Neolithic living and cemetery site located in Ninh Binh province, northern Vietnam. Man Bac, dated to circa 3800–3600 BP, was excavated during several seasons: 1999, 2001, 2004–2005, and 2007 (Oxenham and Matsumura 2011). The Man Bac community was engaged in broad-spectrum foraging (including a significant marine component) and farming subsistence activities, with evidence for both extensive trading networks and very high levels of fertility (Oxenham and Matsumura 2011; Willis and Oxenham 2013; McFadden et al. 2018). The Man Bac sample shows evidence of significant levels of genetic exchange between more northerly originating migrants and local indigenous groups, or the descendants of Da But culture populations (Matsumura and Oxenham 2014; Lipson et al. 2018).

## Materials and Methods

From Con Co Ngua, a total of 40 individuals (16 males, 21 females, 3 subadults) recovered during the 1979–1980 excavation season were assessed for  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios in tooth enamel (third molars; second molars when third molars were not available) and 38 individuals (10 males, 22 females, 6 subadults) were assessed for dental nonmetric trait expression. From Man Bac, 27 individuals (15 males, 10 females, 2 subadults) were assessed for  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios (third molars; second molars when third molars were not available), while cranial nonmetric traits for 65 individuals (18 males or probable males, 14 females or probable females, 33 subadults) were sourced from Huffer (2012) (see [Table 11.1](#)).

INSERT TABLE 11.1 HERE

Nonmetric Trait Assessment and Cluster Analysis

For reasons of sample availability, we use a full set of cranial trait (including dental) data from Man Bac ( $N = 65$ ), but only permanent dentition traits from Con Co Ngua ( $N = 38$ ). Because we analyze each site separately, we need to consider the different forms of evidence when comparing our interpretations about kinship at each site. The osseous and dental nonmetric traits were first recorded using ordinal (highest-score) scales where appropriate with respect to standard trait lists and methodologies given for infracranial traits (Finnegan 1978), cranial traits (Hauser and DeStefano 1989), adult dental traits (Turner et al. 1991; Scott and Turner 1997) and additional deciduous and permanent dental traits (McClelland 2003). All of the traits selected are known from previous studies to be at least moderately heritable and minimally correlated with each other (e.g., Hauser and DeStefano 1989; Turner et al. 1991; Scott and Turner 1997; McClelland 2003). All traits were recorded macroscopically, with bilateral traits initially scored on both sides and the highest ordinal expression used.

As indicated in [Table 11.1](#), some of the recorded traits were converted to dichotomized present/absent scores at the outset (0 or 1 respectively), while others were not, due to being continuous in expression. [Table 11.1](#) also lists the thresholds used to determine the presence or absence for each of the dichotomized traits, which include congenital absence of the lateral incisors, delta-shaped deciduous first mandibular molars, protostylid, and others. The trait frequencies, defined as the number of individuals expressing the trait out of the total number of individuals for which that trait could be assessed, are given in [Table 11.2](#). We controlled for intra-observer error by comparing trait frequencies (cranial, dental, and infracranial) between a randomly selected adult subsample and a rescored of that same subsample, using only traits with at least ten pairs of scores. The estimate of intra-observer error (Shennan 1997; McClelland 2003) is a function of the number of pairs scored, fraction of traits scored in only one session, the differences between paired scores, and the  $p$  value for

each trait where applicable. Our analysis of intra-observer error removed very few traits from the initial battery (Table 11.1).

INSERT TABLE 11.2 HERE

We used the cluster analysis program *Clustan* (v. 6.03, June 2003, using tree visualization software *ClustanGraphics 6*) to generate hundreds of clusters from a given dataset—including both nondichotomized- and dichotomized data—under a variety of controllable conditions. Cluster analysis sorts cases (in this case individual skeletons) into groups by strength of association in terms of a selected set of traits. To quantify similarity using ordinal data that include dichotomous characters, *Clustan* uses Gower’s coefficient, which allows the different characters to be weighted according to their contributions (Podani 1999). After converting the Gower coefficients into dissimilarity observations, the clustering algorithm applies Ward’s (1963) method to progressively agglomerate the observations into larger and larger clusters, until all observations are in one cluster. Each individual has a certain likelihood of belonging to a specific cluster, with clusters forming due to shared high probabilities. This generates a dendrogram whose significance—the null hypothesis being that the partitioning of a given tree is random—can be tested in *Clustan* using a Monte Carlo simulation on a randomized data matrix that preserves the hierarchy of sampling as given by the dendrogram.

To test further the significance of clustering, we removed the very low variance traits from the Man Bac and Con Co Ngua matrices (see Table 11.2) and then randomized the proximity of individuals (as determined by number of scores in common). For Man Bac adults and subadults, numerous separate cluster analyses were performed on the combined cranial, dental, and infracranial trait battery (with nonvariant traits removed), with undichotomized trait data given preferential weight in order to capture the most variance (Huffer 2012). Although the combination of dental, cranial, and infracranial traits within the

same matrix is statistically powerful, the undichotomized cranial trait battery was chosen here as the most representative, as it includes almost the entire skeletal assemblage ( $n = 65$ ), including subadults, and therefore provides the most complete assessment of spatial proximity between hypothetical kin.

## Strontium Isotopic Analysis

Isotopic mapping is still in its infancy in northern Vietnam, so our map of biologically available  $^{87}\text{Sr}/^{86}\text{Sr}$  is necessarily sketched at this point on the bedrock geology (Nam 1995). Underneath the Quaternary sediments indicated in [Figure 11.1](#), northern Vietnam is underlain by marine karst limestone (Day and Ulrich 2000); typical limestones ought to yield  $^{87}\text{Sr}/^{86}\text{Sr}$  about 0.7075. Immediately southwest of Hanoi in northeast Vietnam is a Devonian-age rift basin, trending NW-SE, filled with Permian to early Triassic marine sediments (Yang et al. 2012). Given the age of these marine sediments, we would expect  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios between about 0.707 and 0.7085. There are significant outcroppings of igneous rocks, which include a group of gabbros with  $^{87}\text{Sr}/^{86}\text{Sr}$  ranging from 0.708 to 0.710 as well the granites, dacites, and rhyolites with substantially higher  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios above 0.720 (Hoa et al. 2006). At this point, we have only one faunal sample from this area of northern Vietnam for baseline  $^{87}\text{Sr}/^{86}\text{Sr}$ , just a single *Canis familiaris* canine tooth, recovered from the fill of the human burial 2007H1M1, reported later.

INSERT FIGURE 11.1 HERE

As Man Bac and Con Co Ngua are located on the alluvial delta south of the Red River Delta ([Figure 11.1](#)), we expect the alluvial fan/delta region mixes the range of sediments from different components of the catchment region. Due to this sediment mixing, we would hypothesize a fairly narrow range of Sr isotope signatures among the human groups at both sites. In this initial study, our best way to estimate the local range at this stage will be the  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios from the archaeological skeletal assemblage of the two sites. To use an



example from Khok Phanom Di (KPD), a coastal site of complex foragers (dating after 2000 BC) a thousand kilometers away in the Gulf of Siam, Thailand, the local  $^{87}\text{Sr}/^{86}\text{Sr}$  established from archaeological teeth of pigs and of infants ranged between 0.7092 and 0.7094 (Bentley et al. 2007).

A total of 27 second and third molars collected from the Man Bac assemblage and 40 third molars from Con Co Ngua, representing every adult or adolescent that had these specific permanent teeth present irrespective of side or arcade, provided the samples for the analysis of  $^{87}\text{Sr}/^{86}\text{Sr}$  in tooth enamel. For each sampled molar, approximately 5–10 mg of enamel was subjected to our established procedure (Bentley et al. 2005, 2007, 2018; Cox et al. 2011; King et al. 2015). Each enamel sample was mechanically cleaned of dirt and dentine with a steel scalpel, then dissolved in 3N ultrapure nitric acid and then purified enamel through columns of Sr-spec resin. Once dried down and loaded onto a tungsten filament, the  $^{87}\text{Sr}/^{86}\text{Sr}$  ratio in the sample was analyzed by thermal ionization mass spectrometry (TIMS) at the National Oceanography Centre (NOC). Seven additional samples (designated by an asterisk after the value in [Table 11.5](#)) were prepared and analyzed at Australian National University (ANU). In the ANU preparation procedure, 2N nitric acid was used to dissolve the enamel samples and run through the Sr columns, and  $^{87}\text{Sr}/^{86}\text{Sr}$  was measured on a Neptune multicollector ICP-mass spectrometer (MC-ICP-MS) within the ANU Research School of Earth Sciences. The consistent measurement of NBS 987 standard ( $^{87}\text{Sr}/^{86}\text{Sr} = 0.71025$ ) in both labs ensures that their respective results are comparable.

## Results

Once those traits with no variance were removed, as well as those traits with significant t-test results indicating marked intra-observer discrepancy, the final trait batteries consisted of 67 for the adult combined cranial, dental, and infracranial trait dataset; 24 for the permanent dentition, 31 for the cranial trait battery that included both adults and subadults, and 12

infracranial traits. [Table 11.1](#) presents the final trait batteries utilized here; 31 cranial traits from Man Bac and 14 permanent dental traits from Con Co Ngua. Additional cranial, dental, and infracranial traits scored and intra-observer error testing methodology are presented and discussed in Huffer (2012).

[Table 11.2](#) presents summary frequencies for those cranial traits (Man Bac) and dental traits (Con Co Ngua) showing even minimal variation in expression. Frequencies range from those in the 3%–5% range (e.g., coronal ossicle, bregmatic ossicle, UI1 lingual spines, UM1 Carabelli’s trait; all with only one individual scored present) to approximately 80% (zygomaxillary tubercle presence; with 20 individuals scored present). For subadults, trait frequency expression ranges from approximately 4% to 5% (all those traits with one individual scored as present), to nearly 86% (zygomaxillary tubercle presence; 12 individuals scored present). In this initial analysis of the Man Bac assemblage, six clusters were produced of mixed demographic profiles and with little spatial segregation. [Figures 11.2 and 11.3](#) show the cluster affiliation and spatial positioning, respectively, of each individual within the resultant dendrogram, while [Table 11.3](#) gives the demographic composition of each cluster.

INSERT FIGURE 11.2 HERE

INSERT FIGURE 11.3 HERE

INSERT TABLE 11.3 HERE

For cluster analysis of the Con Co Ngua sample, a total of fourteen adult dental traits were retained (see [Table 11.1](#)), with the resultant dendrogram shown in [Figure 11.4](#), and the demographic composition of each suggested kin group provided in [Table 11.4](#). Five clusters were suggested based on the dental data alone. The trait frequency ([Table 11.2](#)) results for Con Co Ngua dental traits are relatively similar to those from Man Bac presented in Huffer (2012). When compared to Man Bac, markedly more maxillary molar crown reduction

(metacone and hypocone), and a greater incidence of incisor shoveling and maxillary molar root variation is seen in the Con Co Ngua sample.

INSERT TABLE 11.4 and HERE

INSERT FIGURE 11.4 HERE

## Strontium Isotopic Results

Table 11.5 details the  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios for Man Bac and Con Co Ngua, respectively. Figure 11.5 shows the mean and distribution (1 and 2 standard deviations) of the  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios for Con Co Ngua and Man Bac by overall sample and by sex (extreme outliers were removed before calculating the sample means). For comparative purposes, a single faunal specimen (*Canis familiaris* maxillary canine) sampled from Man Bac as well as the value for seawater has been added. The mean  $^{87}\text{Sr}/^{86}\text{Sr}$  ratio for the Con Co Ngua sample as a whole (including indeterminate sex adults) is 0.70947 ( $N = 40$ , SD 0.00017), with males 0.70952 ( $N = 16$ , SD 0.00017) and females 0.70946 ( $N = 21$ , SD 0.00013) having similar means ( $p = 0.256$ , two-tailed t-test) and distributions of values. In terms of these group statistics from Con Co Ngua, the mean  $^{87}\text{Sr}/^{86}\text{Sr}$  ratio is within two standard deviations of the seawater  $^{87}\text{Sr}/^{86}\text{Sr}$  ratio (0.7092). For context, the mean among adults at Con Co Ngua is virtually identical to the mean among adult females at the coastal site of Khok Phanom Di.

At Man Bac, the mean  $^{87}\text{Sr}/^{86}\text{Sr}$  ratio among the 26 individuals assessed (including adults of indeterminate sex) is 0.70916 (SD = 0.00010), with the male mean being 0.70913 ( $N = 14$ ; SD = 0.00012) and the female mean being 0.70921 ( $N = 10$ , SD = 0.00005). Both means are lower than the mean at Con Co Ngua, and the female mean at Man Bac is indistinguishable from the seawater  $^{87}\text{Sr}/^{86}\text{Sr}$  ratio. The means for the complete sample, males, females, and the isolated *Canis* value ( $0.709181 \pm 0.000009$ ), recovered from human burial MB2007H1M1, are all quite similar to the seawater value. The mean among females is higher than that observed among males, and this difference is nearly statistically significant ( $t$

= 1.961,  $p = 0.063$ , df 22). More notably, the standard deviation among the Man Bac female  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios is only 0.00005, whereas among the males it is 0.00012 excluding the outlier male (0.0074 including it). Even when we exclude the male outlier, the variance among males is significantly larger ( $p < 0.01$  by F-Test;  $p = 0.01$  by Levene's test).

INSERT TABLE 11.5 AND HERE

INSERT FIGURE 11.5 HERE

Figure 11.6 combines the strontium isotope ratios with the trait clusters for each site.

At Man Bac, this shows that males and females pooled from Groups 1–3 have significantly different  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios. Among Groups 1–3 at Man Bac (Figure 11.6, upper panel), the mean  $^{87}\text{Sr}/^{86}\text{Sr}$  among the six Man Bac females is  $0.70922 \pm 0.00005$ , whereas among the four males it is  $0.70906 \pm 0.00009$ . These means are different ( $p = 0.006$ , 2-tailed t-test). By contrast, no significant differences in  $^{87}\text{Sr}/^{86}\text{Sr}$  are present at Con Co Ngua (Figure 11.6, lower panel), either between groups or between sexes within groups.

INSERT FIGURE 11.6 HERE

## Discussion

The mean  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios from Man Bac, which are close to the seawater value ( $\sim 0.7092$ ) for both sexes and essentially identical among the females, are consistent with the coastal setting and a seafood component to the diet. While situated a little south of Man Bac, Con Co Ngua is also believed to have been coastal or relatively close to the sea during the time when the site was occupied. Nevertheless, the samples display slightly higher  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios, which suggest greater consumption of terrestrial foods from outside the immediate coastal zone. Preliminary (and unpublished) dietary isotope values for Man Bac indicate a significant sea food component to the diet, while the faunal assemblage at Con Co Ngua is dominated by wild buffaloes and cattle. The latter may have had similarly “coastal”  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios if those large herbivores fed on grasses growing on soils enriched in seawater strontium, as is

common in coastal environments (e.g., Whipkey et al. 2000). Considering the factors gravitating the  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios toward the seawater value at these two estuarine sites, the difference in mean values between Con Co Ngua and Man Bac is significant. The  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios can only tell us so much, however (e.g., Montgomery 2010), and the difference in faunal assemblages is probably stronger evidence that the diets consumed by the inhabitants of these two sites were different.

In terms of mobility, both communities were logistically mobile and reliant on broad-spectrum hunting-gathering-fishing, although rice agriculture and animal husbandry were underway at Man Bac (Oxenham and Matsumura 2011). The isotopic results may reflect patterns of migration, sex-based partner sourcing or foraging mobility. The relatively tight range of  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios for both Man Bac and Con Co Ngua (e.g., only two 2 standard deviation outliers at CCN and one at Man Bac) meant that little could be gained in comparing isotopic values to putative kin group clusters. Notwithstanding, two patterns are worth further exploration. The tight range of values observed for females at Man Bac as compared to the dispersed pattern for males might be indicative of a number of possible scenarios: differential patterns of food sourcing for males and females; greater levels of mobility for males; or sex-based residency rules with numerous possible permutations. What can be said, however, is that the same pattern of significantly smaller variation in  $^{87}\text{Sr}/^{86}\text{Sr}$  among females has been seen at Khok Phanom Di (Bentley et al. 2007) and at Ban Chiang (Bentley et al. 2005) in Southeast Asia, and that this pattern has almost never been observed in Neolithic continental Europe, where larger variation in  $^{87}\text{Sr}/^{86}\text{Sr}$  among females is found at regional and site-specific scales (e.g., Bentley 2013; Bentley et al. 2012).

In terms of trait clusters, the most notable feature of the Man Bac cranial trait cluster analysis is that age and sex demographic distributions within each cluster are suggestive of small family groups (i.e., first- to third-degree kin), assuming the burials were close to each

other in date. Although not every burial could be included due to a paucity of assessable traits, these data suggest that the Man Bac community consisted of extended-family lineages with relatively even numbers of males and females, and varying numbers of subadults. The spatial distribution of each cluster appears somewhat more segregated when subadults are included. The relatively unstructured distribution of purported lineage/kin group members within the Man Bac community is unsurprising, given that high mortality and fertility rates (Oxenham et al. 2008; Domett and Oxenham 2011) may have necessitated frequent burials, especially for subadults. Alternatively, an unstructured cemetery could also indicate that familial affiliation was irrelevant in death, or that kinship was expressed through means other than spatial proximity. Although enough time elapsed during the lifetime of the Man Bac community for mortuary ritual to develop (Huffer 2005; Oxenham et al. 2008), distinguishing at least somewhat separate genetic lineages allows further investigation of these questions.

The Con Co Ngua cemetery also appears to be composed of several kin groups, in a similar manner to Man Bac. The majority of groups derived from the *Clustan* analysis, except for cluster 2, are of mixed sex, suggesting that they comprise the adult members of extended families or lineages. Although cluster 2 contains all females (except for the indeterminate individual), this distribution was not significant ( $\chi^2 = 1.85$ ;  $p = 0.6$ ). Demographically, the Con Co Ngua clusters do not have significantly different numbers of males and females.

An alternative interpretation of the dendrograms is that we are observing random interindividual variation between lineages within a small population over the many generations represented by these samples. Even if some individuals were not genetically more related to others, clusters would still result, given the likely high degree of both inter- and intraindividual relatedness between lineages (*Clustan* deliberately highlights those clusters and dendrograms with significance at or below alpha). Nevertheless, in any community for which a cemetery was used to demarcate a claim to ancestral land or

resources, being able to identify kin groups should not be surprising, as it is likely that every family in a community would seek to obtain equal claims due to inclusion of their own kin or lineage members. Only in rare situations, such as the interment of war casualties from an army in a mass grave, might a lack of kinship among a (presumably) all-male cemetery assemblage be expected (Stojanowski and Schillaci 2006). In the case of Man Bac, the presence of at least somewhat distinguishable kin groups who were for the most part not buried in close proximity, segregated by lineage, or rigidly defined by mortuary treatment further suggests communality. This is reminiscent, on a much smaller scale, of the distinction between genetic and social/practical kin groups that Pilloud and Larsen (2011) argue existed for Çatalhöyük in Turkey, in which burial under the floor of a specific house was only minimally correlated with genetic kinship, and the site as a whole was not arranged into so-called neighborhoods of related families.

General genetic population affinities may reflect two distinct genetic populations (Australo-Papuan and East Asian) present at Man Bac (see Matsumura et al. 2008, Matsumura and Oxenham 2014; Lipson et al. 2018), rather than the presence of first- or second-degree kin (i.e., brothers, sisters, uncle-nephew, aunt-niece). This does not rule out the possibility that second- or third-degree kin (i.e., cousins) from different natal communities belonging to the phenotypically distinct Australo-Melanesian population integrated into Man Bac independently. The demographic composition of most of the groups extracted using cluster analysis was found to be substantially mixed, containing primarily mature adult individuals less suggestive of descent-based consanguine kin.

Comparison between the two samples suggests that general social organizational patterns did not change much during the Neolithic agricultural and demographic transition in northern Vietnam. Even though interment form changed from a more mixed pattern of single, double, and mass burials at Con Co Ngua to solely individual extended supine interments at

Man Bac, spatial organization remained unstructured; genetically related interments tend not to cluster together. The suggested lack of marked change is somewhat surprising, but if early farming remained a somewhat marginal activity (see Oxenham 2015; Oxenham and Buckley 2016) not controlled by specific elite individuals or their families, then the rise of incipient hierarchies need not eliminate communal burial.

Even though interment form changed from a more mixed pattern of single, double, and mass burials at Con Co Ngua to exclusively single individual extended supine interments at Neolithic Man Bac, spatial organization within these cemeteries appears to have remained unstructured. The main objective of this chapter was to throw light on any potential changes in social organization, particularly with respect to biosocially mediated kin group organization (using nonmetric dental traits and  $^{87}\text{Sr}/^{86}\text{Sr}$  signatures) in two cemetery samples from northern Vietnam: pre-Neolithic Con Co Ngua and early Neolithic Man Bac. Indeed, one of the chief emergent patterns seen in this study is the identification of putative biologically defined kin groups in both the pre-Neolithic hunter-gather Con Co Ngua series as well as the Neolithic Man Bac assemblage. Moreover, spatial propinquity does not appear to have been an important factor in the layout of the Man Bac cemetery. One obvious reason for this may simply relate to the observation that affinal kin were presumably an important part of whatever kin-mediated relationships operated at Man Bac in antiquity. Given the relative homogeneity of grave furnishings, which appear more related to age-based status than any other biosocial variable (Oxenham et al. 2008), it is unlikely that we will ever be able to disentangle the issue of archaeologically invisible affines. For Con Co Ngua the task is made the more difficult due to a lack of any spatial information regarding the burials themselves, in addition to an almost complete dearth of burial furnishings. Notwithstanding, a recent re-excavation of Con Co Ngua by one of us (MFO), which uncovered over 160 additional burials, may help us address this issue in the near future. An intriguing situation



has emerged in that little change seems to have occurred, in terms of kin-based social organization, following the NDT if the evidence from Man Bac and Con Co Ngua are anything to go by.

## Conclusions

It is reasonable to assume that kinship was the primary social organizing principle of past human societies (e.g., Fox 1983). We should expect kinship lineage systems, maintained over numerous generations, often to have influenced prehistoric mortuary practices. For example, matrilineal or patrilineal residence patterns make it more likely that nonlocal males or females, respectively, would be buried along with the local community burial grounds. In Neolithic Europe, for example, the within-site consistency of position and cardinal orientation of burials, usually consistent within a cemetery or settlement, were probably of fundamental importance (e.g., Jeunesse 1997; Bradley 2001, Nieszery 1995; Veit 1993) and most likely underwritten by a patrilineal kinship system (Bentley et al. 2002, 2008:9; Haak et al. 2008; Lacan et al. 2011; Fortunate and Jordan 2014). By contrast, in parts of Neolithic Thailand, a matrilineal kinship system appears to have determined burial contents, sexes represented, and spatial arrangements of cemetery populations (Higham and Thorsorat 1994; Bentley et al. 2005, 2007).

Kinship and community organization during the transition to agriculture in northern Vietnam might be put into perspective by comparison with Neolithic Europe, where there exists a vast amount of evidence from multiple disciplines. For Neolithic Europe, multiple forms of evidence—including skeletal, isotopic, genetic, and linguistic—the prevailing hypothesis is one of widespread patrilineal kinship systems (e.g., Bentley 2013; Brandt et al. 2014, and references therein), even if local variation in those systems can never be completely understood. In mainland Southeast Asia, by contrast, kinship inferred by linguistic, genetic, and skeletal-isotopic evidence from Thailand and mainland Southeast Asia

have suggested matricentric kinship systems were present, if not necessarily the rule in all places and among a larger range of variation. Given the landscape of different forms of evidence, a reasonable hypothesis is that kinship systems underlie—whether through diet, marital residence and/or gender-specific subsistence practices—the smaller variance in strontium isotope signatures among females that is observed at Man Bac.

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Table 11.1

Final retained trait battery for both Man Bac and Con Co Ngua. Most traits were designated as absent (0) or present (1), while some (bottom of table) were designated absent, partial, or complete. For those traits that had an ordinal value converted to a presence/absence state, the threshold value is indicated: for example “2+ = present” means that the trait was scored by whole number values and any score equal to or greater than 2 was counted as present, and less than 2 counted absent.

Cranial Traits (Man Bac)	Dental Traits (Con Co Ngua)
<b>Present/absent traits</b>	
Apical ossicle	LM1 3 root variant
Asterionic ossicle	LM1 cusp 6 (2+ = present)
Bregmatic ossicle	LM1 cusp 7 (2+ = present)
Coronal ossicle	LM2 cusp 5 (2+ = present)
Infraorbital suture	LPM2 premolar lingual cusp (present = 2+ cusps)
Lambdoid ossicle	UI1 lingual spines
Mastoid foramen	UI2 labial convexity (3+ = present)
Mastoid foramen number	UI2 shoveling 2+ = present)
Mental foramen number (2+ = present)	UM enamel extension
Metopic suture	UM1 Carabelli’s trait (2+ = present)
Multiple infraorbital foramina (2+ = present)	UM2 hypocone reduction (4+ = present, i.e., reduced)
Mylohyoid bridge	UM2 metacone reduction (4+ = present, i.e., reduced)
Occipito-mastoid ossicle	UM2 root number (absent = 3 roots)
Palatine articulation (curved = present)	UPM1 double root
Palatine torus (1–3 = present)	
Parietal foramen	
Parietal notch bone	

Pterion ossicle	
Sagittal ossicle	
Supraorbital foramen (1–4+ = present)	
Supraorbital notch	
Trochlear spur	
Zygomatic foramen	
Zygomaxillary tubercle	
Zygomaxillary tubercle location	
<b>Three-category traits (absent, partial, or present)</b>	
Condylar canal	UI2 pegging
Divided hypoglossal canal	UM3 pegging
Foramen ovale incomplete	
Foramen spinosum incomplete	
Mylohyoid bridge degree	
Tympanic dehiscence	

Table 11.2

Male, Female, and Combined Trait Frequencies; Man Bac and Con Co Ngua

Trait	Cranial traits; Man Bac			Trait	Dental traits; Con Co Ngua	
	Male	Female	Combined		Male	Female
Metopic suture	n.d.	2/12 (16.6%)	2/29 (6.8%)*	UI2 shoveling	2/6 (33.3%)	n.d.
Supraorbital notch	13/18 (72.2%)	7/13 (53.8%)	36/58 (62%)	UI2 labial convexity	3/7 (42.8%)	3/8 (37.5%)
Supraorbital foramen	8/18 (44.4%)	7/12 (58.3%)	22/58 (37.9%)	UI1 lingual spines	1/6 (16.6%)	n.d.
Infraorbital suture	4/13 (30.7%)	n.d.	6/25 (24%)	UI2 pegging	1/7 (14.2%)	n.d.
Multiple infraorbital foramina	4/13 (30.7%)	2/9 (22.2%)	7/37 (18.9%)	UM1 Carabelli's trait	n.d.	n.d.
Zygomatic foramen	18 (72.2%)	6/11 (54.5%)	19/55 (34.5%)	UM2 hypocone reduction	7/11 (63.6%)	17/21 (80.9%)
Parietal foramen	4/18 (22.2%)	n.d.	5/40 (12.5%)	UPM1 double root	1/15 (6.6%)	4/16 (25%)
Trochlear spur	n.d.	1/9 (11.1%)	2/22 (9%)	UM2 metacone reduction	4/15 (26.6%)	4/21 (19%)
Zygomaxillary tubercle	13/16 (81.2%)	7/9 (77.8%)	32/39 (82%)	UM2 root number	3/9 (33%)	7/17 (41.2%)
Zygomaxillary tubercle location	8/16 (50%)	6/13 (46.1%)	21/43 (48.8%)	UM3 pegging	7/10 (70%)	9/21 (42.9%)

Pterion ossicle	2/9 (22.2%)	n.d.	2/9 (22.2%)*	LM2 cusp 5	3/9 (33.3%)	3/20
Coronal ossicle	1/17 (5.8%)	n.d.	1/17 (5.8%)*	LM1 cusp 6	1/4 (25%)	n.d.
Bregmatic ossicle	1/17 (5.8%)	n.d.	1/17 (5.8%)*	LM1 cusp 7	1/9 (11.1%)	1/17
Saggital ossicle	2/18 (11.1%)	2/13 (15.3%)	4/31 (12.9%)*	LM1 3 root var	2/7 (28.5%)	1/15
Apical ossicle	2/17 (11.7%)	1/11 (9%)	4/45 (8.8%)			
Lambdoid ossicle	9/17 (52.9%)	8/12 (66%)	23/45 (51.1%)			
Asterionic ossicle	4/15 (26.6%)	3/11 (27.2%)	7/26 (26.9%)*			
Occipito-mastoid ossicle	2/15 (13.3%)	1/10 (10%)	3/25 (12%)*			
Parietal notch bone	3/16 (18.7%)	1/11 (9%)	5/27 (13.5%)			
Palatine articulation	3/10 (30%)	2/7 (28.5%)	8/24 (33.3%)			
Palatine torus	2/18 (11.1%)	n.d.	3/30 (10%)			
Mental foramen number	1/19 (5.2%)	n.d.	6/49 (12.2%)			
Mylohyoid bridge	6/18 (33.3%)	2/12 (16.6%)	12/50 (24%)			
Mylohyoid bridge degree	4/18 (22.2%)	2/12 (16.6%)	10/50 (20%)			
Condylar canal	3/6 (50%)	2/7 (28.5%)	11/23 (47.8%)			
Divided hypoglossal canal	6/15 (40%)	n.d.	7/36 (19.4%)			
Foramen ovale incomplete	9/12 (75%)	10/13 (76.9%)	21/38 (55.2%)			
Foramen spinosum incomplete	3/9 (33.3%)	6/11 (54.5%)	13/40 (32.5%)			
Tympanic dehiscence	7/17 (41.1%)	4/13 (30.7%)	17/48 (35.4%)			
Mastoid foramen	8/19 (42.1%)	4/12 (33.3%)	12/31 (38.7%)*			
Mastoid foramen number	8/19 (42.1%)	4/12 (33.3%)	12/31 (38.7%)*			

\* = Combined frequency percentage calculated from sexed adolescent/adult subassemblage only; trait not scorable in subadults.

Table 11.3

Demographic Composition of Kin Groups, Undichotomized Cranial Traits for Man Bac

Burial #	Age Estimate	Age Class	Sex	Kin Group #	Burial #	Age Estimate	Age
ClassSex	Kin Group #						
MB1999M1	16–18 months	YC	Indt.	1	MB2007H1M1	12–13 yrs	OC
MB2001M1	9–10 yrs	C	Indt.	1	MB2007H1M3	12–18 yrs	OC
MB2001M9	N/A	A	F	1	MB2007H2M8	18–24 months	YC
MB2005M9	40–49 yrs	MA	F	1			
MB2007H2M13	4–5 yrs	YC	Indt.	1	MB1999M5a	4–5 yrs	YC
MB2007H2M24	40–49 yrs	MA	F	1	MB2005M5	1–2 yrs	YC
MB2007H2M30	30–39 yrs	MA	M	1	MB2005M10	9–10 yrs	C
MB2007H2M31	4–5 yrs	YC	Indt.	1	MB2005M12	2–3 yrs	YC
					MB2005M13	16–18 yrs	OC/YA
MB2001M10	38–40 yrs	MA	M	2	MB2005M28	15–29 yrs	YA
MB2005M4	2–3 yrs	YC	Indt.	2	MB2005M29	30–39 yrs	MA
MB2007H2M1	40–49 yrs	MA	M	2	MB2005M34	40–49 yrs	MA
MB2007H2M7	18–24 months	YC	Indt.	2	MB2007H1M5	40–49 yrs	MA
MB2007H2M12	50+ yrs	MA	F	2	MB2007H1M8	30–39 yrs	MA
MB2007H2M27	30–39 yrs	MA	M	2	MB2007H1M9	20–29 yrs	YA
					MB2007H1M11	50+ yrs	MA
MB2005M15	17–18 yrs	YA	F?	3	MB2007H2M19	20–24 yrs	YA
MB2005M18	18–20 months	YC	Indt.	3	MB2007H2M32	25+ yrs	YA
MB2005M30	6 months	YC	Indt.	3			
MB2005M31	20–29 yrs	YA	M	3	MB2001M4a	6–8 months	YC
MB2007H1M4	30+ yrs	MA	F	3	MB2001M5	50–60 yrs	MA
MB2007H1M6	6–9 months	YC	Indt.	3	MB2005M3	6–8 months	YC
MB2007H2M2	12–18 yrs	OC	Indt.	3	MB2005M7	neonate	YC
MB2007H2M16	18–24 months	YC	Indt.	3	MB2005M14	2–5 yrs	YC
MB2007H2M18	18–24 yrs	YA	F	3	MB2005M21	5–6 months	YC
MB2007H2M26	18–24 months	YC	Indt.	3	MB2007H1M10	40–49 yrs	MA
MB2007H2M28	neonate	YC	Indt.	3	MB2007H2M5	20–29 yrs	MA
					MB2007H2M6	2–3 yrs	YC

MB1999M2	18–20 yrs	YA	F	4	MB2007H2M10	30–39 yrs	MA
MB1999M3	18–20 yrs	YA	F	4	MB2007H2M14	neonate	YC
MB1999M5b	30–50 yrs	MA	M	4	MB2007H2M15	4–5 yrs	YC

MA mature adult, A adult, YA young adult, C child, YC young child, F female, M male, Indet. Indeterminate

Table 11.4

Demographic Composition of Kin Groups, Undichotomized Dental Traits for Con Co Ngua

Burial #	Age Class	Sex	Kin Group #	Burial #	Age Class	Sex	Kin Group #
CCNM2	MA	F	1	CCNM58	MA	M	3
CCNM25	MA	Indt.	1				
CCNM31	MA	F	1	CCNM3	MA	M	4
CCNM33e	MA	M	1	CCNM17	MA	F	4
CCNM35a	MA	F	1	CCNM26	MA	F	4
CCNM35b	Indt.	F	1	CCNM33a	MA	M	4
CCNM37	MA	F	1	CCNM39	MA	M	4
CCNM48	MA	F	1	CCNM62	MA	F	4
CCNM49	YA	Indt.	1	CCNM66	MA	F	4
CCNM71	YA	F	1				
CCNM72	MA	Indt.	1	CCNM14a	YA	M	5
CCNM87	MA	Indt.	1	CCNM47	OC	Indt.	5
CCNM33b	MA	M	1	CCNM79	MA	F	5
CCNM36	MA	M	1	CCNM18	MA	F	5
CCNM75R	MA	F	1	CCNM43	MA	M	5
CCNM44	MA	F	1	CCNM64	MA	F	5
CCNM53	MA	F	1	CCNM85	MA	M	5
				CCNM97	MA	F	5
CCNM11	YA	Indt.	2				
CCNM74	MA	F	2				
CCNM81	MA	F	2				
CCNM30	YA	F	2				
CCNM82	MA	F	2				

MA mature adult, YA young adult, F female, M male, Indet. Indeterminate

Table 11.5

## Strontium Isotopic Results for Man Bac and Con Co Ngua

Man Bac							
Burial #	Sex	87Sr/86Sr*	± 2 S.E.	Burial #	Sex	87Sr/86Sr*	± 2 S.E.
MB2005M9	F	0.709178*	0.00016	MB2007H1M13b	Indt.	0.709047*	0.00018
MB2005M11	M	0.71197	0.00001	MB2007H2M1	M	0.709	0.00001
MB2005M15	F	0.70919	0.00001	MB2007H2M2	Indt.	0.70922*	0.00001
MB2005M20	M	0.70919	0.00001	MB2007H2M5	F	0.70924	0.00000
MB2005M28	F	0.70912	0.00001	MB2007H2M10	M	0.70939	0.00004
MB2005M29	M	0.70899	0.00001	MB2007H2M12	F	0.70919	0.00001
MB2005M31	M	0.70907	0.00001	MB2007H2M18	F	0.709195*	0.00015
MB2005M32	M	0.70927	0.00001	MB2007H2M19	M	0.70903	0.00001
MB2005M34	F	0.70923	0.00001	MB2007H2M22	F	0.709209*	0.00026
MB2007H1M4	F	0.70928	0.00001	MB2007H2M24	F	0.70928	0.00001
MB2007H1M5	M	0.709184*	0.00015	MB2007H2M27	M	0.70918	0.00015
MB2007H1M8	M	0.709124*	0.00001	MB2007H2M30	M	0.70898	0.00001
MB2007H1M9	M	0.70924	0.00001	MB2007H2M32	M	0.70916	0.00001
MB2007H1M10	M	0.70903	0.00001				
Con Co Ngua							
Burial #	Sex	87Sr/86Sr*	± 2 S.E.	Burial #	Sex	87Sr/86Sr*	± 2 S.E.
CCNM2 ILM3	F	0.709252	0.00012	CCNM36 ILM3	M	0.709405	0.000017
CCNM3 ILM3	M	0.709412	0.00013	CCNM38 rNUM3	M	0.709372	0.000012
CCNM5a ILM3	F	0.709282	0.00012	CCNM39 ILM3	M	0.709585	0.000013
CCNM7a rLM3	M	0.709623	0.00012	CCNM44 rLM3	F	0.709619	0.000005
CCNM8a ILM3	M	0.709481	0.00027	CCNM45 ILM3	F	0.709543	0.000010
CCNM12 rUM3	M	0.709356	0.00021	CCNM48 ILM3	Indt.	0.709385	0.000012
CCNM14a rUM3	M	0.709741	0.00018	CCNM52 ILM3	F	0.709383	0.000011
CCNM15 rLM3	M	0.709393	0.00016	CCNM53 rLM3	F	0.709362	0.000021
CCNM16 ILM3	M	0.709666	0.00017	CCNM58 ILM3	M	0.709459	0.000017
CCNM17 rLM3	F	0.709482	0.00019	CCNM62 ILM3	F	0.709635	0.000015
CCNM18 rLM3	F	0.709333	0.00018	CCNM63 ILM3	F	0.709431	0.000019
CCNM22 ILM3	M	0.709457	0.00016	CCNM65 ILM3	M	0.709744	0.000010
CCNM23 rUM3	M	0.709338	0.00018	CCNM67 ILM3	Indt.	0.709556	0.000020
CCNM27 ILM3	F	0.709391	0.00020	CCNM71 rUM3	F	0.709267	0.000024
CCNM30 rLM3	F	0.709418	0.00013	CCNM74 ILM3	F	0.709520	0.000010
CCNM31 ILM3	F	0.709318	0.00012	CCNM75R ILM3	F	0.709587	0.000013
CCNM33a ILM3	M	0.709327	0.00016	CCNM81 rUM3	F	0.709562	0.000011
CCNM33b ILM3	Indt.	0.709005	0.00019	CCNM82 rLM3	F	0.709528	0.000012
CCNM33c ILM3	F	0.709495	0.00016	CCNM85 rLM3	M	0.709896	0.000010
CCNM35a ILM3	F	0.709481	0.00015	CCNM97 ILM3	F	0.709735	0.000020

Figure 11.1



Geologic map of northern Vietnam, showing known bedrock variation. Dots mark locations of Man Bac (orange) and Con Co Ngua (gold). Original from Nam (1995).

Figure 11.2

Kin group dendrogram, Man Bac undichotomized cranial traits.

Figure 11.3

Spatial distribution of kin groups, undichotomized cranial traits.

Figure 11.4

Kin group dendrogram, Con Co Ngua undichotomized dental traits.

Figure 11.5

Mean and distribution (1 and 2 standard deviations) of the  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios for Con Co Ngua and Man Bac by overall sample and by sex.

Figure 11.6

Strontium isotope ratios combined with the trait clusters for each site. Circles, females, triangles, males, and crosses for indeterminate sex.