Dental Morphological Analysis of Roman Era Burials from the Dakhleh Oasis, Egypt

Scott Donald Haddow

Institute of Archaeology

University College London

PhD Thesis

2012

I, Scott Donald Haddow, confirm that the work presented in this thesis is my own. Where information has been derived from other sources, I confirm that this has been indicated in the thesis.

_____

ABSTRACT

Ismant el-Kharab (ancient Kellis) is an archaeological site in the Dakhleh Oasis, Egypt, which dates from the late Ptolemaic to the late Roman period. Previous studies of skeletal material from Kellis and other oasis sites suggest that the ancient population of the Dakhleh Oasis was largely homogenous and inbred as a result of geographic isolation. Archaeological and textual evidence however, indicates a record of contact with the Nile Valley and regions further afield since the Neolithic. In order to test these apparently conflicting narratives, descriptive and multivariate statistical methods are employed in an analysis of heritable dental morphological variants in 186 individuals from Kellis. Variation in dental morphological trait frequencies are commonly used in biological distance studies to assess phenetic relationships between groups. The present study has two main components: 1) an intra-cemetery assessment of inter-sex and inter-group morphological variation in order to identify related individuals within the Kellis 2 cemetery and provide evidence for post-marital residence patterns; and 2) an inter-regional comparison between the Kellis skeletal assemblage and groups from Egypt, Nubia, North and Sub-Saharan Africa in order to place the ancient Dakhleh Oasis population within a broader regional context.

The results of the intra-cemetery analysis demonstrate low levels of inter-sex phenetic variation consistent with an isolated and possibly interbred population. Spatial analysis within the Kellis 2 cemetery has tentatively identified one area containing individuals with distinctive dental trait frequencies. This may indicate a kin-structured area of the cemetery, or alternatively, an area reserved for individuals who are not native to the Dakhleh Oasis. The results of the inter-regional comparison of trait frequencies demonstrate an overall affinity with North African populations, especially with several early Upper Egyptian and contemporary Lower Nubian groups. Despite these similarities, however, the Kellis assemblage remains relatively distinct in relation to the comparative groups. This is consistent with a geographically isolated population experiencing limited gene-flow.

Acknowledgements

I am extremely grateful to the following people, without whose support and assistance this thesis could not have been completed. I am forever indebted to Professor Simon Hillson, my PhD supervisor, for his guidance and support, as well as his patience and good humour. I'd like to thank Dr. Anthony Mills for allowing me to join the Dakhleh Oasis Project and Dr. Joseph "El" Molto for granting me permission to study the skeletal material from Kellis. I thank Professor Joel Irish for graciously allowing me to use his dental morphological data in my comparative analyses and providing useful feedback. I am grateful to Professor Clive Orton for helping me immensely when I was struggling with the statistical component of my thesis and Professor John Tait for giving me advice regarding Egyptology. I also thank Professor Nancy Lovell for providing helpful comments on the final draft of this thesis and my examiners Dr. Sonia Zakrzewski and Dr. Richard Bussman for their constructive criticisms during my viva. Finally, I thank my family and especially my wife Camilla for providing me with the inspiration, motivation and support (both financial and emotional) I needed in order to finish after so many years!

This research was partially funded by a Social Sciences and Humanities Research Council of Canada (SSHRC) Doctoral Fellowship.

Table of Contents

List of Tables

List of Figures

Chapter 1

Introduction

The aim of the present study is to examine biological variability within a late Roman period cemetery (Kellis 2) in the Dakhleh Oasis, Egypt, through the observation of hereditary morphological dental traits. Additionally, the Kellis assemblage will be compared with dental trait data for other Egyptian sites and for non-Egyptian populations within a broader regional context. The burials derive from the site of Kellis (modern Ismant el-Kharab), a large town in existence from the Ptolemaic through to the late Roman period (Hope 2001). As part of a larger program of ongoing bioarchaeological research in the Dakhleh Oasis, the present study will contribute significantly new and complementary data to the biological analysis of this ancient population. By virtue of its size and exceptional preservation, the Kellis skeletal assemblage is an ideal assemblage for studies of this kind. In addition, the geographically isolated nature of the Dakhleh Oasis and its population provides an excellent opportunity for assessing gene flow between the Western Desert, the Nile Valley and beyond. The present study has two main components: 1) an intracemetery analysis of biological variation between Late Roman individuals within Kellis; and 2) an intercemetery analysis of biological variation between the Kellis assemblage and comparative assemblages within a wider regional context.

Based on previously conducted analyses of the Kellis skeletal assemblage (c.f. Molto 2002), the organization of the Kellis 2 cemetery appears to

represent familial groupings. The work of Corrucini and others (e.g. Corrucini 1998; Corrucini and Shimada 2002; Fix 1993; Howell and Kintigh 1996) suggests that kin-groups are likely to share more hereditary skeletal and dental morphological traits than non kin-group members. Additionally, other researchers have used morphogenetic traits to analyze intracemetery variation between males and females relating to postmarital residence patterns (e.g. Schillaci and Stojanowski 2003; Konigsberg 1988). An analysis of inter-sex and inter-group spatial variation of dental morphological traits within the Kellis 2 assemblage is aimed at addressing these issues.

While the Dakhleh Oasis has cultural associations with the Nile Valley and regions further afield which date back to the Neolithic, the biological relationships between the inhabitants of the oasis and other North African populations is not well understood. Comparisons with regional groups are undertaken in order to assess the Kellis assemblage's biological affinities. As such, the present study aims to test the following hypotheses:

1. *Phenotypic variability between Kellis males and females will indicate post-marital residence status, whereby one sex is more mobile (marrying into the community from elsewhere) and the other stationary (resident to the community from birth).*

2. *Burials located closer together will share more dental traits than those located further apart. Such clustering of dental traits will represent kin group burial areas within the Kellis 2 cemetery.*

3. *The Kellis assemblage will share genotypic/phenotypic features with Nile Valley groups as a result of cultural, political and economic ties between the two regions beginning in the Neolithic period.*

4. *The Kellis sample will contain a Nubian/Sub-Saharan genotypic/phenotypic component as a result of north-south gene flow.*

1.1 Materials and methods

The first systematic archaeological exploration of Kellis began in 1981 by members of the Dakhleh Oasis Project (Knudstad and Frey 1999). Early work focused on the survey and mapping of the entire settlement; later, test excavations of prominent architectural remains such as churches and temples were carried out (Knudstad and Frey 1999). Mortuary complexes associated with Kellis were found within the town itself, and in cemeteries immediately northwest (Kellis 1) and north (Kellis 2) of the townsite (Birrell 1999; Hope and McKenzie 1999; Knudstad and Frey 1999). Human remains from Kellis 1 were interred in rock-cut tombs dating to the Ptolemaic and Early Roman Periods, while the Kellis 2 burials and others recovered from within the settlement are associated with the Late Roman Period, between 300 and 400 AD (Molto 2001). The Kellis 1 burials are clearly interred in the mortuary tradition of the Late Pharaonic Period (i.e. mummification, elaborate wrappings and cartonnage, ample grave goods), with up to 33 individuals occupying a single tomb (Molto 2001:84). The townsite burials and the Kellis 2 cemetery, however, represent a departure from traditional

Pharaonic Egyptian burial practice. Burials consist of simple east-west extended inhumations with minimal grave inclusions and little evidence for mummification, all of which are indicative of early Christian burial practices (Birrell 1999; Hope and McKenzie 1999; Molto *et al.* 2003).

Because the majority of burials from Kellis 1 are mummified (n=44), and many of them from disturbed contexts (Molto 2001), they are unsuitable for dental morphological analysis as this would require invasive action to access the teeth. They are not, therefore, included in the present study. The majority of the burials employed in the present study derive from the Kellis 2 cemetery, which has yielded 701 individuals to date. Of an estimated 3000 to 4000 burials, this represents between 18 to 23% of the total cemetery population (Molto 2002). At the time of data collection for the present study (2003-2004), 581 individuals had been excavated and were available for study. Of these, however, observations of the permanent dentition could only be made on 172 individuals, due to the number of juveniles and older adults which make up a sizeable proportion of the assemblage. With the addition of 14 contemporaneous individuals from tombs within the Kellis settlement itself, the total number of individuals used in the present study rises to 186.

In order to assess the biological relationships between individuals within the late Roman Kellis skeletal assemblage, observation and scoring of 30 permanent dental morphological (or nonmetric) traits has been conducted. Various studies have demonstrated that dental morphology is influenced by the microevolutionary forces of admixture (e.g. Turner 1969), mutation (e.g.

Morris *et al.* 1978), genetic drift (e.g. Turner 1969; Scott and Dahlberg 1982), and selection (e.g. Dahlberg 1963; Scott and Turner 1988). The underlying assumption in all non-metric trait analyses is that trait expression, or phenotype, will approximate the underlying genotype, and thus allow for the delineation of biological relationships within and between groups (Schwartz 1995).

Previously conducted analyses on portions of the Kellis skeletal assemblage have demonstrated spatial concentrations of certain hereditary nonmetric cranial traits (accessory optic canal, trochlear spur, metopism, and fronto-temporal articulation) within the site which have been interpreted as evidence for familial ties (Molto 2001). In addition, Henderson's (1993) study of craniometric data from Kellis and other sites within the oasis is suggestive of a largely homogeneous population with limited inter-regional gene flow. The high occurrence of *spina bifida occulta* in the oasis is another indicator of an inbred, isolated population (Parr 2002). In contrast to the picture of a remote, isolated population, however, is archaeological and textual data which indicate extensive links between the oasis and the Nile Valley during the Greco-Roman period (Gardner *et al*. 1999; Mills 1999; Worp 1995), which would have provided ample opportunity for the exchange of peoples as well as goods. This is borne out by a preliminary analysis of mitochondrial DNA sequences derived from a small subset of the Kellis 2 skeletal sample, which demonstrates high levels of maternal genetic diversity (Parr 2002).

In order to help address these apparently conflicting results, dental morphological data for the Kellis assemblage will be compared with comparative groups from Egypt, Nubia, North Africa and Sub-Saharan Africa. The aim is to identify those groups which share the closest phenetic relationships with the Kellis assemblage.

1.2 Significance of the present study

Ongoing research has revealed important new information on the cultural, political and economic relationships between the Dakhleh Oasis and the Nile Valley. The biological relationships between the oasis and its neighbours, however, remain unclear. Who were the people of the Dakhleh Oasis? Does the population expansion witnessed during the Roman period represent the influx of newcomers to the oasis, or a natural increase resulting from improvements in irrigation techniques? The addition of dental morphological trait frequencies for the entire Late Roman Kellis assemblage will help to address these questions by providing complementary data to compare with the previously conducted skeletal and mitochondrial DNA studies. By assessing inter-sex levels of biological variability within the Kellis assemblage, the present study will also contribute to an assessment of postmarital residence patterns, another important factor in evaluating the biological structure of the ancient Dakhleh Oasis population and their relationships to the wider region.

Chapter 2

The Culture-history of the Dakhleh Oasis, Egypt

2.1 Geography and environment

The Dakhleh (English: *Inner*) Oasis is one of the five principal oases located in the Western Desert of Egypt, and situated approximately 550 km south-southwest of Cairo at roughly the same latitude as Luxor in the Nile Valley (Figure 2.1). Like the other oases in the Western Desert (Siwa, Bahariya, Farafra and Kharga), Dakhleh is essentially a large depression in the desert floor covering an area between 3000 and 2000 km^2 of flat, clay plain, bounded to the north by a steep limestone escarpment (Figure 2.2). The southern, western and eastern boundaries of the oasis are less distinct, as the gradually rising floor of the depression disappears beneath the shifting sand dunes of the surrounding desert. It is roughly 60 km long from east to west, and a maximum of 25 km from north to south (Kleindienst *et al.* 1999). Dakhleh's nearest neighbour is Kharga Oasis, located roughly 120 km to the east, followed by Farafra Oasis, approximately 200 km to the northwest. In ancient times, the Dakhleh and Kharga Oases were often collectively referred to as the Great Oasis (Oasis Magna) and this is mirrored today in the Egyptian government's designation of the region as "The New Valley" (Arabic: *El-Wadi el-Gedid).*

The oases of the Western Desert are made habitable through access to water, although this access derives not from the skies, in the form of precipitation, but rather from below. Lying deep beneath much of the

Western Desert is one of the largest groundwater reserves in the world (Schild and Wendorf 1977). This massive underground reservoir, which forms part of the basal stratigraphic unit known as the Nubian Formation, consists of several deep water-bearing sandstone strata which are overlain by impervious shale beds nearer the surface. These shale strata essentially seal the water within the porous sandstone; it is only in the oasis depressions, often more than 100m below the desert plateau level, that these vast reservoirs are near enough to the surface to escape via artesian pressure through cracks in the shale bed (Giddy 1987). These natural spring mounds or vents would have attracted and sustained a variety of flora and fauna, including humans. Evidence for rudimentary well-digging has been identified in Dakhleh as far back as the Palaeolithic (Schild and Wendorf 1977), and by the 5th century AD, historian Olympiodorus of Thebes noted that the oasis dwellers of the Western Desert were skilled in drilling for water (Wagner 1987).

With the arrival of immigrants from the Nile Valley over 4000 years ago, agriculture has been the primary source of subsistence for the oasis peoples. In this system, ground water is collected by farmers in basins at spring mounds or bore holes and distributed through a series of elaborate irrigation canals and ditches for the cultivation of crops such as rice, sorghum, and wheat (Mills 1999). Techniques for crop cultivation and irrigation remain essentially unchanged from this time onwards, even into the modern era (Mills 1999).

Within the oasis, there are two distinct zones of cultivation and habitation, the existence of which can be attributed to the location of water sources (Figure 2.2). The larger of the two zones takes up most of the western and central portion of the oasis stretching from Mahoub to Ismant; the smaller eastern zone is centred around the villages of Balat, Bashendi and Teneida. The two areas are separated by approximately 15km of arid desert. The majority of ancient settlement sites in Dakhleh are located within these two zones, meaning that little has changed in terms of access to water sources over the last 4000 years.

The Dakhleh Oasis is linked to neighbouring oases, the Nile Valley and beyond through a network of caravan routes which traverse the Western Desert of Egypt. Many of these routes are extremely ancient and provided the inhabitants of the isolated oases with a connection to the outside world and a means to obtain goods and materials which were not readily available locally (Darnell 2002; Kuper 2002). These routes also served as conduits for the flow of people and ideas.

The *Darb el-Tawil* (English: The Long Road) is the only route which provides a direct link between the Dakhleh Oasis and the Nile Valley. It runs from the northeast corner of the oasis and reaches the Nile Valley at Manfalut near Assyut in Middle Egypt. Archaeological evidence attests to its use as far back as the Old Kingdom, although it was probably in use much earlier (Giddy 1987).

The Dakhleh Oasis is connected to Kharga Oasis to the east by two routes, the *Darb 'Ayn Amur* (English: Road of the Lovely One), and the *Darb el Ghubari* (English: The Dust Road). Several routes leading from Kharga connect the oases with the Nile Valley at Abydos to the northeast, and Upper Egypt and Sudan to the south via the *Darb el-Arbein* (English: The Forty Days Road). In Pharaonic times these routes were important trade corridors for the exchange of goods between Egypt, Sudan, Libya and Central and Western Africa. During the Roman Period, the *Darb el-Arbein* was dotted with military forts in order to protect trade and control access to Egypt during periods of unrest and foreign incursion (Giddy 1987). Other routes from Dakhleh include the *Darb el-Farafra* and *Darb Abu Minqar*, which lead to Farafra Oasis to the northwest, and the Abu Ballas Trail, which leads southwest to the Gilf Kebir and possibly beyond to Gebel Uweinat and northern Sudan, and the Libyan oasis of Kufra to the west (Förster 2007; Kuper 2001).

2.2 Human occupation in the Dakhleh Oasis

2.2.1 Prehistory

Archaeological evidence for the earliest human occupation of the Dakhleh Oasis dates back to the Paleolithic, appearing in the form of Upper Acheulian lithics between ca. 350,000 and 400,000 years BP (Schild and Wendorf 1977; Kleindienst 1999). During the Late Pleistocene (ca. 60,000 to 11,000 years BP), at the height of the Würm glacial maximum, the Saharan Western Desert was gripped by a period of increased aridification (Wiseman 1999). Based on these climatological data, in association with archaeological

evidence, many scholars have argued for an occupational hiatus throughout the Western Desert during this period (Close and Wendorf, 1992; Schild 1987). New evidence based on lithic technologies, however, suggests that this was not necessarily the case for the region in and around the Dakhleh Oasis, instead supporting the opinion that humans may have continued to occupy at least some areas of the Western Desert during the Late Pleistocene (Wiseman 1999).

Based on sedimentological, archaeobotanical, and zooarchaeological evidence, the Western Desert appears to have been a more habitable environment during the onset of the Holocene wet period, ca. 11,000 years BP (McDonald 1998, 1999). During this time, the region is characterized as a semiarid or savannah environment with higher rainfall levels and a wider variety of fauna than is known today; brief climatic fluctuations between dry and wet phases occurred throughout the first half of the Holocene epoch, however (Churcher 1999; McDonald 1998).

Three distinct late prehistoric indigenous cultural units have been distinguished for the early Holocene period of the oasis region: the *Masara,* from the early ninth millennium BC, the *Bashendi,* ca. 7500–5500 years BP, and the *Sheikh Muftah,* which appears to overlap with both the Bashendi unit and the later occupation of the oasis by peoples from the Nile Valley during the Old Kingdom (Hope 2002; McDonald 1998). These three cultural units are characterized by increasing sedentism and an increasingly centralized focus on activity within the oasis region itself; Masara sites occur mainly on

the fringes of the oasis, Bashendi sites are found both within and beyond the oasis, while Sheikh Muftah sites occur almost exclusively within the oasis itself (McDonald 1999). This changing settlement pattern appears to coincide with a period of aridification that characterizes the end of the early to mid-Holocene wet phase, rendering the desert region increasingly uninhabitable (Hassan 1986; McDonald 1999; Wendorf and Schild 1980). By the period of the Bashendi and Sheikh Muftah cultures, the oasis would have become a permanent refuge for displaced fauna and humans alike, with environmental conditions remaining relatively stable into the present day (Churcher 1999). While little is yet known about the subsistence patterns of the Masara unit, the Neolithic Bashendi and Sheikh Muftah cultures appear to have been cattle-herding pastoralists (McDonald 1998, 1999). In an analysis of imported ceramic types found at Bashendi and Sheikh Muftah sites in the oasis, Hope (2002:52) sees evidence of far-reaching contact between the inhabitants of Dakhleh and the Nile Valley, as well as regions to the west, south and southeast.

2.2.2 Pharaonic Period

While evidence of contact between the Western Desert and the Nile Valley appears to date as far back as the early and mid Holocene (Hope 2002), the earliest indications of contact between the Dakhleh Oasis and the nascent Pharaonic civilization occur in the Archaic Period (ca. 2920-2650 BC) in the form of imported Nile Valley ceramic types (Hope 1980). It is not until the late VI Dynasty (ca. 2300 BC), however, that evidence for permanent, settled habitation by Pharaonic Egyptians occurs within the oasis near the modern

village of Balat, where a large Late Old Kingdom/First Intermediate Period settlement (‘Ayn Asil) and mortuary complex (Qila’ el Dabba) has been extensively excavated by the French mission (IFAO) since 1977 (Osing *et al.* 1982; Valloggia and Henein 1986). The settlement appears to have been the administrative capital of the oasis for the period in question; this is borne out by the discovery of fortified installations and large-scale buildings (Giddy 1987). Complex political organization and social stratification are evident in the funerary inscriptions and large mastaba tombs at Qila’ el Dabba (Valloggia and Henein 1986). Subsequent surveys by the Dakhleh Oasis Project have discovered smaller Late Old Kingdom and First Intermediate Period sites in the oasis (Mills 1979, 2002, 2003), but the complex near Balat remains the largest and best excavated (Mills 1999). Abandonment of the sites near Balat appears to have occurred by the end of the First Intermediate Period (Giddy 1987) and probably coincides with the disintegration of the Pharaonic state at the end of the Old Kingdom.

During the Middle Kingdom through to the Late Period (ca. 2040-332 BC), archaeological evidence for Pharaonic Egyptian activity in the oasis is sparse in comparison with the preceding periods (Giddy 1987; Mills 1999). The site of Mut el-Kharab, in the central oasis region, contains the only large-scale evidence for an Egyptian presence until the Ptolemaic period, although a number of satellite sites and cemeteries are known throughout the oasis (Mills 1979, 1999). Another source of evidence for contact with the Nile Valley during this time exists in the form of two Pharaonic stelae which were recovered from the oasis at the end of the 19th century and now in the

possession of the Ashmolean museum in Oxford. The first dates to the 22nd Dynasty and records the visit of a governor, a relative of the Pharaoh, to settle a dispute over water rights during a period of war and turmoil (Gardiner 1933:22); such a visit implies an ongoing political connection to the Nile Valley. The second stela, dating to the 25th Dynasty, makes reference to the presence of Libyan tribes in the oasis (Janssen 1968). An explanation for the lack of a strong Pharaonic presence in the oasis during the first and second millennia BC remains tentative, especially as Nile Valley sources continue to make mention of contact and trade with the oases of the Western Desert, particularly during the New Kingdom (Giddy 1987; Hope 2002; Redford 1976). It may be that sites dating to these periods have yet to be discovered.

2.2.3 Greco-Roman Period

It is not until the Ptolemaic and Roman Periods (ca. 332 BC – 323 AD) that the Dakhleh oasis witnesses a period of renewed contact with the Nile Valley (Mills 1999; Worp 1995), and it is from these periods that the majority of archaeological sites derive (Mills 1999). This period of re-integration with the Egyptian state may be due, in part, to the introduction of the camel as a pack animal in the first millennium BC (Bulliet 1975; Rowley-Conwy 1988). The domesticated camel greatly facilitated travel and trade between the desert oases, the Nile Valley and beyond. Despite these improvements, however, textual data recovered from Kellis indicate that while travel between the oasis and the Valley occurred regularly, the journey was still considered long and arduous (Gardner *et al.* 1999:12).

During the Ptolemaic and Roman Periods, foreign trade became a central feature of Egyptian economic policy. The introduction of a monetary system by Alexander the Great greatly facilitated trade with other regions of the Mediterranean and beyond (Bowman 1986). In this period the number of goods imported and exported from Egypt increased dramatically, as did the geographical range within which these exchanges took place (Bagnall 1993; Bowman 1986). In addition, the Egyptian state became increasingly reliant on foreigners to fill the ranks of its military. Ptolemy I recruited a large number of Greeks and Macedonians, settling them along the Nile as farmers and herders but ready to be called upon in times of war (Bevan 1968). The practice of foreign recruitment continued into the Roman Period with the establishment of military garrisons at strategic locations throughout Egypt, although the army appears to have relied less on foreigners as a source of manpower after the 2nd century AD (Alston 1995).

As a result of improved irrigation techniques introduced during the Ptolemaic Period (Bowman 1986), the amount of arable land in the oasis was dramatically increased (Thanheiser *et al.* 2002). Such improvements led to a profusion of new settlements, especially during the Roman Period when intensified agricultural practices aimed at boosting exports led to a dramatic increase in population levels throughout Egypt (Bagnall and Frier 1994; Mills 1984). Commodities produced for export in the Dakhleh Oasis include dates and olives (Bagnall 1997; Wagner 1987). Mills (1984) has speculated that government incentives may have been introduced at this time to encourage

new migrants to the oasis. Large Roman Period settlements, cemeteries and field systems occur throughout the oasis and are preserved to a remarkable degree by the accumulation of windblown sands (Mills 1979, 1999). One such settlement, Kellis, has been the focus of continued excavation by members of the Dakhleh Oasis Project since 1986 (Knudstad and Frey 1999).

2.3 Ancient Kellis (Ismant el-Kharab)

The ancient village of Kellis (Greek: Κελλις; Arabic: *Ismant el-Kharab*), located in the south-central area of the Dakhleh Oasis (Figure 2.2), dates from the Late Ptolemaic through to the Late Roman period and was an important centre for commerce, politics and religion (Hope 1995, 2001). Several large religious complexes, bath houses, administrative buildings and field systems (Figure 2.3), in addition to a wealth of artifactual and textual data, attest to the relative affluence and self-sufficiency of this community (Bagnall 1997; Bowen 2002; Hope 1995, 2001; Knudstad and Frey 1999; Gardner 1996). During the early 4th century AD, the emergence of a sizeable Christian community at Kellis is demonstrated by the construction of several purpose-built church complexes (Bowen 2002), textual data (Gardner 1996), and by the establishment of new mortuary sites (Figure 2.4) wherein burial customs deviate substantially from those of the traditional Pharaonic Period (Birrell 1999; Bowen 2003). Estimates of the maximum population size at Kellis range from between 1000 and 1500 persons (Molto 2002). Archaeological evidence suggests the site was abandoned at the end the 4th century AD, possibly as the result of increased salination and sand dune

action which would have made continued occupation and agricultural activity untenable (Hope 2001; Knudstad and Frey 1999). Following the Late Roman/early Byzantine Period, the population of the Dakhleh Oasis seems to have declined until the modern era (Mills 1999).

2.4 Kellis mortuary sites

2.4.1 Pagan (pre-Christian) tombs

The earliest burials at Kellis are found in a series of chamber tombs which riddle the low rising hills northwest of the settlement. This mortuary complex is known as Kellis 1. The tombs contain burials dating to the Late Ptolemaic and Early Roman periods, as evidenced by mortuary practices which adhere to standard Late Pharaonic traditions, i.e. mummification, cartonnage, iconography and grave goods (Birrell 1999; Molto 2001). The tombs appear to have been used for successive inhumations, as later burials were often placed on top of earlier ones; loose and disturbed human remains were also pushed aside in order to make room for new inhumations (Birrell 1999). A total of 44 individuals have been recovered from 15 tomb chambers. Most of the tombs and some of the mummies contained within show evidence of disturbance at some point in the past (Molto 2001).

2.4.2 Christian tombs and cemeteries

Burials pertaining to the Christian period are found in two locations at Kellis. The first are the so-called “townsite” burials which have been discovered in several locations on the settlement perimeter. North Tombs 1 and 2 are a series of large mudbrick mausolea located on the northwestern edge of the

settlement. The construction of the North Tombs dates to the Early Roman period (1st - 2nd century AD), but the burials recovered *in situ* appear to follow Christian mortuary practices, thus suggesting re-use in the Late Roman period (Hope 2003). Highly disturbed skeletal remains were recovered from both tombs; these remains likely represent the original occupants of the tombs who were disinterred during its re-use, as well as some Christian burials disturbed more recently (Hope 2003). The minimum number of individuals is 31 for North Tomb 1, and 23 for North Tomb 2 (Dupras and Tocheri 2003). Eleven Christian burials dating to the fourth century AD have also been recovered from several tombs in areas D/6 and D/7 located on the western perimeter of the settlement in association with a church complex (Hope and McKenzie 1999; Hope 2003; Molto *et al.* 2003).

The second, and largest, source of Christian-era burials is the Kellis 2 cemetery, located to the northeast of the settlement. Since 1992 when systematic work in the cemetery began (Birrell 1999), 701 individuals have been excavated and recorded. Based on surveys and test excavations, the cemetery appears to cover an area of approximately 9000m^2, comprising an estimated 3000 to 4000 burials (Molto 2002). Thus, the current excavated skeletal assemblage represents approximately 18 to 23% of the total cemetery population. The burials consist of simple rectangular pits dug into the bedrock at an average depth of 1.3m (Birrell 1999). All burials are oriented east-west, with the head to the west. Slight deviations from this orientation do occur and appear to represent seasonality in the timing of interments (Williams 2008). In terms of grave construction, three distinct

types of burial are observable. The first and most elaborate consists of a vaulted mudbrick ceiling which begins approximately 35cm above the floor of the grave and terminating at surface level. The grave is then covered with a mudbrick mastaba superstructure. The second type consists of a rectangular pit with sides sloping towards the floor. Grave fill is deposited directly onto the body and sealed with a false mudbrick floor which is again covered by a mastaba superstructure. The third type consists of a simple pit, the fill of which is covered by a low earthen mound coated in gypsum. The presence of some type of grave superstructure, however minimal, seems to have prevented earlier burials from disturbance by later interments as there is no evidence for overlapping grave cuts, even within areas of densely packed graves. Several large mudbrick tomb enclosures containing males, females and juveniles in separate graves have also been identified and may represent family groups (Birrell 1999; Bowen 2003).

The burials are all single interments, with the exception of grave 92, which contained the bodies of two infants (Birrell 1999). Bodies were wrapped in a linen shroud, secured by ties and deposited directly onto the floor of the grave pit in a supine position, with the hands to the side of the body or across the pelvic region (Birrell 1999). There appears to have been no attempt to mummify the dead in the typical Pharaonic manner (Birrell 1999), although what appears to be natural resins and other, as-yet unidentified, materials have been found adhering to the bones of some individuals. Burial goods are minimal and, where found, consist of beads, a re-used glass vessel, an occasional ceramic bowl, and rosemary and myrtle sprays

(Bowen 2003). In some cases, broken ceramic pots were placed over the body (Birrell 1999). Nearly 65% of the individuals recovered from Kellis 2 are juveniles, with infant burials occurring throughout the cemetery; their graves consisting of shallow pits oriented on an east-west axis (Birrell 1999). Based on these mortuary practices, the cemetery appears to be that of an early Christian community (Birrell 1999; Bowen 2003; Davies 1999). Multiple bone samples from Kellis 2 individuals were submitted to IsoTrace Laboratory at the University of Toronto where human bone collagen was extracted for accelerated mass spectrometry (AMS) radiocarbon dating; the results suggest the cemetery was in use between 50 and 450 AD (Stewart *et al.* 2003; Molto *et al.* 2006). This is disputed by archaeological evidence (e.g. ceramic typologies), however, and the fact that separate cemeteries for Christians do not appear in the Mediterranean world until the third century AD (Bowen 2003; Hope 2001). This discrepancy between the radiocarbon dates and archaeological evidence has yet to be resolved satisfactorily, despite testing and re-testing of the multiple bone samples.

2.5 Previous osteological research in the Dakhleh Oasis

The earliest studies of archaeological skeletal material from Dakhleh emerge from the French excavations near Balat in the eastern part of the oasis. Tadeusz Dzierżykray-Rogalski, a Polish anthropologist, published a series of brief papers analyzing the human remains from Old Kingdom, Late Period and Ptolemaic sites excavated since 1977 under the direction of the *Institut Français d'Archéologie Orientale (IFAO).* These reports deal mainly with observed pathological conditions, both skeletal and dental *(*Dzierżykray-

Rogalski 1979a,b, 1981; Dzierżykray-Rogalski and Szlatchetko 1980), as well as basic demography (Dzierżykray-Rogalski 1978). The authors have argued based on the skeletal evidence that the Old Kingdom remains show greater signs of physiological stress than those of the later periods (Dzierżykray-Rogalski 1980, 1981).

Of particular interest to the present study are two reports which deal with the "racial" classification of the skeletal remains (Dzierżykray-Rogalski 1980; Dzierżykray-Rogalski 1983). Here, the Old Kingdom remains are described as belonging to an Eastern Mediterranean type with Berber additions (Dzierżykray-Rogalski 1983:313), while the Late Period and Ptolemaic remains are characterized as Europoid or Caucasian (Dzierżykray-Rogalski 1980:72; Dzierżykray-Rogalski 1983:313). The author states that these skeletal remains probably represent an elite ruling class with ethnic origins outside the oasis: "since it is well known that the southern Oases of Egypt were inhabited by a Negroid population" (Dzierżykray-Rogalski 1980:72). Despite this claim, however, no references are provided to support this assertion, and the means by which Dzierżykray-Rogalski characterizes the Balat skeletal material are not clearly described. His assessments appear to be based on cranial morphology: in an analysis of a skull from Mastaba V (Old Kingdom), he characterizes the individual as belonging to a "*variété blanche*" with a small component of "*variété noire*" based on the position of the articular surface of the mandibular heads (Dzierżykray-Rogalski 1979b:482). In current practice, this would not be considered a valid method for determining biological ancestry. Assigning individuals to broad

typological categories such as “Europoid” or “Negroid” based on a visual assessment of cranial morphology can only provide a very crude approximation of population affinity and does not take into account the significant amount of variation that occurs within populations. At any rate, it is not the aim of the present study to assign the Kellis skeletal assemblage to a “Caucasoid” or “Negroid” typology. This sort of essentialist taxonomy is no longer considered a valid approach to the study of human variation (Ousley *et al.* 2009; Relethford 2009). More importantly, the phenotype of a particular ancient population is unlikely to correspond to any of the socially-constructed racial archetypes of our modern era. Nor would ancient peoples likely recognise themselves within such archetypes.

Lastly, Promiñska (1981) compared average stature and life expectancies between the Late and Ptolemaic period individuals at Balat. While average age-at-death was estimated to be 3.5 years higher in the Ptolemaic assemblage, average height (using the methods of Trotter and Gleser 1952, 1958) was 6cm lower than the Late Period assemblage. Because of the higher average age-at-death, Promiñska rejects a lower “*niveau de vie*” (standard of living) as a cause of reduced stature in the Ptolemaic group; instead she proposes ethnicity as an explanation for the differences, with the shorter Ptolemaic era individuals perhaps being Greek in origin (Promiñska 1981:279). As with Dzierżykray-Rogalski above, this type of analysis belongs to an older and outmoded era of physical anthropology and would not be considered a valid method of assessing biological variability in human skeletal populations.

Another oasis site which has produced skeletal material for analysis is ‘Ein Tirghi, located 8km southwest of Balat. This large cemetery, excavated under the aegis of the Dakhleh Oasis Project (DOP) in the 1980’s, comprises a number of rock-cut tombs dating primarily to the Late Period (Frey 1986; Molto 2000). A number of studies were conducted on this material, including a comparison with the Roman period Kellis burials of cribra orbitalia rates and other paleoepidemiological indicators (Fairgrieve and Molto 2000; Molto 2001). These studies have demonstrated that overall health, as reflected in infection and cribra orbitalia rates, among other indicators, improved during the Roman period (Molto 2001). Based on similar frequencies of hereditary morphological cranial traits, Henderson (1993) and Molto (2001) also argue for population continuity and genetic homogeneity between the two cemeteries, and by extension the oasis region, throughout the Late and Roman periods. The skeletal assemblage from ‘Ein Tirghi would have made an ideal comparative collection in the present study, but due to a lack of storage space at the time, the remains were reburied after having been studied (Molto, personal communication 2002).

The skeletal remains of six individuals dating to the mid-Holocene (late Neolithic to Old Kingdom) have been recovered between 1997 and 2000 (Thompson and Madden 2003). The dating of these individuals is based on their association with artifacts linked to the Sheikh Muftah Cultural Unit (McDonald 1998, 1999). Five of these individuals were found near Sheikh Muftah, a small village in the central oasis region; the sixth individual was

recovered near Balat. These remains, though poorly preserved, have yielded important information regarding diet, health and environmental stress during the Neolithic (Thompson 2008; Thompson and Madden 2003, 2006).

Finally, the substantial collection of burials from Kellis has generated numerous studies on a wide range of topics. These include paleopathology (Cook *et al.* 1988; Molto 2000, 2001; Wheeler 2012), paleodemography (Dupras *et al.* 2001; Tocheri and Molto 2002; Tocheri *et al.* 2005), as well as isotopic studies of diet (Dupras 1999; Dupras *et al.* 2001; Dupras *et al.* 2008), migration (Dupras and Schwarcz 2001) and seasonal mortality (Williams 2008). Because the majority of individuals recovered from the Kellis 1 tombs are mummified, and many are still wrapped, standard osteological analyses of these burials have not been carried out. A selection of the Kellis 1 mummies has been autopsied, however, and analyses of the embalming techniques were conducted (Aufderheide *et al.* 1999; Aufderheide *et al.* 2004).

Lastly, paleogenetic studies on the Kellis 2 and townsite skeletal assemblages have demonstrated spatial concentrations of several hereditary nonmetric cranial traits (accessory optic canal, trochlear spur, metopism and fronto-temporal articulation) that have been interpreted as evidence for kin-group burial areas (Kron 2007; Molto 2001). The high occurrence of *spina bifida occulta* at Kellis and other oasis sites has been interpreted as further indication of an inbred, isolated population (Molto 2001).

In contrast to the picture emerging from osteological analyses, however, is archaeological and textual data which indicate extensive links between the southern oases and the Nile Valley (Gardner *et al.* 1999; Worp 1995). While texts from Kellis indicate that the inhabitants of the oasis considered themselves as separate from Egypt, personal correspondence and receipts for economic transactions recovered from several houses indicate that male residents of Kellis often travelled to the Nile Valley for work and trade (Gardner *et al*. 1999:13). Close links between the oasis and Middle Egyptian centres such as Aphrodite, Antinopolis, Hermopolis and Siaout (modern Assyut) are evident in the papyri, with some Kellis males apparently residing permanently in the Nile Valley (Gardner *et al.* 1999; Worp 1995). Such links would have provided ample opportunity for the exchange of genes as well as goods. This perspective is supported by a preliminary analysis of mitochondrial DNA sequences derived from a subset (N=13) of the Kellis 2 skeletal sample, which appears to demonstrate a high level of maternal genetic diversity (Parr 2002). Two isotopic studies also indicate that at least eight individuals from the Kellis 2 cemetery came from outside of the oasis (Dupras 1999; Dupras and Schwarcz 2001). In light of these previous studies, the primary aim of the present study is to explore the biological relationships of the Kellis skeletal assemblage to other ancient groups in Egypt and beyond, as well as to provide new data for the analysis of kin-group areas and sex-based differences within the Kellis skeletal assemblage.

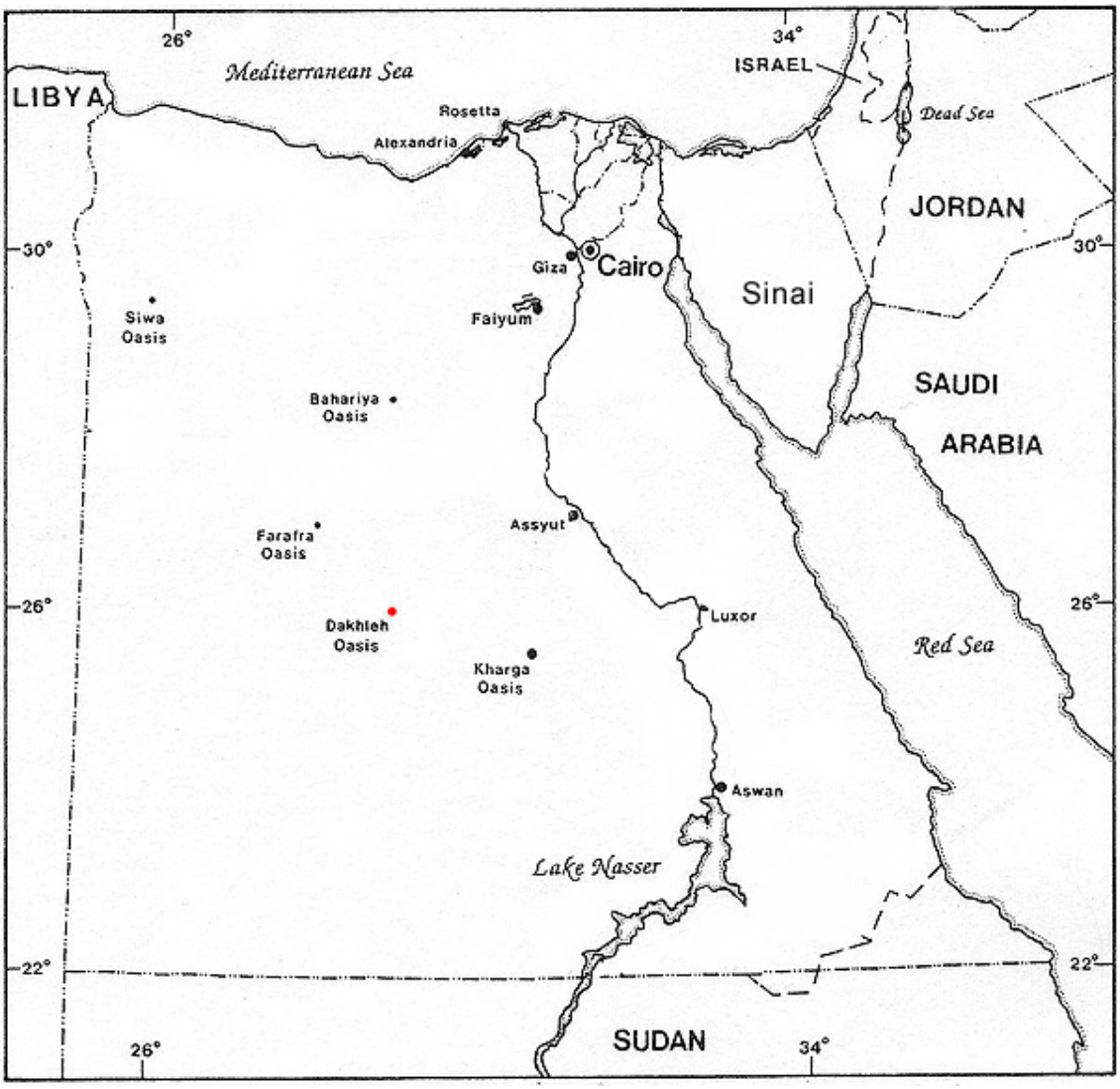


Figure 2.1. Map of Egypt, showing location of Dakhleh Oasis.

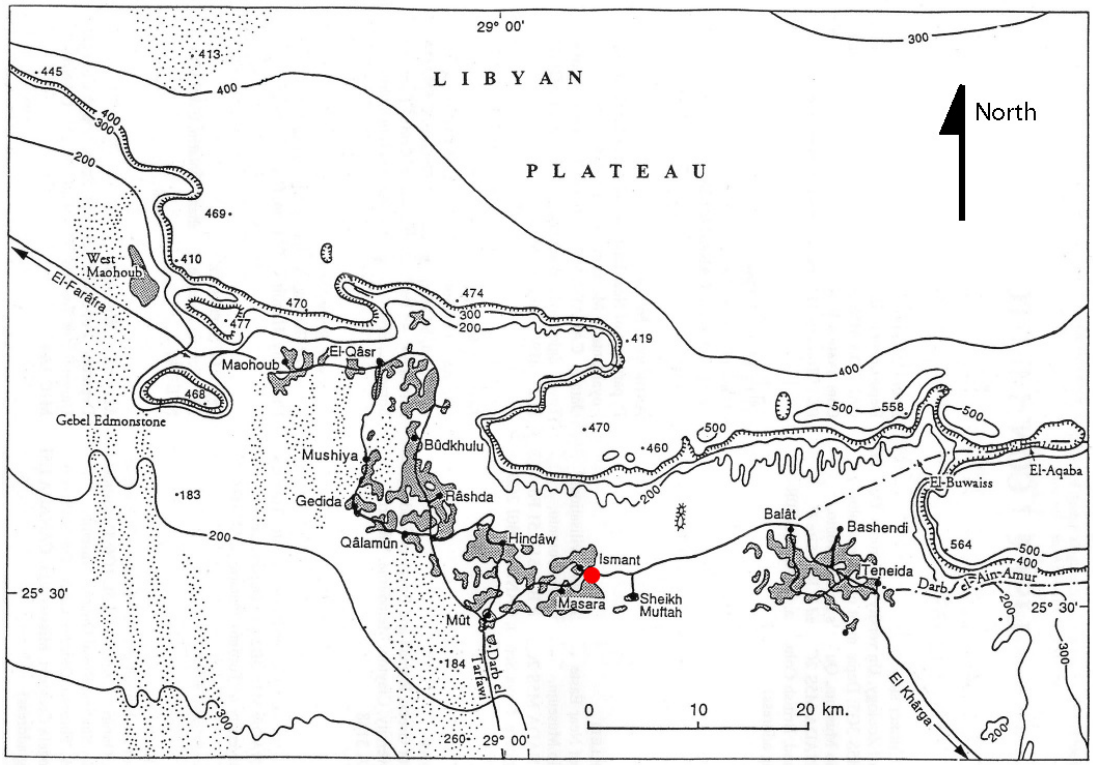


Figure 2.2. Map of Dakhleh Oasis showing location of Kellis in red (Ismant el-Kharab). Grey areas represent areas under cultivation.

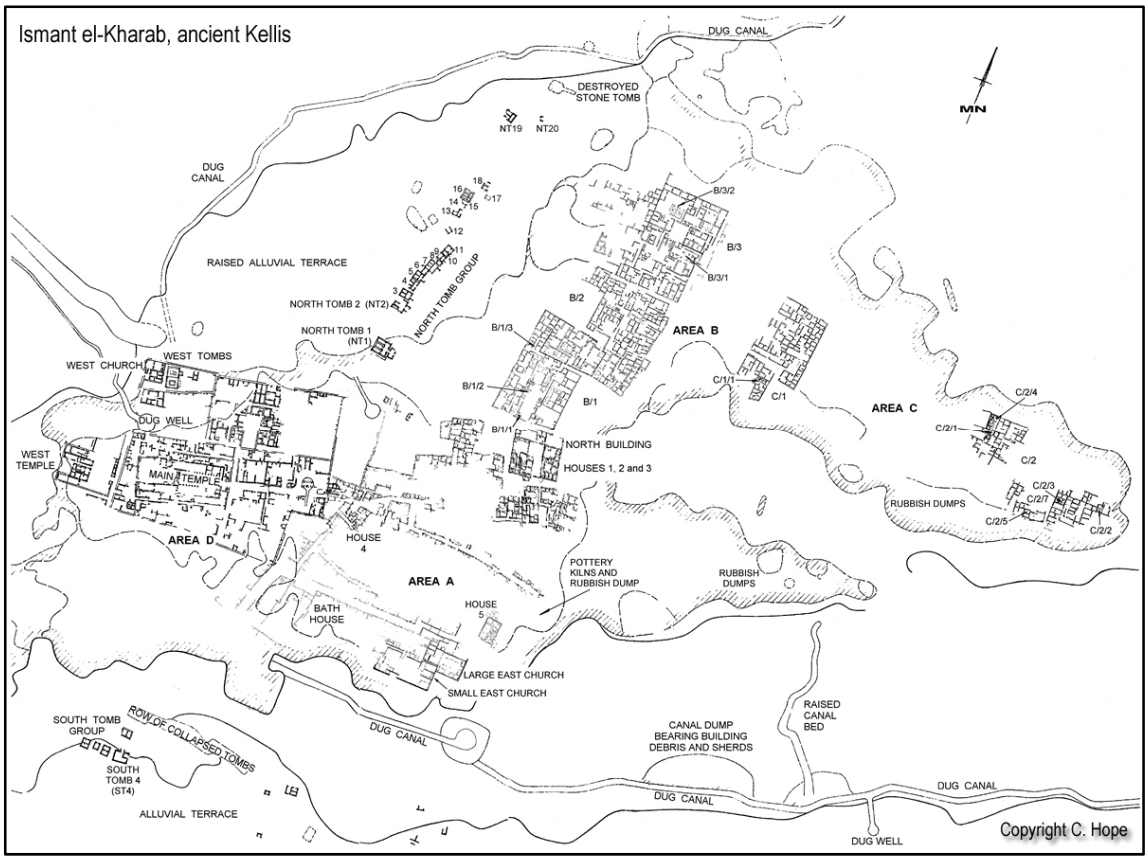


Figure 2.3. Map of Kellis settlement. The Kellis 2 cemetery is located just off this map to the north. The townsite burials were recovered from the North Tomb Group located in the upper centre of the map (Reproduced with the permission of Dr. Colin Hope).

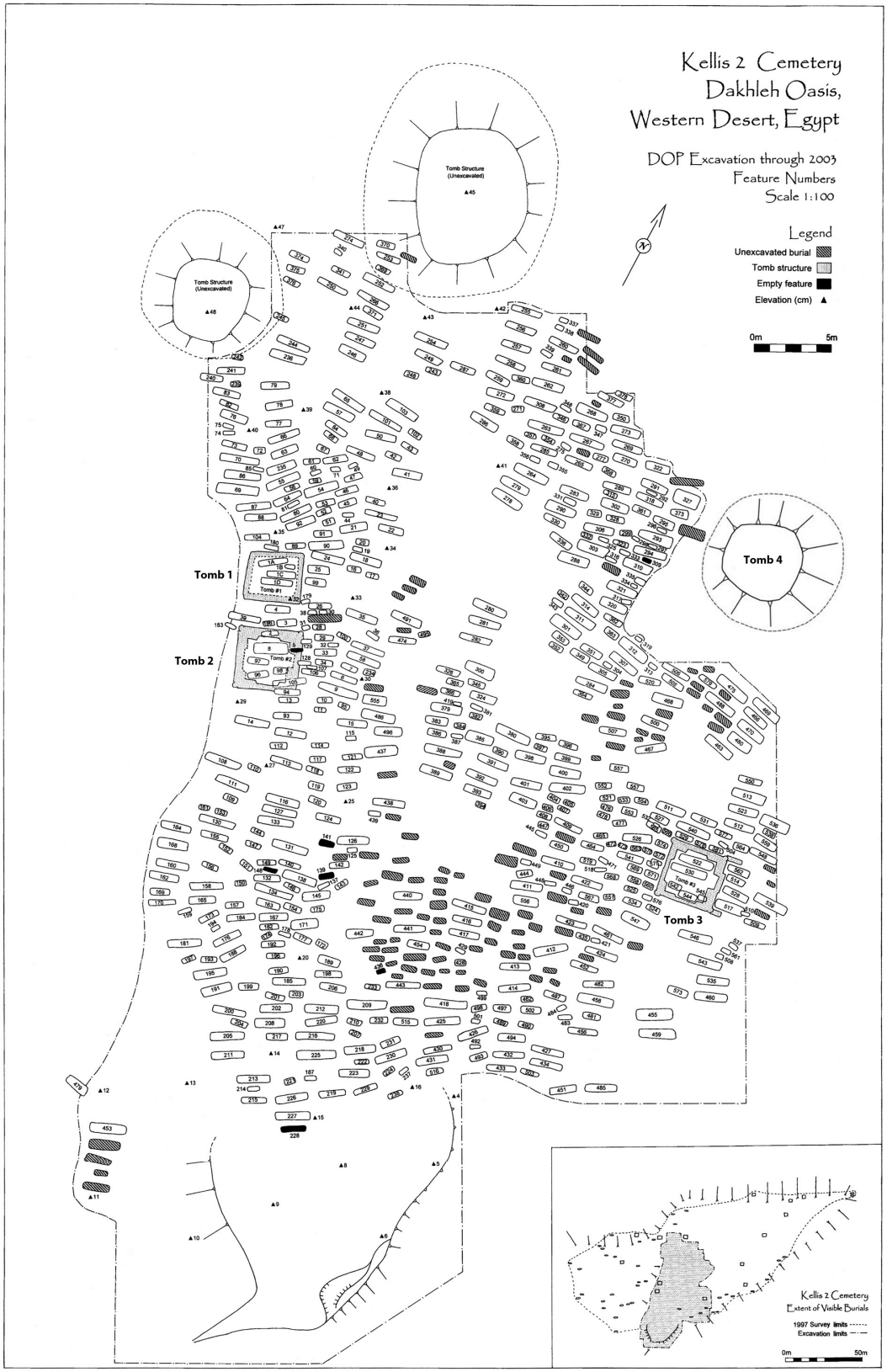


Figure 2.4. Map of Kellis 2 cemetery located northeast of the settlement.

Chapter 3

Dental Morphological Traits and Biological Distance: Methodological Background

3.1 Introduction

Teeth are formed early in life and once their development is complete their basic morphology is not subject to the physiological alterations that affect the rest of the skeleton in the course of a lifetime. By nature of their structural composition, they are a more durable tissue than bone, and thus more likely to survive the often harsh conditions of the post-depositional environment. As a result, dental assemblages often comprise the majority of material available for study by osteologists and archaeologists.

In relation to their size, teeth contain an extraordinary amount of information. Studies of the dentition can provide numerous insights into cultural, biological and ecological aspects of human behaviour, environments, and living conditions in the past, as well as the present. Such insights include information on age, sex, dietary practices and health patterns. In addition, many hominid phylogenetic theories are based largely on fossilized teeth (Kieser 1990; Alt *et al.* 1998). Because of the ease with which the dentition can be observed (in both living populations and archaeological assemblages), and of the increasing number of fossil teeth available for analysis, evolutionary studies based on the hominid dental variation have become increasingly common in the twentieth century and continue into the twenty-first century. These studies have focused on two primary aspects of

dental variation: tooth shape and tooth size, i.e., dental morphometrics. The present study aims to employ the analysis of tooth shape -dental morphology- for the purposes of assessing biological relationships within the Late Roman period skeletal assemblage at Kellis, as well as its affinities with other Egyptian groups and a number of regional populations as well. Before presenting the results of the study, however, it is necessary to provide an overview of basic dental anatomy and terminology, as well as to review the history of dental morphological research and its applicability to the present study. Finally, the four hypotheses for the present study are put forward, followed by a presentation of the materials analyzed and a critical overview of the methodologies employed.

3.2 Structure and function of the human dentition

Humans, like most mammals, have two sets of dentition during the course of their life: the primary or deciduous teeth, which typically begin to emerge one year after birth and are retained into late childhood, and the permanent teeth, which gradually replace the exfoliated deciduous teeth beginning in mid-childhood. The smaller deciduous teeth, whilst performing the same functions as that of their successors (i.e. mastication, speech), also act as place holders for the larger permanent teeth, allowing the bones of the jaws sufficient time to grow in order to accommodate them. The first permanent teeth to appear (erupt) are typically the first molars, which emerge in the jaws just behind the deciduous premolars around the age of six. By the age of 12, the deciduous dentition will normally have been replaced by that of the permanent. The entire set of permanent teeth is not complete, however, until

late adolescence/early adulthood when the final pair of upper and lower third molars, or wisdom teeth, emerge.

Deciduous and permanent teeth are composed of two main regions: a crown and a root (Figure 3.1). The crown is the enamel coated portion of the tooth which protrudes from the jaw into the oral cavity, whilst the root is anchored firmly in the sockets, or *alveolae*, of the jaw bones. Each tooth, crown and root, is comprised primarily of a hard-wearing core of tissue known as dentin. The dentin portion of the tooth crown is encased in a thick sheath of dental enamel which is the most highly mineralized tissue in the body. This sturdy coating provides the durability required for a life's worth of exposure in the mouth. The tooth root does not have an enamel component but is instead covered in a thin layer of bone-like cementum. Cementum provides an anchor for the periodontal ligament which fastens the tooth root firmly to the *alveolus*. The external boundary between crown and root is known as the cemento-enamel junction or CEJ. This area is also known as the cervix or neck of the tooth. At the centre of each tooth is a pulp chamber containing nerve and blood vessels which lead in through the root tips and provide nourishment to the dentin. The tip of each root is referred to as an apex (apices, pl.). Unseparated root-like divisions within the primary tooth root are referred to as 'radicals'.

There are four permanent tooth types which are classified according to their form and position within the jaws. These types are incisors, canines, premolars and molars (Figures 3.2 and 3.3). Incisors and canines, located at

the front of the jaw, comprise the anterior dentition, while premolars and molars, located at the back of the jaw, are known as the posterior dentition or cheek teeth. In the deciduous dentition, there are three tooth types: incisors, canines and premolars. Deciduous premolars are sometimes referred to as deciduous molars, typically by anthropologists, but from a paleontological view the former is considered a more accurate terminology as these teeth are replaced by permanent premolars (Hillson 2005).

A standard terminology is employed by dental workers when describing specific regions or aspects of the dentition. This helps to orient oneself within the dentition, and makes it easily understood when describing morphological variation in a specific tooth. The upper (maxillary) and lower (mandibular) jaws are often individually referred to as the dental arcade or arch (Figure 3.4). The two arches may be partitioned into left and right quadrants by an imaginary line extending from the front of the jaw through to the back (imagine dividing the letter “U” down the middle). This dividing line is called the median sagittal plane or midline. Within each dental arcade, the vertical aspect of the tooth which faces anterior, or towards the midline, is known as the mesial surface. Conversely, the aspect of the tooth which faces away from the midline is known as the distal surface. The area between two contiguous teeth in the dental arcade is known as the approximal or interproximal surface. The lingual surface refers to the side of the tooth that faces the inside of the oral cavity, while the outer aspect of the tooth is referred to as the buccal (in the case of molars and premolars) or labial (in the case of incisors and canines) surface. When the jaws are closed, the

portion of the tooth crown that comes into contact with its upper or lower opposite is known as the occlusal surface and it is this site that provides the cutting and grinding planes required for mastication. The lower section, or base, of the crown is called the cervical margin. In this region there may occur a prominence or bulge known as the *cingulum*. In the anterior dentition, this cingulur bulge is known as the tuberculum.

The main structural components of the tooth crown are protrusions known as cusps which vary in number according to tooth class (i.e. incisor vs. molar). Smaller cusplets or tubercles may also occur. Cusps are separated from one another by a series of grooves and furrows which, taken together, form the topographic landscape of the crown surface.

For the deciduous dentition, each dental quadrant normally comprises two incisors, one canine and two premolars, making for a total of twenty teeth. For each half of the upper and lower dental arches, this arrangement can be expressed in the following dental formula (where *di* stands for deciduous incisors, *dc* is for deciduous canines, and *dp* is for deciduous premolars):

$$\mathrm{di}\frac{2}{2},\ \mathrm{dc}\frac{1}{1},\ \mathrm{dp}\frac{2}{2}$$

In the permanent dentition, each quadrant is typically comprised of two incisors, one canine, two premolars, and three molars. Thus, there are normally 32 teeth which make up the permanent dentition. The dental formula (where *I* stands for incisors, *C* for canines, *P* for premolars, and *M* for molars) for the permanent teeth is:

$$I\frac{2}{2}, C\frac{1}{1}, P\frac{2}{2}, M\frac{3}{3}$$

3.2.1 Description of tooth types

3.2.1.1 Incisors

Incisors, the most anterior of the four tooth types, are characterized by their spatulate morphology and their incisive occlusal surface. The blade-like edge of the incisors is used for cutting and shearing during mastication. Within each dental quadrant there are two incisors. The first or central incisor is the more mesial of the two, whilst the second or lateral incisor is distal to the first. In both the deciduous and permanent incisors, the upper or maxillary first incisors are appreciably larger than the second incisors. In the lower or mandibular incisors, the first incisor is slightly smaller than the second. For both deciduous and permanent teeth, the upper first and second incisors are always larger than the lowers. The labial surface of the incisors is convex in shape, although more so in upper incisors than lowers, and the lingual surface is concave. On newly erupted or unworn incisors, the incisal edge contains three to five small cusplets called mamelons, which are rapidly worn down once the tooth comes into occlusion. On the lingual surface, two ridges run down the mesial and distal margins and meet at the cervix, forming the tuberculum on the cingular region (Figure 3.5). These marginal ridges are usually more pronounced in the upper incisors than in the lowers. In some cases the labial marginal ridges are so pronounced they produce a shovel-shaped appearance. This particular form of incisor morphology has been demonstrated to cluster along population lines (Hanihara 1998, Scott and Turner 1997), and is one of several tooth traits

used in the present study. Upper incisors tend to demonstrate more variation in form than lower incisors. This is especially true of the upper second incisor which is more variable in size and shape than any other tooth, and -after the third molars- has the second highest frequency of congenital absence (Scott and Turner 1997). Incisors are normally single-rooted teeth whose apices are frequently skewed distally.

3.2.1.2 Canines

As with the incisors, canines are typically single-rooted spatulate teeth with marginal ridges on the labial surface. With canines, however, the crown is more tubular in shape, with the central third of the occlusal surface forming a pointed cusp. Two strongly developed lingual marginal ridges, one mesial and one distal, run down from the central cusp; the distal ridge is the longer of the two and slightly curved, whilst the mesial ridge is more prominent and perpendicular to the jaw line (Figure 3.6). This lends the crown of the canine an asymmetrical silhouette when seen from the lingual or buccal aspect. This asymmetry helps to differentiate canines from incisors. Canine crowns are also taller and have longer roots than incisors. The arrangement of the marginal ridges is the same in deciduous and permanent canines, except for the deciduous upper canine where their orientation is reversed. In addition, a central ridge or buttress runs down the centre of the lingual surface and merges with the prominent bulge of the tuberculum in the cingular region. Occasionally, the tuberculum may take the form of a small cusplet. Permanent lower canines are occasionally two-rooted. A shallow furrow

known as the developmental groove runs down the mesial and distal surface of the root of the permanent canines.

3.2.1.3 Premolars

Premolars are often referred to as bicuspids because of their typically double-cusped crown morphology (Figure 3.7). Upper premolars have two major cusps, one buccal and one lingual. The buccal cusp is the larger of the two and is centred on the midline of the crown, while the slightly smaller lingual cusp is offset mesially. The two cusps are divided by a mesial-distal oriented furrow. Ridges on the mesial and distal margins of the crown join the two cusps, with the mesial ridge being slightly more prominent than the distal. In both the deciduous and permanent dentitions there are two premolars per quadrant. In upper premolars the second tooth is usually smaller than the first, although average crown diameters for upper premolars are similar (Hillson 1996). When viewed from the occlusal surface, upper third premolar crowns are slightly triangular, while the fourth is more rectangular. Root number, length, separation and prominence of upper premolars are highly variable. Upper premolars may have one, two or three roots. Single-rooted premolars have developmental grooves on the mesial and distal surfaces of the root. In two-rooted premolars, the roots are oriented in the same way as the cusps: buccal and lingual, with the buccal root being the larger of the two. Three-rooted premolars, which are rarer, have a lingual root, and a distobuccal and mesiobuccal root.

Lower premolars may have two or three cusps, with the buccal cusp being the most prominent, and one or two smaller cusps located lingually. The fourth premolar usually has three cusps, while the third has two. Marginal ridges on the mesial and distal rim of the crown run down from the main buccal crown and join the smaller lingual cusp or cusps. A mesial-distal fissure divides the buccal and the lingual cusps, while a prominent buttress runs lingually from the centre of the buccal cusp, creating two dimples on the occlusal surface. When viewed occlusally, lower premolar crowns are circular in form in relation to uppers (although fourth premolars are slightly squarer in comparison with third premolars), which are more ovoid. The third lower premolar is typically smaller than the fourth. Lower premolars typically display a single conical root with grooves of varying depth on the mesial and distal surfaces. Occasionally these grooves are of sufficient depth to create two roots, one buccal and one lingual. This variation is referred to as a Tome's root. The double-rooted form, when it occurs, almost always appears on the lower third premolar. Multiple-rooted lower fourth premolars are extremely rare.

3.2.1.4 Molars

The permanent molar teeth are the largest of the four tooth types, and have correspondingly broad occlusal surfaces with complex arrangements of cusps and furrows which act as grinding surfaces for the act of mastication. There are usually three molars per dental quadrant, with the first molar typically the largest of the series, followed by the second and the third. The third molars, or wisdom teeth, are the most variable in size and cusp

arrangement. In some individuals, some or all of the third molars may fail to develop; this phenomenon is known as third molar agenesis, or congenital absence.

Upper permanent molar crowns (Figure 3.8) have four primary cusps, the protocone (mesiolingual), paracone (mesiobuccal), hypocone (distolingual) and metacone (distobuccal). The tips of the buccal cusps, paracone and metacone, are higher than the lingual protocone and hypocone, and the lingual crown surface is more swollen outward in comparison to the buccal, whose surface is split by a groove which divides the bases of the paracone and metacone. The distolingual cusp, or hypocone, is the most variable in size, typically being largest in first molars, reduced in second molars, and often not present in third molars. Similarly, the distobuccal cusp, or metacone, is often reduced or absent in third molars. A small fifth cusp known as the metaconule is occasionally present on the distal marginal ridge between the hypocone and metacone. Additionally, a cusplet known as the cusp of Carabelli may occur on the base of the protocone and varies considerably in size and expression. When this cusp occurs, it appears most often on the first molar. This accessory cusp is often used by researchers to distinguish between population groups (Scott and Turner 1997). Rarer still, a second accessory cusp known as the parastyle, or paramolar tubercle, may occur on the base of the paracone. Upper molars are normally three-rooted, with one large lingual root and two smaller buccal roots. The apices of the buccal roots tend to curve towards one another, whilst the lingual root tip tends to curve distolingually. In some instances, the three roots may fuse

into one with deep grooves betraying the fused lingual and buccal root lengths. This occurs most commonly in third molars, where the fused roots take on a conical appearance.

Lower permanent molar crowns (Figure 3.8) tend to be rectangular in form when viewed from the occlusal surface, with the long axis running mesiodistally. As with the upper molars, crown size is largest in lower first molars, and decreases as one moves distally through the series. There are commonly four main cusps, one in each corner of the rectangle: the protoconid (mesiobuccal), the metaconid (mesiolingual), the hypoconid (centrobuccal) and the entoconid (distolingual). In lower first molars, a smaller fifth cusp known as the hypoconulid often occurs between the centrobuccal and distolingual cusps. Second lower molars typically have four cusps, whilst third molars may have four or five cusps. Additionally, a distal sixth cusp, the *tuberculum sextum*, may occur alongside the hypoconulid and a seventh lingual cusp occurs infrequently between the disto- and mesiolingual cusps. Rarely, a seventh cusp, the *tuberculum intermedium*, may occur between the mesiolingual and distolingual cusps. Lastly, lower molars normally have two broad, flattened roots, one mesial and one distal, with apices curving distally. The mesial root is larger than the distal and has more prominent grooving.

3.3 History and development of Dental Anthropology

The modern study of the human dentition begins with the work of nineteenth century geologists and biologists (Dahlberg 1991). Charles Lyell's

establishment of the earth's antiquity paved the way for far-reaching concepts such as Charles Darwin's theory of evolution, which influenced scientists in a wide array of fields, from biology and zoology, to comparative anatomy and palaeontology. Richard Owen's *Odontography* (1840-1845) was the first comprehensive monograph on the comparative dental anatomy of living and fossilized animals and remained the foundation for subsequent comparative investigations for many years (Alt *et al.* 1998). With fossil hominid remains emerging in Europe and Africa in the nineteenth and early twentieth century, teeth became recognized as valuable tools for assessing ontogenetic and phylogenetic questions such as mammalian development and evolution (Alt *et al.* 1988). Researchers such as E.D. Cope (1840-1897), H.F. Osborn (1857-1935), and W.K. Gregory (1876-1970), were pioneers in the study of growth and evolutionary factors, establishing much of the framework for future inquires (Dahlberg 1991; Alt *et al.* 1998). The beginnings of the independent development of dental anthropology are marked by the emergence of population-based studies of particular ethnic groups or fossil assemblages during the early half of the twentieth century (Hillson 1996). These dental studies were known as "odontographies", examples of which include the analysis of the dentition of Australian Aborigines by Campbell (1925), Bantu tribesman of Africa by Shaw (1931), and Chinese *Homo erectus* by Weidenreich (1937; cited in Hillson 1996). A.A. Dahlberg's paper, *The Changing Dentition of Man* (1945), further refined and developed the concept of population studies based on the teeth and set the stage for a dramatic increase in the number of anthropological dental studies in the second half of the twentieth century (Dahlberg 1991;

Hillson 1996). Later, D.R. Brothwell's (1963) edited symposium volume, *Dental Anthropology*, established the scope of dental anthropological research, and included papers on tooth morphology, growth and development, and dental pathology in both living populations and archaeological skeletal assemblages.

Today, dental anthropology is considered a sub-field of physical anthropology, encompassing a wide variety of research pursuits. Some researchers concentrate on post-eruptive changes such as tooth wear and cultural modification (reviewed by Milner and Larsen 1991), while others concentrate on pathological afflictions of the dentition such as caries and periodontal disease (reviewed by Brothwell 1963; Koritzer 1973). Such research has revealed a great deal of information on diet and habitual activities involving the teeth. Another avenue of inquiry is the study of developmental patterns in the dentition, including tooth germ formation and developmental defects (reviewed by Hillson 1996). Finally, researchers interested in the genetic and evolutionary aspects of the dentition study tooth shape and size (reviewed by Hillson 1996; Kieser 1991; Scott and Turner 1988, 1997). This particular branch of dental anthropology, tooth shape (morphological variation) and tooth size (metric variation), generates more literature than any other topic in dental anthropology (Mayhall 2000). In the present study, tooth shape, or dental morphology, is used to assess biological variation within an ancient Egyptian skeletal assemblage and to test for biological relationships between this assemblage and regional

population groups. This type of analysis is commonly referred to as the study of biological distance.

3.4 Biological distance analysis

Biological distance analyses assess human biological variation through the observation and recording of phenotypic data, most often from the cranium or dentition. “Phenotype” is commonly defined as the physical characteristics of an organism resulting from the interaction between its genes and the environment. The basic theoretical assumption of any biological distance study is that phenotypic similarity, or dissimilarity, between individuals or populations will provide an approximation of genetic relatedness (Buikstra *et al.* 1990; Konigsberg 2006; Larsen 1997; Stojanowski and Schillaci 2006). In order for a physical characteristic, or trait, to have utility in biological distance studies, it should be demonstrably heritable, while environmental effects should be minimal or randomly distributed within the groups being compared (Stojanowski and Schillaci 2006).

Biological distance studies most commonly aim to reconstruct the origins, affinities and movements of human populations at both the regional (local) and inter-regional (continental) levels. In this sense, the term “distance” should not be taken to imply spatial or geographical proximity except in the sense that population groups physically closer to one another are more likely to be related to one another than they are to groups thousands of kilometres away (Konigsberg 1990; Sewell 1943). When populations exchange mates through migration or smaller-scale cultural processes, they tend to become

more similar, both phenotypically and genetically, over time. In evolutionary terms, this phenomenon is known as gene flow. Conversely, where populations are separated from one another, thus preventing mate exchange, they tend to become less similar over time. This occurrence is referred to as genetic drift. Impediments to the exchange of mates between populations may be physical in nature, e.g., geography, or cultural, e.g., religion, socioeconomic status, etc. The ease with which modern populations circulate globally means that groups once separated both geographically may now live next door to one another. Cultural barriers, however, may still exist which prevent mate exchange.

Examples of this regional and inter-regional approach to biological distance using dental morphology include C.G. Turner's study of the origins of Native Americans (Turner 1971, 1983, 1984), J.R. Lukacs and co-workers' studies of prehistoric populations in Pakistan and India (Lukacs 1983, 1987; Lukacs and Hemphill 1991; Lukacs and Walimbe 1984), and J.D. Irish's analysis of African population groups (Irish 1993, 1997, 1998a,b,c,d, 2000, 2006). Turner noted similarities in dental crown and root morphology between Native Americans and East Asians which, in conjunction with genetic and linguistic evidence, led to the formulation of the three-wave model for the peopling of the Americas from Northeast Asia (Greenberg *et al.* 1985, 1986). Lukacs and co-workers' research led to the development of a model for the peopling of South Asia (Lukacs 1984; Lukacs and Hemphill 1991), while Irish's work identified a series of dental morphological traits which

characterizes Sub-Saharan African populations (Irish 1997), and lends tentative support to the Out-of-Africa model of human origins (Irish 1998a).

Other researchers have used biological distance studies to assess genetic relationships within a single site. These intracemetery approaches to biological variation, while less prevalent in the literature, are providing deeper and complementary insights into cultural behaviours previously accessible only through the study of artifactual data (Stojanowski and Schillaci 2006). Such behaviours include mortuary practices, mating patterns, kinship structures and socioeconomic status (Alt and Vach 1998). At the intracemetery level of analysis, phenotypic data can be used to compare individuals in order to assess their level of relatedness via the non-random spatial patterning of rare traits (Alt and Vach 1998). This form of kin-group analysis assumes that related individuals will be buried together within particular areas of a cemetery or other mortuary site. Alternatively, the summed frequencies of phenotypic data for groups of individuals may be compared in the same way as regional groups.

Examples of intracemetery analyses using dental morphological traits include Johnson and Lovell's (1994) study of social inequality in an Upper Egyptian Predynastic cemetery, Corruccini and Shimada's (2002) kinship analysis of individuals from Huaca Loro, Peru, and Tomczak and Powell's (2003) research on postmarital residence patterns at the prehistoric Windover site in Florida.

3.5 Dental morphological variation

Dental morphological traits are commonly referred to as “non-metric” variations in external morphological structures that occur at a particular site on one or more members of a tooth class or classes (i.e. incisors, premolars, molars). As opposed to metric analysis of the dentition, which typically concerns the measurement of individual tooth dimensions such as crown height, root length, occlusal area, etc., the term non-metric implies structural variations of individual crown and root forms that are visually scored in two ways: (1) “presence-absence” characters such as furrow patterns, accessory ridges, supernumerary cusps and roots, or (2) as differences in form such as curvature and angles (Hillson 1996; Scott and Turner 1997). While many of these traits are typically characterized as either present or absent, most non-metric traits vary in the degree to which a particular morphological structure is expressed (e.g. cusp/ridge size) (Scott and Turner 1997). In this sense, while they are sometimes referred to as discrete or discontinuous traits, most dental morphological variants are more accurately characterized as quasi-continuous, because they occur along a gradient of expression which cannot easily be divided into distinct stages. The concept of quasi-continuous variation was first developed by Grüneberg (1952) as a result of his laboratory studies on mice.

The earliest study of human dental morphological variation comes from the dental anatomist Georg von Carabelli, who published a paper in 1842 on his observations of a small mesiolingual accessory cusp on the upper molars (cited in Scott and Turner 1997). Carabelli noted the common occurrence of

this cusp in European dentitions. In 1920, Aleš Hrdlička published a study of shovel shaped incisors in the *American Journal of Physical Anthropology* which is considered by many as the foundation of the modern study of human dental morphology (Scott and Turner 1997). Hrdlička was the first to attempt to classify the degree of expression of a morphological dental trait and to examine its variation among human populations (Turner *et al.* 1991; Alt *et al.* 1998). His research on the geographic distribution of shovel shaped incisors lent increasing weight to the argument for the close biological relationship between East Asians and Native Americans. W.K. Gregory, in his major work *The Origin and Evolution of the Human Dentition* (1922), furthered the comparative study of human dentition by noting that, among other things, apart from some minor variations, differences in morphology between human populations were minimal (cited in Scott and Turner 1997). Some minor variations observed by Gregory include shovel-shaped incisors, *tuberculum dentale* of the anterior maxillary teeth, molar cusp number, lower molar groove pattern, and Carabelli's cusp. Despite these advances, however, subsequent studies of dental morphological variation were in short supply until the arrival of two key researchers, A.A. Dahlberg and P.O. Pederson, in the mid-twentieth century.

Dahlberg and Pederson, both of whom began their careers as dentists, made great strides in the advancement of dental morphological studies during the second half of the twentieth century; Dahlberg, through the collection and study of large numbers of dental casts from living White and Native Americans, and Pederson, through his studies of living and

archaeological Greenlandic Eskimo dentitions (Hillson 1996). Working together, Dahlberg and Pederson also organized several Dental Morphology Symposia beginning in the mid-1960s. Over the years these symposia have promoted the study of tooth variation and the discipline of dental anthropology as a whole (Dahlberg 1991; Hillson 1996). Dahlberg advocated the comparative study of dental morphology unceasingly through these symposia, and through his own research (e.g. Dahlberg 1963). Through his introduction and distribution of a series of 17 standardized reference plaques which presented the classification of permanent dental traits and their variations, Dahlberg also helped to overcome one of the major problems of dental morphological studies: the classification of traits and standardization of scoring procedures (Dahlberg 1991; Scott and Turner 1997; Mayhall 2000). Some of the traits represented in Dahlberg's series include plaques for upper incisor shovelling and double-shovelling, Carabelli's cusp, the upper second molar hypocone, and the protostylid.

Building on Dahlberg's efforts to standardize the classification of permanent dental morphological variation, researchers at the Dental Anthropology Laboratory of the Arizona State University developed a procedure for the graded scoring of key morphological traits of the permanent dentition, complete with reference plaques and detailed descriptions of trait expression for each scoring grade (Turner *et al.* 1991; Mayhall 2000). Known as the Arizona State University (ASU) Dental Anthropology System, this method standardizes scoring for over 40 crown, root, and jaw variants, many of them based on the earlier works of Hrdlička and Dahlberg. Most traits in this

system are scored by reference to a graded scale which reflects the degree to which the trait is expressed. Zero represents trait absence, while the highest number represents full trait expression. Other traits, such as cusp and root number, interruption groove, molar groove pattern and congenital tooth absence are recorded as either present or absent. Due to the comprehensiveness of the system and the widespread distribution of the reference plaques, the ASU system is the most widely employed method in use today and is also the recommended standard for scoring dental non-metric traits (Buikstra and Ubelaker 1994). In Japan, Kazuro Hanihara and co-workers devised similar reference plaques and scoring procedures for the deciduous dentition and, at the same time, developed and defined the characteristics of the “Mongoloid dental complex” based on living populations (Hanihara 1963; Hanihara and Minimidate 1965; Hanihara *et al.* 1974). Unfortunately, these plaques are not widely available and the comparative study of deciduous dental morphological variation has lagged behind that of the permanent dentition (Mayhall 2000).

3.6 The Arizona State University Dental Anthropology System

A description of each Arizona State University Dental Anthropology System (ASUDAS) dental morphological trait used in the present study is given below. A summary of the geographical distribution for each trait is also provided. While the precise mode of inheritance for these traits is not well-understood, most researchers now conclude that dental morphological trait variation is governed by complex polygenic factors, rather than simple dominant/recessive modes of inheritance (Scott and Turner 1997; Scott

2008). As such, trait frequencies cannot be directly equated with gene frequencies. While twin and family studies (e.g. Sofaer *et al.* 1972; Townsend and Martin 1992; Townsend *et al.* 1992) have shown that environmental factors may influence individual trait expression, they do not have a significant effect on overall population trait frequencies (Scott and Turner 1997). Studies of traits used in the ASU system have shown that they respond to microevolutionary forces of gene flow (e.g. Turner 1969), genetic drift (e.g. Turner 1969; Scott and Dahlberg 1982), mutation (e.g. Morris *et al.* 1978), and selection (e.g. Dahlberg 1963; Scott and Turner 1988), thus evincing their high degree of genetic control and suitability for use in biological distance studies.

3.6.1 Maxillary crown and root traits

Central incisor winging

Winging of the upper central incisors is not a true crown trait in the sense that the morphology of the individual tooth is not at issue. The trait is expressed as a bilateral rotation of the central incisors within their sockets so that the mesial crown margins are oriented towards the palate. From an occlusal view they form a V-shape. This trait may be expressed in a variety of ways including bilateral winging, unilateral winging of either the left or right central incisor, and counterwinging, in which the mesial margins of the teeth are rotated outwards rather than inwards (Enoki and Dahlberg 1958). Unilateral winging and counterwinging are typically disregarded in population studies, however, as they are usually the result of anterior tooth crowding and not reflective of underlying genetic factors (Scott and Turner 1997).

Lumholtz (1902) is credited with the first observation of bilateral incisor winging during his ethnographic work among several Mexican Indian groups. Other early observations of the trait include Nelson's (1938) work with the Pecos Pueblo Indians, and Wright's (1941) study of the Jivaro of South America.

Bilateral winging occurs in low frequencies (0-15%) among Western Eurasian, Sub-Saharan African and Sahul-Pacific populations. It occurs in moderate frequencies (15-30%) among East and Central Asian, American Arctic and Sunda-Pacific populations. Its highest rate of occurrence (30-50%) is among Northeast Siberian and North and South American populations (Scott and Turner 1997). The ASU system employs Enoki and Dahlberg's (1958) four-point trait classification which includes bilateral winging, unilateral winging, counterwinging and trait absence (no winging) (Turner *et al.* 1991). Winging may also be expressed in the mandibular central incisors, although this is not recorded in the ASU system (Turner *et al.* 1991).

Shovelling of the incisors and canines

In both upper and lower incisors and sometimes canines, pronounced mesial and distal marginal ridges of the lingual tooth surface may occur, creating a lingual fossa in which the tooth has the appearance of a coal-shovel. Shovel-shaping of the incisors and canines spans a range of expression, from slight/trace shovelling to heavily-buttressed marginal ridges which give the tooth a barrel-shaped appearance. Ales Hrdlička's seminal paper (1920) on

shovel-shaped teeth is the first to systematically describe variation of the trait, as well as defining four categories of trait expression: shovelling absent, trace-shovelling, semi-shovelling and full-shovelling. Albert Dahlberg later elaborated on Hrdlička's work by creating, among others, a three-dimensional reference plaque which adopted the four grades of trait expression for shovel-shaped teeth (Scott and Turner 1997). While Dahlberg's plaque and grading system are still used by anthropologists today, researchers at Arizona State University (ASU) have developed a seven-grade scale and reference plaque (Figure 3.9) which provides finer distinctions between Hrdlička and Dahlberg's original scoring system (Turner *et al.* 1991).

Shovel-shaped teeth have been studied extensively by researchers working in various regions of the world (e.g. Abrahams 1949; Carbonell 1963; Greene 1982; Hellman 1928; Suzuki and Takai 1964), and have been shown to be one of the most reliable dental traits for distinguishing between major geographical populations (Scott and Turner 1997). When the frequencies of shovel-shaped incisors are dichotomized into presence-absence, the highest rates of expression (>90%) are seen in East and North Asian and American Indian populations (Sino-Americans), while the lowest rates of expression (<20%) are observed in European and Sub-Saharan African populations (Carbonell 1963; Scott and Turner 1997). Other geographic groups such as Sunda-Pacific populations (Southeast Asia and the East Indian archipelago) occupy an intermediate position in terms of trait expression (Scott and Turner 1997). While shovel-shaping of the anterior dentition may be

observed on both maxillary and mandibular teeth, the trait tends to occur most often on the upper incisors (Hanihara 1963). In the ASU system, Turner *et al.* (1991) state that the key tooth for population comparisons of the shovelling trait should be confined to the upper teeth, especially the central incisors. An example of trace shovelling (grade 2) in the upper lateral incisors from the Kellis skeletal assemblage is given in Figure 3.10.

Labial convexity (upper central incisors)

The labial surface of the upper central incisors, when viewed occlusally, may range from extremely convex to relatively flat in appearance. Nichol *et al.* (1984) have developed a five-grade scaling plaque (Figure 3.11) for the purposes of scoring the trait and it has been incorporated into the ASU Dental Anthropology System (Turner *et al.* 1991). Nichol and co-workers (1984) have demonstrated that the degree of labial convexity is inversely correlated with double-shovelling. As these two traits are highly correlated, they should not be used in tandem for population analyses (Turner *et al.* 1991).Significant differences occur between populations in relation to trait expression. African and Asiatic Indian groups exhibit the strongest amount of labial convexity, while American Indians have low convexity frequency levels. Interobserver error levels for recording of this trait have been shown to be relatively high (Nichol *et al.* 1984, Nichol and Turner 1986), and as such, labial convexity trait frequencies, while recorded, are not used for population comparisons in the present study.

Double-shovelling of the upper incisors and canines

The term double-shovelling refers to the occurrence of pronounced mesial and distal ridges on the labial surface of the upper incisors (lateral and central) and canines. The trait was first characterized by Dahlberg and Mikkelson (1947). The mesial labial ridge is often more strongly developed than the distal labial ridge, and in some cases there is no development of the distal ridge at all (Scott and Turner 1997). Although double-shovelling can occur on any of the upper anterior teeth, (incisors and canines), the trait is typically most strongly expressed on the central incisors. The first attempt at standardizing the classification of this trait was made by Albert Dahlberg (1956). The ASU scoring rationale and reference plaque (Figure 3.12) was developed by Turner and Laidler Dowda in 1979 (Turner *et al.* 1991).

In terms of geographic distribution, double-shovelling is most commonly observed (45-65%) in Sino-American populations (Scott and Turner 1997). The trait is relatively rare in other populations, and is at its lowest frequency in Western Eurasian, Sub-Saharan African, Sahul-Pacific and Sunda-Pacific groups (Scott and Turner 1997). The key tooth for comparative population studies is the upper central incisor (Turner *et al.* 1991).

Interruption grooves (upper incisors)

Interruption grooves (*dens invaginatus*) are vertical developmental furrows which may occur on the lingual surface of the cingulum and roots of upper incisors. These grooves can start at the cingulum and proceed down the length of the root, or may be restricted largely to the enamel portion of the

cingulum with minimal involvement of the root. CG Turner II (1967) was the first person to systematically study this trait. In the ASU system there are no reference plaques; scoring is based on the location of the interruption groove on the lingual surface of the tooth (i.e. mesial lingual surface, distal lingual surface, medial lingual surface, etc.).

While interruption grooves are found to varying degrees in all major world populations, they occur most frequently in Sino-American groups (45-65%), and least frequently in Sub-Saharan and Sahul-Pacific populations (10-20%) (Scott and Turner 1997). The trait is most often expressed in the upper lateral incisors and it is this tooth that is recommended by Turner *et al.* (1991) for population comparisons. An example of the trait from the Kellis skeletal assemblage is shown in Figure 3.13.

Tuberculum dentale

Tuberculum dentale are cingular structures occurring on the lingual surface of the upper anterior teeth. They are sometimes referred to as lingual tubercles or cingular ridges (Scott and Turner 1997). They appear as vertical crests known as mediolingual ridges, or small tubercles or cusplets. The upper lateral incisor exhibits the greatest variety of cingular expressions ranging from single ridges to multiple cusplets. When these cusps occur on the canines they are known as canine tubercles (Scott and Turner 1997). W.K. Gregory (1922) was one of the earliest researchers to describe this trait in his magnum opus *The Origin and Evolution of the Human Dentition*. Classification and scoring of this trait has proven difficult, however, and the

levels of intra and interobserver error in recording this trait has been shown to be extremely high (Nichol and Turner 1986). The ASU system recommends focusing on trait expressions on the upper lateral incisors when conducting comparative population studies (Turner *et al.* 1991). The reference plaques for scoring this trait on the upper incisors and canines are shown in Figure 3.14.

Canine mesial ridge

In the upper canines, the mesiolingual and distolingual marginal ridges are normally equal in size. In rare instances, a strongly developed mesiolingual marginal ridge of the upper canine may fuse with the *tuberculum dentale*. This feature was first described by Morris (1975) as the “Bushman canine” due to its high occurrence among the Bushmen and other Sub-Saharan African groups. The trait has been observed in other populations however, although the highest rates (12-35%) of expression are confined to Sub-Saharan Africa (Scott and Turner 1997). The canine mesial ridge is least often seen (0-3%) among the indigenous peoples of the Americas (Scott and Turner 1997). The ASU scale (Figure 3.15) for recording of the trait was developed by Turner and Dale Klausner in 1979 (Turner *et al.* 1991).

Canine distal accessory ridge

There are typically three distinct ridges on the lingual surface of the upper and lower canines: a median ridge, and a mesiolingual and distolingual marginal ridge. Occasionally, an accessory ridge may occur between the median and distolingual ridges and this polymorphism is known as the

canine distal accessory ridge (Morris 1965; Scott 1977). The trait occurs more often and is more strongly expressed in upper canines than in lowers (Scott and Turner 1997). The canine distal accessory ridge is the most sexually dimorphic crown trait, with male expressions being more strongly developed and occurring in higher frequencies (Scott and Turner 1997).

Because there is no dentin involvement, this trait is difficult to record in older individuals where even slight attrition may obliterate any trace of its occurrence. For this reason, trait frequencies for children and young adults with unworn teeth should be used exclusively in population studies (Turner *et al.* 1991). Scoring for this trait was first developed by G.R. Scott (1973, 1977). The ASU reference plaque for this trait is shown in Figure 3.16.

Premolar mesial and distal accessory cusps (upper premolars)

First described by Turner (1967), these small cusps are occasionally observed at either end of the occlusal sagittal groove. For recording purposes, true accessory cusps must be distinctly separate from the buccal and lingual cusps. As these cusps are easily worn down, observations should be limited to younger individuals (Turner *et al.* 1991). Because it is so easily obliterated in older individuals, this trait is rarely used in population comparisons although it has been recorded for the present study. There is no reference plaque for this trait.

First premolar distosagittal ridge (Uto-Aztecan premolar)

This rare upper first premolar trait was first observed in the dentition of southwestern American Indians (Morris *et al.* 1978) and given the term Uto-Aztecan premolar. It is now known to occur among other American Indian populations but is not seen anywhere else (Turner *et al.* 1991). It is characterized by a strongly defined ridge extending from the apex of the buccal cusp to the distal occlusal border. The buccal surface is rotated mesially and the cusp is expanded buccolingually. Because of the geographic specificity of this trait, it is not usually employed in population comparisons outside of the Americas. The reference plaque for this trait is shown in Figure 3.17.

Metacone reduction (upper molars)

The third (distobuccal) cusp of the upper molars is known as the metacone. Reduction or absence of the distobuccal cusp is atypical in the first and second molars, but can occur on the third molars (Turner *et al.* 1991). Because of the infrequency of reduced or absent metacone expressions worldwide, the trait is rarely used for comparative population studies, although it has been recorded in the present study. The reference plaque for this trait is shown in Figure 3.18.

Hypocone reduction (upper molars)

The fourth (distolingual) cusp of the upper molars is known as the hypocone. It is the most variable of the four main upper molar cusps, and can range from a large, fully developed cusp, most often seen on the first molars, to a

reduced or absent cusp on the second and third molars (Hillson 1996; Scott and Turner 1997). Anthropologists and palaeontologists have for many years been interested in the number of cusps in both upper and lower molars as they relate to hominid dental evolution (Scott and Turner 1997). The evolutionary trend towards hypocone reduction and loss in the hominid line has long been noted by researchers (e.g. Campbell 1925; Shaw 1931). Dahlberg (1951), building on the work of early twentieth-century scholars, developed a cusp counting system which takes into account the reduction of the hypocone: 4 (fully expressed hypocone; i.e. 4 cusps), 4- (slightly reduced hypocone), +3 (drastically reduced hypocone), and 3 (hypocone absent; i.e. 3 cusps). In the ASU system (Turner *et al.* 1991), a six grade system of scoring hypocone expression has been developed along with an accompanying reference plaque (Figure 3.19).

Because the hypocone is almost always present in the upper first molars, any trait comparisons between populations should focus on the upper second molars, as they are more variable in terms of cusp retention (Turner *et al.* 1991). The worldwide variation of three-cusped (hypocone absent) upper second molars is quite limited in range. Sub-Saharan and Sahul-Pacific populations appear to have the lowest occurrence of three-cusped upper second molars (<10%), While Western Eurasian and Sino-American groups show the highest frequencies (10-30%) (Scott and Turner 1997). An example of second molar hypocone reduction in the Kellis skeletal assemblage is shown in Figure 3.20.

Carabelli's trait (upper molars)

The cusp of Carabelli is a supernumerary cusp which occurs on the mesiolingual surface of the protocone on the upper molars. While the trait may be present on all three upper molars, it is most commonly seen on the upper first molar (Scott and Turner 1997). The trait runs a gamut of expression from small pit and furrow features, to large tubercles with free-standing apexes. As one of the most intensively studied of all dental morphological variants (e.g. Bang and Hasund 1972; Hassanali 1982; Kolakowski *et al.* 1980; Reid *et al.* 1991; Scott 1980; Turner *et al.* 1998), the trait has been the subject of numerous attempts at classification (reviewed in Scott and Turner 1997). Of these, the eight-grade scale and reference plaque (Figure 3.21) developed by Albert Dahlberg (1956) has become the most commonly employed standard for scoring expression of the trait, and it is the method that is used in the ASU system (Turner *et al.* 1991).

Carabelli's trait has long been associated with western Eurasian (Caucasoid) populations, and Scott and Turner (1997) have demonstrated that it is this group which shows the highest incidence of cusp and tubercle forms (grade 5-7), followed by Sub-Saharan Africans. The trait does occur less frequently, however, in other populations (Scott 1980; Turner and Hawkey 1998). An example of a large Carabelli's cusp from the Kellis dental assemblage is given in Figure 3.22.

Cusp 5 (metaconule, distal accessory tubercle)

There are normally four main cusps on the occlusal surface of the upper molars: the protocone (mesiolingual cusp), paracone (mesiobuccal cusp), metacone (distobuccal cusp) and hypocone (distolingual cusp). In certain individuals, a small accessory cusp of variable size known as the metaconule occurs on the distal occlusal surface of the upper molars between the metacone and the hypocone (Scott and Turner 1997). Harris (1977) and Harris and Bailit (1980) were the first to attempt to classify this trait for scoring purposes, including trait absence and five grades of trait expression. The ASU scoring scale is similar to Harris' (1977), while the plaque (Figure 3.23) for Cusp 5 was developed by C.G. Turner and Richard Warner in 1977 (Turner *et al.* 1991).

The key tooth for population studies is the upper first molar (Turner *et al.* 1991; Scott and Turner 1997). In terms of geographic distribution, low frequencies of Cusp 5 occur in Western Eurasian and Sino-American groups (10-25%); Sunda-Pacific and certain Sub-Saharan African groups occupy an intermediate position (30-40%), while Sahul-Pacific and Western Sub-Saharan African groups have the highest rates of occurrence (45-60%) (Scott and Turner 1997). An example of the metaconule from the Kellis population is shown in Figure 3.24.

Parastyle (paramolar tubercle)

The parastyle is a cingular accessory cusp which occurs on the buccal surface of upper molar paracones (mesiobuccal cusp). Expression of this

trait can range from a small pit or attached cusp to a very large cusp with a free-standing apex. Rarely, the trait is expressed as a supernumerary conical or peg-shaped tooth which is fused to the buccal surface of the tooth (Scott and Turner 1997; Turner *et al.* 1991). The parastyle most commonly occurs on the upper third molars, although the trait is sometimes observed on the first and second molars as well (Scott and Turner 1997). The reference plaque for this trait is shown in Figure 3.25.

Enamel extensions

The contour of the cemento-enamel junction is normally horizontal along the buccal and lingual surfaces of the molars. Enamel extensions are thin lines of enamel which project downward from the buccal and/or lingual cervical enamel borders towards the root bifurcations of both upper and lower molars. Enamel extensions may also occur on upper and lower premolars as well. The trait was first systematically described and classified by Pedersen in his study of Greenland Eskimo teeth (1949), although earlier observations of the trait do exist in the literature (e.g. Chappel 1927; Leigh 1928, 1929). In the ASU scoring system there are three categories of trait presence: slight, moderate and pronounced (Turner *et al.* 1991). While enamel extensions can occur on both the lingual and buccal surfaces of the molars, the ASU system records only those extensions present on the buccal surface (Turner *et al.* 1991). There is no reference plaque for this trait.

In terms of geographic distribution, enamel extensions occur in low frequencies (0-10%) among Western Eurasian, Sub-Saharan African, Sahul-

Pacific and Jomon (Japan) populations. The trait occurs most often (40-60%) in American and East and North Asian populations. Sunda-Pacific and South Siberian groups occupy an intermediate position with regards to trait expression (20-30%) (Scott and Turner 1997). The key tooth for population studies is the upper first molar (Turner *et al.* 1991).

Premolar root number

Upper premolars may have one, two or three radicals. Single-rooted upper premolars are not bifurcated but may show developmental grooves which separate the root into two radicals, one lingual and one buccal. When the lingual and buccal radicals are separated by a root bifurcation, the tooth is considered double-rooted. The rare three-rooted upper premolar has three completely separated radicals, one lingual, one mesiobuccal and one distobuccal. In order for the tooth to be considered double or triple rooted, the roots must be separated at least one-fourth of the total root length (Turner *et al.* 1991). There is no reference plaque for this trait.

In terms of geographic distribution, Sub-Saharan African populations exhibit the highest rates of multi-rooted upper premolars (>60%). Intermediate groups include Western Eurasian, Sunda-Pacific, Sahul-Pacific, East Asian and Jomon populations (20-60%), while North Asian and American populations have the lowest rates of multi-rooted upper premolars (5-15%) (Scott and Turner 1997). The key tooth for population comparisons is the third premolar, as it more likely to have multiple roots than the fourth premolar (Turner *et al.* 1991).

Molar root number

Both upper and lower molars vary in terms of root number. Upper molars are typically three-rooted, while lower first molars are typically two-rooted. Environmental factors such as space restrictions at the back of the jaw may influence the number of roots on third molars; this precludes their use in dental morphological studies. The upper second molar is the most variable in terms of root number and is the key tooth for population studies (Turner *et al.* 1991). For lower molars, variation in root number is recorded for first and second molars. The scoring procedure for these traits was developed by Turner (1967). There is no reference plaque for this trait.

Peg-shaped upper lateral incisors and third molars

Reduced forms of upper lateral incisors and third molars may occasionally occur. These small peg- or cone-like teeth lack standard crown morphology and appear to exist at the threshold of a continuum that culminates with congenital absence of the tooth (Turner *et al.* 1991). Dahlberg (1956) was one of the first researchers to attempt a classification of upper lateral incisor variation. Usage and standardization for both tooth traits was developed by Turner for the ASU scoring system (Turner *et al.* 1991). This trait is rare for both upper lateral incisors and third molars (0-5%) and its utility in population comparisons remains uncertain (Scott and Turner 1997). As such, although both traits are recorded in the present study, they are not used in inter-population analyses. An example of a peg-shaped upper third molar from the Kellis dental assemblage is shown in Figure 3.26.

Odontomes (occlusal tubercles)

Odontomes are enamel and dentin spicules which may occur on the occlusal surface of both upper and lower premolars. This trait was first described by Pedersen (1949) in his study of the East Greenland Eskimo dentition. Three distinct geographic clusters are discernible among world populations. The trait is nearly absent (0-1%) among Western Eurasian, African, New Guinean, South Siberian and Jomon groups, while Sino-Americans, especially North American Indians, display the highest frequencies (4-7%); Australian, Melanesian and Sunda-Pacific groups occupy an intermediate position (1-3%) vis-à-vis the other groups (Scott and Turner 1997). In the ASU scoring system, odontomes are recorded as present or absent, although variation does occur in size and shape (Scott and Turner 1997). Because of the dentin component of this trait, odontome presence can be readily observed even in teeth with moderate cusp wear. There is no reference plaque for this trait.

Congenital absence (hypodontia)

Upper lateral and lower central incisors, lower fourth premolars and upper and lower third molars commonly fail to develop (agenesis) in some individuals (Hillson 1996). Such anomalies are thought to be inherited (Davies 1967, Lasker 1951). Congenital absence of teeth was first studied by Montagu (1940), who focused on upper lateral incisor variation, while Garn and co-workers (1962) studied third molar agenesis in relation to other anomalies of dental formation and eruption. Agenesis of the third molar is the most common form of congenital absence with up to one-third of a

population displaying the trait; absence of other tooth types is usually a much rarer occurrence (Hillson 1996). Without the use of x-rays, however, it may be impossible to determine whether a particular tooth is completely absent or unerupted/impacted and still lurking within the jaw. Teeth may also have been lost antemortem (i.e. before death) due to disease or injury, and thus care must be taken to determine the circumstances for each missing tooth. Because the use of x-ray machines is rare for the examination of archaeological skeletal assemblages, the potential for misdiagnosis of congenital absence is high and caution must be taken when comparing frequencies of tooth agenesis between groups.

3.6.2 Mandibular crown and root traits

Premolar lingual cusp variation (lower premolars)

While upper premolars have a single lingual cusp, lower premolar lingual cusp number is highly variable. One, two or three lingual cusps of varying size are common. A number of researchers have attempted to classify the considerable amount of variation in lower premolar crown morphology, including Pedersen (1949) and Kraus and Furr (1953). The ASU Dental Anthropology System, with its eleven-grade scoring scale, focuses strictly on variation in the number of lingual cusps and their relative size (Turner *et al.* 1991). The procedure, with slight modification, was developed by Scott (1973). The lower fourth premolar is considered the key tooth for use in population studies (Scott and Turner 1997). The reference plaques for scoring the trait in lower premolars are shown in Figure 3.27.

Anterior fovea (precuspidal fossa)

The anterior fovea, or precuspidal fossa, is a deep triangular indentation distal to the mesial marginal ridge that often occurs on lower first molars. The trait was first described in detail by Hrdlička (1924) who believed it to have evolutionary significance as it features in many fossil hominid dentitions as well as in anatomically modern humans. While anterior foveae are also known to occur on lower third molars, especially among fossil hominids, the lower first molar is considered the key tooth for population studies in the ASU Dental Anthropology System (Scott and Turner 1991). Nichol and Turner (1986), however, have shown that inter- and intraobserver error levels for scoring this trait are often unacceptably high; the trait is also extremely susceptible to occlusal wear, precluding observation in individuals above the age of twelve years (Turner *et al.* 1991). For this reason, although it has been recorded, the trait is not used for comparative purposes in the present study. The ASU scoring procedure was developed by C.G. Turner and S.M. Chilton in 1979 (Turner *et al.* 1991). The reference plaque is shown in Figure 3.28.

Lower molar cusp number

W.K. Gregory (1916) was the earliest researcher to categorize variation in the lower molar cusp number. Lower molars can have anywhere from three to seven cusps, although three-, four- and five-cusped molars are the most common. An example from the Kellis dental assemblage is shown in Figure 3.29. The distolingual cusp (entoconid) is omitted in three-cusped molars, while five-cusped molars have an additional distobuccal cusp (hypoconulid).

A sixth cusp (entoconulid) may occur between the entoconid (distolingual cusp) and hypoconulid (distobuccal cusp). Finally, a lingual seventh cusp (metaconulid) may occur between the metaconid (mesiolingual cusp) and entoconid (distolingual cusp). This seventh cusp, however, is not counted when scoring lower molar cusp number in the ASU system as Cusp 7 may occur without Cusp 6 (Turner *et al.* 1991). The ASU scoring system is based on Gregory's (1916) classification, with slight modification. There is no reference plaque for this trait.

Lower first molars typically have five cusps, while second molars typically have four. Lower third molars are more variable but are usually four or five-cusped. The relatively rare absence of the fifth cusp (hypoconulid) on lower first molars (world range: 0-20.0%) has a fairly clear geographic distribution as follows: Western Eurasian populations show the highest occurrence of hypoconulid absence (10-20.0%), while most other populations have frequencies of less than 3% (Scott and Turner 1997:211).

Lower second molars exhibit a much higher level of variation with regard to cusp number (world range: 10-80%) and for this reason it is the key tooth in population studies (Turner *et al.* 1991). 4-cusped lower second molars occur with regularity among many populations with Western Eurasian groups showing by far the highest frequencies (>80%). The Sub-Saharan San, Northeast Siberians, Native Americans and indigenous Australians have the lowest frequencies (10-30%) (Scott and Turner 1997:211).

Lower molar groove pattern

In lower molars, each of the main and accessory cusps is divided from the other by a series of fissures which form one of three common configurations: the Y, the X and the + patterns. In the Y groove pattern the fissure arrangement allows the mesiolingual (metaconid) and centrobuccal (hypoconid) cusps to abut one another, whilst the mesiobuccal and distolingual cusps are separated by a short length of fissure. In the X groove pattern, the arrangement is reversed so that the mesiobuccal and distolingual cusps abut one another and the mesiolingual and centrobuccal cusps are separated. In the + groove pattern the fissures dividing the main cusps meet at the same point in the centre of the crown surface forming a cross. The Y groove pattern, designated by W.K. Gregory (1916) as the *Dryopithecus* pattern, is found in fossil and extant hominoid dentitions and retained to varying degrees in modern human populations. In modern dentitions, the Y groove pattern occurs most commonly on the first molars. Because of the common tendency of modern humans to retain the ancestral Y groove pattern in the first molars, the lower second molar is the focal tooth for comparative studies of groove pattern (Turner *et al.* 1991). An example of the Y and + molar groove patterns from the Kellis assemblage is shown in Figure 3.30, and an example of the X pattern is shown in Figure 3.31. There is no reference plaque for this trait.

In terms of geographical distribution, the retention of the Y groove pattern on the lower second molars occurs most often among the San peoples of Sub-Saharan Africa (60-70%). East and South African, Melanesian and New

Guinean groups occupy an intermediate position (25-40%), while low frequencies of trait expression occur among Western Eurasian, Sino-American, Sunda-Pacific and Australian groups (5-20%) (Scott and Turner 1997).

Deflecting wrinkle (lower first molars)

The deflecting wrinkle is a deviation of the median occlusal ridge on the lower first molar, which normally follows a straight line from the tip of the metaconid (mesiolingual cusp) to the central fossa. In such cases, the median occlusal ridge is deflected mesially before continuing into the central fossa. Full expressions of this trait lend the median occlusal ridge a distinctive 'L' shape. Weidenreich (1937) was the earliest researcher to identify this occlusal variant, while Morris (1970) was the first to categorize the trait's occurrence geographically.

The deflecting wrinkle rarely occurs on lower second and third molars; thus, the lower first molar is the key tooth for population studies. The trait does not show any distinctive geographic patterning (world range: 5-55%). Native American groups and Northeast Siberians have the highest frequency of trait occurrence (35-55%), while Western Eurasians have the lowest incidence (5-15%). Intermediate groups (20-35%) include Sub-Saharan Africans and East Asians (Scott and Turner 1997). As with other occlusal crown traits without a dentin component, the deflecting wrinkle can easily be obliterated by attrition. For this reason, it is recommended that only juveniles be scored for this trait as it may be missed in older individuals with high levels of tooth

wear (Turner *et al.* 1991). The reference plaque for this trait is shown in Figure 3.32.

Protostylid (lower molars)

The protostylid is the term used to describe a cingular variation which occurs on the buccal aspect of the mesiobuccal cusp in lower molars. The trait ranges in expression from a small pit located in the buccal groove, to a secondary fissure which emanates mesially from the buccal groove, and culminating in a large free-standing cusp (Dahlberg 1950). The trait most commonly occurs on the lower first and third molars (Scott and Turner 1997). Dahlberg (1950) was the earliest researcher to assess the evolutionary significance of the protostylid, which had been commonly observed in fossil hominids and living apes but rarely seen in modern humans until his seminal research on the Pima Indians of the American southwest (Dahlberg 1945). He later produced a reference plaque and eight-grade scale (Dahlberg 1956) for scoring expressions of the trait which is still used in the ASU system (Figure 3.33). The lower first molar is considered the key tooth for population studies utilizing the protostylid (Scott and Turner 1997). Expressions of this trait may occur in up to 40% of a population (Hillson 1996).

Cusp 5 (lower molars)

The fifth (distobuccal) cusp of the lower molars, also known as the hypoconulid, occurs most frequently on first molars, while second molars exhibit greater variation in terms of hypoconulid retention (Scott and Turner 1997). When the fifth cusp is present it may vary from a small tubercle to a

large cusp equal in size to that of the hypoconid and entoconid. The ASU Dental Anthropology System employs a six-grade scale with corresponding reference plaque (Figure 3.34) developed by C.G. Turner and R. Warner in 1977 (Turner *et al.* 1991).

Cusp 6 (lower molars)

A sixth cusp, also known as the *tuberculum sextum* or entoconulid, may occur on lower molars between the hypoconulid (Cusp 5) and the entoconid (Cusp 4). It is a rare trait in modern human populations, although it occurs frequently in fossil hominids (Robinson 1956) as well as primates, especially pongids (Swindler 1976). If there is only a single distal cusp occurring between Cusp 4 and Cusp 3, it is impossible to determine whether or not it is Cusp 5 or 6. Typically, if there is only a single distal cusp, it is considered the fifth cusp. Consequently, Cusp 6 can only be determined in the presence of Cusp 5 (i.e. two distal cusps). When two distal cusps occur, Cusp 6 is always lingual to Cusp 5. In most cases, Cusp 6 is smaller than Cusp 5, although it is occasionally equal in size or larger (Scott and Turner 1997).

In the ASU scoring system, the size of Cusp 6 is scored on a six-grade scale in relation to Cusp 5 (Figure 3.35). The reference plaque and scale were developed by Turner in 1970 (Turner *et al.* 1991). The key tooth for trait frequency comparisons is the lower first molar. The world range for the expression of this trait is 4.7-61.7%, with Western Eurasian populations having the lowest rates of occurrence (Scott and Turner 1997). Sino-

American, Polynesian and Australian populations have the highest frequencies of Cusp 6 presence.

Cusp 7 (lower molars)

Cusp 7, also known as the *tuberculum intermedium* or metaconulid, is a supernumerary wedge-shaped cusp which may occur in the lingual groove between the metaconid (cusp 2) and the entoconid (cusp 4) of the lower molars. Like Cusp 6, the *tuberculum intermedium* is rare in modern human groups but common in living primates and some fossil hominids, e.g. *Paranthropus* (Hillson 1996). This trait occurs most often on the lower first molars and thus it is the key tooth for recording trait frequencies. The ASU system uses a six-grade scoring scale and reference plaque (Figure 3.36) that was developed by Turner in 1970 (Turner *et al.* 1991). In terms of geographical distribution, Cusp 7 occurs most frequently among Sub-Saharan African populations (25-40%); all other groups exhibit uniformly low frequencies of expression for this trait (0-10%) (Scott and Turner 1997). An example of a large Cusp 7 from the Kellis dental assemblage is shown in Figure 3.37.

Canine root number

Permanent lower canines are typically single-rooted teeth. In rare instances, however, the lower canine may be bifurcated into two roots, one buccal and one lingual (Alexandersen 1962, 1963). For scoring purposes, the tooth root must be separated for at least one-fourth of the total root length in order to

be considered double-rooted (Turner *et al.* 1991). There is no reference plaque for this trait.

In terms of geographic distribution, European groups exhibit the highest expression rates (>5%). North African and South Siberian groups occupy an intermediate position (2-4%), while Sub-Saharan African, Sino-American, Sunda-Pacific and Sahul-Pacific groups rarely exhibit the trait (0-1%) (Scott and Turner 1997).

Tome's root (third premolar)

C.S. Tomes (1889) was the earliest researcher to describe the occurrence of deep developmental grooves on the mesial surface of the lower third premolar root surface. It is now known that this phenomenon is part of a morphological continuum from a single to a double-rooted tooth (Scott and Turner 1997). In the ASU scoring procedure for this trait, there are six grades including trait absence (no developmental grooving), several grades of progressively deep developmental grooving, culminating in complete radical separation (two-roots) (Turner *et al.* 1991). The reference plaque for this trait is shown in Figure 3.38. Multiple-rooted lower premolars are far less common than multiple-rooted upper premolars (Scott and Turner 1997). Lower fourth premolars are not scored for Tome's root as they rarely display bifurcated radicals.

In terms of geographic distribution, the trait is relatively rare in Western Eurasian, Jomon, American Arctic and New Guinea groups (0-10%), while

high frequency groups include Sub-Saharan Africans and Aboriginal Australians. Groups occupying intermediate positions include North and East Asians, North and South American Indians, Melanesians, South Siberians and Sunda-Pacific peoples (Scott and Turner 1997).

Lower molar root number

Lower molars are typically two-rooted teeth. Single-rooted lower molars occur less often as the result of incomplete separation of the mesial and distal roots. In some situations, both the lingual and buccal root surfaces fail to separate, while in others it is only the buccal or lingual root surface which is involved (Scott and Turner 1997). Single-rooted lower first molars are exceedingly rare. Lower third molars are quite often single-rooted as the root complex is compacted due to space constrictions in the mandible. For these reasons, the lower second molar is the key tooth for scoring the single-rooted trait in the ASU system (Turner *et al.* 1991). A smaller supernumerary third root, conical in form, may also occur on the lingual aspect of the distal root. This three-rooted form occurs most often on the first molar and it is this tooth which is typically scored for the trait (Scott and Turner 1997). There is no reference plaque for this trait.

With regards to geographic distribution, single-rooted lower second molars are most commonly observed in Sino-American groups (30-40%). North African, Sunda and Sahul-Pacific and European groups occupy an intermediate position in terms of trait frequency (10-30%), while the trait rarely occurs among Sub-Saharan African, Jomon, and Aboriginal Australian

populations (0-10%) (Scott and Turner 1997). Three-rooted lower first molars occur most often among American Arctic and North and East Asian groups (>20%). Intermediate groups include Sunda-Pacific and American Indian groups (5-15%), while low frequency groups are comprised of Western Eurasians, Sub-Saharan Africans, Jomon, South Siberian and Sahul-Pacific peoples (Scott and Turner 1997).

Additional morphological traits not recorded in the present study

There are several additional crown, root and jaw morphological variants used in the ASU system which were not recorded for the Kellis assemblage. These include tooth root radical number, lower molar distal and middle trigonid crests, lower third molar torsomolar angle, palatine torus, mandibular torus and rocker jaw. Tooth root radical number is a difficult trait to score, and because the majority of the teeth recorded for the Kellis assemblage are still in their sockets, the number of potentially observable cases was deemed to be minimal. The distal and middle trigonid crests are rare traits which are notoriously difficult to score with even the slightest occlusal wear (Turner *et al.* 1991). Finally, the three traits based on the bony morphology of the palate and mandible were also left out because they do not directly involve the dentition. For these reasons, and the fact that none of these traits are commonly used in comparative studies of dental morphological data, I feel justified in excluding them from the present study.

3.7 Previous biological distance studies in Egypt and Nubia

The origins of ancient Egyptian civilization continue to be a major focus of Egyptologists and archaeologists alike. Early theories of large-scale population migration from western Asia (e.g. Derry 1956; Emery 1961; Petrie 1920, 1939) compete with more recent proposals of indigenous cultural evolution (e.g. Hassan 1986, 1988; Kemp 2006; Trigger 1983; Wendorf and Schild 2002). As such, the ancestry of the ancient Egyptians has been an Egyptological obsession since the birth of the discipline. Beginning with the likes of Samuel G. Morton (1844), many early anthropologists used the burgeoning collections of ancient Egyptian and Nubian skeletons to classify the ancient peoples of the Nile Valley using a largely outdated racialist/essentialist typology characteristic of the era (reviewed by Keita 1993). These early studies largely focused on cranial dimensions (e.g. Batrawi 1945, 1946; Morant 1925; Smith 1915, 1923; Smith and Wood Jones 1910), a methodology which flourished in the late 19th and early 20th centuries and continues to be used by physical anthropologists today, albeit in a far more sophisticated fashion (see for example: Angel 1972; Brace *et al*. 1993; Keita 1990; 1992; Zakrzewski 2007). In the second half of the twentieth century, physical anthropologists also began to use non-metric traits of the skeleton, especially of the cranium, to assess the biological affinities of the ancient Egyptians (see for example: Berry and Berry 1972; Prowse and Lovell 1995; Strouhal and Jungwirth 1979; Van Gerven *et al*. 1977).

One of the first systematic attempts to use dental morphological traits to examine the biological affinities of the ancient Egyptians was by D.L. Greene (1966, 1972, 1982) who compared dental traits amongst early Egyptian and Nubian skeletal collections. With the development of the Arizona State University Dental Anthropology System (Turner and Scott 1991), further studies of dental morphological trait variation in Egypt emerged during the 1990's. Johnson and Lovell's (1994) study of the Predynastic cemetery at Naqada is one of few papers to utilize dental morphological traits in order to understand the phenetic relationships within an intracemetery assemblage. A diachronic approach to dental trait variation was also conducted by Johnson and Lovell (1995) on A-Group and C-Group Nubians. Recently, J.D. Irish (2006) conducted an extensive survey of Egyptian archaeological dentitions in order to assess the population structure of the region from the prehistoric through the post-Pharaonic periods. His work, like that of Greene (1972), Brace *et al.* (1993), and Zakrzewski (2007), suggests a relatively high degree of population stability before, during and after the Egyptian Predynastic and Dynastic periods, while still allowing for small-scale genetic contributions from outside the immediate region. A later study by Schillaci and Irish (2009) using the same trait data in combination with new statistical methods draws similar conclusions. Irish (2005) has also examined Nubian dental trait variation from the Late Paleolithic to the Christian era in an attempt to estimate the biological affinities of the ancient peoples of Upper and Lower Nubia. This study also makes a strong case for Nubian population continuity in the Post-Pleistocene period (Irish 2005), although an earlier study demonstrated evidence for some Egyptian gene flow into Nubia

(Irish 1998b). Finally, Irish and Friedman (2010) used dental morphological traits to determine whether C-Group Nubians resident at Hierakonpolis during the Middle Kingdom and Second Intermediate Period remained genetically distinct from local Egyptians or became increasingly similar as a result of gene flow between the two groups. The results indicate that C-Group Nubians maintained their genetic distinctiveness throughout their occupation at Hierakonpolis despite being becoming culturally "Egyptianised" over time (Irish and Friedman 2010:98).

3.8 The present study: materials

At the time of data collection for the present study (2003-2004), 581 individuals had been recovered from the Kellis 2 cemetery since excavations began in 1992. Of these, however, only a much smaller subset of permanent dentitions was available for observation, due to the fact that nearly 65% of the skeletal assemblage is comprised of juveniles whose permanent teeth are either undeveloped or unerupted. There are also a sizeable number of older adults who are either completely edentulous (having lost all teeth antemortem), or whose teeth are too worn for observation. Consequently, only 172 individuals from Kellis 2 could be observed for permanent dental morphological traits. To bolster the study collection, 14 individuals with observable permanent teeth recovered from several tomb sites within the Kellis settlement itself have been recorded, bringing the total number of individuals to 186. These additional individuals are collectively referred to as the "townsite" burials. Before combining the two assemblages for use in the

regional and inter-regional comparative analysis, however, they will be tested for significant differences.

Based on grave goods, mortuary treatment and other archaeological indicators, the townsite burials have been tentatively assigned to the Late Roman period and thus are contemporary with the Kellis 2 cemetery. Multiple samples from Kellis 2 were submitted for accelerated mass spectrometry (AMS) radiocarbon dating with the results suggesting the cemetery was in use between 50 and 450 AD (Stewart *et al.* 2003; Molto *et al.* 2006). Others, however, have argued based on artifactual and mortuary evidence that the cemetery could not have existed earlier than the fourth century AD (Bowen 2003; Hope 2003).

The demographic structure of the Kellis assemblage is shown in Figure 3.39. Age at death estimation for the Kellis subadult assemblage is based on Ubelaker's (1989) dental eruption standards and regression formulas for long bone lengths developed by Sheuer and co-workers (1980). For adults, cranial suture closure (Meindl and Lovejoy 1985) and changes to the symphyseal surface of the pubic bone (Brooks and Suchey 1990) were used. Assessment of sex for the adult skeletal assemblage is based on the observation of sexually dimorphic indicators in the pelvis (e.g. sciatic notch, subpubic angle and presence/absence of the ventral arc) and skull (e.g. nuchal crest, mastoid process, supraorbital margin, glabella and mental eminence) (see Bass 1995; Phenice 1969; White and Folken 2005 for details of these methods). An individual skeleton can be assigned to one of five sex

categories: male, possible male, indeterminate, possible female and female; none of the adults used in the present study, however, were assigned to the possible male or female category. For the majority of burials analysed in the present study, all individuals are represented by a complete, well-preserved skeleton; as such, the demographic information can be presented with confidence. 13 individuals (7% of the overall sample), however, were missing either the mandible or cranium as a result of disturbances to the burial through looting activity. The sex distribution for Kellis, 64 males and 82 females, is shown in Figure 3.40. The distribution of burials by sex within the Kellis 2 cemetery is illustrated in Figure 3.41. Because all age categories are well-represented, the Kellis 2 assemblage appears to provide an accurate demographic profile of the population (Molto 2002), although the noticeably higher number of females than males is unusual. Perhaps their involvement in the caravan trade meant more males died away from home.

The data collection took place in Egypt over a period of two months between 2003 and 2004. During this phase, all available permanent teeth were scored individually, but only the antimere exhibiting the highest degree of trait expression was used in the analysis, according to the individual count method (Scott 1977, 1980; Turner and Scott 1973). This technique accounts for the fluctuating asymmetric effects of environmental factors (Van Valen 1962a, b; Staley and Green 1971; Sciulli *et al.* 1979), and maximizes sample sizes in dental series obtained from archaeological contexts where remains are often fragmentary. All traits are described in the Arizona State University (ASU) Dental Anthropology System, which presents well-established criteria

for scoring intra-trait variation (Turner *et al.* 1991). The traits were recorded with the aid of standardized ASU and Dahlberg Zoller Laboratory rank-scaled reference plaques. Intraobserver variation, the testing of which is recommended by Nichol and Turner (1986), was assessed by re-scoring 21 maxillary and 13 mandibular traits in a 10% sub-sample (18 individuals) of Kellis adults. The test of intraobserver variation took place at the end of the data collection season. Scoring inconsistencies were observed in only 3% of either maxillary or mandibular tooth-trait combinations. Scoring inconsistencies occurred during observations of the hypocone on the maxillary molars, and of shovelling on both maxillary and mandibular incisors. None of these inconsistencies, however, affect the dichotomized expression frequencies presented in this study.

3.9 Hypotheses

With an eye to addressing issues raised by previously conducted osteological studies, as well as more general archaeological issues concerning the Dakhleh Oasis within a broader regional context, the following hypotheses have been formulated:

1. *Phenotypic variability between Kellis males and females will indicate post-marital residence status, whereby one sex is more mobile (marrying into the community from elsewhere) and the other stationary (resident to the community from birth).*

2. *Burials located closer together will share more dental traits than those located further apart. Such clustering of dental traits will represent kin group burial areas within the Kellis 2 cemetery.*

3. *The Kellis assemblage will share genotypic/phenotypic features with Nile Valley groups as a result of cultural, political and economic ties between the two regions beginning in the Neolithic period.*

4. *The Kellis assemblage will contain a Nubian/Sub-Saharan genotypic/phenotypic component as a result of north-south gene flow stemming from historically known trade/exchange routes with northern Sudan and other parts of the Sahara.*

The first two hypotheses deal with the Kellis assemblage in an intracemetery (i.e. single site) context, while Hypotheses 3 and 4 necessitate an inter-regional approach. The methodologies for assessing both sets of hypotheses are described below.

3.10 Hypotheses 1 and 2: intracemetery analysis

3.10.1 Inter-sex trait variation

Biological distance studies which attempt to assess postmarital residence patterns work under the assumption that mates marrying into a community from elsewhere will be more phenotypically variable than mates who are resident in the community from birth (reviewed in Stojanowski and Schillaci 2006). Thus, if significant inter-sex differences in trait expressions are found

within an assemblage, they may indicate that one sex is more mobile than the other. According to Roman-era census data, the overwhelming majority of marriages in Egypt resulted in patrilocal residency (Bagnall and Frier 1994:121), in which the wife resides in the husband's household. In a cemetery assemblage deriving from a society which practices patrilocal residence, one would expect that females, having married into the community from elsewhere, would be the more variable sex in terms of dental morphology. Endogamy, however, the practice of choosing marriage partners from within a community, class or kin group, is also a common characteristic of ancient Egyptian society (Bagnall and Frier 1994). As such, if mates were chosen from within Kellis, one would not expect to see major inter-sex differences in trait frequencies because both sexes derive from the same local population. Instead, differences between male and female trait frequencies may pattern spatially within a cemetery, assuming that groupings of burials represent the accretion of patrilocal kin-groups over time. If the assumption holds, one would expect that within a cluster of burials males would be morphologically more similar than adult females, as they share the same genetic make-up (fathers, sons, grandsons, cousins, etc.). A complicating factor in this equation is that endogamous marriage between close kin (lineage endogamy) was a regular occurrence in Greco-Roman Egypt (Bagnall and Frier 1994; Hopkins 1980; Lewis 1983; Middleton 1962; Scheidel 1996a, 1997). Roman census data indicates that one-fifth of all Egyptian marriages with determinable kinship were between full siblings, half-siblings or first cousins (Bagnall and Frier 1994:127). If lineal endogamy was practiced at Kellis, it might make the task of observing inter-sex trait

variation more difficult as males and females would be equally related as a result of inbreeding.

3.10.2 Spatial analysis

In their review of intracemetery approaches to biological distance analysis, Stojanowski and Schillaci (2006:56) identify three cemetery contexts, each of which affect the methodologies employed in identifying closely-related individuals or groups: 1) small grave contexts containing a limited number of individuals such as crypts, tombs or double burials, 2) spatially structured large cemeteries containing distinct burial areas or differences in mortuary practices, 3) large cemeteries which are not spatially structured or contain no differences in mortuary practices. The Kellis 2 cemetery contains attributes of the second and third categories, as there is very little difference in mortuary practices among burials and, while there does appear to be spatial clustering of burials in certain areas of the site, there is considerable overlap between these burial groupings. In such circumstances, kin-structured cemeteries will be indentified through the positive correlation of spatial and phenotypic proximity (Stojanowski and Schillaci 2006). Thus, if kin-group burial areas exist at Kellis, they can potentially be identified by the non-random spatial distribution of traits, as individuals who are closely related will share similar trait frequencies.

In the present study, two methods are employed in an attempt to identify kin-groups within the Kellis 2 cemetery. The first method is to plot the spatial distribution of individual dental traits in order to assess whether or not they

are non-randomly distributed. A similar type of analysis has been conducted at Kellis using rare skeletal nonmetric traits (Kron 2007; Molto 2002). Alt and Vach (1998) recommend the use of rare or genetically anomalous traits when conducting intra-cemetery kinship analyses as these are more useful in identifying closely related individuals than commonly occurring dental traits. Such traits might include premolar odontomes, peg-shaped molars/incisors, talon cusps or incisor twinning. Unfortunately, rare traits such as talon cusps and incisor twinning are not recorded in the ASU system, while premolar odontomes and peg-shaped maxillary lateral incisors do not occur at all in the Kellis assemblage.

As such, a selection of traits which occur in low frequencies at Kellis have been chosen for this analysis in the hopes that non-random spatial patterning can be observed. While they are not considered rare or genetically anomalous, it is worth attempting to map their distribution. These traits are Y-groove pattern on mandibular second molars, Cusp 6 and 7 on mandibular first molars, 4-cusped mandibular first molars, 5 or more cusps on maxillary second molars, reduced maxillary second molar hypocone and metacone, shovel shaped maxillary lateral incisors, interruption grooves on maxillary lateral incisors and peg-shaped maxillary third molars. Each of these traits' occurrence is plotted on the map of the Kellis 2 cemetery.

The second approach is to divide the cemetery into four colour-coded groups of burials based on their location. Red corresponds to the northern group of burials, brown to the western group, blue to the southern group, and green to

the eastern and central burials (see Figure 3.42). The assumption is that these four groups will correspond to kin group burial areas. This is based on the observation that many of the burials tend to cluster around a number of large mudbrick tomb structures; these tombs may represent founding family groups with descendants or extended family members buried adjacent to them in simpler pit graves (Birrell 1999; Bowen 2003). Group assignation is based on a visual analysis of burials which appear to cluster together. The decision to include some burials in a particular group was often arbitrary as there are not always clear delineations between clusters of burials. The West group burials, however, appear to cluster around two large mudbrick tomb structures (Tomb 1 and 2) which predate them. The same is evident for the East group burials, which cluster around mudbrick Tomb 3. The North group represents a well-defined area of burials that appear to cluster around Tomb 4 (unexcavated at the time of data collection). The South group burials do not appear to have a focal point, and the graves appear more haphazardly lain, although a focal point may lie outside the area of excavation. Dental trait frequencies can then be compared between these areas to determine whether statistically significant differences can be observed and plotted. In addition, the combined dental trait frequencies for each group can be analyzed in order to see how they relate to one another in the same way the inter-regional groups are compared (i.e. MMD values and hierarchical cluster).

3.11 Hypotheses 3 and 4: regional trait comparisons

In order to assess the biological relationships of the Kellis assemblage to regional and inter-regional groups, dental trait frequencies obtained from studies of ancient Egyptian (Irish 2006) and Nubian (Irish 2005) groups are used as the basis for the present study's regional comparison. Additional comparative data for North and Sub-Saharan African groups derive from studies conducted by Irish (1993) and Irish and Konigsberg (2007), respectively. Table 3.1 provides a list of the skeletal assemblages used in the comparative study, along with their origin, time period and number of individuals. Finally, a comparison between the Kellis assemblage and those of broader-based regional groups will be undertaken using frequencies for thirteen commonly observed dental traits.

3.11.1 Egyptian comparative material

The Egyptian comparative data derives from Irish's (2006) study of dental traits from nine Upper Egyptian and six Lower Egyptian sites ranging from the Final Neolithic through to the Byzantine period (Table 3.1). The Upper Egyptian material is comprised of skeletal material from Gebel Ramlah, Badari, Naqada, Hierakonpolis, Abydos, Thebes, Qurneh, El Hesa and Kharga oasis. The Lower Egyptian material is comprised of skeletal material from Tarkhan, Saqqara, Lisht, Giza, and Hawara. The Greek Egyptian sample consists of Ptolemaic individuals from Saqqara and Manfalut in Middle Egypt. See Figure 3.43 for the locations of these sites. These data represent a total of 996 individuals (Irish 2006:530). The observation and recording of the dental trait frequencies were conducted entirely by Irish.

3.11.2 Nubian comparative material

The Nubian comparative data derive from Irish's (2005) study of dental traits from ten skeletal assemblages from Upper and Lower Nubia ranging from *ca*. 3000 BC to the 14th century AD. Nubian groups are commonly described as having a mix of Western Eurasian and Sub-Saharan African craniofacial and dental characteristics (Billy and Chamla 1981; Gill 1998; Irish 1993; Nielson 1970). The Upper Nubian material consists of skeletal remains from Kawa, Kerma, and Soleb. The Kushite group is comprised of Meroitic and Post-Meroitic era individuals from Kawa and Gabati. The Lower Nubian material consists of A-Group, C-Group and Pharaonic Nubian skeletal remains from Faras and Gamai. The Meroitic, X-Group, and Christian Nubians also derive from Faras and Gamai, with the addition of several individuals from Semna. See Figure 3.43 for the locations of these sites. These groups represent a total of 545 individuals (Irish 2005:522). The observation and recording of the dental trait frequencies were conducted entirely by Irish.

3.11.3 North African comparative material

The North African comparative data (Table 3.1) is taken from Irish's (1993) unpublished PhD thesis and consists of one ancient and four recent skeletal assemblages (Table 3.1). The total number of individuals is 164 (Irish 1993:78). They are used in the present study to test the Kellis assemblage for affinities with Saharan groups west of the Nile Valley. The Carthaginian assemblage consists of skeletal remains from the ancient Phoenician city of

Carthage located on the coast of Tunisia. The Carthaginians are a West Asian-derived population who most likely experienced some degree of admixture with indigenous Berber groups (Wysner 1945). The Algerian assemblage is comprised of recent Shawia Berber skeletal remains. The Shawia Berbers are known to have considerable admixture with Bedouin Arab and other Eurasian populations, i.e. Phoenicians, Greeks, Romans, Turks, Spanish and French (Wysner 1945). The Bedouin assemblage consists of recent skeletal remains from Morocco, Tunisia and Libya. North African Bedouin groups are typically classified as Arab peoples who first entered the region during the Muslim conquests of the 7th century AD (Julien 1970; Hiernaux 1975). The Kabyle assemblage consists of the recent skeletal remains of Kabyle Berbers from Algeria. Unlike other Berber groups, the isolated Kabyle were not exposed to high levels of foreign admixture, making them the most representative of indigenous North Africans (Wysner 1945). Finally, the Chad assemblage consists of the recent skeletal remains of several ethnic groups from this eastern Saharan country. The people of Chad are generally described as having Sub-Saharan physical characteristics, although some individuals may have lighter skin and Caucasoid facial features (Lebeuf 1959). The observation and recording of dental trait frequencies were conducted by Irish. See Figure 3.44 for the locations of the comparative groups.

3.11.4 Sub-Saharan African comparative material

In order to test for biological relationships between Kellis and Sub-Saharan Africa, dental trait frequencies from five West and two East African recent

skeletal assemblages are employed. The Sub-Saharan African comparative data (Table 3.1) derives from Irish and Konigsberg's (2007) comparative study of the inhabitants of Jebel Moya, an ancient Upper Nubian site. The West African material derives from Congo, Nigeria/Cameroon, Ghana, Gabon and Togo/Dahomey (Figure 3.44). The East African material derives from Kenya/Tanzania and Ethiopia (Figure 3.44). The total number of individuals is 374 (Irish and Konigsberg 2007:141). The observation and recording of dental trait frequencies were conducted by Irish.

3.11.5 Inter-regional comparative material

Dental trait frequency data for Western Europe, North Africa and three Sub-Saharan African groups (West Africa, South Africa and Khoisan) are used to situate the Kellis assemblage within a broader regional context. The comparative data for the inter-regional analysis are derived from Scott and Turner's (1997) compilation of dental trait frequencies from several independent studies conducted by Turner and Irish (Scott and Turner 1997:318). The Western European (WE) group is comprised of trait frequency data from Finnish, English, Dutch and Danish populations. While trait frequencies for Mediterranean Europeans would be more appropriate for comparisons with Kellis, such data are not currently available. Comparable data for western Asia are also nonexistent. The North African group (NAF) is comprised of combined trait frequency data from Algerian, Bedouin, Carthaginian, Canary Islander, Chadian, Nubian and Egyptian populations. Three Sub-Saharan African groups: West Africa (WAF), South Africa (SAF) and Khoisan (KHO) are comprised of trait frequency data from Congo,

Gabon, Nigeria, Cameroon, Pygmy, South Africa, Senegambia, Sotho, Tanzania, Togo/Benin, Tukolor, San and Khoikhoi.

3.12 Trait selection for comparative studies

While many comparative studies of dental morphology have demonstrated that the distribution of certain trait frequencies such as incisor shovelling and Carabelli's cusp tends to pattern along major geographical population lines (e.g. Swindler 1976; Brues 1977), more recent studies have shown that attempts to classify populations based on one or two traits are inadequate, as they do not sufficiently discriminate between groups (Scott 1980; Turner and Hawkey 1998). As such, Turner and Hawkey (1998) have recommended that, whenever possible, all traits in the ASU system be employed in assessments of biological affinities. In practice, however, especially when dealing with archaeological skeletal assemblages, it is rarely possible to score all 42 traits, given factors such as post/antemortem tooth loss, and attrition.

Another consideration when comparing trait frequencies between groups is to avoid using traits with low numbers of observable cases, as these may adversely affect the outcome of statistical analyses. These typically include the deflecting wrinkle, distal trigonid crest, anterior fovea and other crown traits which can be obscured by even small amounts of tooth wear. Traits which do not vary across comparative groups (i.e., 100% present or absent in all groups) should also be avoided as they lack discriminatory value in biological distance studies (Irish 2005). Intra- and inter-trait correlations are

another consideration in choosing the appropriate set of traits for comparative purposes (Scott 2008; Scott and Turner 1997). Examples of strong intra-trait correlations are shovelling of maxillary and mandibular incisors and canines, or hypocone and metacone expression on maxillary molars. In these cases, while the trait is recorded for each tooth in which it occurs, population comparisons should only compare trait frequencies for a specific tooth to avoid redundancy (Scott 2008). An example of an inter-trait correlation is the link between Carabelli's Cusp and hypocone expression on maxillary molars (Scott 1979). In this case, population comparisons typically employ frequencies for Carabelli's Cusp on the maxillary first molar where the trait is usually most strongly expressed, while frequencies for the hypocone are taken from the maxillary second molar as the trait is more variably expressed on this tooth (Turner *et al.* 1991). As a result, the number of traits used in comparative studies of dental morphology is usually a much-reduced subset of the total range of tooth-trait combinations; in some studies this number may be as low as nine (e.g. Johnson and Lovell 1994).

To facilitate the comparison of dental trait frequencies between groups, each trait's expression is dichotomized into binary presence/absence categories, a practice which is required before submitting the data for multivariate analyses (Sjøvold 1977). Because most traits are expressed quasi-continuously, however, it is not always a simple matter of characterizing a trait as present if it has a score above zero on the rank-scale; sometimes a trait is considered present only if it reaches a certain level of expression (Scott and Turner 1997). As such, the cut-off or breakpoint which determines

presence or absence is based on the morphological threshold of each trait (Scott and Turner 1997). These breakpoints have been established and standardized by Scott (1973) and Nichol (1990) through segregation analysis studies. Some researchers, however, may vary the breakpoints used in a particular study in order to emphasize or de-emphasize particular traits within a population for the purposes of intra-regional comparisons, for example lower molar Cusp 7 among Sub-Saharan populations (Irish 1993, 1997, 1998a). Thus, it essential to ensure that the same breakpoints are employed when comparing dichotomized dental trait data between researchers, as raw scores for dental traits are rarely published.

3.13 Statistical analyses

Sophisticated analyses of large numbers of traits can be analyzed profitably through the use of multivariate statistics, which allows the discernment of finer levels of biological distance between groups (Scott and Turner 1997). For those generating quantitative data such as tooth crown or cranial measurements, techniques such as principal coordinates, principal components and factor analysis are typically utilized (Keiser 1990; Relethford and Lees 1982; Stojanowski and Schillaci 2006). Those workers who deal in qualitative data such as cranial and dental morphological trait frequencies typically employ methods such as the chi-square statistic, angular transformations of frequencies or kinship coefficients (Harris and Sjøvold 2004; Scott and Turner 1997). Biological distance values calculated using quantitative data are based on differences in intergroup means, while those

generated from qualitative data are based on differences in frequencies or proportions.

Distance values calculated by researchers looking at dental morphology are typically measures of dissimilarity. Any value generated by biological distance analysis is a relative measure of relationship generated when a common set of variables are compared between groups (Scott and Turner 1997). Thus, two groups with identical trait frequencies will have a pairwise distance coefficient of 0.0. Similarity between groups as indicated by a small intergroup distance value implies a close biological relationship and a recent common ancestry (Scott and Turner 1997). As differences in trait frequencies increase, the distance coefficient will increase from zero, which implies population divergence. When many groups are compared in matrix format the pairwise distance coefficients between groups will indicate their relative relatedness. The more similar or related a group across all compared traits, the smaller the distance value will be, while dissimilar groups will have a larger distance value. These distance matrices are often plotted in a dendrogram (tree diagram) chart which visually represents the relatedness of multiple comparative groups. Groups which are more closely related (with small distance coefficients) will be linked at the lowest rungs of the dendrogram, while less related groups will diverge at higher levels on the dendrogram.

The morphological data for the Kellis permanent dentition are presented as follows. Variation in trait frequencies for males and females are analysed

through the use of the chi-square and Fisher's Exact tests in order to test for significant intersex differences from which inferences on post-marital residency at Kellis can be made. If no significant differences are apparent between Kellis 2 males and females, the trait frequencies for both sexes can be lumped and compared with trait frequencies for other geographic populations in order to assess the biological affinities of the Kellis skeletal assemblage. In the comparative section, the dichotomized tooth trait frequencies for each trait are presented and compared with data for major regional groups in order to position the Kellis assemblage within a global context. Following this, the Kellis tooth trait data are subjected to a series of statistical analyses in order to quantify in a more precise manner the assemblage's biological affinities with several regional groups. These statistical methods are outlined below.

3.13.1 Mean Measure of Divergence (MMD)

While there are a number of multivariate statistical approaches to quantifying biological distance, for example, Penrose's size and shape coefficients (1954) and more recently the use of the Mahalanobis D^2 distance (1936) for nonmetric data, the Mean Measure of Divergence (MMD) statistic is the most commonly used method for comparing both skeletal and dental discrete trait frequencies within and between skeletal assemblages (e.g. De Souza and Houghton 1977; Greene 1982; Greene *et al.* 1979; Guatelli-Steinberg *et al.* 2001; Irish 1997, 1998a,b,c,d, 2000, 2006; Johnson and Lovell 1995; Prowse and Lovell 1996; Ullinger *et al.* 2005).

The MMD statistic was formulated by Cedric A.B. Smith for use in genetic studies of inbred laboratory mice by M.S. Grewal (1962). Grewal used the MMD statistic to quantify the level of genetic divergence among successive generations of lab mice through the observation and recording of a series of skeletal nonmetric traits (Grewal 1962). The use of the Mean Measure of Divergence statistic has since become fashionable in anthropological studies as a result of seminal research papers by A.C. and R.J. Berry among others (e.g. Berry 1968; Berry and Berry 1967; Berry *et al.* 1967; Berry 1974, 1976).

The Mean Measure of Divergence statistic is a dissimilarity measure which produces values based on pair-wise comparisons of non-metric biological data between two groups. In the present study, dichotomized frequencies for individual dental morphological traits comprise the pair-wise comparisons. Low MMD values imply phenetic similarity between groups, while high values imply phenetic divergence. MMD values may be adversely affected by insufficient numbers of recorded individuals (i.e. small sample size), which are typical of studies employing archaeological data; as a result, a number of modifications to the original formula have been developed for dealing with this problem (Sjøvold 1977). The present study employs the Freeman and Tukey (1950) angular transformation which stabilizes variance between small samples and corrects for trait frequencies which are either very low (≤5%) or very high (≥95%). Other researchers use the Anscombe (1948) transformation, which produces similar results to the Freeman and Tukey (1950) formula (Harris and Sjøvold 2004); however, Greene and Suchey

(1976) have shown that that the latter method works better with small, archaeologically derived assemblages.

The Mean Measure of Divergence statistic is expressed as follows:

$$\mathrm{MMD} = \frac{\sum_{i=1}^{r} (\theta_{1i} - \theta_{2i})^2 - (1/(n_{1i} + 1/2) + 1/(n_{2i} + 1/2))}{r}$$

Where:

r = number of uncorrelated traits

n = number of individuals examined for trait ‘‘i’’

Θ = angular transformation of Freeman and Tukey (1950):

$\Theta = 1/2\sin^{-1}(1-(2k)/(n+1)) + 1/2\sin^{-1}(1-2(k+1)/(n+1))$

Where:

k = number of positive observations for trait ‘‘i’’

n = number of individuals examined for trait ‘‘i’’

The variance formula is expressed as:

$$\mathrm{var}\,(\mathrm{MMD}) = \frac{2\sum_{i=1}^{r} (1/(n_{1i} + 1/2) + 1/(n_{2i} + 1/2))^2}{r^2}$$

The standard deviation of the MMD is the square root of its variance:

$$\mathbf{SD}_{\mathrm{MMD}} = \sqrt{\mathbf{Var}_{\mathrm{MMD}}}$$

Sjøvold (1973:216, 1977) states that if an MMD value is greater than twice its standard deviation, a statistically significant difference exists between the two groups. Thus, the null hypothesis that both groups are drawn from the same population can be rejected at the 0.025 confidence level. Such tests of significance are commonly employed in biodistance studies using the MMD statistic (e.g. Greene 1982; Johnson and Lovell 1995; Irish 2005, 2006, 2010; Ullinger *et al*. 2005). However, as pointed out by Harris and Sjøvold (2004:92) in a review of the MMD statistic, no statistically significant difference between groups does not imply that these groups can be assumed to represent the same population, only that it is impossible to distinguish between them on the basis of the data at hand. Archaeological skeletal assemblages, so often separated by temporal and spatial distances, already represent distinct populations by their very nature. As a result of these considerations, the test of significance in biodistance studies must be used as part of a broader range of statistical approaches in order to obtain a more accurate depiction of the biological relationships between skeletal assemblages. These additional approaches are discussed in detail in the next section.

While the use of the MMD statistic has come under criticism in recent years in terms of its modification by various researchers and the corresponding lack of specificity when reporting their results (c.f. Harris and Sjøvold 2004; Harris 2008; Kongisberg 2006), several authors have recently attempted to

clarify and defend the use of the MMD in biodistance studies (Harris and Sjøvold 2004; Irish 2010). These authors explicate the proper formula for calculating the MMD statistic, while jettisoning some of the statistical baggage the formula has accumulated over the years, including the recent tendency for standardization of the MMD statistic (Harris and Sjøvold 2004). Irish (2010) goes further and lays out some of the major considerations that should be taken into account before using the MMD statistic, including trait selection and testing for inter-trait correlations. In direct comparisons between the Mahalanobis D^2 distance and MMD statistic, Edgar (2004) and Irish (2010) demonstrate that both methods are appropriate for nonmetric traits and produce highly concordant results. Irish (2010:391) posits that the MMD statistic may be the more robust of the two methods, as the MMD statistic uses summary count data, unlike the Mahalanobis D^2 distance which can be adversely affected by missing data. Based on these findings, I feel justified in employing the Mean Measure of Divergence statistic, using the formulas stated above, for the present study. As the MMD formula is currently not available as a module in SPSS (or any widely available statistical software package) the MMD statistic is calculated by programming the formula in MS Excel.

3.13.2 Hierarchical cluster analysis

Hierarchical cluster analysis is a useful tool for visually representing the relationships between different populations. It is a form of multivariate analysis which attempts to find structure in the relationships between cases defined by a set of variables (Drennan 2009). To begin, the MMD value for

each pairwise case (in the present study case = comparative group) comparison is used to produce a distance matrix. A distance matrix is a two-dimensional array (table) containing the pairwise values of a set of points – in this case the intercemetery comparative groups. The matrix is entered into a statistical software package which analyzes the data and generates a cluster analysis output in the form of a dendrogram. Hierarchical cluster analysis typically proceeds by linking individual groups to form larger clusters. In the first step, the two most similar groups are linked to form the first cluster; then two more groups are linked to form a second cluster, or a third group is added to the pre-existing cluster. Gradually, more groups are added to the hierarchy of agglomeration until all groups are incorporated into the finalized dendrogram (Drennan 2009). Within the dendrogram, groups that are closely related to one another will cluster together, while less related groups will appear in separate clusters. Groups linked at lower branches of the dendrogram will be more closely related than groups separated at higher branches of the dendrogram. SPSS 17 was used to run the hierarchical cluster analysis with Ward's linkage as the clustering method and Squared Euclidean distance as the measure. Ward's linkage (Ward 1963) is commonly used in biological distance cluster analyses (e.g. Hallgrimsson et al. 2004; Irish 1993, 1997; Irish and Hemphill 2004; Lukacs 2007; Ricaut and Waelkens 2008; Sutter and Mertz 2004). This method differs from other clustering methods in that it uses an analysis of variance (ANOVA) approach to evaluate distances between clusters. Ward's method attempts to minimize the Sum of Squares of any two clusters that can be formed at each step and has the effect of creating clusters of smaller size (Ward 1963). This is

considered advantageous in analyses of biological distance as closely related groups tend to stand out within the resulting dendrogram. It should be noted, however, that hierarchical clustering programs – by their nature – often force outliers into clusters that do not necessarily reflect reality. In addition, this method is not as useful as multidimensional scaling or principal components analysis for observing patterns of variation within a dataset (Drennan 2009). As such, while hierarchical cluster analysis is a useful tool for representing variation, many researchers consider multidimensional scaling as a more accurate method for plotting biological distance matrices (Irish, pers. comm.).

3.13.3 Multidimensional Scaling (MDS)

Multidimensional scaling is similar to hierarchical clustering in that it facilitates the visual representation of data generated from multivariate analyses of biological distance (Kruskal and Wish 1978). Like hierarchical clustering, a multidimensional scaling algorithm uses the distance matrix produced from the pairwise MMD values for each group and plots them in relation to one another. Each point on the plot represents one of the intracemetery comparative groups used in the MMD calculation. Multidimensional scaling plots the comparative groups as if they were Euclidean distances in such a way that “the rank order of the distances between pairs of points corresponds as well as possible to the rank order of the similarity coefficients in space” (Drennan 2009:285). In the present study, the similarity coefficient used is the MMD value generated for paired comparative groups. Thus, those groups that have smaller MMD values (i.e.

are more similar to one another) will be plotted closer together, while those that have larger MMD values (i.e. are less similar) will be placed further apart from one another. The spatial arrangement of groups is a trial-and-error process in which the scaling algorithm attempts to produce an initial configuration of points and then continuously adjusts them until no further improvements can be made.

As the name implies, multidimensional scaling can visualize data in any number of dimensions, although interpreting the results becomes difficult beyond three dimensions. Two- and three-dimensional plots are the most common in analyses of biological distance. Two important considerations in the interpretation of these plots are: 1) Kruskal's stress formula 1 value, which is a measure of the "goodness of fit" of the data; and 2) the r^2 value, which represents the proportion of variance of the scaled values accounted for by their corresponding distance values (Kruskal and Wish 1978). These values are generated as part of the multidimensional scaling output for the range of dimensions chosen. The values should be compared for each plot (e.g. two-dimensional vs. three-dimensional plots) to determine which number of dimensions provides the best representation of the data. Lower stress values imply a better fit between data values, while high r^2 values imply a truer representation of the spatial relationships between data values, i.e. comparative groups (Kruskal and Wish 1978). Typically, a higher number of dimensions used in a plot will produce a better representation of the data, but interpreting the output becomes increasingly difficult beyond three

dimensions. For the present study, multidimensional scaling is restricted to two- and three-dimensional plots as they are the easiest to interpret.

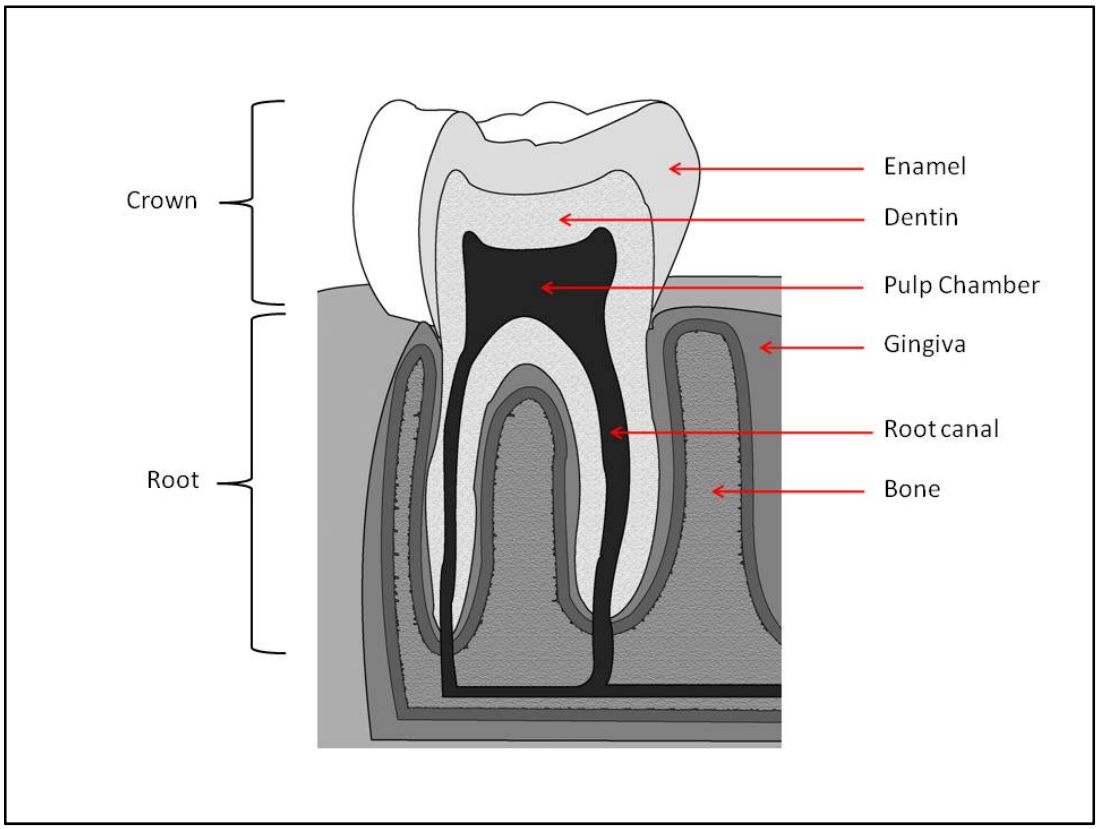


Figure 3.1. Cross-section of molar tooth with anatomical terminology.

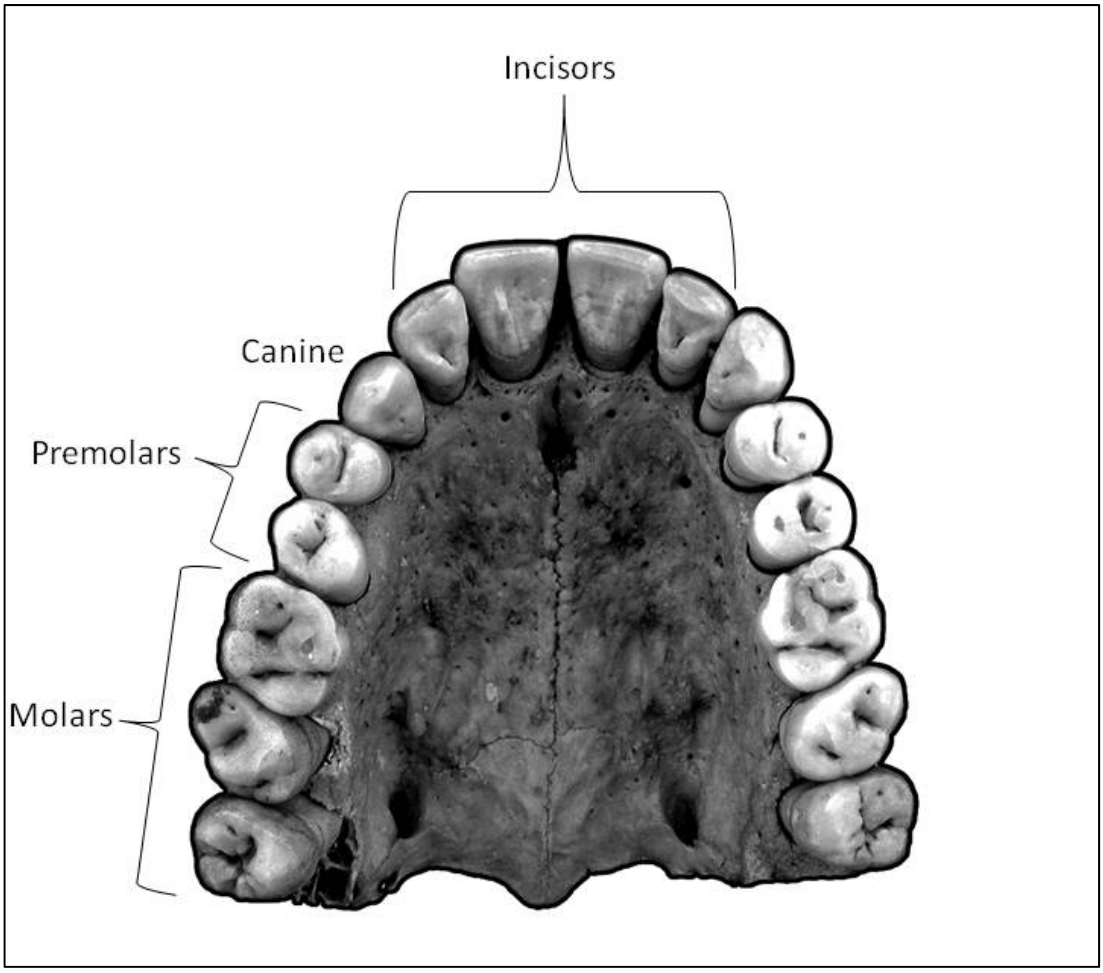


Figure 3.2. The four tooth types (Occlusal view).

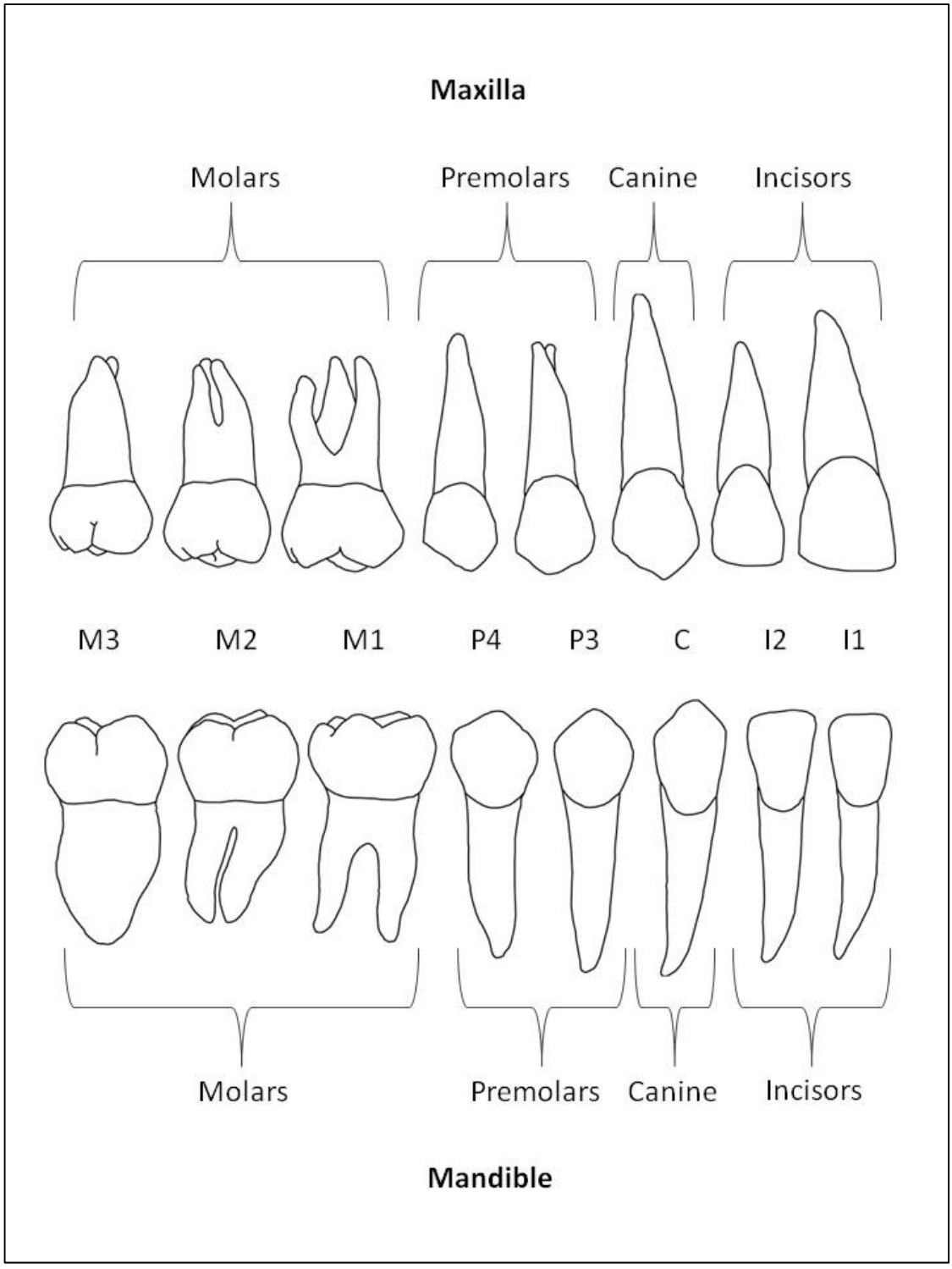


Figure 3.3. The four tooth types (buccal/labial view).

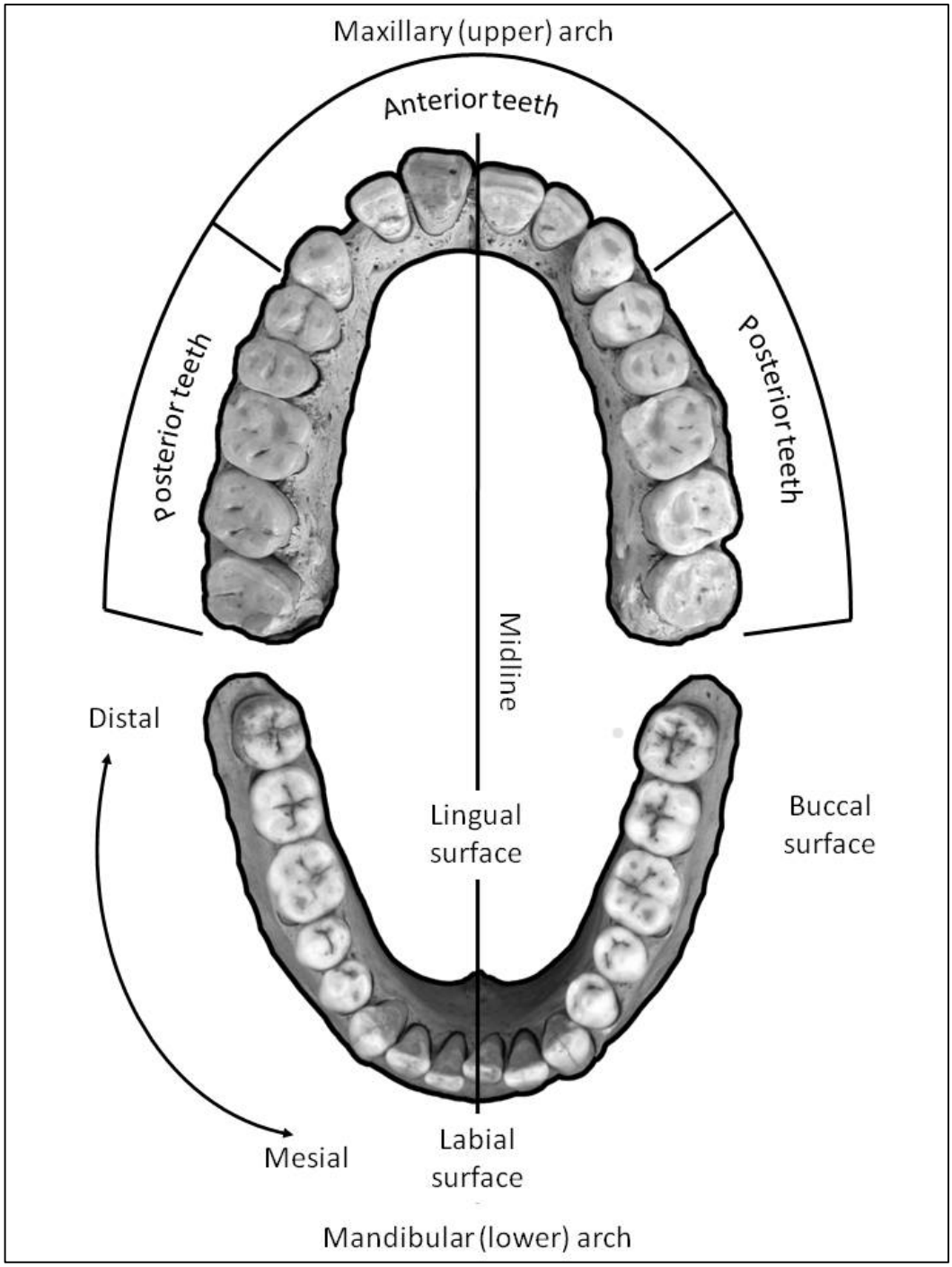


Figure 3.4. Positional terms for the teeth and jaws.

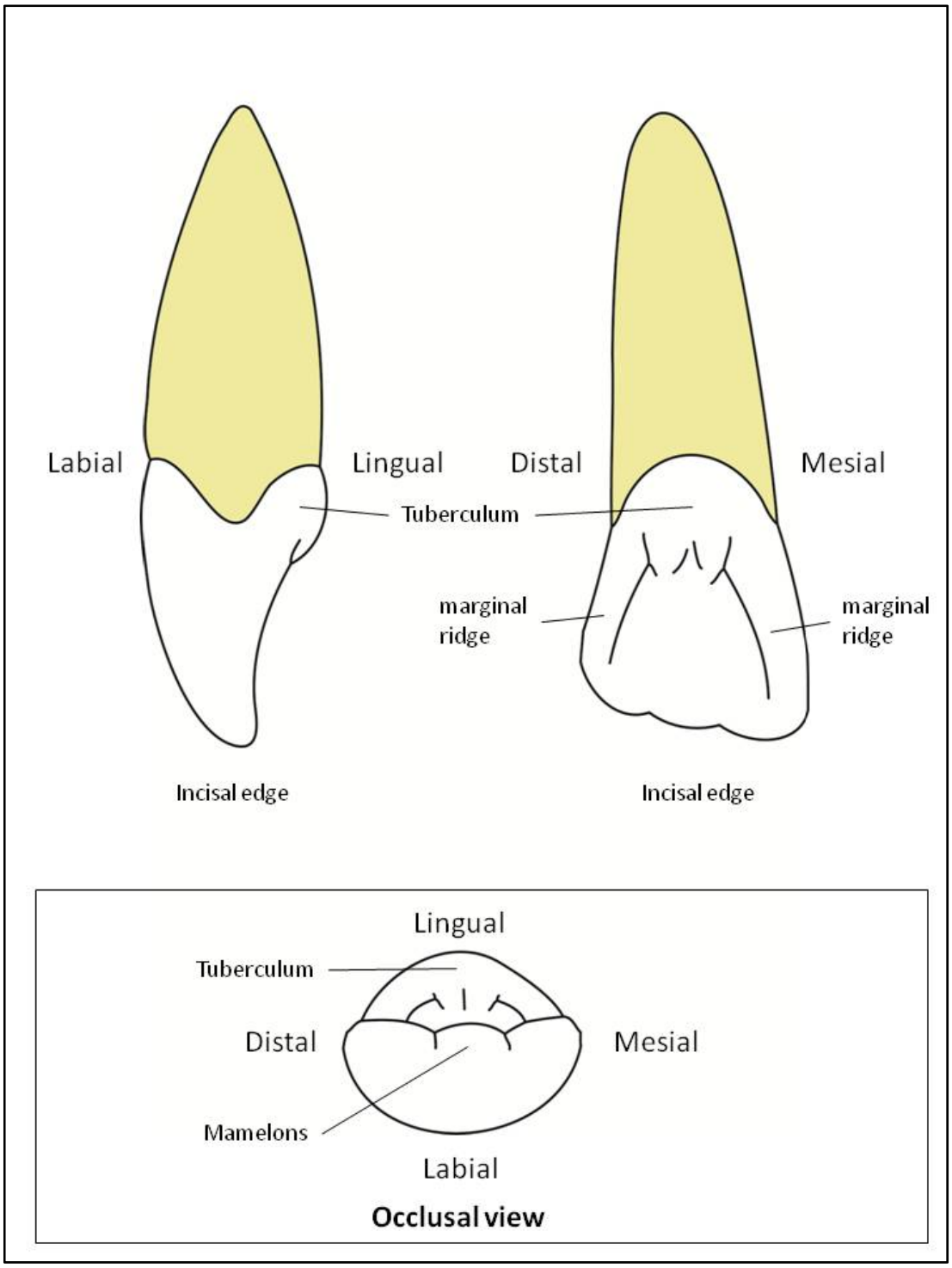


Figure 3.5. Left maxillary central incisor showing anatomical features (modified from Hillson 1996).

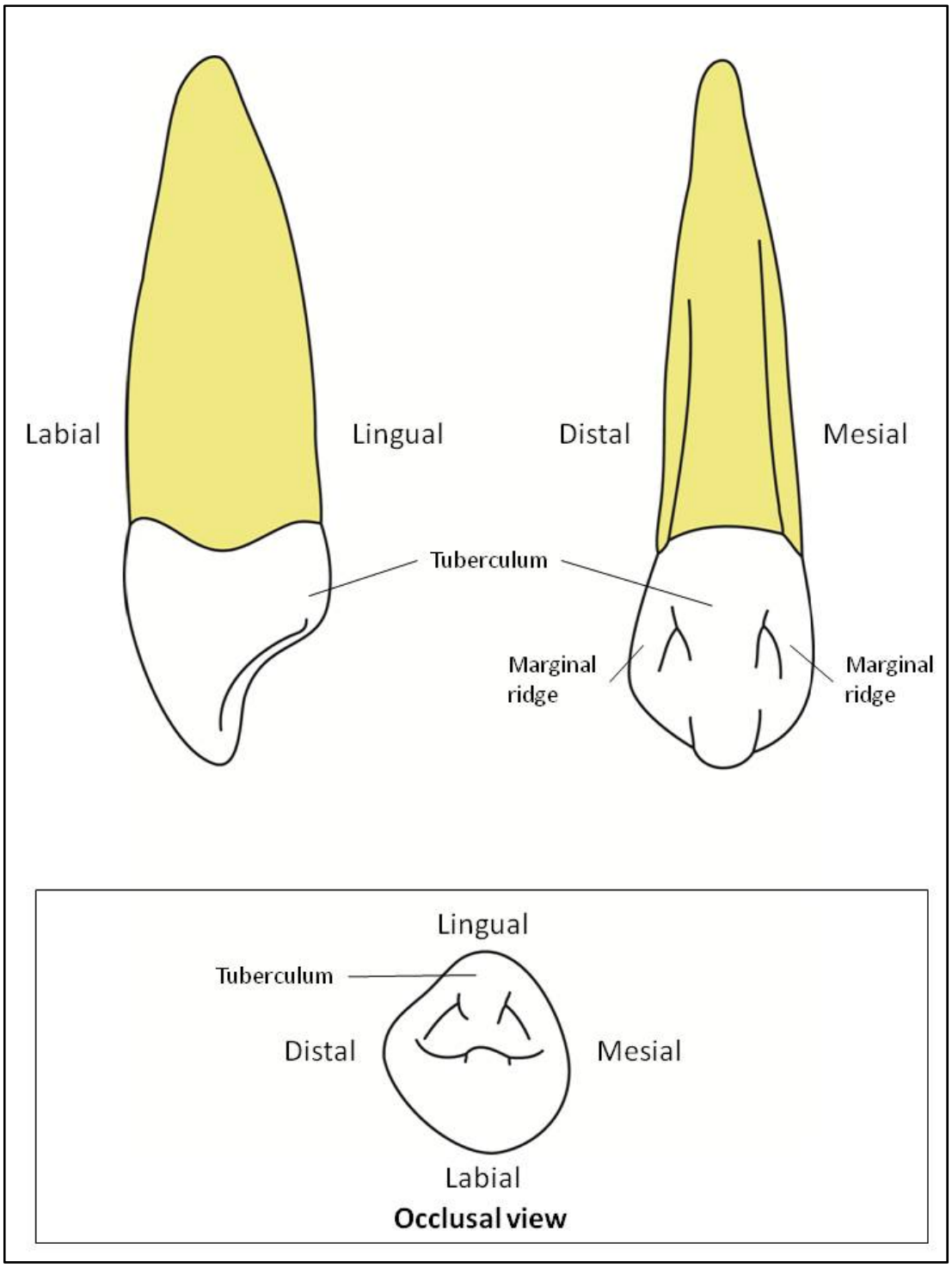


Figure 3.6. Left maxillary canine showing anatomical features (modified from Hillson 1996).

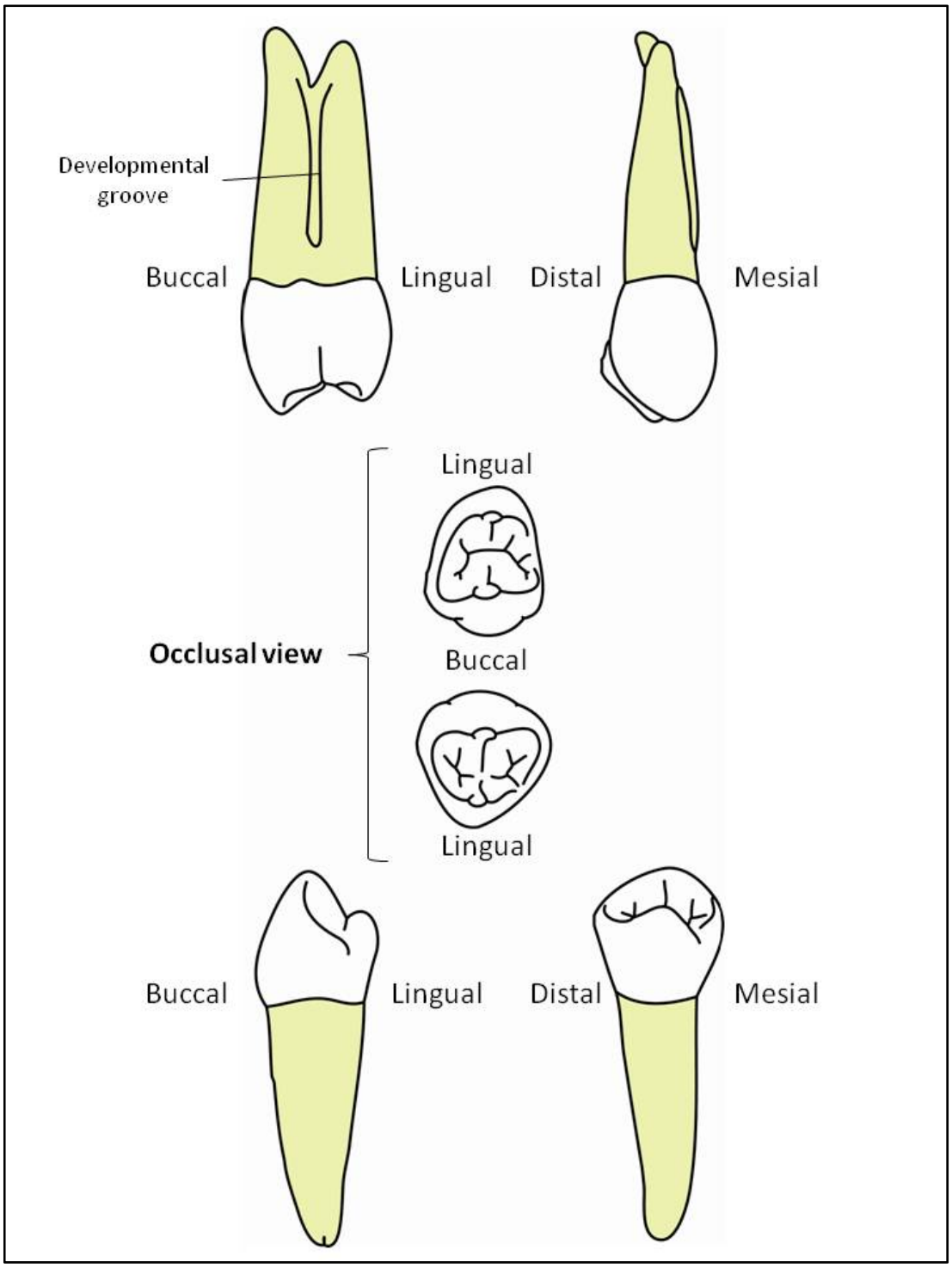


Figure 3.7. Left maxillary and mandibular premolars showing anatomical features (modified from Hillson 1996).

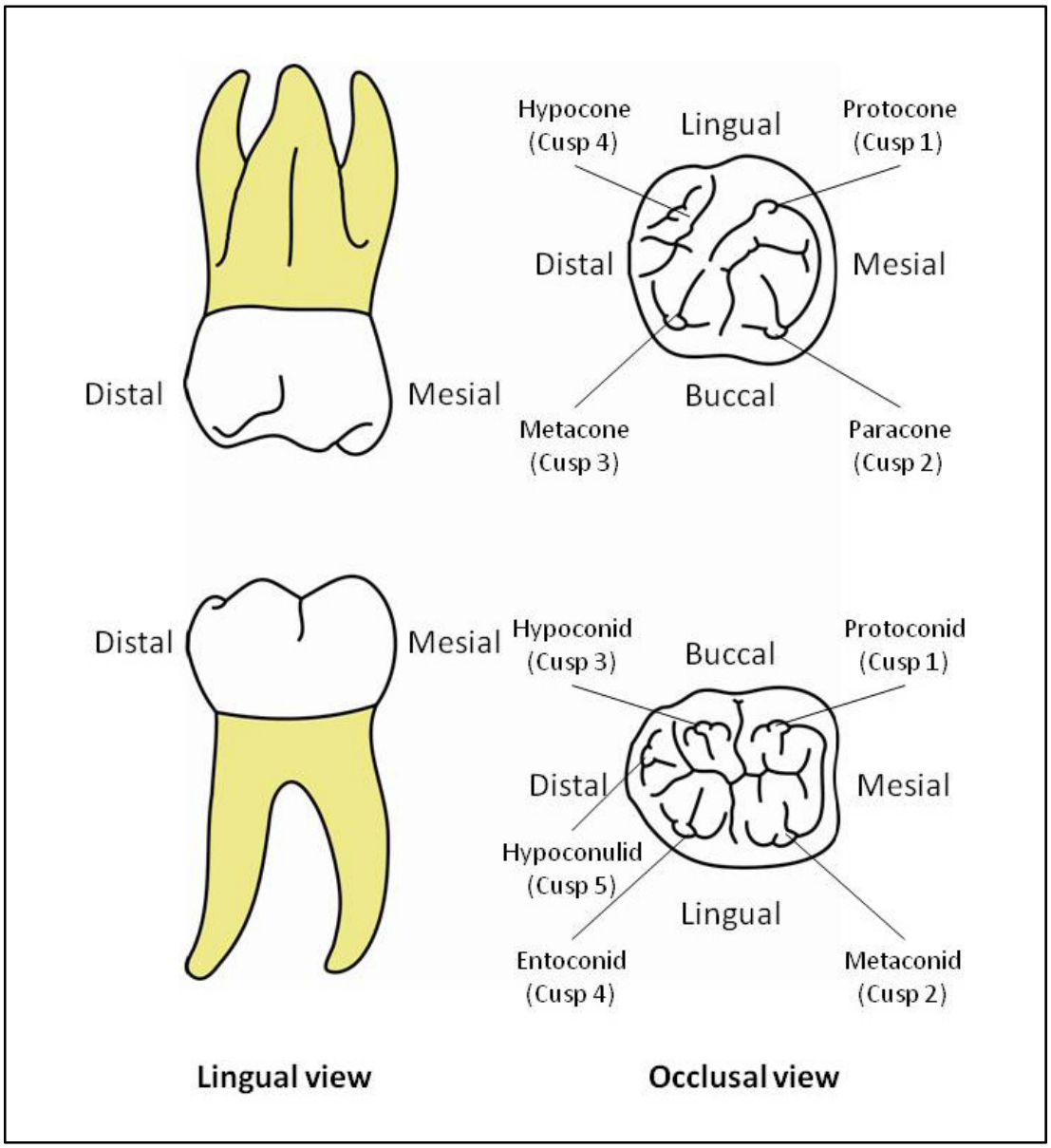


Figure 3.8. Maxillary and mandibular left molars showing anatomical features (modified from Hillson 1996).

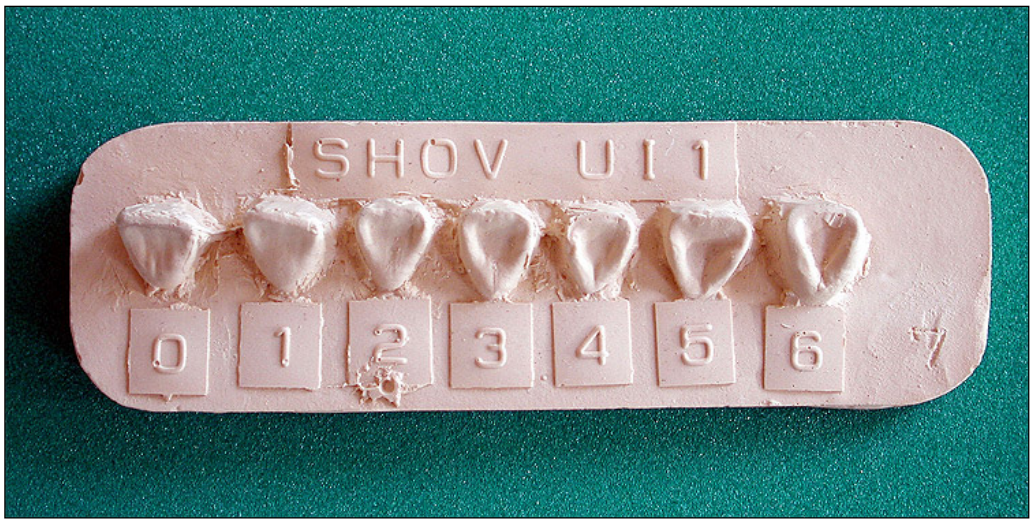


Figure 3.9. ASU Dental Anthropology System reference plaque showing different grades of shovelling in the permanent upper central incisor.

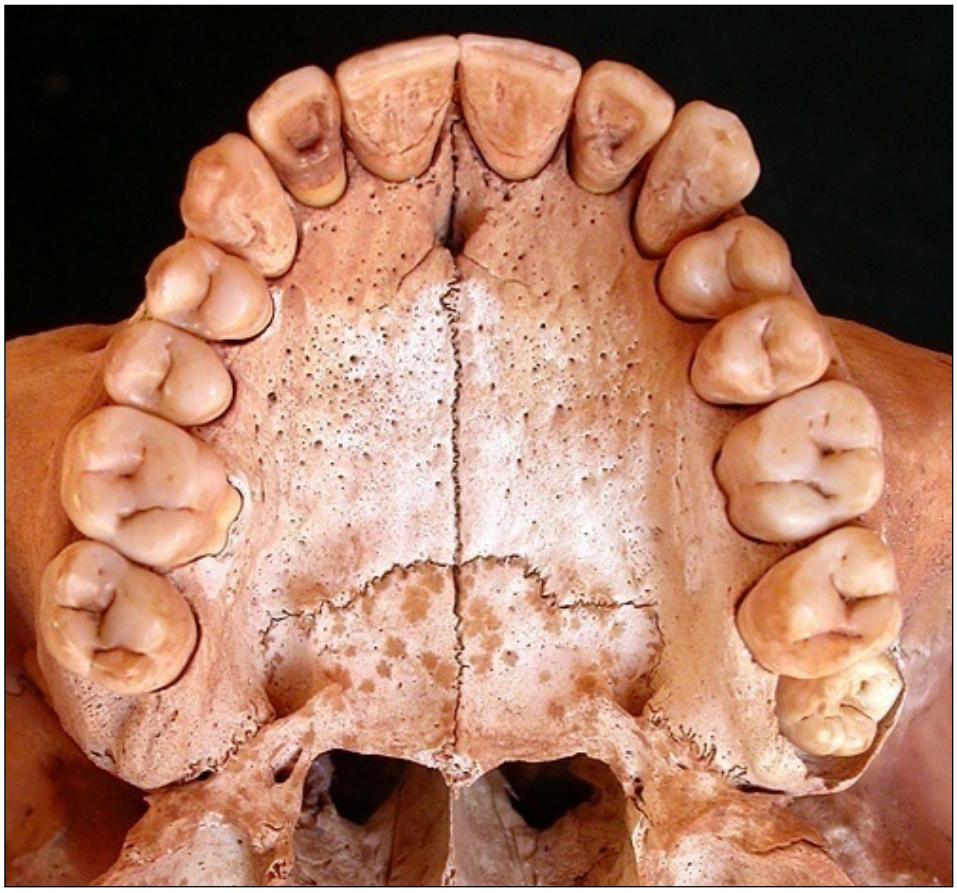


Figure 3.10. Grade 2 shovelling on the lateral incisors. Kellis North Tomb (townsite) burial 3 maxillae.

Figure 3.11. ASU Dental Anthropology System reference plaque for upper central incisor labial convexity.

Figure 3.12. ASU Dental Anthropology System reference plaque for upper incisor double shovelling.

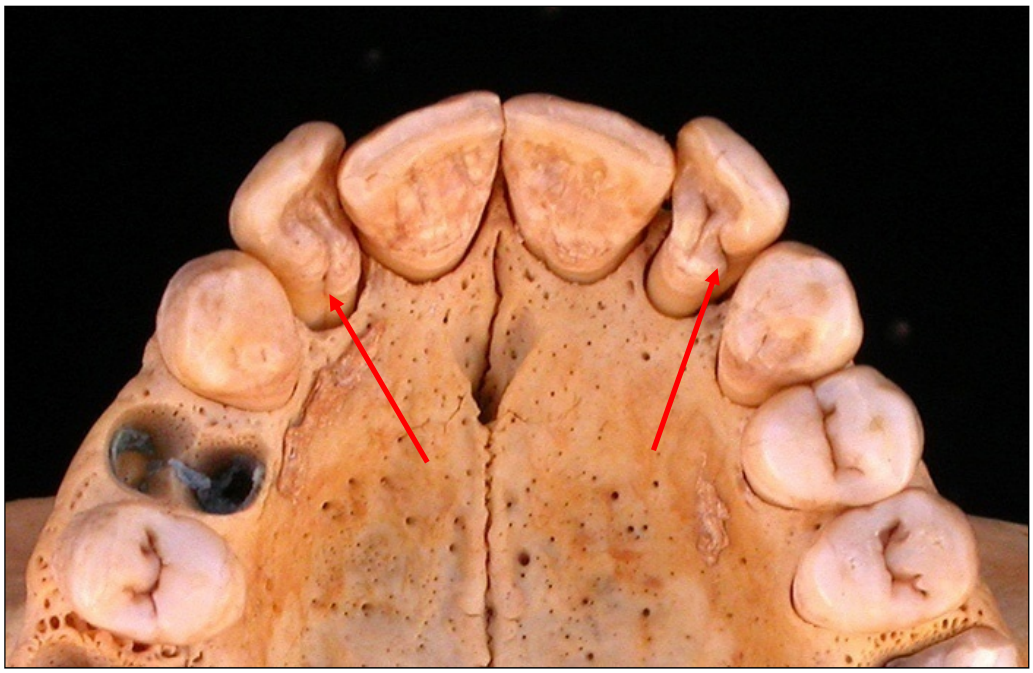
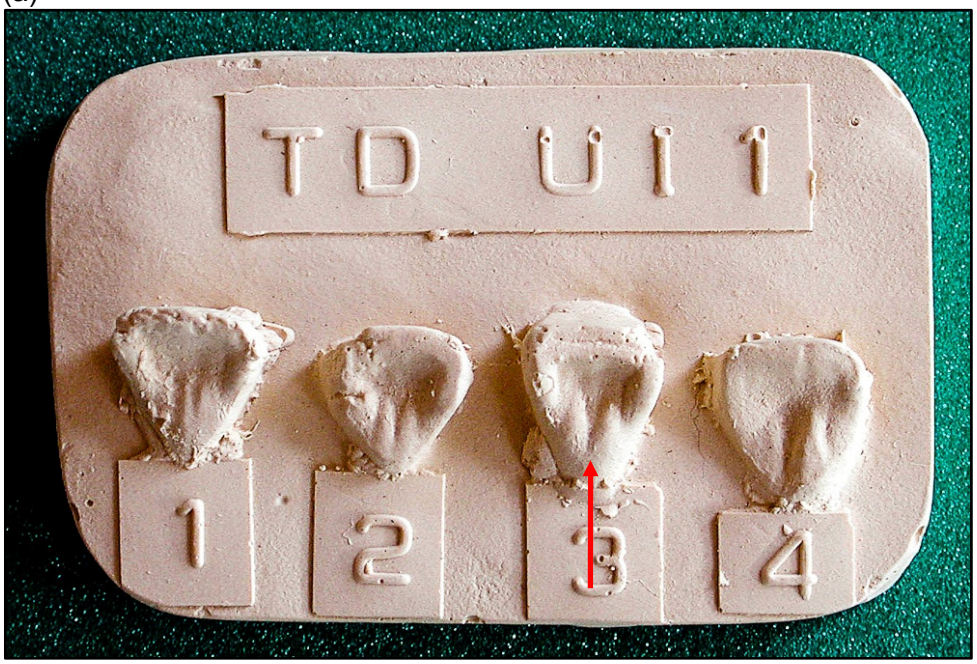


Figure 3.13. Interruption grooves on lateral incisors. K2 burial 169 maxillae.

(a)



(b)

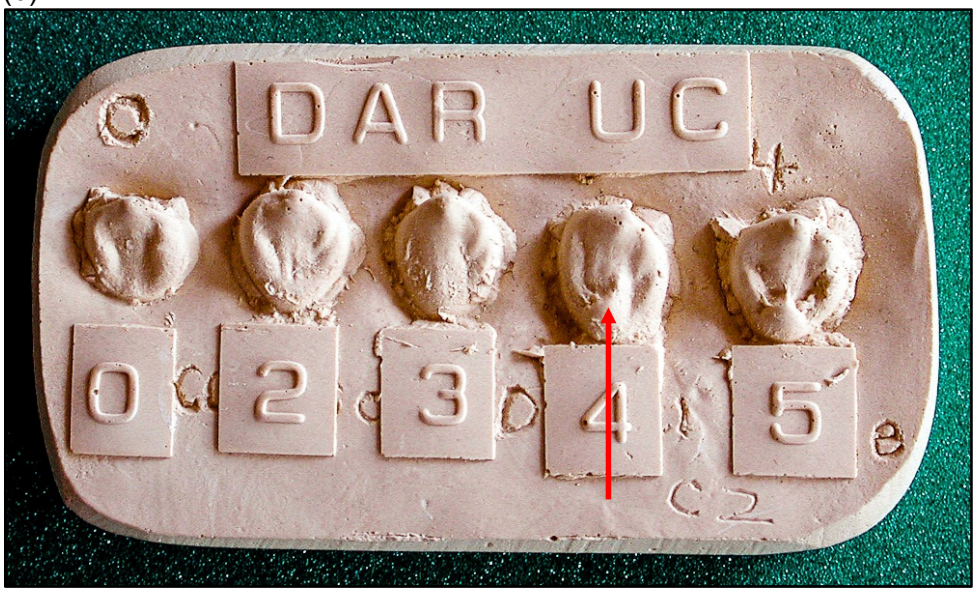


Figure 3.14. ASU Dental Anthropology System reference plaques for scoring *tuberculum dentale* on: (a) upper central incisors and (b) upper lateral central incisors and canines.

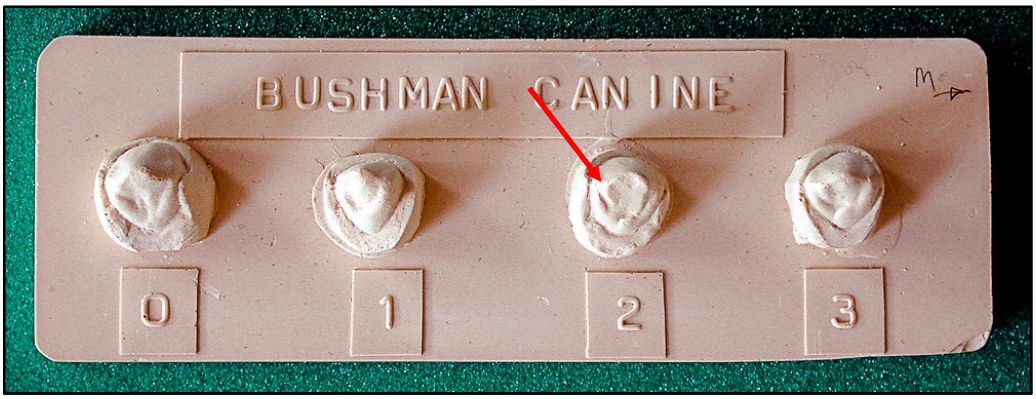
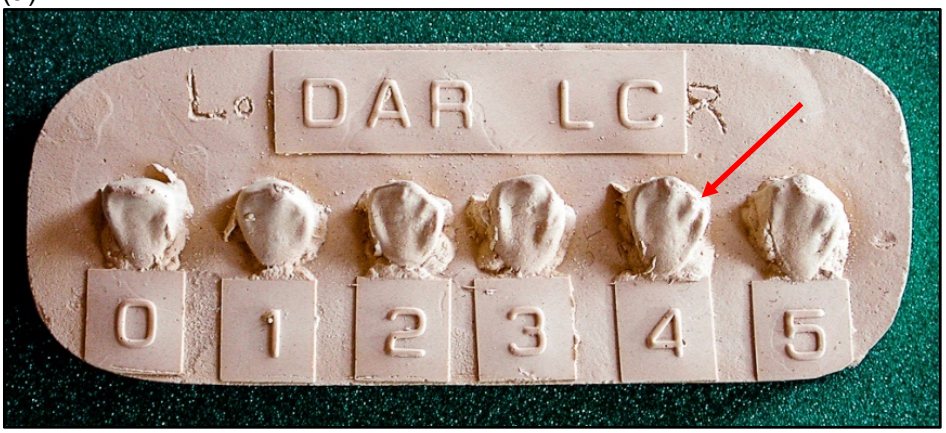


Figure 3.15. ASU Dental Anthropology System reference plaque for upper canine mesial ridge ("Bushman canine").

(a)



(b)

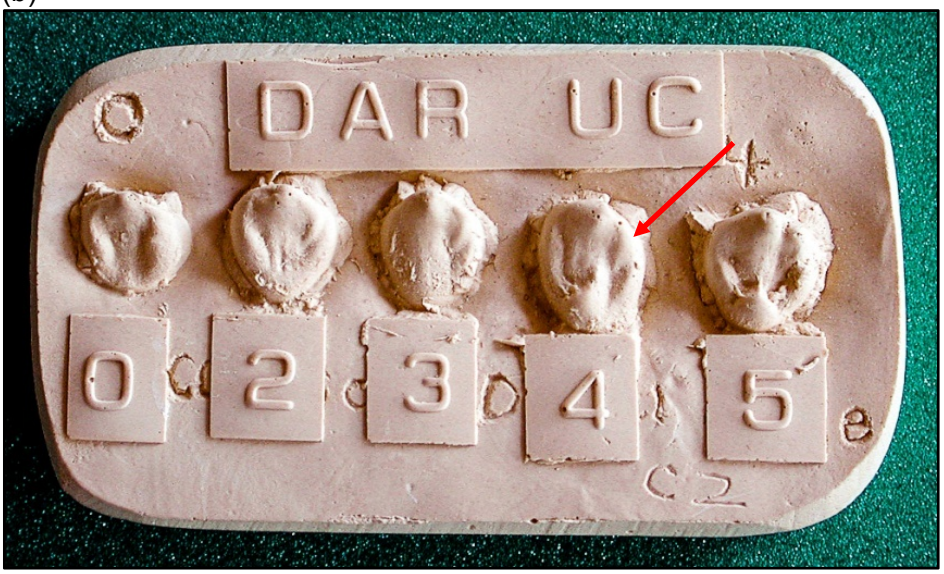


Figure 3.16. ASU Dental Anthropology System reference plaques for scoring canine distal accessory ridge on: (a) lower canines, and (b) upper canines.

Figure 3.17. ASU Dental Anthropology System reference plaque for upper third premolar distosagittal ridge ("Uto-Aztecan" premolar).

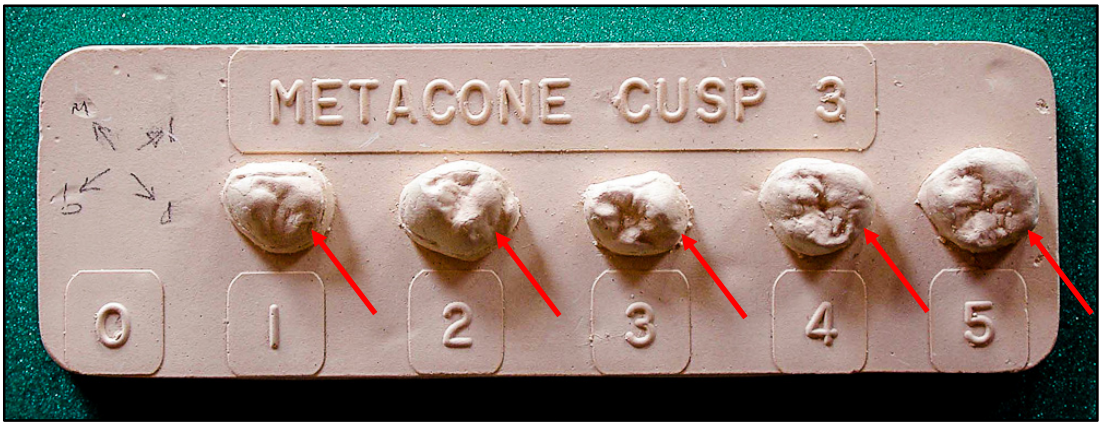


Figure 3.18. ASU Dental Anthropology System reference plaque for upper molar metacone.

Figure 3.19. ASU Dental Anthropology System reference plaque for upper molar hypocone.

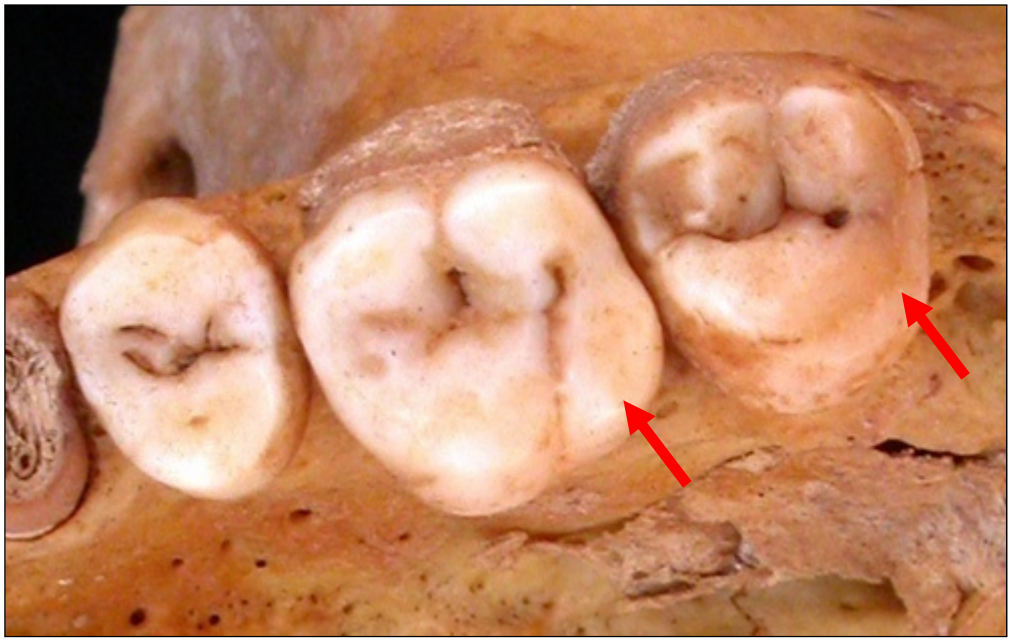


Figure 3.20. Reduction in hypocone (distolingual cusp) size from M1 to M2. K2 burial 491 (upper left molars).

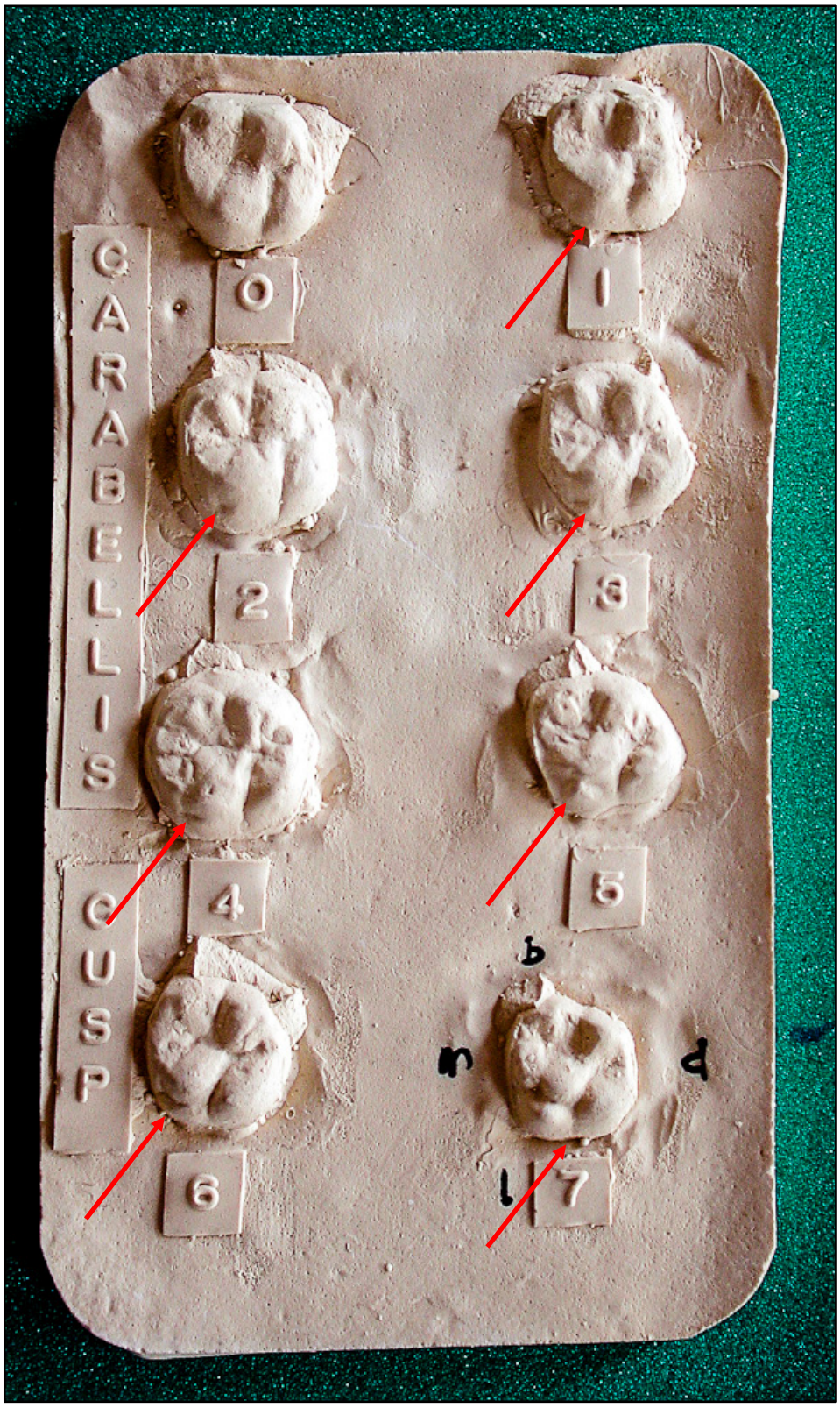


Figure 3.21. Dahlberg's eight-grade reference plaque for Carabelli's trait in the upper molars.

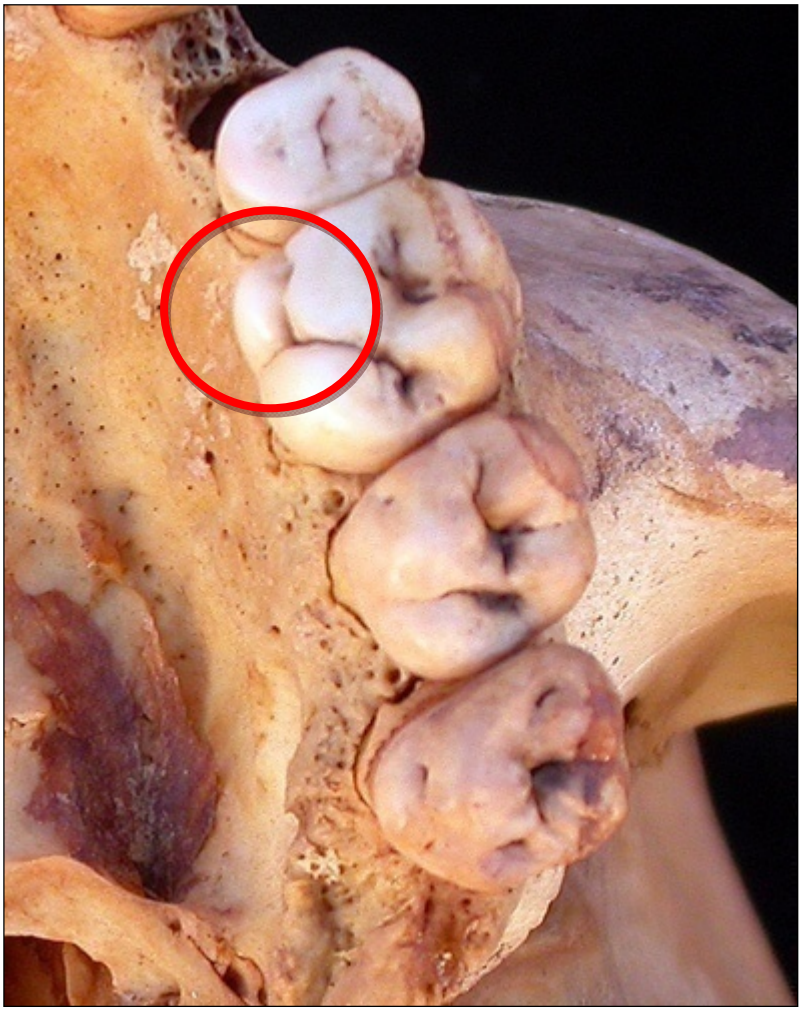


Figure 3.22. Grade 7 Carabelli's cusp on M1. Note rare presence of low-grade Carabelli's cusp on M2 and M3. K2 burial 284.

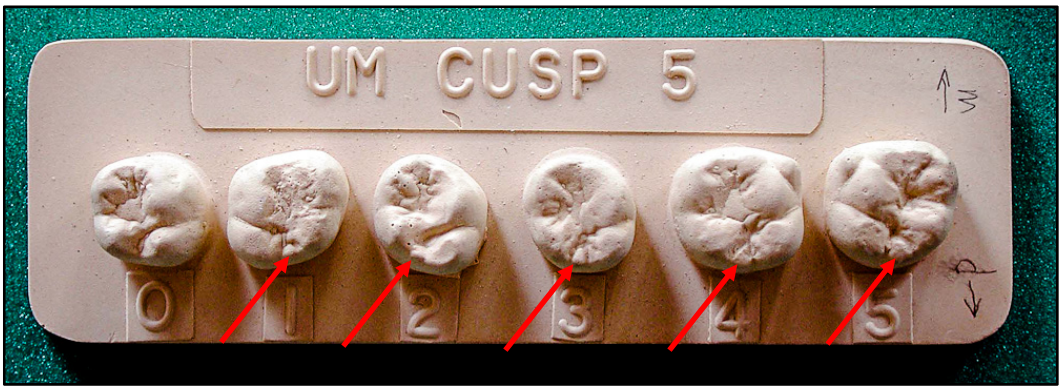


Figure 3.23. ASU Dental Anthropology System reference plaque for upper molar cusp 5 (metaconule).

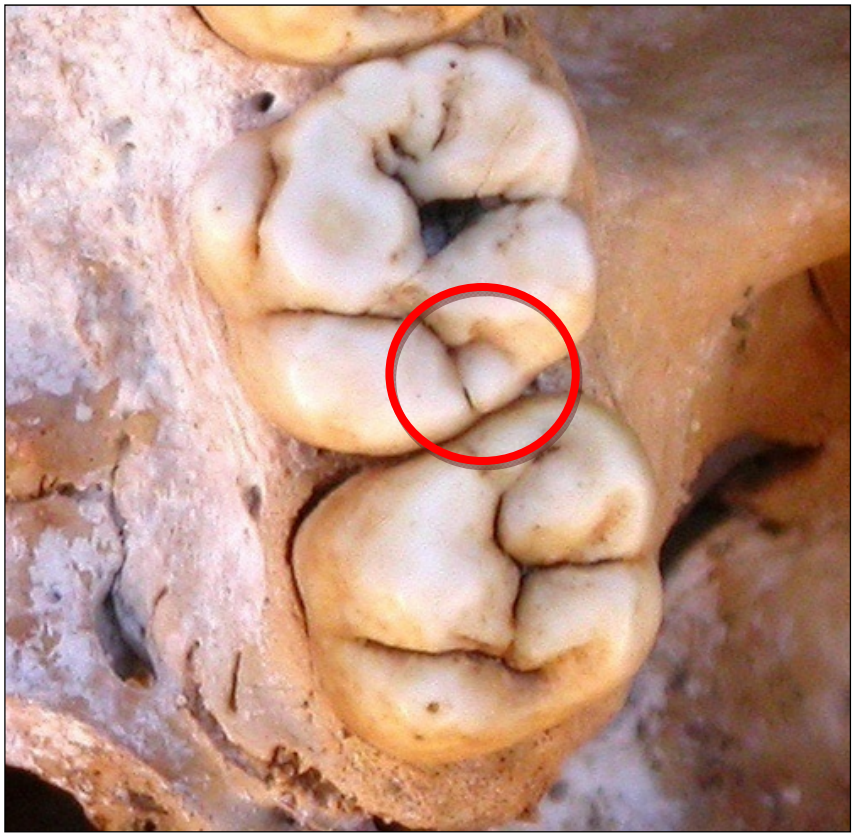


Figure 3.24. ASU Grade 3 cusp 5 (metaconule) on left upper first molar. Note the large Carabelli's cusp on the first molar. K2 burial 287.

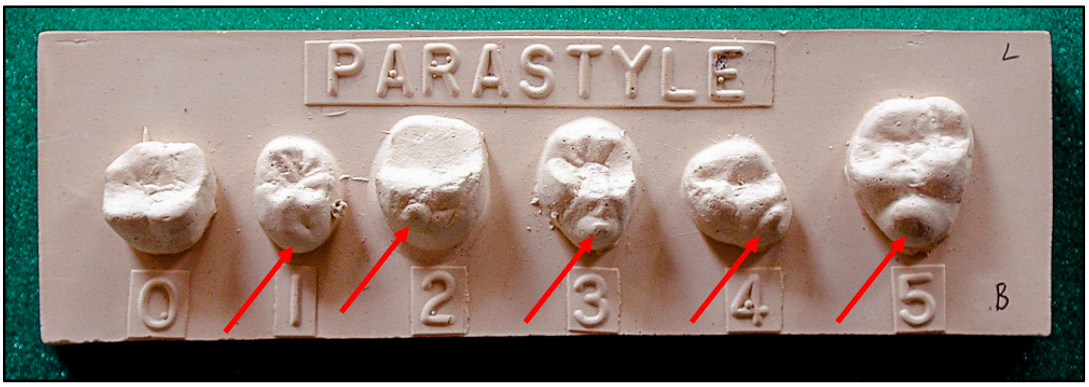


Figure 3.25. ASU Dental Anthropology System reference plaque for upper molar parastyle.

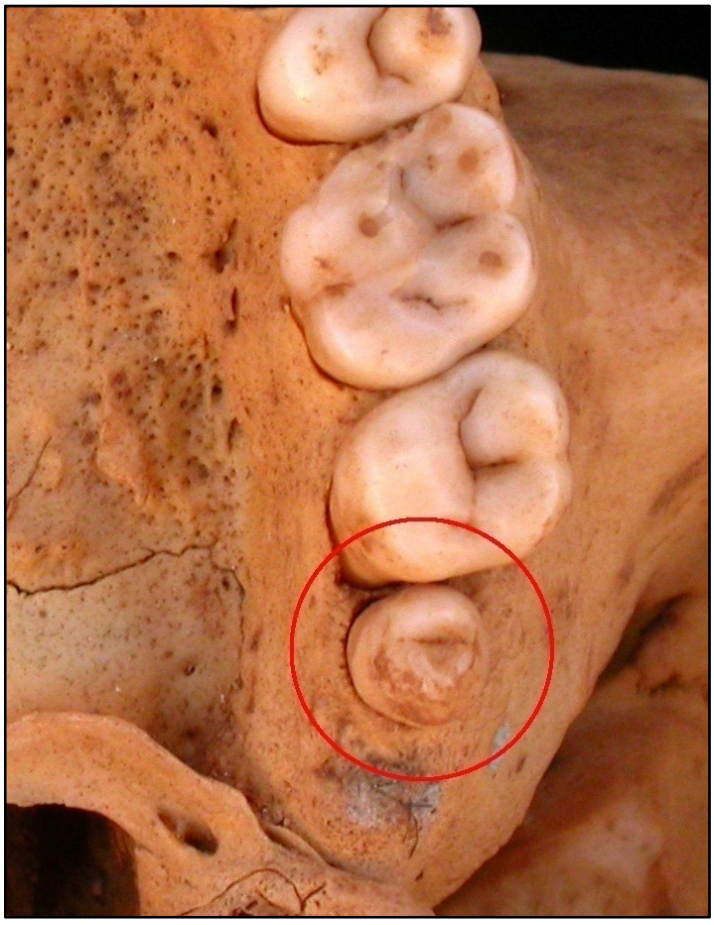
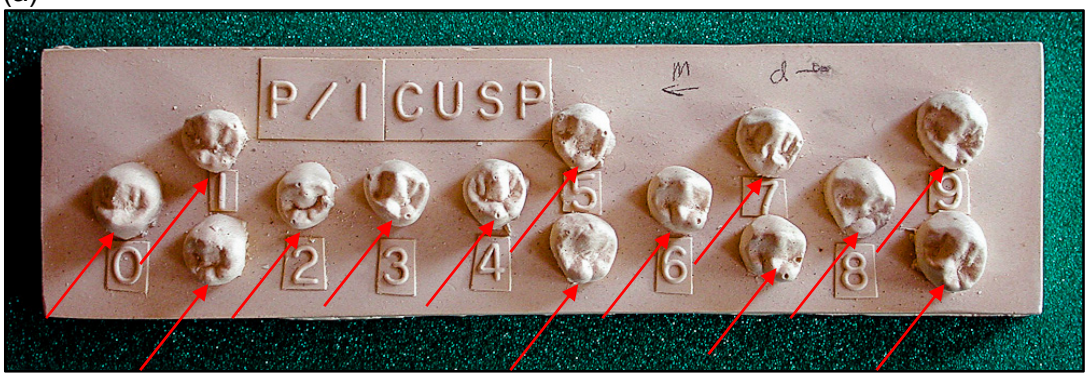


Figure 3.26. Left maxilla showing peg-shaped third molar. K2 Burial 274.

(a)



(b)

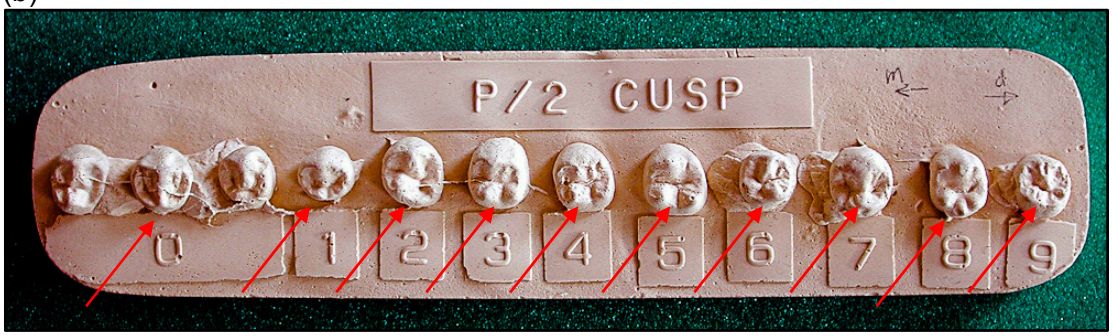


Figure 3.27. ASU Dental Anthropology System reference plaques for lower premolar lingual cusp variation on: (a) third premolars; (b) fourth premolars.

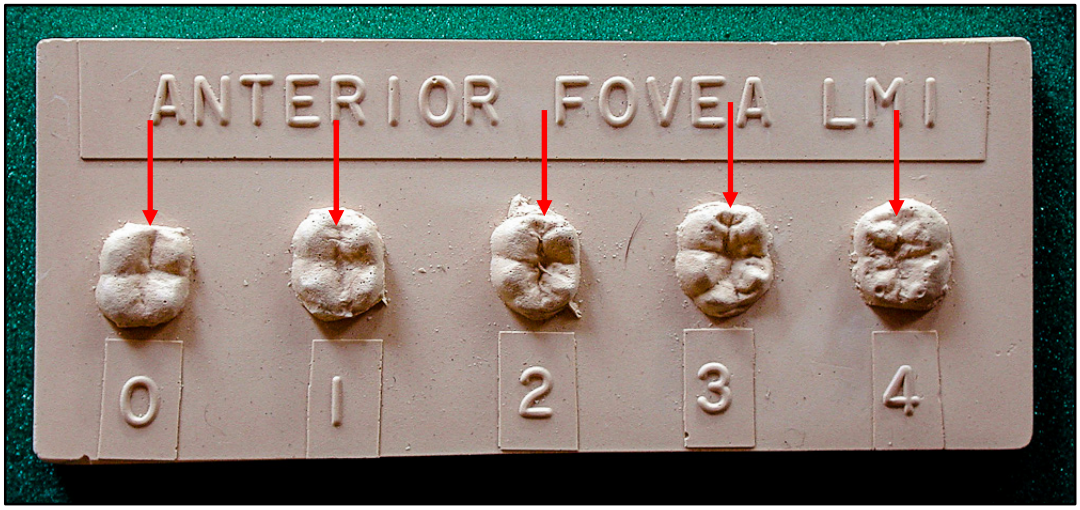


Figure 3.28. ASU Dental Anthropology System reference plaque for lower first molar anterior fovea.

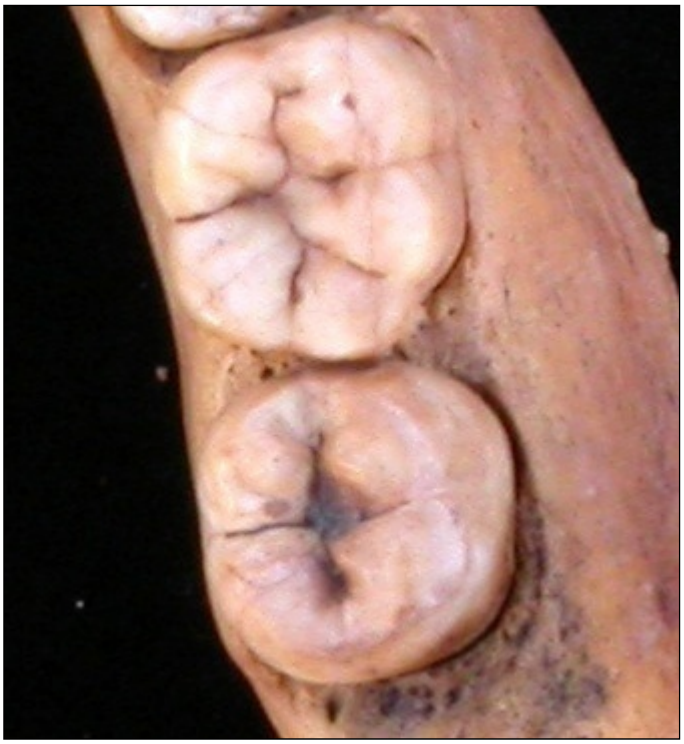


Figure 3.29. 5-cusped M1 and 4-cusped M2. Lower molars. K2 burial 258.

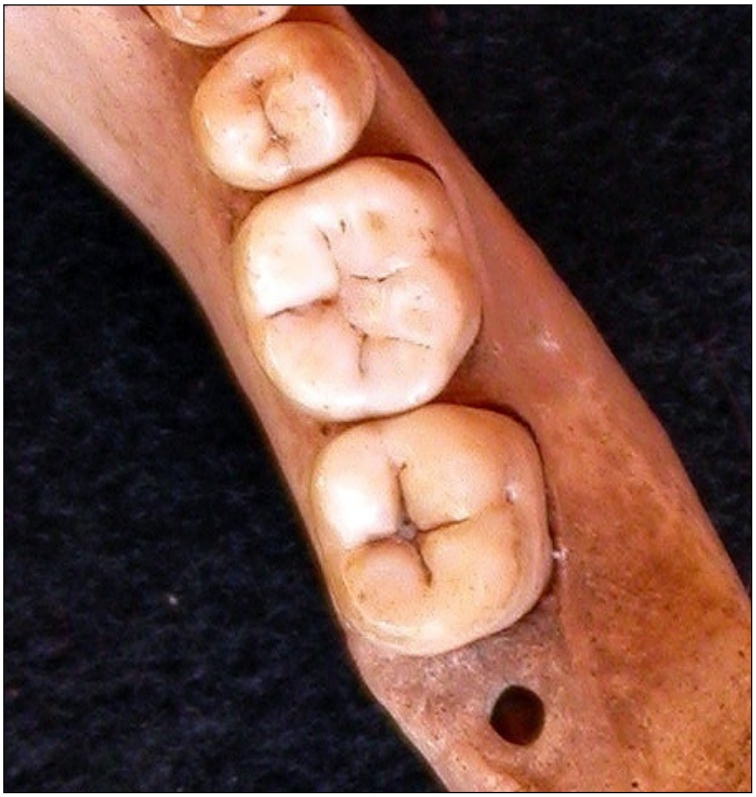


Figure 3.30. Lower right molars. Y-groove pattern on M1 (5 cusps), and +-groove pattern on M2 (4 cusps). Kellis North Tomb (townsite) burial 3.

Figure 3.31. Lower left molars. X-groove pattern on M2 and M3. K2 burial 522.

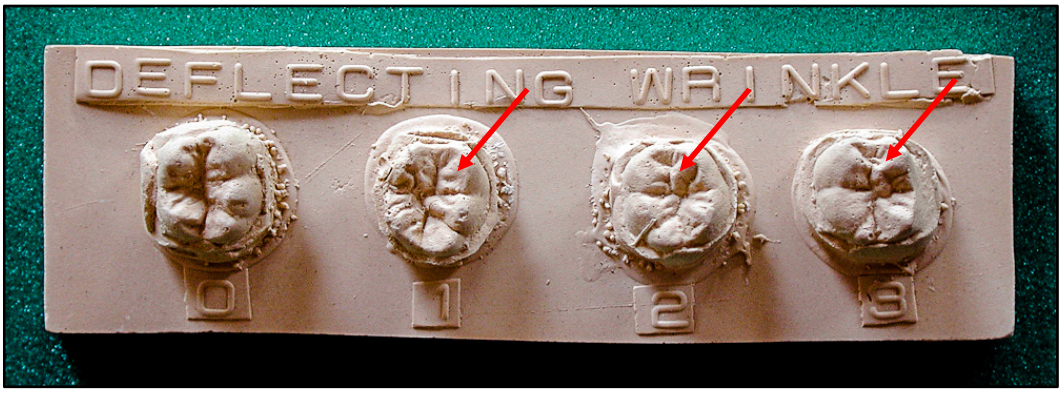


Figure 3.32. ASU Dental Anthropology System reference plaque for lower molar deflecting wrinkle.

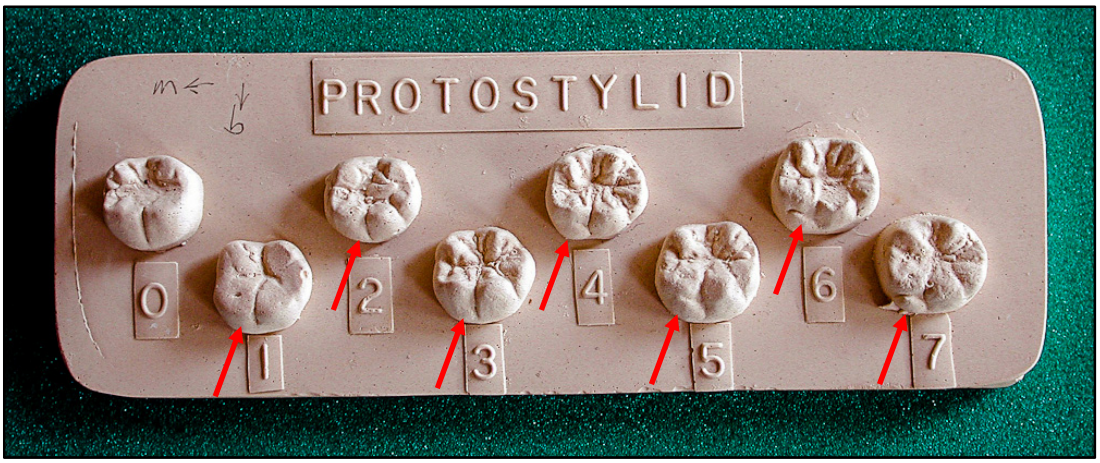


Figure 3.33. ASU Dental Anthropology System reference plaque for lower molar protostylid.

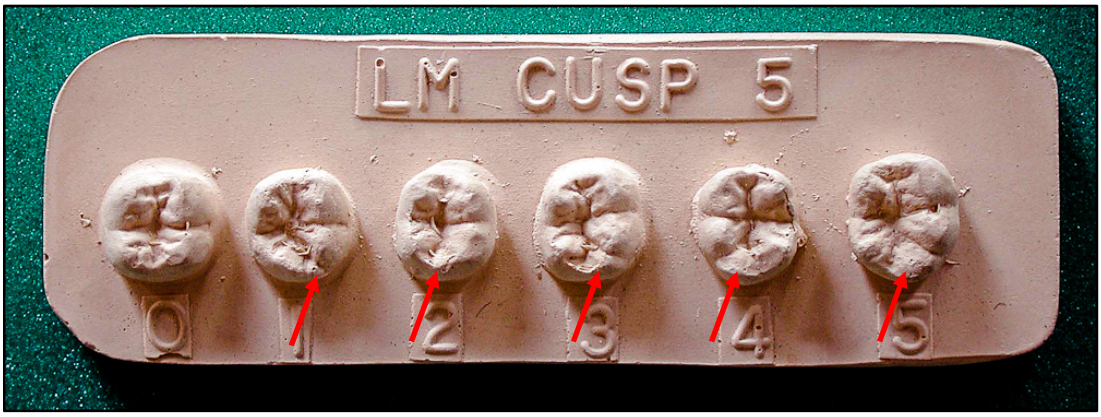


Figure 3.34. ASU Dental Anthropology System reference plaque for lower molar Cusp 5.

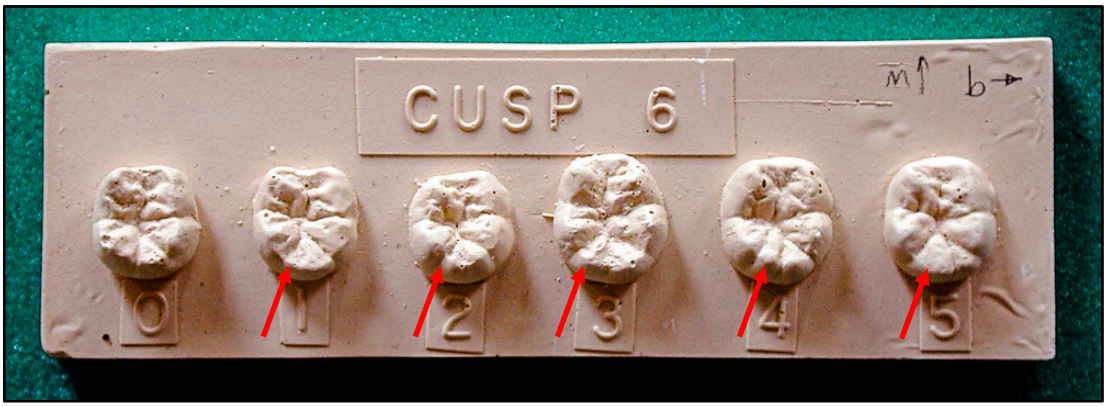


Figure 3.35. ASU Dental Anthropology System reference plaque for lower molar Cusp 6.

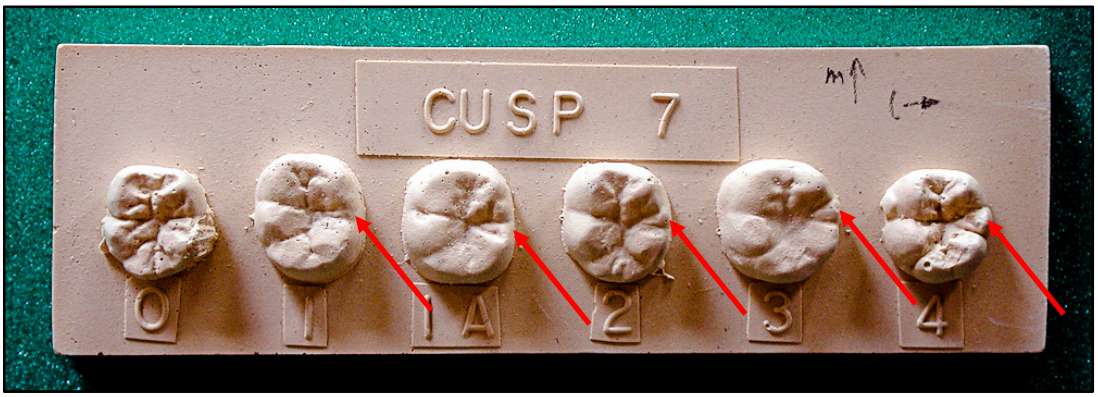


Figure 3.36. ASU Dental Anthropology System reference plaque for lower molar Cusp 7.

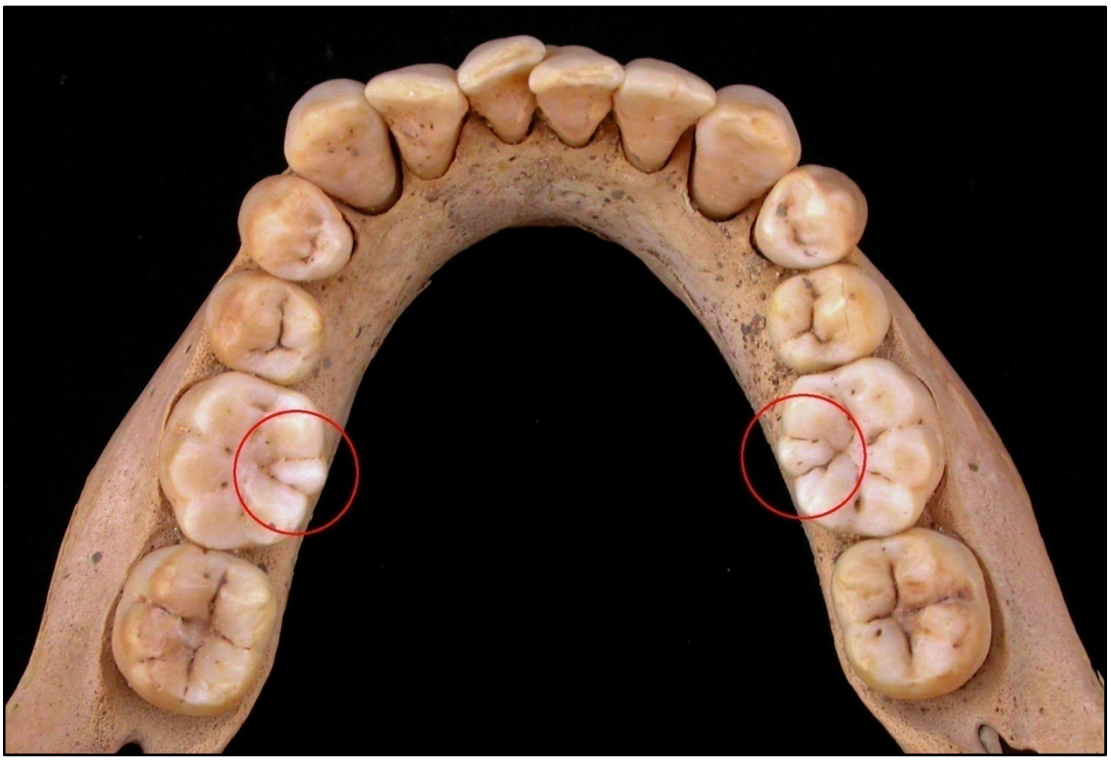


Figure 3.37. Mandible with large Cusp 7 on left and right lower first molars. K2 Burial 559.

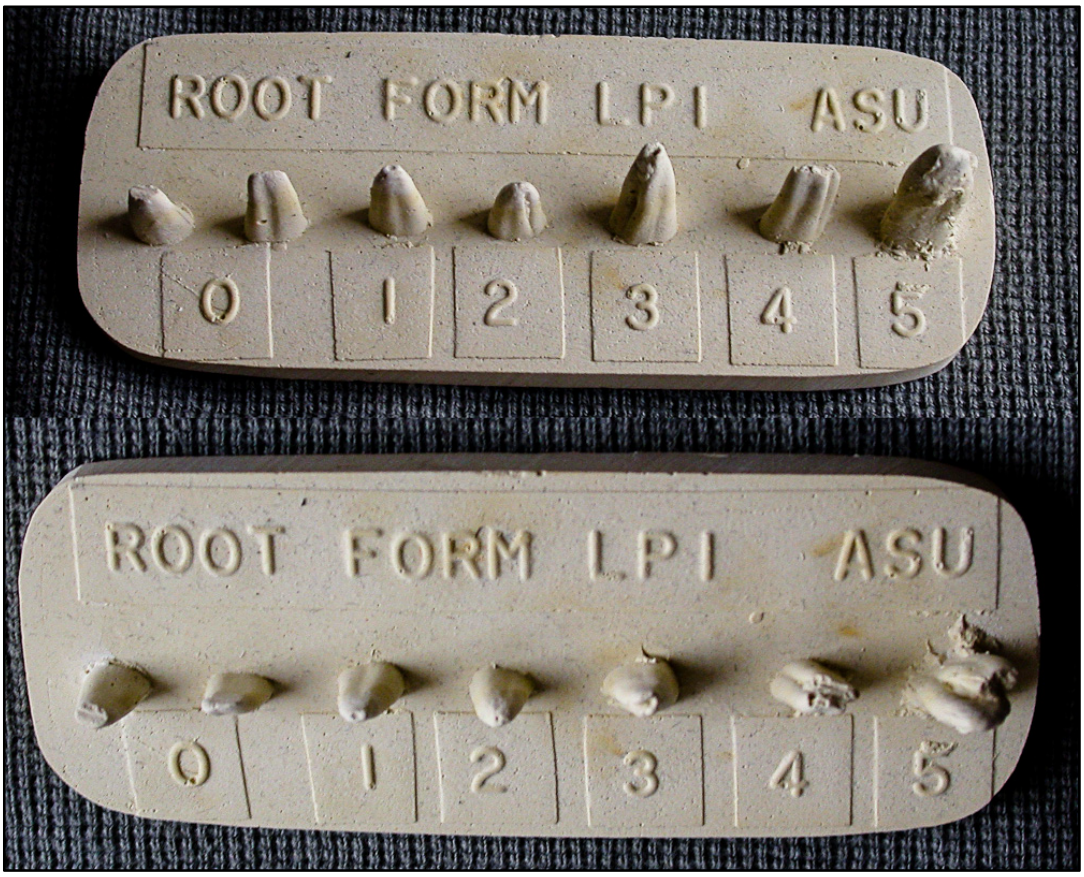


Figure 3.38. ASU Dental Anthropology System reference plaque for lower third premolar Tome's root.

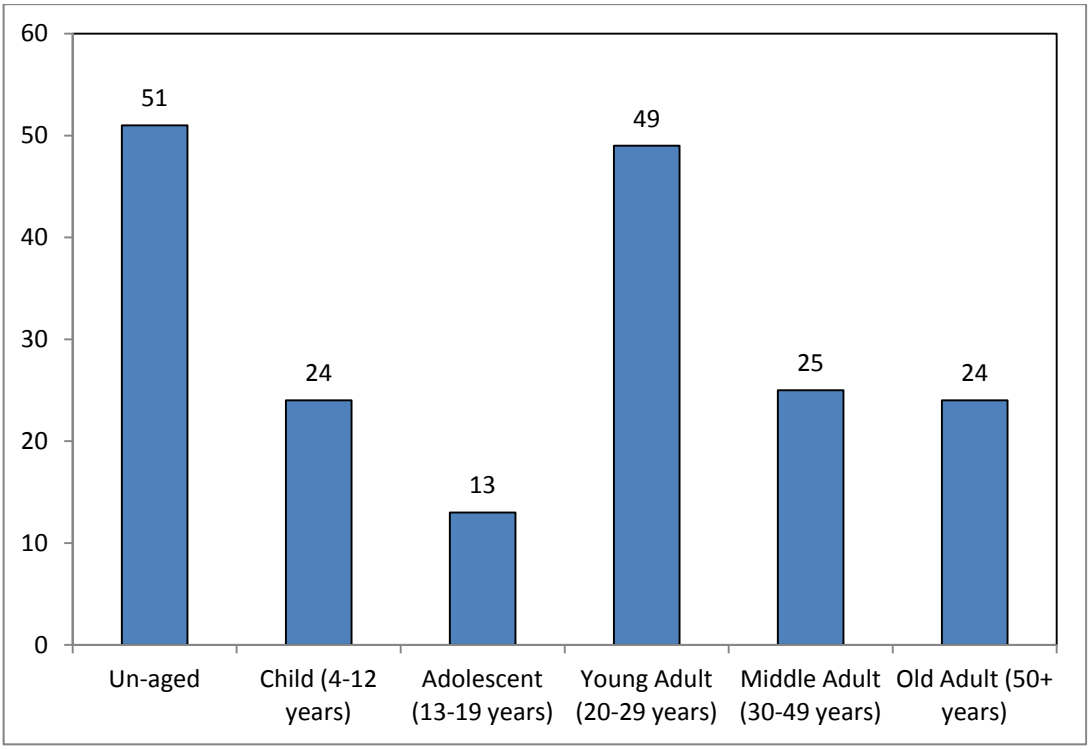


Figure 3.39. Kellis age distribution (N=186) (individuals with observable permanent teeth only).

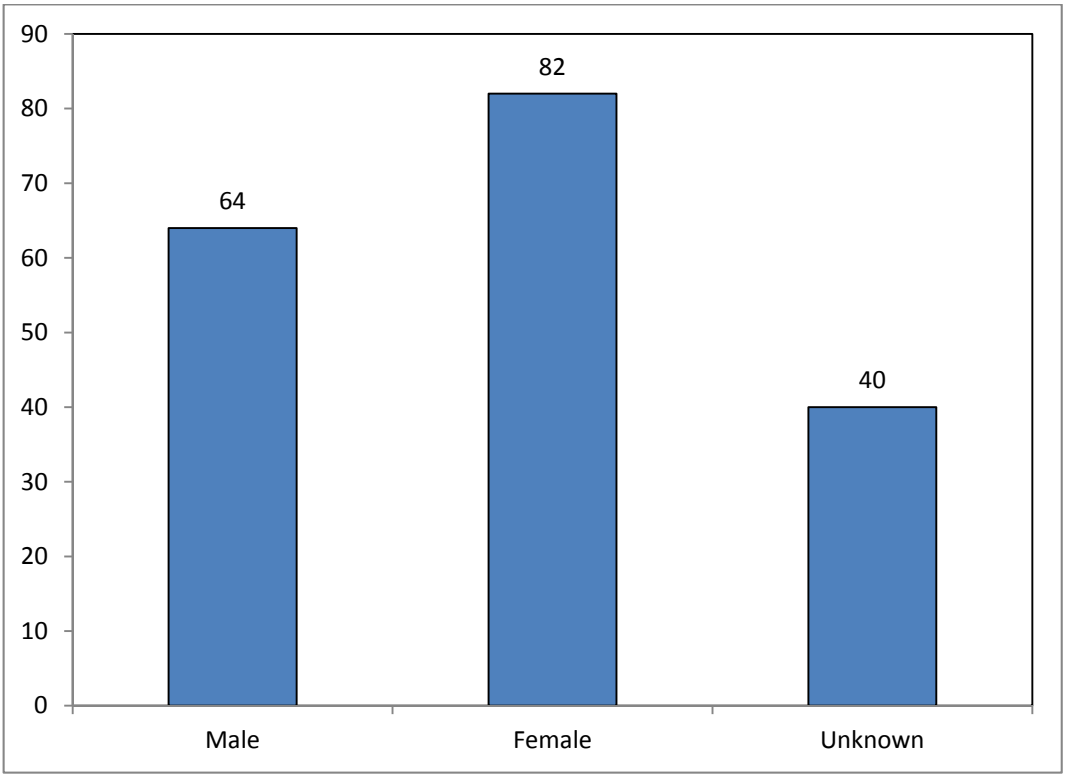


Figure 3.40. Kellis sex distribution (N=186) (individuals with observable permanent teeth only).

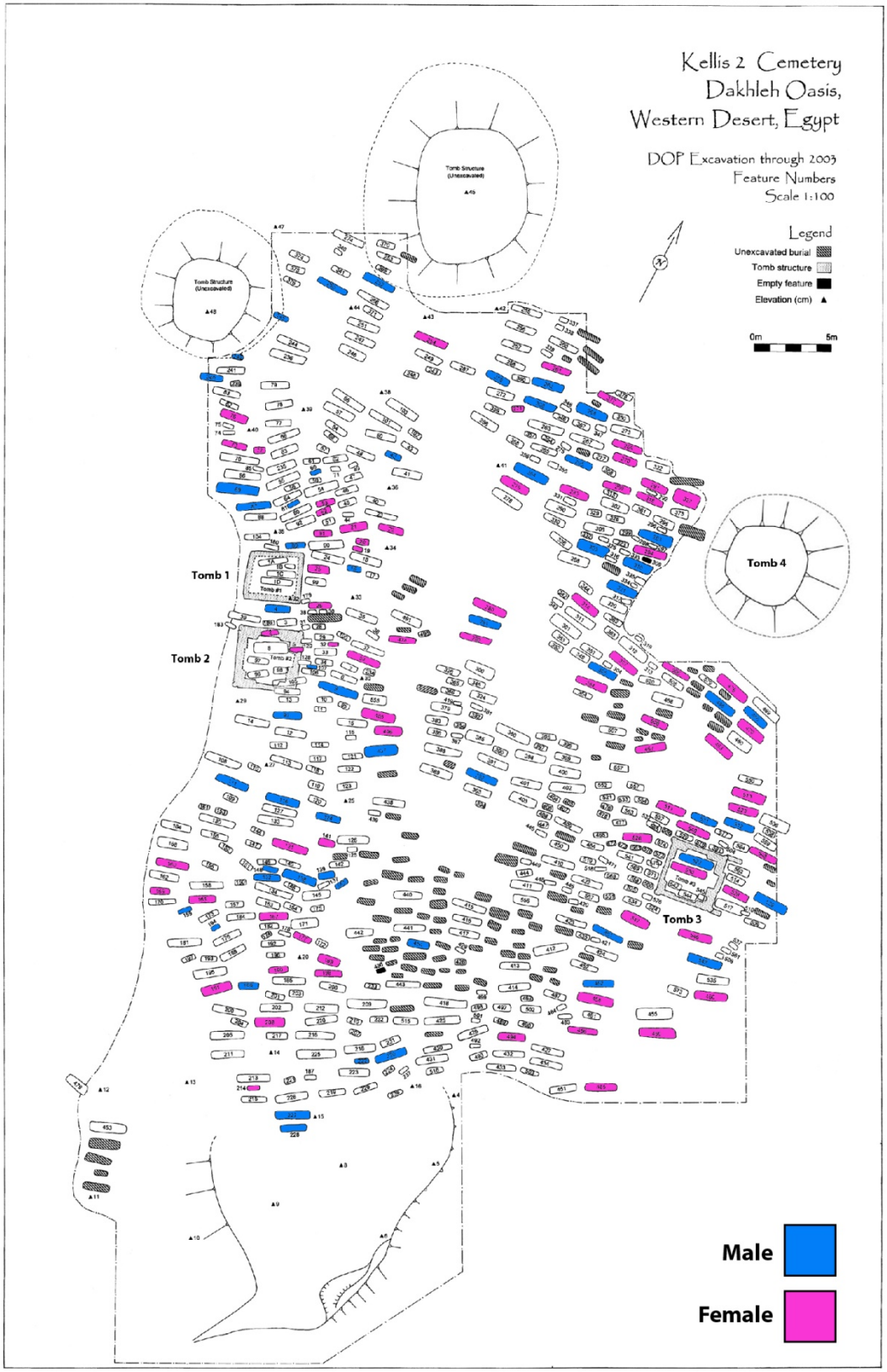


Figure 3.41. Kellis 2 cemetery sex distribution (individuals with observable dentitions only).

Table 3.1. Comparative groups used in the present study.

Assemblage name	Origin/Site	Period	Date	N	Source
UPPER EGYPT					
Gebel Ramlah (GRM)	Gebel Ramlah	Final Neolithic	c. 4650-4400 BC	**59**	Irish, 2006
Badari (BAD)	Badari	Predynastic (Badarian)	c. 4400–4000 BC	**40**	Irish, 2006
Naqada (NAQ)	Naqada	Predynastic (Naqada I & II)	c. 4000-3200 BC	**65**	Irish, 2006
Hierakonpolis (HRK)	Hierakonpolis	Predynastic (Naqada II)	c.3500-3200 BC	**247**	Irish, 2006
Abydos (ABY)	Abydos	Early Dynastic (Dynasty 1-2)	c. 3000-2686 BC	**54**	Irish, 2006
Thebes (THE)	Thebes	Middle Kingdom (Dynasty 11-12)	2055-1773 BC	**54**	Irish, 2006
Qurneh (QUR)	Qurneh	New Kingdom (Dynasty 19)	1295-1186 BC	**67**	Irish, 2006
El Hesa (HES)	El Hesa	Roman	AD 200-400	**72**	Irish, 2006
Kharga (KHA)	Kharga Oasis	Roman (Byzantine)	AD 500-600	**26**	Irish, 2006
LOWER EGYPT					
Tarkhan (TAR)	Tarkhan	Early Dynastic (Dynasty 1)	c. 3000-2890 BC	**51**	Irish, 2006
Saqqara (SAQ)	Saqqara	Old Kingdom (Dynasty 4)	2613–2494 BC	**41**	Irish, 2006
Lisht (LIS)	Lisht	Middle Kingdom (Dynasty 12)	1985-1773 BC	**61**	Irish, 2006
Giza (GIZ)	Giza	Late Dynastic (Dynasty 26-30)	664-332 BC	**62**	Irish, 2006
Greek Egyptians (GEG)	Saqqara, Manfalut	Ptolemaic	332–30 BC	**46**	Irish, 2006
Hawara (HAW)	Hawara	Roman	AD 50-120	**51**	Irish, 2006
UPPER NUBIA					
Kawa (KAW)	Kawa	Kerma Ancien/Moyen	2500–1750 BC	**37**	Irish, 2005
Kerma (KER)	Kerma	Kerma Classique Nubian	c. 1750–1500 BC	**63**	Irish, 2005
Soleb (SOL)	Soleb	Pharaonic (Dynasty 18)	1550–1380 BC	**32**	Irish, 2005
Kushite (KUS)	Kawa, Gabati	Meroitic/Post-Meroitic	c. 600 BC-550 AD	**63**	Irish, 2005
LOWER NUBIA					
A-Group (AGR)	Faras to Gamai	A-Group Nubian	c. 3000 BC	**52**	Irish, 2005
C-Group (CGR)	Faras to Gamai	C-Group Nubian	c. 2000–1600 BC	**62**	Irish, 2005
Pharaonic (PHA)	Faras to Gamai	Pharaonic	1650–1350 BC	**38**	Irish, 2005
Meroitic (MER)	Semna; Faras/Gamai	Meroitic Nubian	100 BC–AD 350	**94**	Irish, 2005
X-Group (XGR)	Semna; Faras/Gamai	X-Group Nubian	AD 350–550	**63**	Irish, 2005
Christian (CHR)	Semna; Faras/Gamai	Christian	AD 550–1350	**41**	Irish, 2005
NORTH AFRICA					
Carthage (CAR)	Tunisia	Phoenician	751-146 BC	**28**	Irish, 1993
Algeria (ALG)	Algeria	Recent	19th cent. AD	**26**	Irish, 1993
Bedouin (BED)	Morocco, Tunisia, Libya	Recent	19-20th cent. AD	**49**	Irish, 1993
Kabyle (KAB)	Algeria	Recent	19-20th cent. AD	**32**	Irish, 1993
Chad (CHA)	Chad	Recent	19-20th cent. AD	**29**	Irish, 1993
SUB-SAHARAN AFRICA					
Kenya (KEN)	Kenya, Tanzania	Recent	19–20th cent. AD	**114**	Irish & Konigsberg, 2007
Ethiopia (ETH)	Ethiopia, Eritrea	Recent	19–20th cent. AD	**40**	Irish & Konigsberg, 2007
Congo (CNG)	Congo, Gabon	Recent	19–20th cent. AD	**52**	Irish & Konigsberg, 2007
Nigeria-Cameroon (NIC)	Nigeria, Cameroon	Recent	19th cent. AD	**57**	Irish & Konigsberg, 2007
Ghana (GHA)	Ghana	Recent	19th cent. AD	**47**	Irish & Konigsberg, 2007
Gabon (GAB)	Gabon	Recent	19–20th cent. AD	**39**	Irish & Konigsberg, 2007
Togo-Dahomey (TOD)	Togo, Benin	Recent	19th cent. AD	**25**	Irish & Konigsberg, 2007

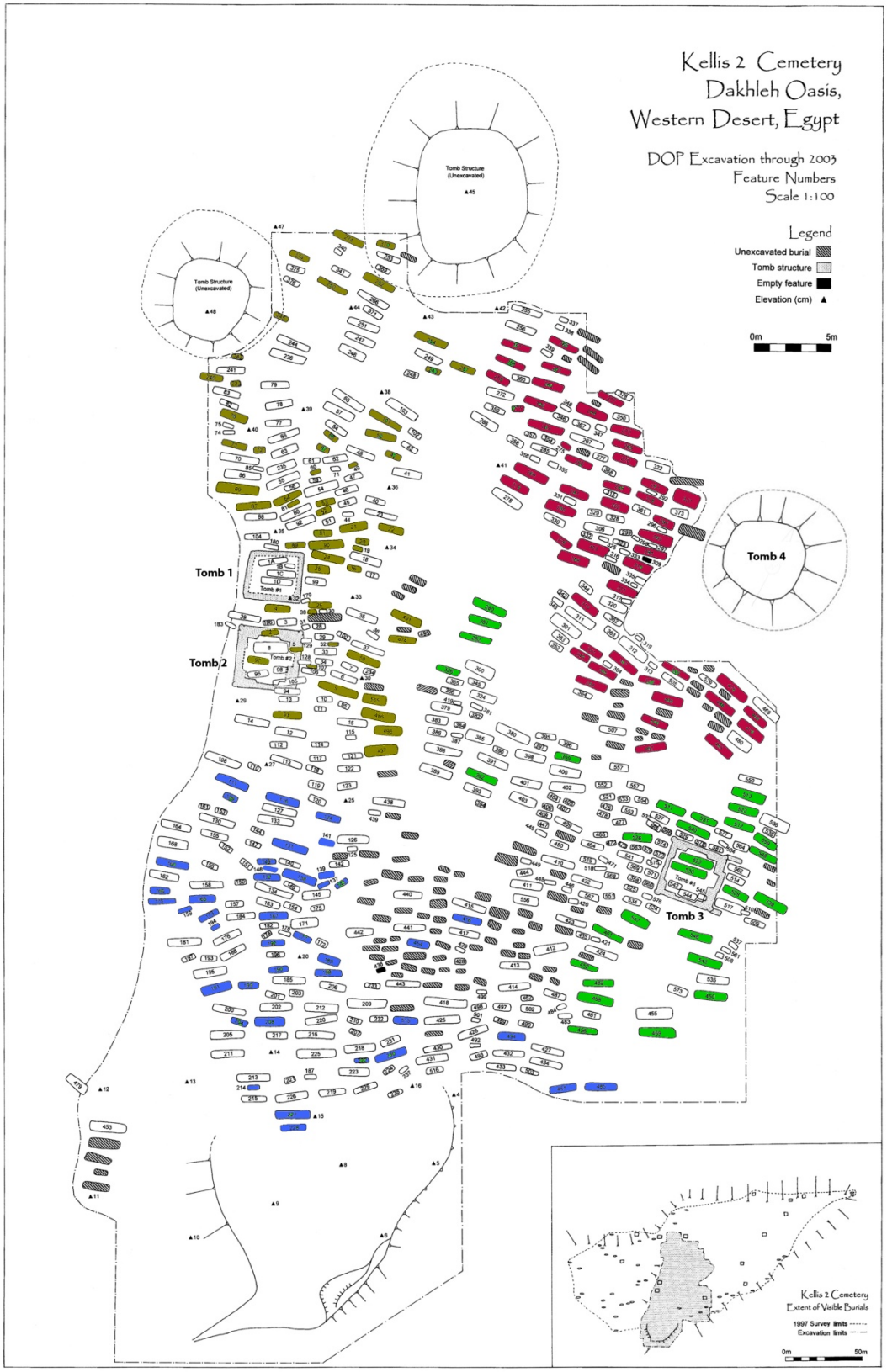


Figure 3.42. Map of Kellis 2 cemetery showing four burial subgroups (green=east; brown=west, red=north and blue=south)

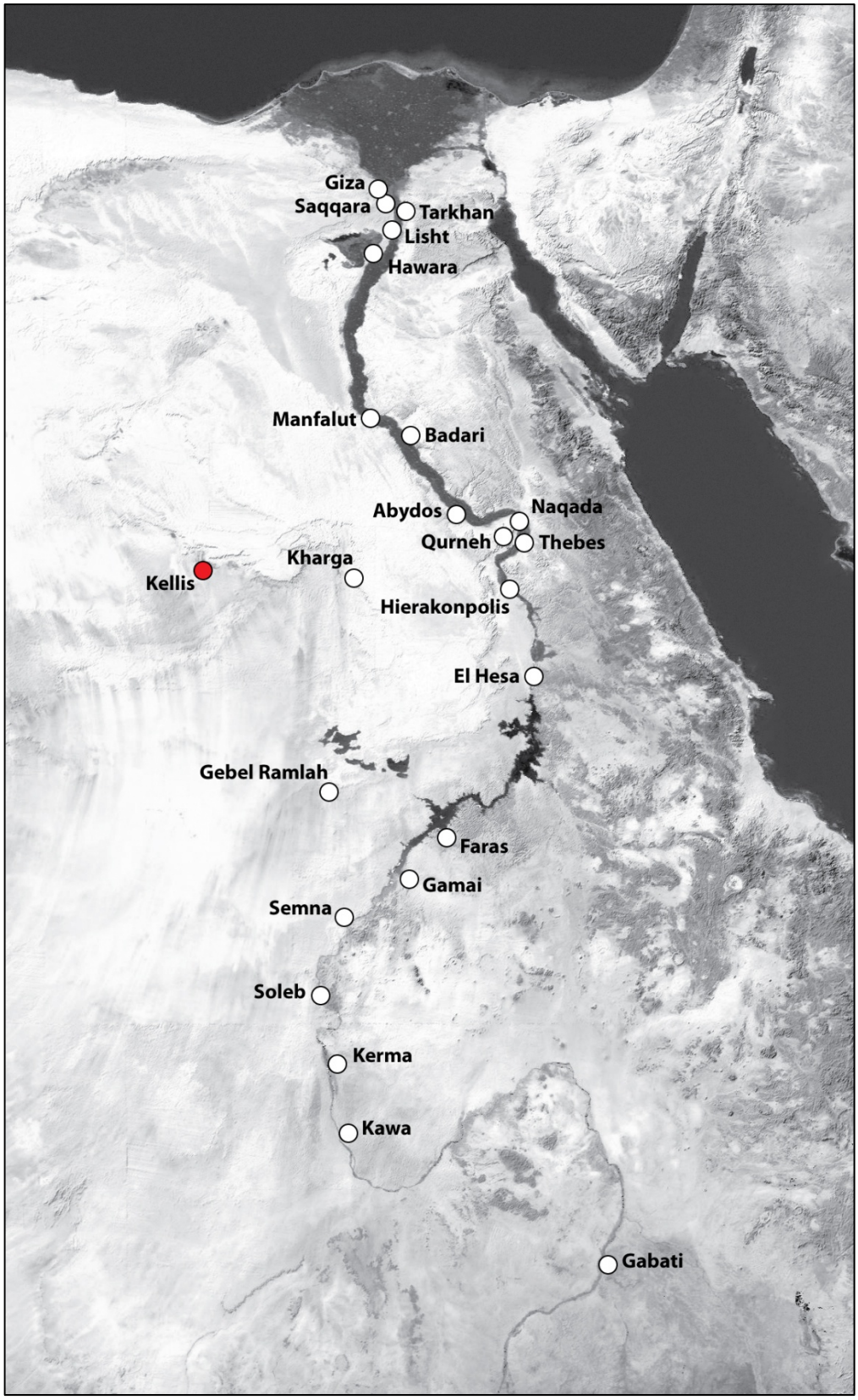


Figure 3.43. Map of northeast Africa showing Egyptian and Nubian sites for comparative groups.

Figure 3.44. Map of Africa showing locations for North African and Sub-Saharan comparative groups.

Chapter 4

Results of the Dental Morphological Analysis

4.1 Introduction

The total number of individuals for which dental morphological observations of the permanent teeth can be made is 186 (172 individuals from the Kellis 2 cemetery, and 14 individuals from the townsite burials). For the present study, seventeen permanent mandibular and twenty-three maxillary tooth-trait combinations have been recorded in accordance with the Arizona State University Dental Anthropology System. Unfortunately, several occlusal traits were often unobservable due to high dental attrition rates, especially for older individuals. These traits are the canine distosagittal and mesial ridges, first molar anterior fovea, molar deflecting wrinkle and distal trigonid crest. Despite this, the majority of dental nonmetric traits were scorable in most individuals.

Despite the fact that the Kellis townsite burials appear to be contemporary with the Kellis 2 cemetery based on archaeological evidence, it is essential to check for significant differences between the two assemblages before combining them for broader regional comparisons. Chi-square and Fisher's Exact tests were conducted using frequency data for the twenty dental traits used in the comparative portion of the present study (see Appendix I). Of the twenty dental trait frequencies observed, two traits showed significant ($P \leq 0.05$) differences between the two assemblages: Carabelli's cusp (Fisher's Exact Test P=0.000) and upper lateral incisor interruption groove (Fisher's

Exact Test P=0.008). However, these significant differences can largely be attributed to the very small number of observable cases within the townsite assemblage. Only eight individuals were observable for upper lateral incisor interruption groove, and eleven individuals for Carabelli's cusp. As such, I feel justified in combining the two groups for the regional and inter-regional analysis. The Mean Measure of Divergence statistic was not used to compare the two groups as the number of observable cases for the townsite burials is below the limit that the formula is designed for.

4.2 Presentation of results

The results of the analysis are presented as follows: a qualitative description of the Kellis dental trait frequencies is presented first. Each recorded dental trait for the Kellis population is described in terms of expression frequencies between the sexes and then for the sex-pooled assemblage as a whole. They are then compared with dichotomized trait frequencies for inter-regional groups (discussed in Chapter 3) in order to give an idea of where the Kellis assemblage fits within a broader geographical context. When available, the world minimum and maximum range for each trait is provided. The trait frequencies for the inter-regional populations and world ranges are taken from Scott and Turner (1997).This is followed by the results of the intracemetery analysis of sex differences and spatial patterning of traits. Finally, the results of the multivariate statistical analysis of biological distance for Kellis and comparative group dental trait frequencies are presented.

4.3 Description of Kellis permanent dentition morphological traits

Tables 4.1 and 4.2 present the raw scores for all Kellis mandibular and maxillary dental traits recorded in the present study. The Kellis dental assemblage is discussed with reference to dichotomized world trait frequencies below. Not all traits recorded for the Kellis assemblage are discussed in this section as comparative data is not always available for particular traits. These data, broken down by sex category, are presented in Table 4.3. Note that for certain traits the ASU scale breakpoints are different from the ones used for the subsequent analysis of sex differences and for the multivariate analysis. This is due to differences between researchers in the way dichotomized trait expression frequencies are presented. The breakpoints for each trait are provided in the descriptions. Comparative data for Nubia and North Africa derives from Irish (2000). Comparative data and world trait frequency ranges for Western and Northern Europe derive from Scott and Turner (1997).

4.3.1 Mandibular dental traits

Fourth premolar lingual cusp variation (presence=2 or more lingual cusps)

Two or more lingual cusps on the lower 4^{th} premolar occur in 57.9% and 76.9% of Kellis males (N=19) and females (N=13), respectively. When the total number of Kellis individuals (including unsexed individuals) observable for this trait is considered (N=46), the expression rate is 69.6%. Of the available comparative data, the Kellis assemblage is most closely related to North African populations, which has an expression rate of 72.6%. This

compares with a trait frequency of 93.3% for the Nubian group. The world range for this trait is not available.

First molar anterior fovea (presence=ASU score 2-4)

Well-developed anterior fovea on the lower first molars occur in 0.0% and 33.3% of Kellis males (N=3) and females (N=3), respectively. When the total number of Kellis individuals observable for this trait is considered (N=31), the expression rate is 54.8%. This compares with trait frequencies of 37.9% and 69.2% for the North African and Nubian groups, respectively. The world range for this trait is not available.

Second molar Y-groove pattern

The Y-groove pattern occurs on the lower second molar in 15.6% and 7.1% of Kellis males (N=45) and females (N=42), respectively. When the total number of Kellis individuals observable for this trait is considered (N=106), the expression rate is 11.5%. In comparison, this frequency is quite low when placed beside neighbouring groups from North Africa, Nubia and Western Europe with frequencies of 30.6%, 62.5% and 27.2%, respectively. The world range of expression for this trait is 7.6% to 71.9%.

First molar hypoconulid absence (presence=4-cusps)

4-cusped lower first molars occur in 10.0% and 8.6% of Kellis males (N=39) and females (N=36), respectively. When the total number of Kellis individuals observable for this trait is considered (N=107), the total expression rate is 6.5%. This compares with trait frequencies of 7.8%, 10.0%

and 10.0% for Western Europe, Northern Europe and North Africa, respectively. The world range for this trait is 0.0% to 10.0%.

Second molar hypoconulid absence (presence=4-cusps)

The absence of the hypoconulid (cusp 5) and the entoconulid (cusp 6) on the lower second molar occurs in 80.4% and 93.0% of Kellis males (N=46) and females (N=43), respectively. When the total number of Kellis individuals observable for this trait is considered (N=108), the expression rate is 85.2%. In comparison, Western and Northern Europeans have an expression rate of 71.1% and 84.4%, respectively, while North Africans have an expression rate of 66.4%. The world range for this trait is 15.6% to 95.6%.

First molar deflecting wrinkle (presence=moderate to strong expression)

The presence of moderate to strong forms of the deflecting wrinkle on the lower first molar occurs in 66.7% of males (N=3) and 100% of females (N=1). Because this trait is extremely sensitive to occlusal attrition, it is typically observed only in younger individuals who cannot be assigned to either sex; in this instance, only three males and one female could be observed for the trait. As such, any interpretation of sex-based differences in the expression of the deflecting wrinkle should be taken with caution, given the extremely limited number of individuals involved. When the total number of individuals observable for this trait is considered (N=24), the expression rate becomes 62.5%. The frequency of this trait at Kellis is almost eight times higher than the North African group (8.2%), and more than doubles the rate for the Nubian group (30.8%). The expression rate for Western and

Northern Europeans is, 5.2% and 16.0%, respectively. The world range for this trait is 4.9% to 39.5%.

First molar protostylid (presence=pit, groove and cusp forms)

The presence of a pit or cusp form of the protostylid on the mesiobuccal cusp of the lower first molar occurs in 43.8% and 41.7% of Kellis males (N=31) and females (N=25), respectively. When the total number of Kellis individuals observable for this trait is considered (N=86), the expression rate is 43.0%. This compares with trait frequencies of 32.5% and 29.2% for the North African and Nubian groups, respectively. The world range for this trait is not available. Expression of the protostylid in the Kellis assemblage is overwhelmingly confined to pit forms (ASU grade 1); cusp forms (ASU grade 4+) are not observable.

First molar cusp 6 (presence=any expression of cusp 6)

A sixth cusp on the lower first molars occurs in 12.8% and 17.1% of Kellis males (N=38) and females (N=36), respectively. When the total number of Kellis individuals observable for this trait is considered (N= 106), the expression rate is 16.0%. This compares with trait frequencies of 8.3%, 16.9%, 7.7% and 31.3% for the Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 4.7% to 61.7%.

First molar cusp 7 (presence=small to large-sized cusp)

A seventh cusp on the lower first molars occurs in 10.0% and 5.4% of Kellis males (N=40) and females (N=37), respectively. When the total number of Kellis individuals observable for this trait is considered (N=110), the expression rate is 9.1%. This compares with trait frequencies of 5.1% and 9.7% for the North African and Nubian groups, respectively. The world range for this trait is 3.1% to 43.7%. Cusp 7 occurs in high frequencies in Sub-Saharan African populations (Scott and Turner 1997), to the extent that it is considered one of several key traits in the Sub-Saharan African Dental Complex (Irish 1997, 1998a).

Canine root number (presence=2 roots)

Two-rooted lower canines occur in 7.3% and 6.7% of Kellis males (N=55) and females (N=75), respectively. When the total number of Kellis individuals observable for this trait is considered (N=146), the expression rate is 6.2%. This compares with trait frequencies of 5.7%, 6.1%, 2.3% and 0.0% for the Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 0.0% to 6.1%.

Third premolar Tome's root (presence=ASU grade 3-5)

The presence of deeply grooved or bifurcated roots on the lower third premolars is observable in 18.5% and 10.4% of Kellis males (N=54) and females (N=67), respectively. When the total number of Kellis individuals observable for this trait is considered (N=137), the expression rate is 14.6%. This compares with trait frequencies of 5.9%, 6.6%, 8.6% and 52.4% for the

Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 0.0% to 38.7%.

First molar root number (presence=three roots)

Three-rooted lower first molars occur in 0.0% and 2.7% of Kellis males (N=39) and females (N=37), respectively. When the total number of Kellis individuals observable for this trait is considered (N=99), the expression rate is 1.0%. This compares with trait frequencies of 0.6%, 0.0%, 1.2% and 13.0% for the Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 0.0% to 31.1%.

Second molar root number (presence=one root)

Single-rooted lower second molars occur in 5.6% and 12.9% of Kellis males (N=36) and females (N=31), respectively. When the total number of Kellis individuals observable for this trait is considered (N= 80), the expression rate is 7.5%. This compares with trait frequencies of 28.0%, 20.8%, 11.7% and 16.3%, for the Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 3.6% to 39.8%.

4.3.2 Maxillary traits

Central incisor winging (presence=bilateral winging)

Central incisor winging occurs in 0% and 3.3% of Kellis males (N=42) and females (N=60), respectively. For all individuals observable (N=121), the trait occurs in 1.7% of Kellis assemblage. This compares with trait frequencies of 7.2%, 4.7%, 7.5% and 29.6% for the Western European, Northern

European, North African and Nubian groups, respectively. The world range for this trait is 4.2% to 50.0%.

Shovel-shaped central incisors (presence=trace- to barrel-shaped shovelling)

Shovel-shaping of the upper central incisors occurs in 18.8% and 24.3% of Kellis males (N=32) and females (N=37), respectively. When the total number of Kellis individuals observable for this trait is considered (N=91), the expression rate is 19.8%. It is important to note, however, that the level of trait expression in the Kellis assemblage does not exceed the slight semi-shovelling stage (ASU grade 3). The Kellis assemblage compares with trait frequencies of 45.8% and 19.5% for the Nubian and North African groups, respectively. The world range for this trait is not available at the breakpoint used here.

Central incisor double-shovelling (presence=trace to extreme double-shovelling)

Double-shovelling of the upper central incisors does not occur in any Kellis individual observable for the trait (N=103). This compares with trait frequencies of 3.8%, 5.0%, 8.6% and 4.3% for the Western European, Northern European and North African groups, respectively. The world range of expression for double-shovelling is 0.0% to 70.5%.

Lateral incisor interruption grooves (presence=total frequency)

The presence of interruption grooves on the upper lateral incisors occurs in 17.5% and 22.6% of Kellis males (N=40) and females (N=53), respectively. When the total number of Kellis individuals observable for this trait is considered (N=109), the expression rate is 20.2%. This compares with trait frequencies of 42.0%, 30.0%, 36.1% and 16.0% for the Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 10.4% to 65.0%.

Lateral incisor tuberculum dentale (presence=trace to pronounced ridging)

The presence of trace to pronounced ridging on the upper lateral incisors occurs in 8.8% and 10.0% of Kellis males (N=34) and females (N=40), respectively. When the total number of Kellis individuals observable for this trait is considered (N=92), the expression rate is 12.0%. This compares with trait frequencies of 38.8% and 38.9% for the North African and Nubian groups, respectively. The world range for this trait is not available for the breakpoint used here.

Canine mesial ridge “Bushman canine” (presence=mesiolingual ridge is larger than distolingual)

The presence of a mesiolingual ridge which is larger than the distolingual ridge on the upper canine crown surface occurs in 0.0% and 3.1% of Kellis males ((N=30) and females (N=32), respectively. When the total number of Kellis individuals observable for this trait is considered (N=78), the expression rate is 1.3%. This compares with trait frequencies of 4.3%, 0.0%,

6.1% and 20.0% for the Western European, Northern European, North African and Nubian groups, respectively. The trait occurs in much higher frequencies in Sub-Saharan groups (Irish 1997; Scott and Turner 1997). The world range for this trait is 0.0% to 35.1%.

Canine distal accessory ridge (presence=weak to pronounced ridge)

The presence of a weak to pronounced distal accessory ridge on the upper canines occurs in 33.3% and 25.0% of Kellis males (N=12) and females (N=12), respectively. When the total number of Kellis individuals observable for this trait is considered (N=38), the expression rate is 31.6%. This compares with trait frequencies of 17.9% and 88.9% for the North African and Nubian groups, respectively. The world range for this trait is not available.

Second molar hypocone absence (presence=3-cusped molars)

The absence of the hypocone (resulting in 3-cusped molars) on the upper second molars occurs in 13.5% and 14.0% of Kellis males (N=37) and females (N=50), respectively. When the total number of Kellis individuals observable for this trait is considered (N=108), the expression rate is 16.7%. This compares with trait frequencies of 24.7%, 19.2% and 10.6% for the Western European, Northern European and North African groups, respectively. The world range for this trait is 3.3% to 30.6%.

First molar cusp 5 (presence=total frequency of occurrence)

The presence of cusp 5 (metaconule) on the upper first molar occurs in 31.0% and 19.0% in Kellis males (N=29) and females (N=42), respectively. When the total number of Kellis individuals observable for this trait is considered (N=105), the expression rate is 31.4%. This compares with trait frequencies of 11.8%, 26.4% and 18.5% for the Western European, Northern European and North African groups, respectively. The world range for this trait is 10.4% to 62.5%.

First molar Carabelli's cusp (presence=tubercle and cusp forms only)

The presence of tubercle and cusp forms of Carabelli's trait on the upper first molars occurs in 44.4% and 56.5% of Kellis males (N=27) and females (N=23), respectively. When the total number of Kellis individuals observable for this trait is considered (N=82), the expression rate is 42.7%. This compares with trait frequencies of 27.3%, 18.1% and 20.0% for the Western European, Northern European and North African groups, respectively. The world range for this trait is 1.9% to 36.0%. As can be seen from the comparative data, the frequency of cusp and tubercle forms of Carabelli's trait in the Kellis population is extremely high.

Third molar parastyle (presence=total frequency of occurrence)

The accessory cusp known as the parastyle on upper third molars occurs in 0.0% and 2.6% of Kellis males (N=27) and females (N=39), respectively. When the total number of individuals observable for the trait (N=70) is taken into account, the rate of occurrence is 1.4%. This compares with trait

frequencies of 1.2% and 0.0% for the North African and Nubian groups, respectively. The world range for this trait is not available.

First molar enamel extensions (presence=medium to lengthy-sized extensions)

Medium- to lengthy-sized enamel extensions on the upper first molars do not occur in any Kellis individuals observable for the trait (N=120). This compares with trait frequencies of 3.8%, 2.2% and 6.8% for the Western European, Northern European and North African groups, respectively. The world range for this trait is 0.0% to 54.6%.

Third premolar root number (presence=two-rooted third premolars)

The presence of two-rooted upper third premolars occurs in 60.0% and 42.6% of Kellis males (N=50) and females (N=61), respectively. When the total number of Kellis individuals observable for this trait is considered (N=126), the expression rate is 50.0%. This compares with trait frequencies of 40.7%, 45.9%, 57.1% and 72.7% for the Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 4.9% to 66.7%.

Second molar root number (presence=three-rooted second molars)

The presence of three-rooted upper second molars occurs in 84.6% and 72.9% of Kellis males (N=39) and females (N=48), respectively. When the total number of individuals observable for this trait is considered (N=99), the expression rate is 77.8%. This compares with trait frequencies of 57.4%,

61.2%, 78.6% and 73.0% for the Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 37.4% to 84.5%.

Premolar odontomes (presence=total frequency of occurrence)

Odontomes on the upper and lower third and fourth premolars do not occur in those Kellis individuals observable for the trait (N=107). This compares with trait frequencies of 0.8%, 0.0%, 0.2% and 0.0% for the Western European, Northern European, North African and Nubian groups, respectively. The world range for this trait is 0.0% to 6.5% (Scott and Turner 1997).

Third molar congenital absence

Congenital absence of the upper third molars occurs in 2.1% and 7.1% of Kellis males (N=47) and females (N=56), respectively. When the total number of Kellis individuals observable for this trait is considered (N=116), the expression rate is 5.2%. This compares with trait frequencies of 15.2% and 0.0% for the North African and Nubian groups, respectively. Figures for Western and Northern Europeans are not available. The world range for this trait is also not available.

4.4 Intracemetery analysis

4.4.1 Kellis inter-sex variation

Chi-square and Fisher's Exact tests were calculated in order to test for significant differences between male and female trait frequencies for the

combined (K2 and TS) Kellis assemblage (see Appendix II for full list). Only one trait, congenital absence of the mandibular third molar, showed a significant difference (Fisher's Exact Test P=0.049) between the sexes. 9% (4/46) of females display this trait, compared with 0% (0/50) of males. No other statistically significant differences ($P \leq 0.05$) were found between the sexes, although maxillary third premolar (UP3) root number (Fisher's Exact Test P=0.063), mandibular second molar (LM2) cusp number (Fisher's Exact Test P=0.082) and maxillary canine (UC) *tuberculum dentale* (Fisher's Exact Test P=0.099) approached the significance threshold. 43% (26/60) of Kellis females exhibit two-rooted maxillary third premolars, while for males the rate of expression is 61% (30/49). Five or more cusps on the mandibular second molar appear in 7% (3/42) of Kellis females, while males have an expression rate of 20% (9/45). *Tuberculum dentale* in maxillary canines occurs in 24% (9/38) of Kellis females and 42% (15/36) of Kellis males. Other researchers have shown statistically significant sex differences for maxillary third premolar root number (Irish 1997; Ullinger 2005). As with the Kellis assemblage, these studies have revealed that females have a greater predilection for reduced root numbers than males.

Additionally, the Mean Measure of Divergence statistic for Kellis males versus females was calculated using all 29 dental traits and again for only the 20 traits used in the comparative analysis (Table 4.4). See the methodology chapter for details regarding trait selection. In both cases, the resulting MMD values (0.000) demonstrate that the two groups are not significantly different from one another.

Because there are few significant differences between the sexes in terms of trait expression, data for males and females are combined for intra- and inter-site comparative analyses. A lack of significant differences between male and female trait expression are typical in morphological dental studies and it is standard practice to pool the sexes, thereby maximizing sample sizes for inter-group comparative purposes (Irish 1997, 2006; Johnson and Lovell 1994; Scott and Turner 1997; Ullinger 2005).

4.4.2 Spatial analysis: individual traits

The distribution of ten low-occurring dental morphological traits is plotted by burial for the Kellis 2 cemetery in order to test for non-random spatial patterning which might indicate the presence of kin-groups. The rationale for selecting choosing these traits is discussed in the methodology chapter. Each trait is plotted separately (Figures 4.1-4.10) and discussed below.

1) Mandibular 2nd molar Y-groove pattern (Figure 4.1)

As seen in Figure 4.1, the trait appears to be distributed randomly. It is notable, however, that there is no occurrence of the Y-groove in the eastern cluster of burials surrounding Tomb 3.

2) Mandibular 1st molar Cusp 6 (Figure 4.2)

Again, the pattern of Cusp 6 distribution appears random at first glance. However, the trait seems to occur more frequently in the southern group of burials, while not at all in the eastern group of burials centred around Tomb

3.

3) Mandibular 1st molar Cusp 7 (Figure 4.3)

Eight of the ten occurrences of Cusp 7 are distributed among the southern and western group of burials, while only once among the north group and once among the eastern group.

4) Mandibular 1st molars: 4 cusps (Figure 4.4)

Four-cusped mandibular molars occur most frequently among the western and southern burials. There are two instances of the trait among the northern burials, while the trait does not occur at all among the eastern group of burials surrounding Tomb 3.

5) Mandibular 2nd molars: 5 or more cusps (Figure 4.5)

Five or more cusps on the mandibular second molar occur most frequently among the northern group of burials. The trait occurs sporadically in the southern and eastern burials while only once in the western group.

6) Maxillary 2nd molar hypocone reduction (Figure 4.6)

Reduction or absence of the hypocone in maxillary second molars occurs most often among the western burials, followed by the southern burials. Seven individuals concentrated in a tight cluster around Tombs 1 and 2 display the trait. This trait also appears randomly distributed throughout the northern and eastern areas of the cemetery to a lesser extent.

7) Maxillary 2nd molar metacone reduction (Figure 4.7)

Reduction or absence of the metacone appears randomly distributed among burials with the cemetery, although the western group of burials has the lowest occurrence of the trait.

8) Maxillary lateral incisor shovel-shaping (Figure 4.8)

Distribution of this trait appears to be random, although there is a lower occurrence of shovel-shaped incisors among the western burial group.

9) Maxillary lateral incisor interruption groove (Figure 4.9)

Interruption grooves on the maxillary lateral incisors occur throughout the cemetery, with the exception of the eastern group of burials surrounding Tomb 3.

10) Maxillary 3rd molar peg-shape (Figure 4.10)

Peg-shaped maxillary third molars do not occur among the southern burials. The trait appears randomly distributed throughout the other areas of the cemetery.

While most of these traits appear randomly distributed throughout the cemetery, some differences do occur spatially. The eastern area of the cemetery containing burials clustering around Tomb 3 lacks any occurrence of mandibular 1st molar Cusp 6, 4-cusped mandibular 1st molars and maxillary lateral incisor interruption grooves. The western group of burials which surround Tombs 1 and 2 have no occurrence of maxillary lateral

incisor shovelling and the lowest occurrence of 5-cusped mandibular 2nd molars. This area of the cemetery also has the highest occurrence of reduced or absent maxillary 2nd molar hypocone.

It would appear, then, that certain areas of the cemetery are more variable in terms of trait occurrence than others. These areas can be roughly divided into four groups based on the observation of clusters of burials in the north, south, east and west of the excavation area. Chi-square and Likelihood Ratio analyses of trait frequency variation by cemetery area (see Appendix III for complete list) reveal that the most spatially variable traits are maxillary canine *tuberculum dentale* (P=0.009), maxillary central incisor shovelling (P=0.067), three-rooted maxillary second molars (P=0.078) and maxillary first molar Cusp 5 (metaconule) (P=0.085). Only the distribution of the *tuberculum dentale,* however, is statistically significant. These four traits are plotted in Figures 4.11-4.14.

4.4.3 Spatial analysis: inter-sex variation

As seen in the previous analysis of individual trait distribution, certain areas of the cemetery appear to have differential rates of expression for particular traits. An assumption can be made that these areas represent groups of closely-related individuals. As such, an alternate method of addressing inter-sex trait variation within the Kellis 2 cemetery is to analyze variation in trait frequencies between males and females within these areas. In this method, chi-square and Fisher's Exact tests are again used to check for significant differences. While there were few significant overall inter-sex differences in

trait frequencies that indicate a pattern of patrilocal post-marital residence at Kellis, when males and females are compared in this way, intra-cemetery spatial variation is observable (see Appendix IV for complete list of traits).

In the northern group of burials there are no significant inter-sex differences in trait expression, but one trait does approach the threshold: mandibular third premolar Tome's root, which occurs in 6% of females and 31% of males (Fisher's Exact Test P=0.138). Among the eastern and western groups of burials there are also no significant differences between males and females.

The southern group of burials, however, has the highest levels of inter-sex variability. As with the other groups, there are no significant differences; there are, however several traits which approach the threshold: maxillary interruption groove and central incisor shovelling, both of which have P values of 0.131 (Fisher's Exact Test). In both cases, females have a higher rate of occurrence than males (interruption groove: females 55%, males 11%; shovelling: females 56%, males 13%). Shovelling of the maxillary lateral incisor also has a Fisher's Exact Test P value (0.132) which approaches significance. Again, females have a higher rate of occurrence than males (shovelling: females 75%, males 25%).

4.4.4 Spatial analysis: combined traits

The sex-combined dental trait frequencies for each burial group will now be compared with one another to see if any significant differences occur between them. In this method, the four groups are treated as if they were

separate assemblages and analysed for inter-group variation. The burials are divided into four groups (see Figure 4.15) which correspond roughly to the areas described above (red=North group, green=East group, blue=South group, brown=West group). The Mean Measure of Divergence statistic was used to generate a proximity matrix for the pairwise comparisons of the four groupings using 20 dental morphological traits (see Table 4.4 for the list of traits used). The MMD proximity matrix is presented in Table 4.5. While there are no statistically significant differences between any of the groupings, the East (green) and South (blue) groups are the most dissimilar with an MMD value of 0.073, markedly higher than any of the other pair-wise group comparisons. The East and West (brown) groups appear to be the most similar with a very low MMD value of 0.000.

When the MMD values are plotted on a dendrogram using hierarchical clustering (Figure 4.16), the West and North groups cluster together as the most closely related, while the East group diverges from them at a slightly higher level. The South group occurs on a highly divergent branch from the other groups. Thus, it would seem that while the North, East and West groups appear similar in terms of dental morphology, the South group is morphologically distinctive. As with the previous analysis of intra-group inter-sex differences, the southern area of the Kellis 2 cemetery is shown to be the most variable in terms of dental morphology.

4.5 Regional and inter-regional comparisons

4.5.1 Descriptive comparisons

When compared with world-wide dental trait frequency data for five maxillary and five mandibular permanent tooth-trait combinations (thirteen traits in total), the biological affinities of the Kellis assemblage become apparent. Table 4.6 presents this comparison, and includes the trait frequencies compiled by Scott and Turner (1997) from studies of several major geographic population groups including Western Europe, North Africa, West Africa, South Africa and Khoisan.

The incidence (2%) of upper central incisor (UI1) shovelling in the Kellis assemblage is most comparable to the Western European group (3%). The frequency (19%) of interruption grooves on upper lateral incisors (UI2), however, places the Kellis assemblage closest to the Sub-Saharan groups (10-16%). Reduction of the maxillary second molar (UM2) hypocone occurs in 17% of the Kellis assemblage, a figure which falls between the Western European (25%) and North African (11%) groups. Cusp and tubercle forms (ASU 5-7) of Carabelli's trait on maxillary first molars (UM1) occur in 43% of observable cases for the Kellis assemblage, a rate almost double that of the highest world population frequency (27%, Western Europe). 31% of Kellis upper first molars (UM1) exhibit 5 cusps (ASU 1-5). This trait places the Kellis assemblage closer to the Khoisan (35%) and South African (22%) groups than to North Africa (19%) or Western Europe (12%). Multi-rooted (ASU 2-3) maxillary third premolars (UP3) occur in the Kellis assemblage at

a rate of 50%, placing it between the Western European (41%) and North African (57%) groups. Only 6% of Kellis mandibular first molars (LM1) exhibit four cusps, an expression rate closest to Western Europe (8%) and North Africa (10%). Four-cusped mandibular second molars (LM2) occur in 85% of observable cases, again placing the Kellis assemblage nearest to the Western European (71%) and North African (66%) groups. Six-cusped lower first molars (LM1) are present in 16% of the Kellis population. The nearest group to Kellis for this trait is South Africa (19%). Seven-cusped lower first molars (LM1) occur in 9% of the Kellis population, compared with 9% and 5% for the North African and Western European groups, respectively. The Y-shaped groove pattern on lower second molars (LM2) occurs only in 12% of Kellis individuals, lower than any other group, but closest to the Western European group (27%). Three-rooted lower first molars (LM1) are rare in the Kellis assemblage (1%), an identical expression rate to Western Europe and North Africa, but also similar to West African (0%) and Khoisan groups (0%). Finally, one-rooted lower second molars (LM2) occur in 7% of the Kellis assemblage, placing it within the range of South and West African groups (4 and 9%, respectively).

As illustrated by this descriptive comparison of dental trait frequencies, the Kellis assemblage mainly exhibits a simplified, mass-reduced dentition characteristic of North African and Western European populations: an unsurprising conclusion given the geographical location of Kellis. It also indicates that there is little affinity with Sub-Saharan African groups. Most of the trait frequencies commonly associated with the “Sub-Saharan African

Dental Complex" (Irish 1997, 1998a), e.g. high incidences of Cusp 7, retained third molars, canine mesial ridge ("Bushman canine"), and second molar Y-groove pattern are not present in the Kellis assemblage.

4.5.2 Trait selection for multivariate comparative study

The dental data for Kellis will now be subjected to multivariate statistical analyses in order to provide a more detailed picture of the population's phenetic relationship to regional and inter-regional groups. First, the Kellis assemblage is compared with 37 regional comparative groups using the dichotomized frequencies for twenty dental morphological traits. These traits were shown by Irish (2006) to have low inter-trait associations and sufficient inter-group variability. Table 4.4 provides a list of these traits along with the breakpoints used to establish trait presence or absence. The second set of multivariate analyses involves the thirteen traits used in the inter-regional comparisons with Western European, North African, West African, South African and Khoisan groups. These thirteen traits were also chosen because they have low inter-trait correlations and sufficient inter-group variability. This comparison uses a smaller set of traits because frequency data were not available for the complete range of morphological traits (Scott and Turner 1997). Table 4.6 provides a list of the traits employed along with the breakpoints used to establish trait presence or absence.

4.5.3 Twenty trait regional comparison

4.5.3.1 Mean Measure of Divergence (MMD)

Table 4.7 presents the MMD distance matrix generated from the pairwise

group comparisons between Kellis and the comparative groups. Low MMD values imply a phenetic similarity between pairwise groupings, while high values imply phenetic divergence. Italicized values represent significant differences between groups when the MMD value is greater than twice its standard deviation. Thus, the null hypothesis that the two samples in question are drawn from the same population (i.e. that they are phenetically identical) can be rejected at the 0.025 confidence level (Sjøvold 1977).

Results of the MMD analysis indicate that there is a statistically significant difference between the Kellis assemblage and all but two of the comparative groups. The two groups which are not significantly different from Kellis are the Kabyle Berber (MMD=0.029) and Kharga Oasis (0.040) groups. Other groups which share low MMD values (≤ 0.100) with Kellis are the Abydos (0.051), Pharaonic Nubian (0.055), Algerian Shawia Berber (0.060), Thebes (0.062), Hierakonpolis (0.073), Badari (0.073), Naqada (0.078), Meroitic Nubian (0.081), Hawara (0.082), Giza (0.085) and Christian Nubian (0.085) assemblages. The Sub-Saharan African groups are among the most divergent from Kellis: Togo/Dahomey (0.348), Nigeria/Cameroon (0.295), Ethiopia (0.295), Gabon (0.224), Ghana (0.209), Kenya (0.207), Chad (0.176) and Congo (0.155). Other groups which are highly divergent from Kellis are the Gebel Ramlah (0.248), Greek Egyptian (0.200), Saqqara (0.197), Soleb Nubian (0.162) and Carthage (0.155) assemblages.

When compared with roughly contemporaneous groups (i.e. Roman Hawara and El Hesa, Byzantine Kharga, Meroitic, X-Group and Christian Nubians), it

is notable that Kellis shares the closest affinity to the Byzantine Kharga Oasis assemblage, followed by the Meroitic Nubian, Roman Hawara and Christian Nubian assemblages. Kellis shares little affinity with the Roman El Hesa, and X-Group Nubian assemblages in terms of pairwise MMD values.

In terms of geography, the Kellis assemblage's nearest neighbour, Kharga Oasis, is also one of the most phenetically similar. Other sites which are near Kellis such as Abydos, Thebes, Badari, Hierakonpolis and Naqada, also share low MMD values, yet Gebel Ramlah and Qurneh, which are also nearby, do not. Strangely, the Kabyle Berber assemblage, which is the most phenetically similar to Kellis, is one of the furthest removed groups from the Dakhleh Oasis in terms of geographical distance. The Algerian Shawia Berber sample is also the fifth most similar group to Kellis. The Berbers, however, are the indigenous inhabitants of North Africa west of the Nile Valley and the phenetic similarities between them and the Kellis assemblage may offer support for the existence of Libyans (i.e. western Saharan peoples) in the Dakhleh Oasis. The Kabyle and Algerian groups share low and insignificant MMD values with most of the Egyptian and Nubian groups however; in some cases much lower than Kellis.

Average MMD values for the Kellis assemblage and regional groups are also instructive. The average MMD value for Kellis and the Upper Egyptian groups is 0.102. For Lower Egypt the average MMD value is 0.132. For the combined Egyptian groups, the MMD value is 0.114. For Kellis and the Upper Nubian groups the average MMD value is 0.137. For Lower Nubia the

value is 0.101. The average MMD value for all Nubian groups is 0.115. The Kellis and North African groups have an average MMD value of 0.104. Finally, the average MMD value for Kellis and the Sub-Saharan African groups is 0.247.

While evaluating MMD values for significant differences are useful for providing a general impression of phenetic similarities between groups on a one-to-one basis, further statistical analysis based on the MMD values is required in order to better elucidate the overall biological affinities of the Kellis assemblage. Hierarchical cluster and multidimensional scaling analysis of the MMD values are presented next in order to facilitate this.

4.5.3.2 Hierarchical cluster analysis of MMD values

Hierarchical cluster analysis is used to compare MMD values for the Kellis assemblage and comparative groups. Ward's linkage (Ward 1963) is the cluster method employed for this analysis. Figure 4.17 presents the dendrogram and it is immediately evident that there is a clear divide between the Sub-Saharan Africans and the Egyptian, Nubian and other North African groups. The Kellis assemblage clusters with the latter grouping. The exceptions to this geographic split are the Final Neolithic Upper Egyptian Gebel Ramlah group which clusters with the Sub-Saharan African groups, and the Ethiopian sample which clusters with several of the Nubian groups. While Irish (1993) includes the Chad group in the North African sample, Chadian peoples are typically classified as a Sub-Saharan population, so it is unsurprising that this group clusters with the other Sub-Saharan African

comparative groups.

Within the North African cluster there are three major sub-clusters, the first and most divergent contains the Saqqara and Greek Egyptian assemblages. The second most divergent cluster contains a mix of Upper and Lower Egyptian groups (El-Hesa, Qurneh, Thebes, Kharga, Tarkhan, Giza, Lisht), along with the Carthage and Upper Nubian Soleb groups. The third largest and most tightly grouped North African sub-cluster is comprised of three sub-clusters all diverging at the same level. The largest of the three contains the Upper Egyptian Predynastic Badari, Naqada, Hierakonpolis, Early Dynastic Abydos and Lower Egyptian Roman Hawara groups, along with the Kawa, C-Group and Pharaonic Nubian groups and the Algerian, Bedouin and Kabyle groups. The second sub-cluster contains the Kerma, Kush and A-Group Nubians along with the east African Ethiopian assemblage. Finally, the Kellis assemblage joins the X-Group, Christian and Meroitic Nubian groups in the third sub-cluster.

Based on the dendrogram, it is clear that the Kellis assemblage is more phenetically similar to the Egyptian, Nubian and North African groups than to the Sub-Saharan African groups. Within the North African range of comparative groups, the Kellis assemblage has the closest affinity to the most recent Nubian groups (i.e. X-Group, Christian and Meroitic). The Kellis assemblage also shares a general affinity with other Nubian groups, as well as with the early Upper Egyptian and recent North African groups.

4.5.3.3 Multidimensional Scaling of MMD values

The same MMD value distance matrix is used as the input (again in SPSS 17) to produce multidimensional scaling plots in two and three dimensions. This method is similar to hierarchical clustering in that it produces plots which allow the observer to better visualize the relationships between groups. The MDS plots were generated using an interval level of measurement, which is deemed appropriate due to the large number of traits used in the analysis causing the MMD distance matrix to approximate continuous values (Irish 2006). The scaling model employed is Euclidean distance.

Figures 4.18 and 4.19 present the MDS plots of the Kellis assemblage and comparative groups in two and three dimensions, respectively. Kruskal's stress formula 1 value for the two-dimensional plot (Figure 4.18) is 0.21713, and the r^2 value is 0.81687. For the three-dimensional plot (Figure 4.19), the stress value is 0.16608 and the r^2 value is 0.85787. Kruskal's stress formula 1 value is a measure of the "goodness of fit" of the data; thus the lower the stress value, the better the fit (Kruskal and Wish 1978). The r^2 value represents the proportion of variance of the scaled values accounted for by their corresponding distance values. In this case, 81.7% and 85.8% of the variation is explained by these distance values for the two dimensional and three dimensional plots, respectively. Based on these results, the three-dimensional MDS plot provides a slightly better representation of the biological affinities of the Kellis assemblage than the two-dimensional plot.

Despite this, the two-dimensional plot is still useful as it is easier to interpret.

As seen in Figures 4.18 and 4.19, the multidimensional scaling plots by and large recapitulate the results of the hierarchical cluster dendrogram presented previously. The Kellis assemblage is most closely linked with the X-Group, Christian and Meroitic Nubian groups as a result of sharing high positive values along the y-axis (dimension 2). Kellis is also near the El Hesa, Abydos, Naqada and Hierakonpolis groups. With the exception of Ethiopia, the Sub-Saharan African and Chad groups form a distinctly separate constellation of points that share the lowest values along the x-axis (dimension 1). Unlike the dendrogram produced by the hierarchical scaling analysis, Kellis appears as an outlier in these MDS plots. This is perhaps a truer representation of the Kellis assemblage's relationship with the comparative groups as multidimensional scaling provides a broader view of multivariate data patterning than hierarchical cluster analysis (Drennan 2009). The Saqqara and Greek Egyptian assemblages are also outliers which share the highest positive values along the x-axis.

4.5.4 Thirteen trait inter-regional comparison

4.5.4.1 Mean Measure of Divergence (MMD)

A final set of comparisons is made using a broader set of comparative groups in order to place Kellis within an inter-regional context encompassing Europe, North and Sub-Saharan Africa. As before, the Mean Measure of Divergence statistic is employed to produce a distance matrix for each set of pairwise group comparisons and is presented in Table 4.8. From the matrix it

can be seen that there is a statistically significant difference between Kellis and all of the comparative groups. Kellis is most similar to the North African group, however (MMD=0.066), followed by the Western European and Khoisan groups (MMD=0.086). The groups with the greatest divergence from the Kellis assemblage are the West and South African groups (MMD=0.373 and 0.233, respectively).

4.5.4.2 Hierarchical cluster analysis of MMD values

When the MMD values from the distance matrix are used to produce a hierarchical cluster dendrogram using Ward's Method (Figure 4.20), two main branches of the dendrogram are apparent, with the Western European, North African and Kellis groups comprising one branch, and the Sub-Saharan African groups comprising the other. Here it can also be seen that the Kellis, Western European and North African groups are tightly linked at the same level on the dendrogram. This implies that the three groups are equally related, although the North African group emerges as an intermediary between Western Europe and the Kellis assemblage, again suggesting a closer link between Kellis and North Africa. The Western European, North African and Kellis cluster are highly divergent from the Sub-Saharan African cluster.

4.5.4.3 Multidimensional scaling of MMD values

Figure 4.21 presents the MDS plots of the Kellis and regional groups in two dimensions. A three-dimensional plot cannot be produced because there are not enough data points to allow for such a representation. Kruskal's stress

formula 1 value is 0.11526, and the r^2 value is 0.88998. The low stress value and high r^2 value suggest this two-dimensional plot is an accurate representation of the data.

The MDS plot serves to corroborate the previous analysis of significant group differences, as well as the hierarchical cluster plot of the MMD values. The Kellis, Western European and North African groups all share positive values along the x-axis, while the Sub-Saharan groups share negative values. This distribution pattern mirrors the divide between the two groups illustrated in the hierarchical cluster plot. However, while the Western European and North African groups share positive values, the Kellis group lies on the negative side of the y-axis. This suggests more of a distinction between the three groups than hinted at in the dendrogram.

Table 4.1. Raw scores for Kellis mandibular dental traits, with total number of individuals observable.

Shovelling	ASU Score								
Tooth	0	1	2	3	4	5	6	7	Total
LI1	97	3	1	0	0	0	0	0	**101**
LI2	105	4	1	0	0	0	0	0	**110**

Double Shovelling	ASU Score							
Tooth	0	1	2	3	4	5	6	Total
LI1	107	0	0	0	0	0	0	**107**
LI2	112	0	0	0	0	0	0	**112**

Distal Accessory Ridge	ASU Score						
Tooth	0	1	2	3	4	5	Total
LC	40	3	2	0	1	0	**46**

Lingual Cusp	ASU Score										
Tooth	A	0	1	2	3	4	5	6	7	8	9	Total
LP3	9	40	6	2	4	4	4	1	0	0	0	**70**
LP4	0	13	1	8	17	5	1	1	0	0	0	**46**

Anterior Fovea	ASU Score					
Tooth	0	1	2	3	4	Total
LM1	7	7	10	6	1	**31**

Groove Pattern	ASU Score			
Tooth	Y	+	X	Total
LM1	89	4	9	**102**
LM2	13	68	25	**106**

Cusp Number	ASU Score			
Tooth	4	5	6	Total
LM1	7	83	17	**107**
LM2	92	13	3	**108**
LM3	44	26	7	**77**

Deflecting Wrinkle	ASU Score				
Tooth	0	1	2	3	Total
LM1	4	5	15	0	**24**

Protostylid	ASU Score								
Tooth	0	1	2	3	4	5	6	7	Total
LM1	49	36	0	1	0	0	0	0	**86**
LM2	58	33	0	0	0	0	0	0	**91**
LM3	54	22	0	0	0	0	0	0	**76**

Cusp 5	ASU Score						
Tooth	0	1	2	3	4	5	Total
LM1	7	2	9	56	29	1	**104**
LM2	92	1	7	7	0	0	**107**
LM3	50	0	8	15	7	2	**82**

Cusp 6	ASU Score						
Tooth	0	1	2	3	4	5	Total
LM1	89	3	11	3	0	0	**106**
LM2	104	0	3	0	0	0	**107**
LM3	74	1	4	2	0	0	**81**

Cusp 7	ASU Score						
Tooth	0	1	1A	2	3	4	Total
LM1	94	2	4	5	4	1	**110**
LM2	101	2	3	1	0	0	**107**
LM3	74	2	0	2	1	2	**81**

Root number	ASU Score		
Tooth	1	2	Total
LC	137	9	**146**

Tome's Root	ASU Score						
Tooth	0	1	2	3	4	5	Total
LP3	98	7	12	20	0	0	**137**

Root number	ASU Score			
Tooth	1	2	3	Total
LM1	2	96	1	**99**
LM2	6	74	0	**80**
LM3	4	36	3	**43**

Congenital Absence	ASU Score		
Tooth	0	1	Total
LI1	164	0	**164**
LI2	158	0	**158**
LC	156	0	**156**
LP3	153	0	**153**
LP4	141	2	**143**
LM1	153	0	**153**
LM2	145	0	**145**
LM3	108	4	**112**

Table 4.2. Raw scores for Kellis maxillary dental traits, with total number of individuals observable.

Winging	ASU Score				
Tooth	1	2	3	4	Total
UI1	2	0	117	2	**121**

Shovelling	ASU Score								
Tooth	0	1	2	3	4	5	6	7	Total
UI1	41	32	16	2	0	0	0	0	**91**
UI2	33	27	21	9	0	0	0	0	**90**
UC	65	13	9	0	0	0	0	0	**87**

Labial Convexity	ASU Score					
Tooth	0	1	2	3	4	Total
UI1	0	16	38	49	0	**103**
UI2	0	1	3	24	73	**101**

Double Shovelling	ASU Score							
Tooth	0	1	2	3	4	5	6	Total
UI1	102	1	0	0	0	0	0	**103**
UI2	100	1	1	0	0	0	0	**102**
UC	104	1	2	1	0	0	0	**108**

Interruption Groove	ASU Score					
Tooth	0	M	D	MD	Med.	Total
UI1	112	1	0	0	4	**117**
UI2	87	10	8	1	3	**109**

Tuberculum Dentale	ASU Score							
Tooth	0	1	2	3	4	5	6	Total
UI1	29	35	22	5	1	0	0	**92**
UI2	64	17	5	1	1	3	1	**92**
UC	50	10	4	2	1	19	4	**90**

Mesial Ridge (Bushman Canine)	ASU Score				
Tooth	0	1	2	3	Total
UC	77	1	0	0	**78**

Distal Accessory Ridge	ASU Score						
Tooth	0	1	2	3	4	5	Total
UC	18	8	9	3	0	0	**38**

Accessory Cusp	ASU Score		
Tooth	0	1	Total
UP3	85	1	86
UP4	81	0	81

Tri-cusped Premolar	ASU Score		
Tooth	0	1	Total
UP3	108	0	108
UP4	109	0	109

Distosagittal Ridge	ASU Score		
Tooth	0	1	Total
UP3	104	0	104

Metacone	ASU Score							
Tooth	0	1	2	3	3.5	4	5	Total
UM1	0	0	0	0	13	118	2	133
UM2	0	2	2	8	57	43	0	112
UM3	1	0	2	26	37	5	0	71

Hypocone	ASU Score							
Tooth	0	1	2	3	3.5	4	5	Total
UM1	0	0	0	0	9	118	4	131
UM2	11	7	9	23	43	14	1	108
UM3	28	9	13	15	4	0	0	69

Cusp 5 (Metaconule)	ASU Score						
Tooth	0	1	2	3	4	5	Total
UM1	72	20	6	6	1	0	105
UM2	75	10	9	3	2	0	99
UM3	45	3	6	6	3	4	67

Carabelli's Cusp	ASU Score								
Tooth	0	1	2	3	4	5	6	7	Total
UM1	11	2	2	20	12	16	8	11	82
UM2	88	0	5	2	0	0	1	0	96
UM3	65	0	1	0	0	1	0	2	69

Parastyle	ASU Score							
Tooth	0	1	2	3	4	5	6	Total
UM1	107	1	0	0	0	0	0	108
UM2	98	2	0	0	0	0	0	100
UM3	69	1	0	0	0	0	0	70

Enamel Extensions	ASU Score				
Tooth	0	1	2	3	Total
UP3	116	2	0	0	**118**
UP4	113	1	0	0	**114**
UM1	114	6	0	0	**120**
UM2	93	2	1	2	**98**
UM3	61	2	2	1	**66**

Root Number	ASU Score				
Tooth	1	2	3	4	Total
UP3	63	63	0		**126**
UP4	109	13	0		**122**
UM1	1	9	118	0	**128**
UM2	7	15	76	1	**99**
UM3	34	18	16	1	**69**

Peg-Shaped Incisor	ASU Score		
Tooth	0	1	Total
UI2	119	0	**119**

Peg-Shaped Molar	ASU Score		
Tooth	0	1	Total
UM3	80	4	**84**

Odontome	ASU Score		
Tooth	0	1	Total
UP3	107	0	**107**
UP4	107	0	**107**

Congenital Absence	ASU Score		
Tooth	0	1	Total
UI2	161	1	**162**
UP4	150	2	**152**
UM3	110	6	**116**

Table 4.3. Selected trait scores (dichotomized) for Kellis dentition by sex category.

	Males		Females		Unsexed		Pooled	
Trait	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
2+ lingual cusps (LP4)	19	57.9	13	76.9	14	78.6	46	69.9
Anterior fovea (LM1)	3	0.0	3	33.3	25	64.0	31	54.8
Y-groove (LM2)	45	15.6	42	7.1	19	15.8	106	11.5
4 cusps (LM1)	39	10.8	36	8.6	32	0.0	107	6.5
4 cusps (LM2)	46	80.4	43	93.0	19	78.9	108	85.2
Deflecting wrinkle (LM1)	3	66.7	1	100.0	20	60.0	24	62.5
Protostylid (LM1)	31	43.8	25	41.7	30	43.3	86	43.0
Cusp 6 (LM1)	38	12.8	36	17.1	32	18.8	106	16.0
Cusp 7 (LM1)	40	10.0	37	5.4	33	12.1	110	9.1
2-rooted canines (LC)	55	7.3	75	6.7	16	0.0	146	6.2
Tome's root (LP3)	54	18.5	67	10.4	16	18.6	137	14.6
3 roots (LM1)	39	0.0	37	2.7	23	0.0	99	1.0
1 root (LM2)	36	5.6	31	12.9	13	0.0	80	7.5
Bilateral winging (UI1)	42	0.0	60	3.3	19	0.0	121	1.7
Shovel shape (UI1)	32	18.8	37	24.3	22	13.6	91	19.8
Double shovelling (UI1)	34	0.0	47	0.0	22	0.0	103	0.0
Interruption groove (UI2)	40	17.5	53	22.6	16	18.8	109	20.2
Tuberculum dentale ((UI2)	34	8.8	40	10.0	18	22.2	92	12.0
Mesial ridge (UC)	30	0.0	32	3.2	16	0.0	78	1.3
Distal accessory ridge (UC)	12	33.3	12	25.0	14	35.7	38	31.6
3 cusps (UM2)	37	13.5	50	14.0	21	28.6	108	16.7
Cusp 5 (UM1)	29	30.0	42	19.0	34	47.1	105	31.4
Carabelli's cusp (UM1)	27	44.4	23	56.5	32	31.3	82	42.7
Parastyle (UM3)	27	0.0	39	2.6	4	0.0	70	1.4
Enamel extensions (UM1)	36	0.0	54	0.0	30	0.0	120	0.0
2 roots (UP3)	50	60.0	61	42.6	15	46.7	126	50.0
3 roots (UM2)	39	84.6	48	72.9	12	75.0	99	77.8
Odontomes (UP3)	40	0.0	48	0.0	19	0.0	107	0.0
Odontomes (UP4)	43	0.0	46	0.0	18	0.0	107	0.0
Congenital absence (UM3)	47	2.1	56	7.1	13	7.7	116	5.2

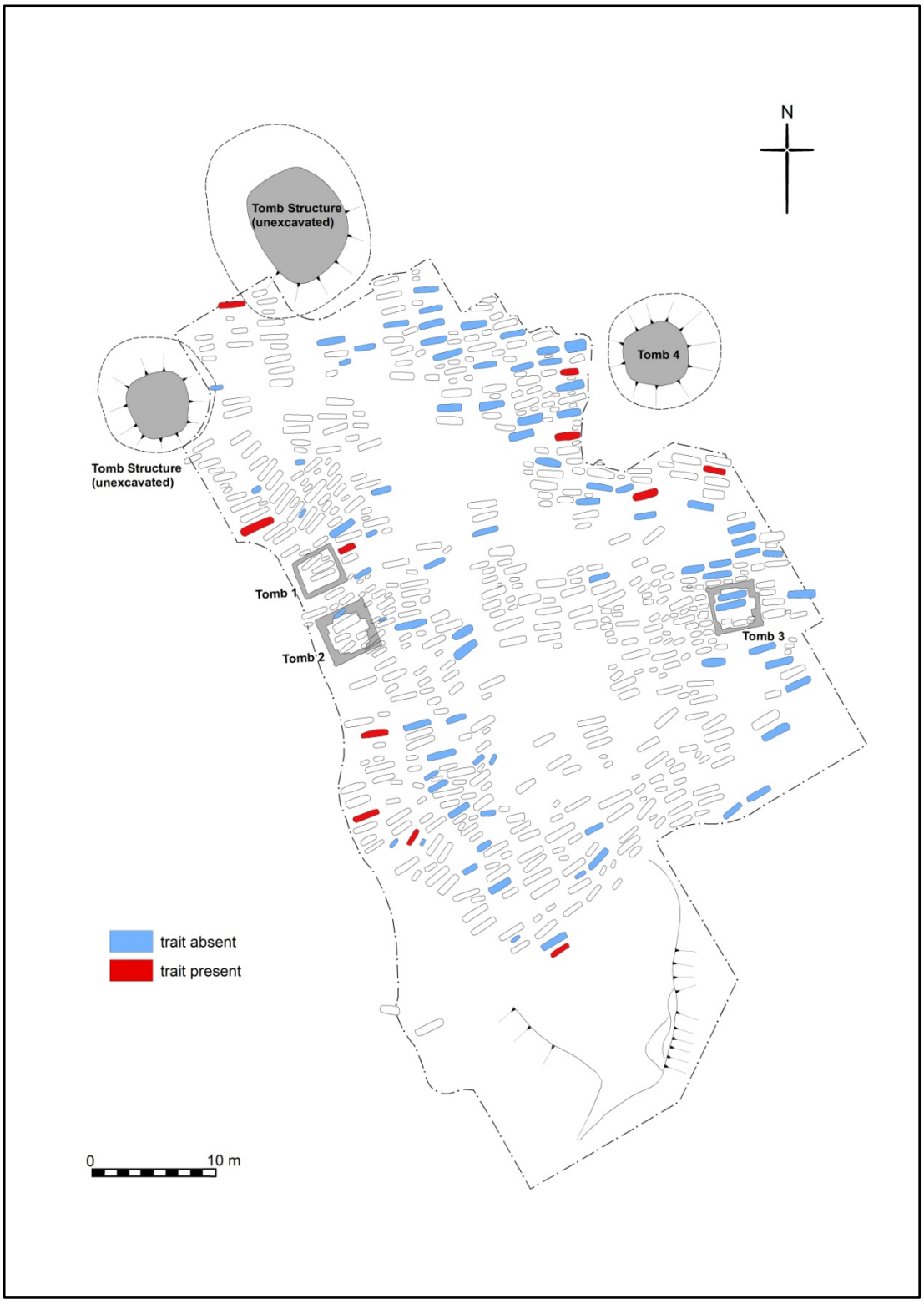


Figure 4.1. Distribution of mandibular 2nd molar Y-groove trait.

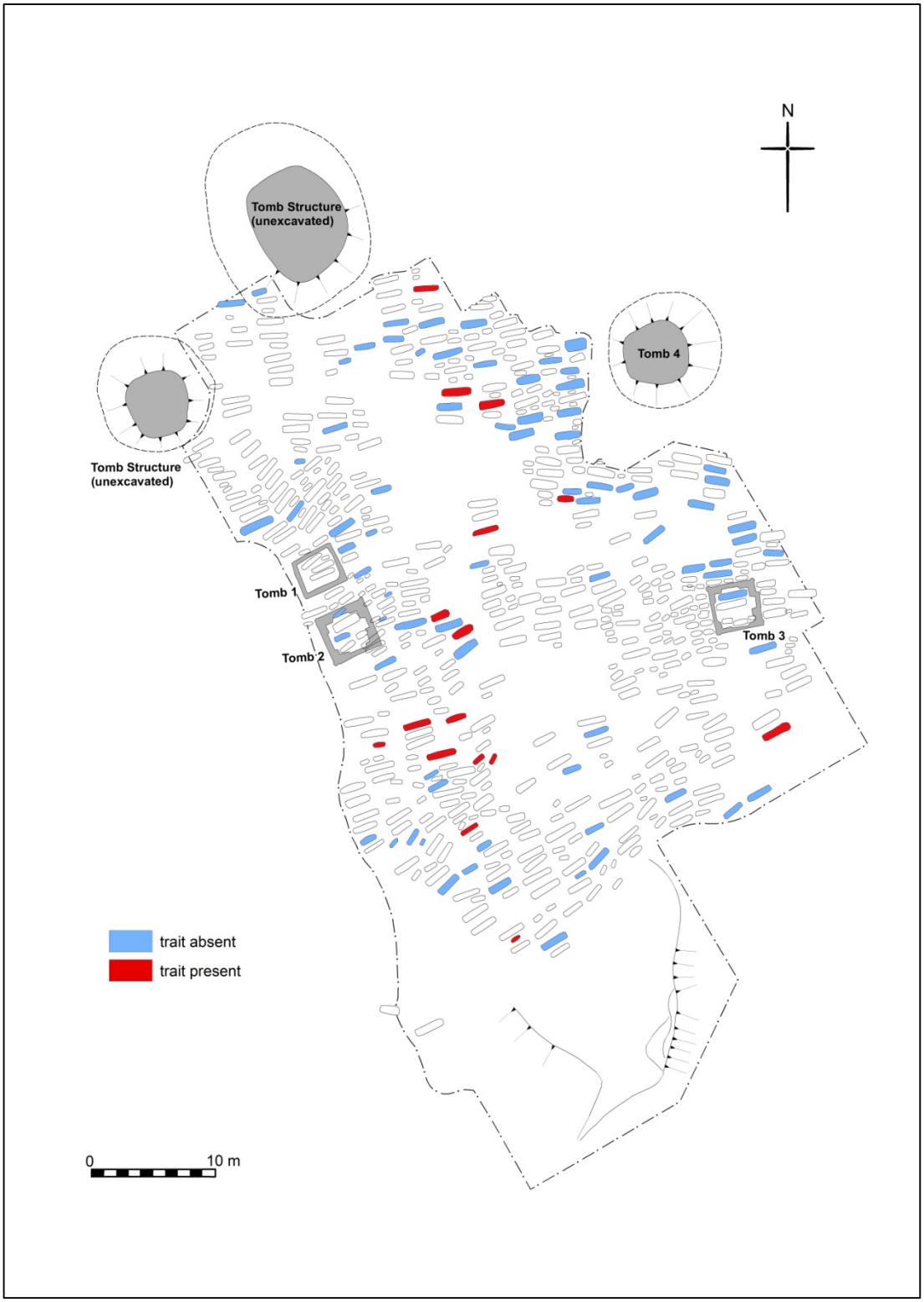


Figure 4.2. Distribution of mandibular 1st molar Cusp 6 trait.

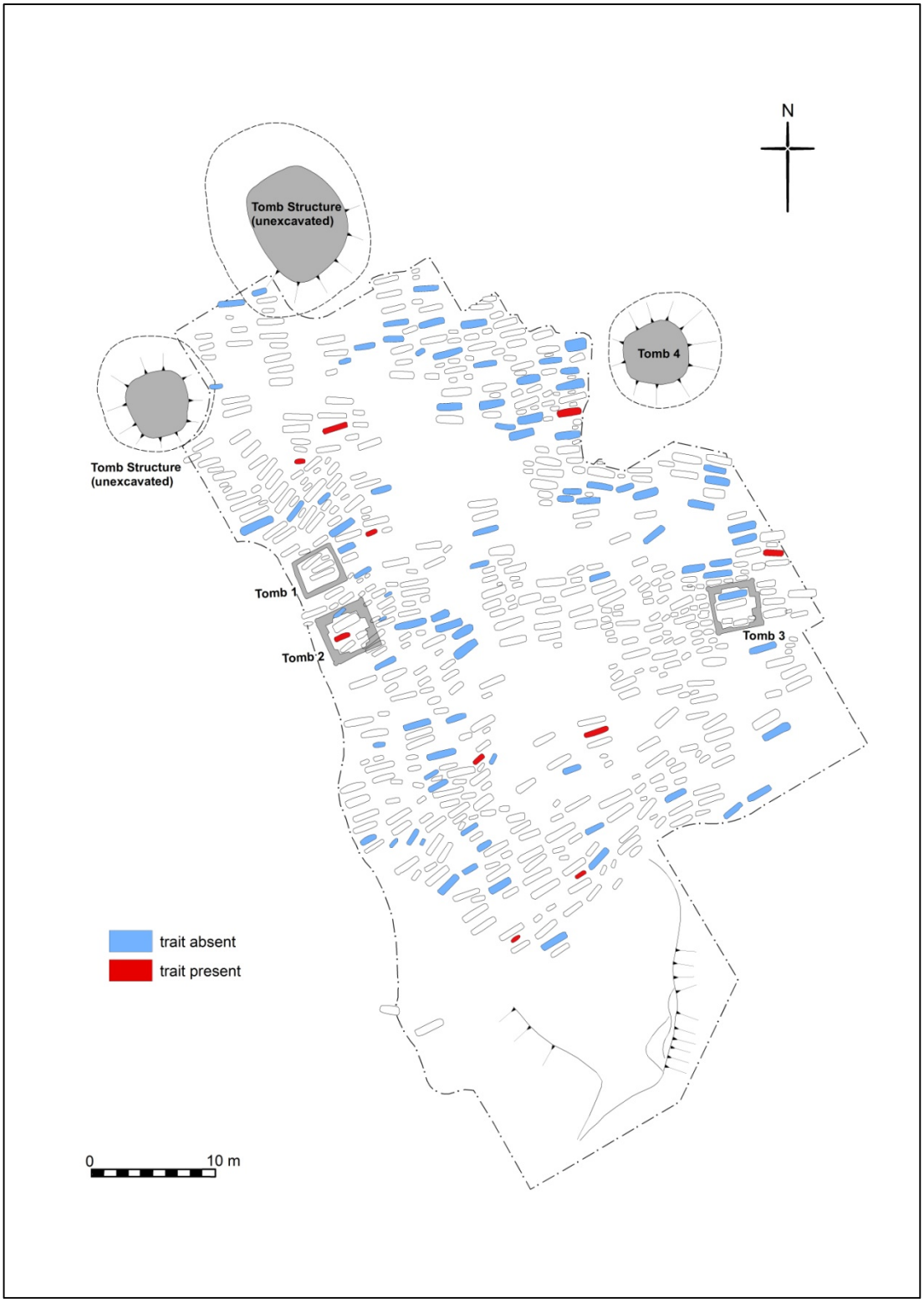


Figure 4.3. Distribution of mandibular 1st molar Cusp 7 trait.

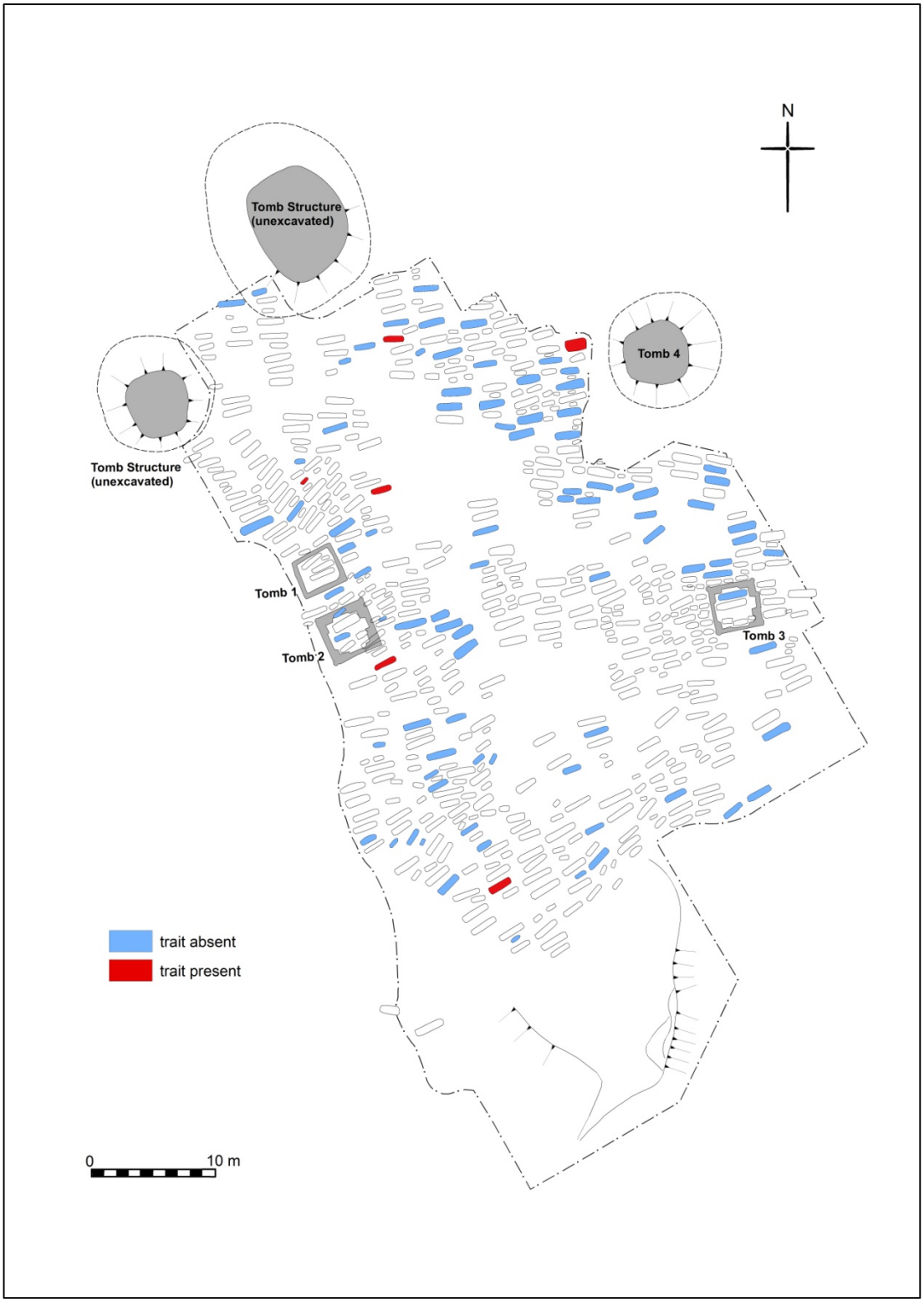


Figure 4.4. Distribution of 4-cusped mandibular 1st molar trait.

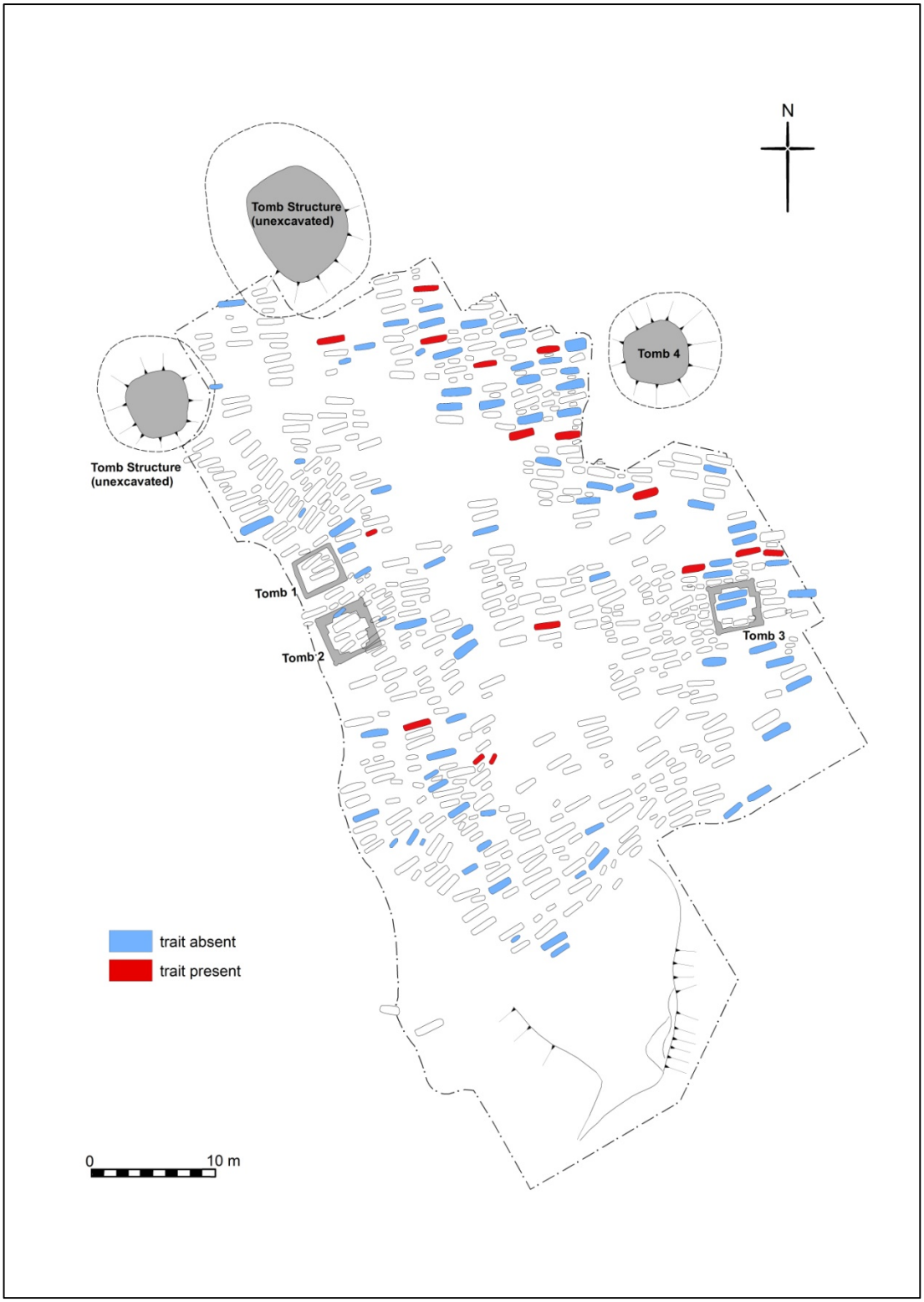


Figure 4.5. Distribution of 5 or more cusps mandibular 2nd molar trait.

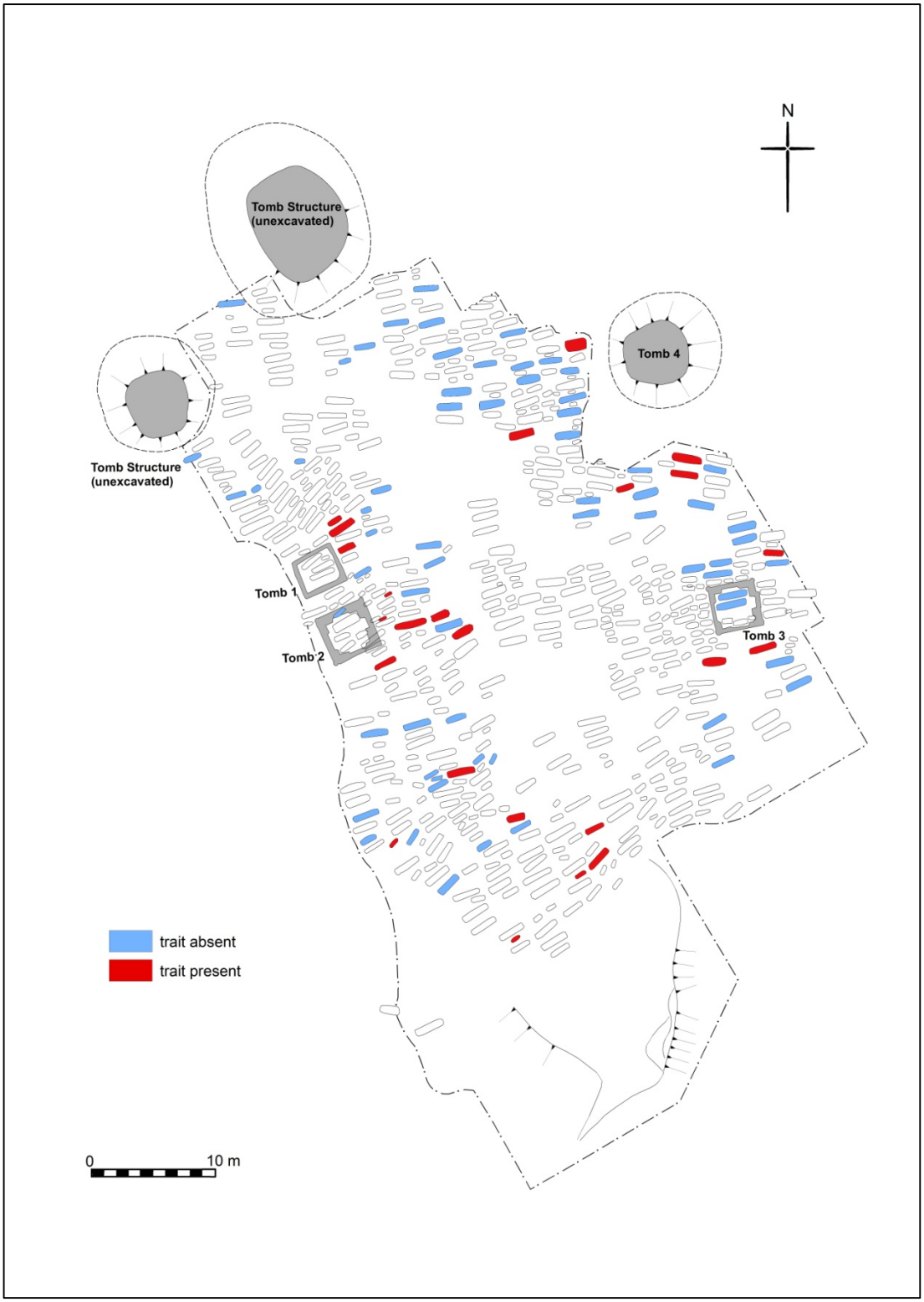


Figure 4.6. Distribution of reduced/absent maxillary 2nd molar hypocone trait.

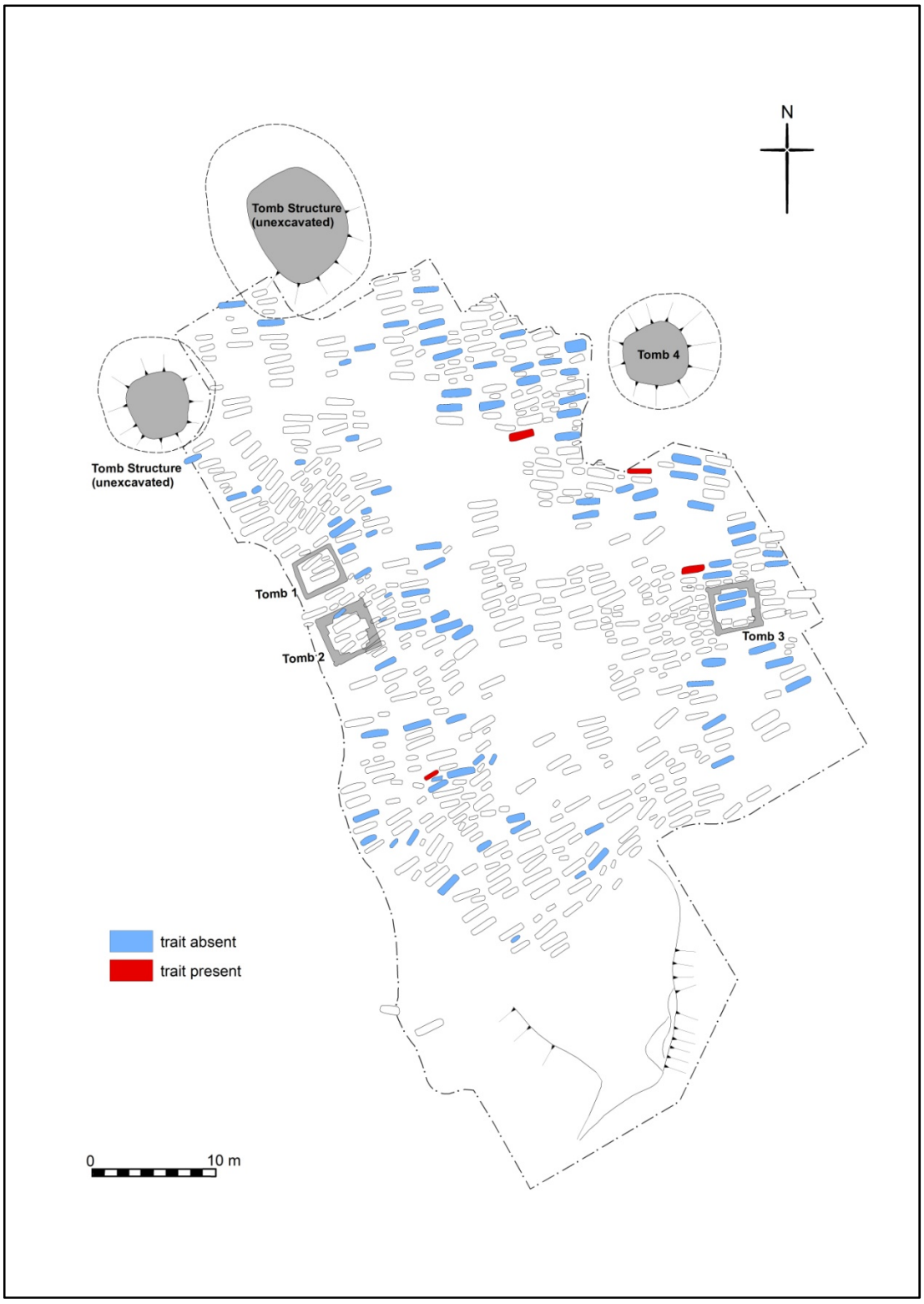


Figure 4.7. Distribution of reduced/absent maxillary 2nd molar metacone trait.

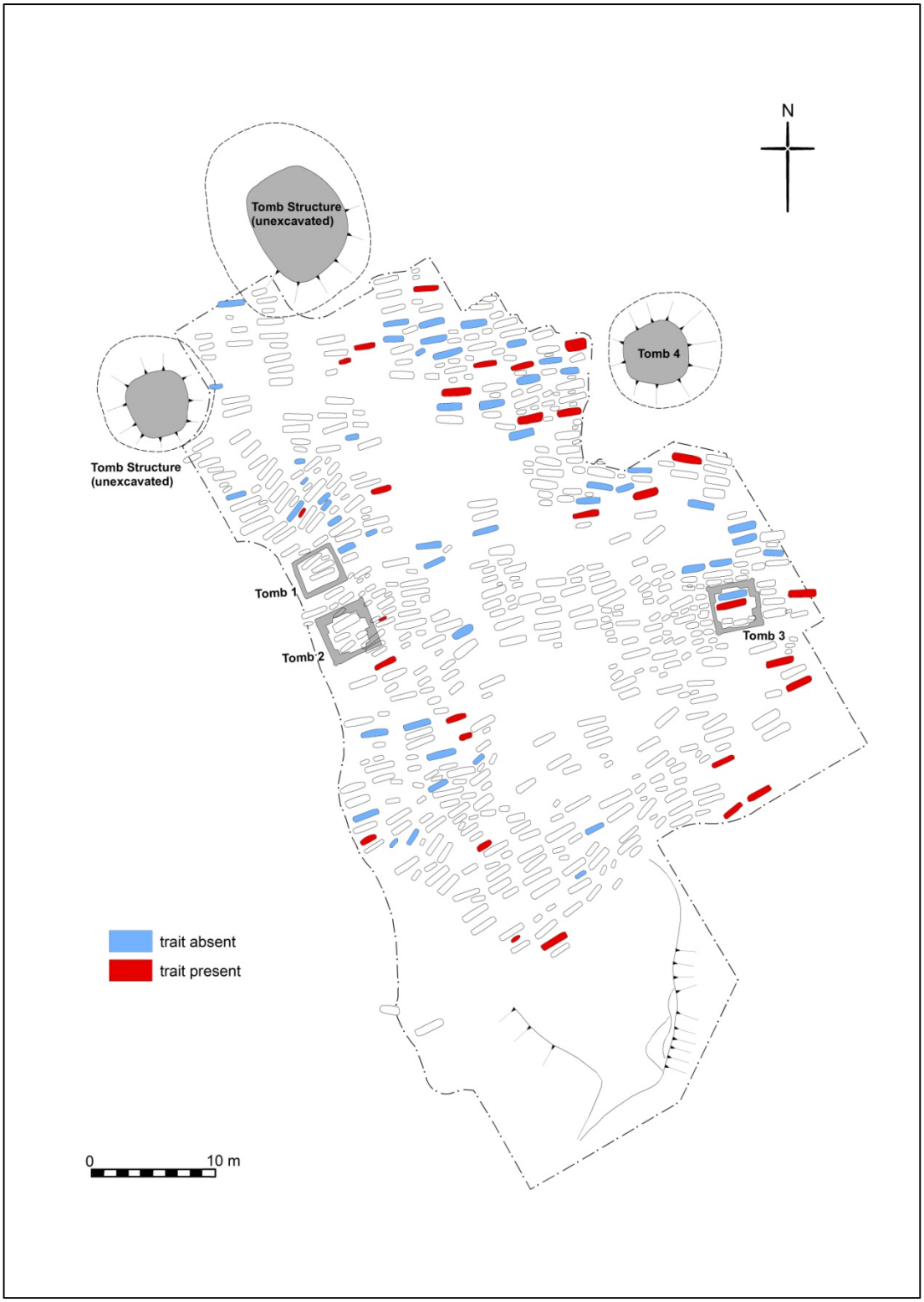


Figure 4.8. Distribution of maxillary lateral incisor shovel-shaped trait.

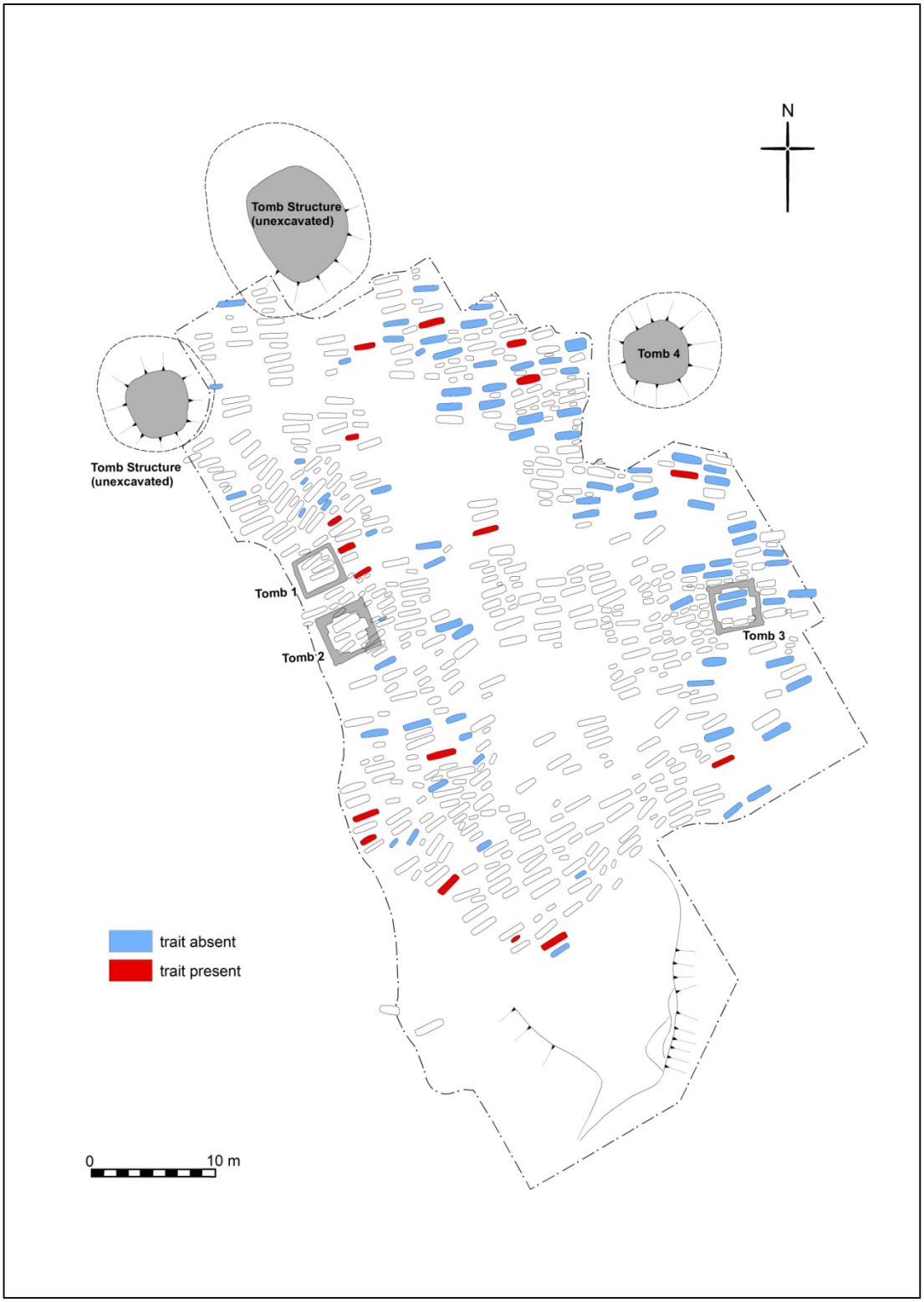


Figure 4.9. Distribution of maxillary lateral incisor interruption groove trait.

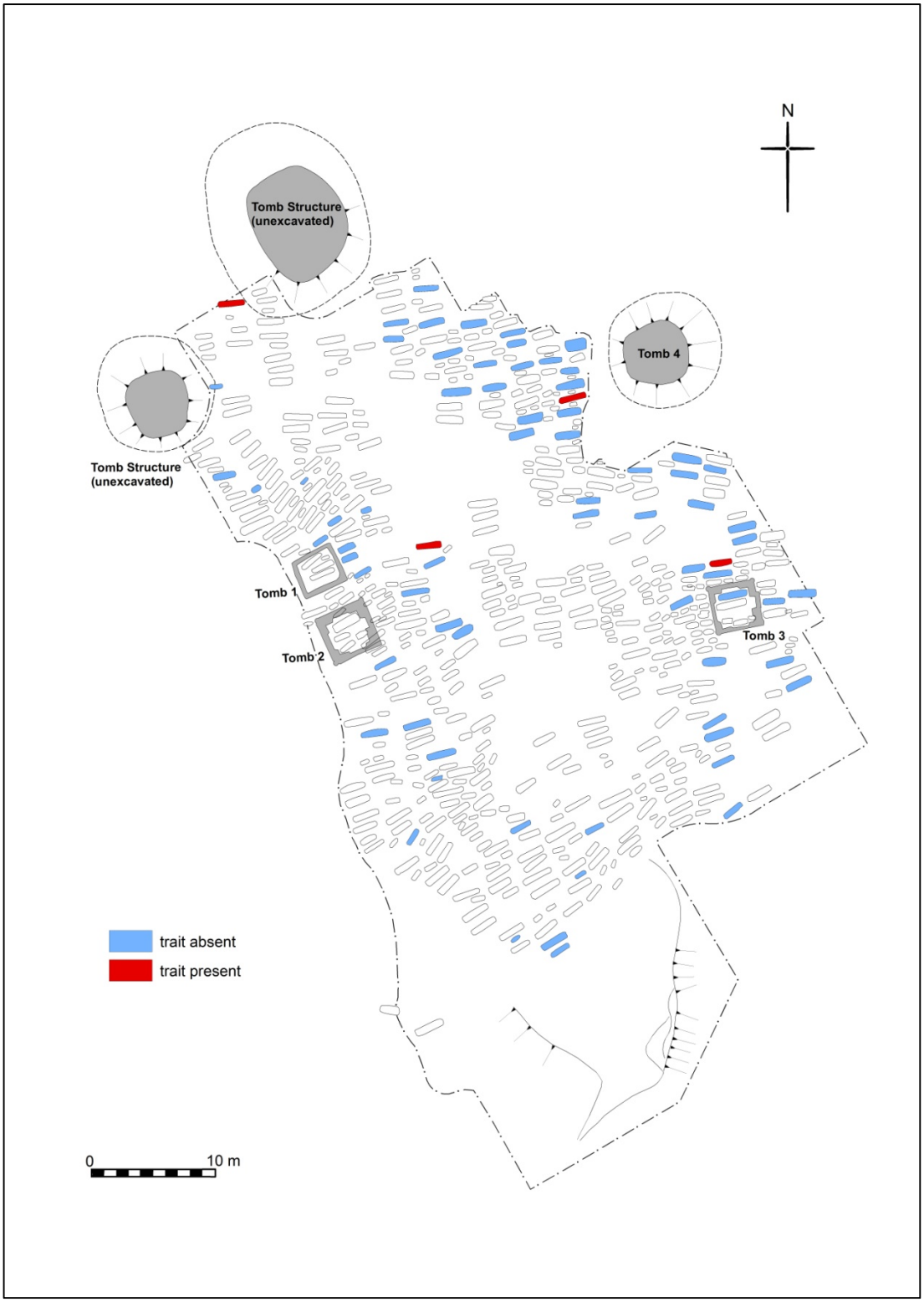


Figure 4.10. Distribution of peg-shaped maxillary 3rd molar trait.

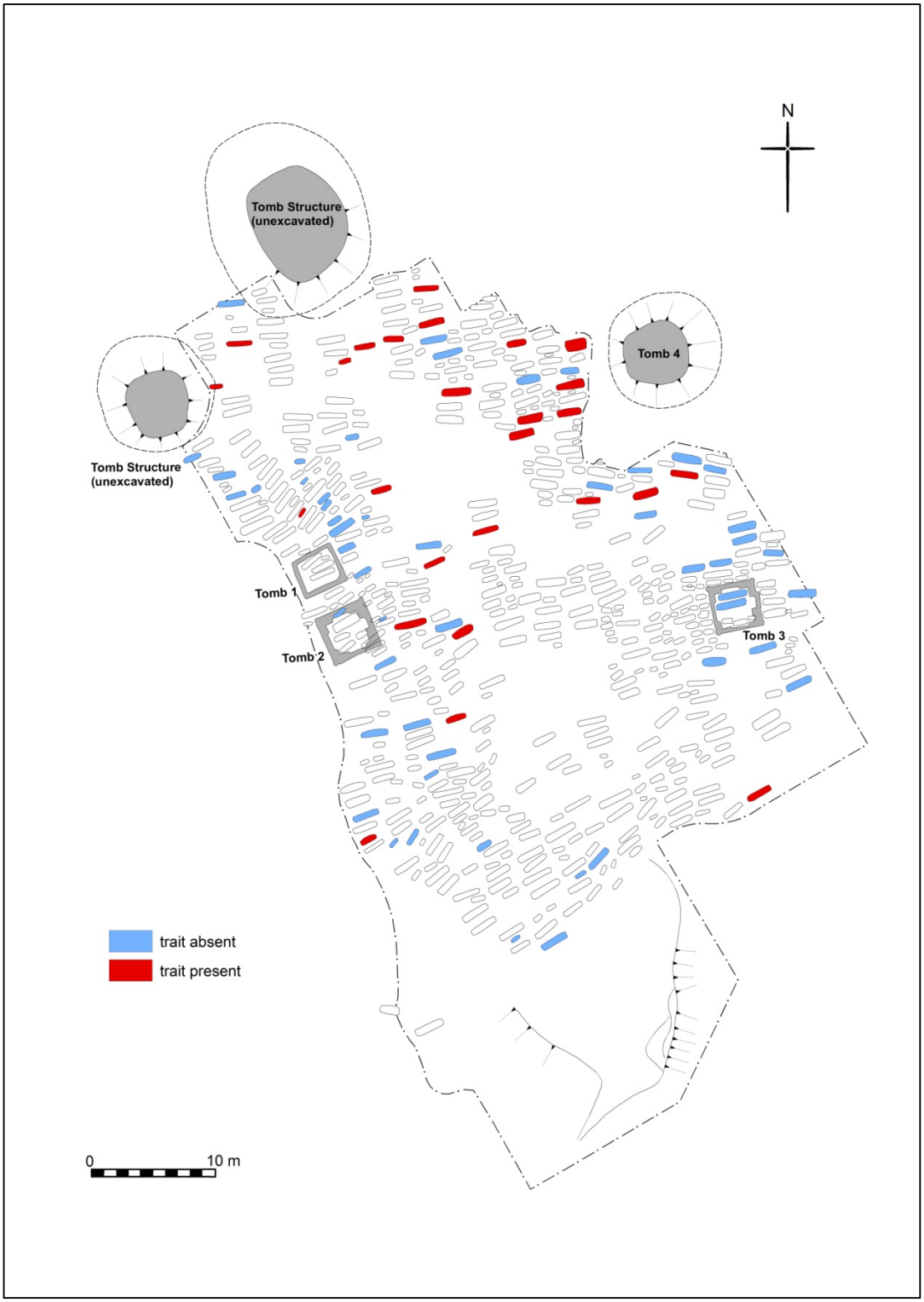


Figure 4.11. Distribution of maxillary canine *tuberculum dentale* trait.

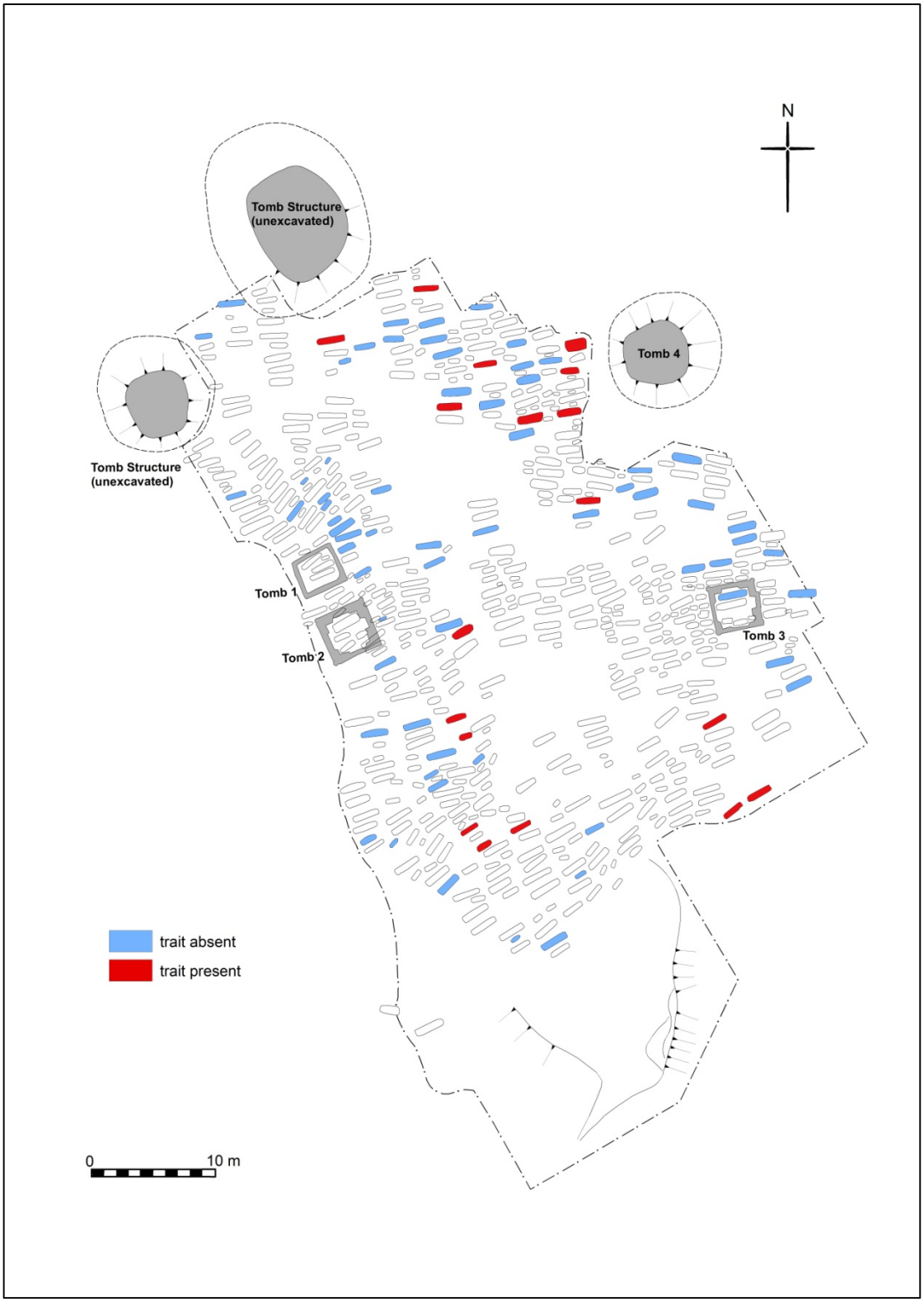


Figure 4.12. Distribution of maxillary central incisor shovelling trait.

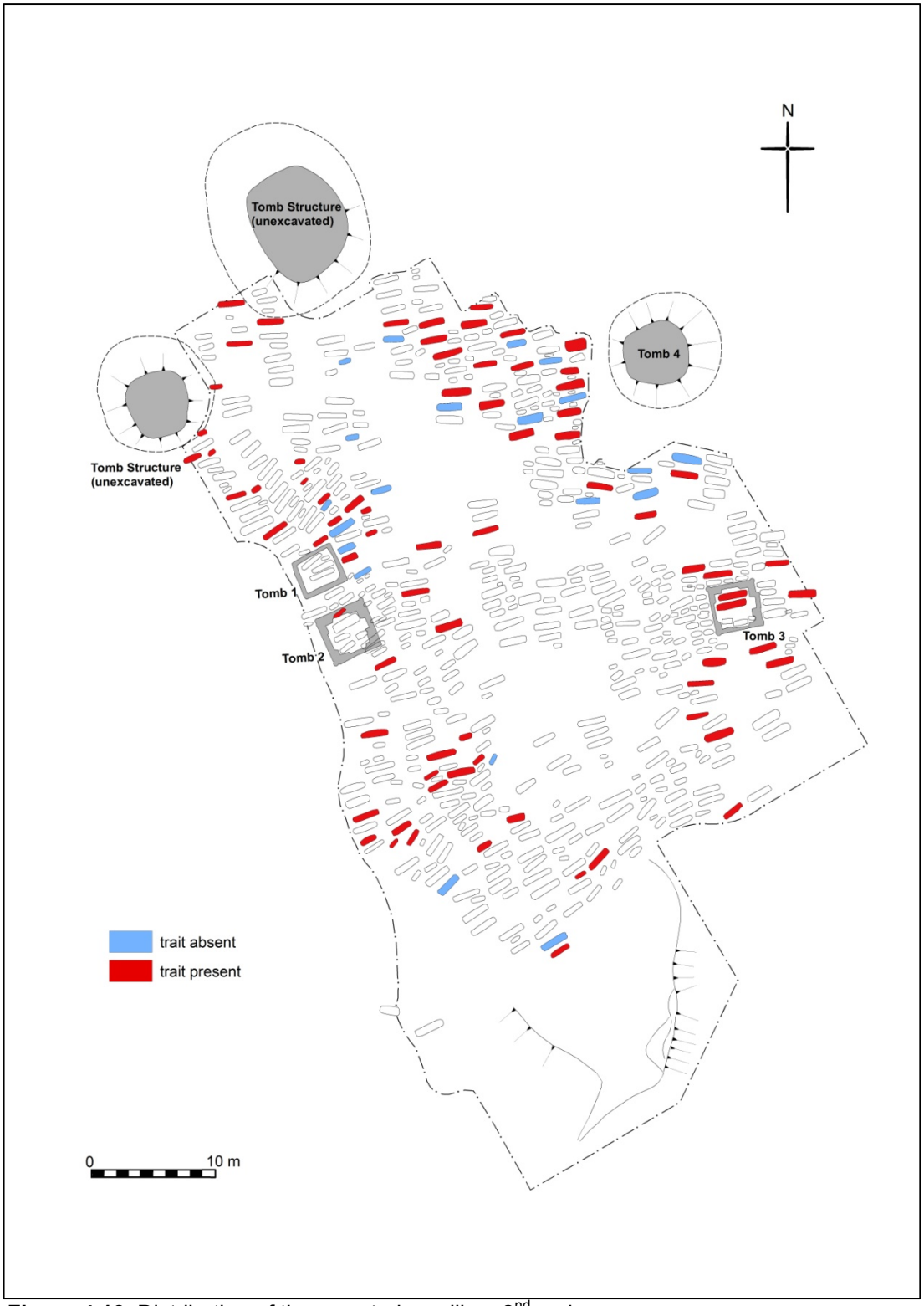


Figure 4.13. Distribution of three-rooted maxillary 2nd molars.

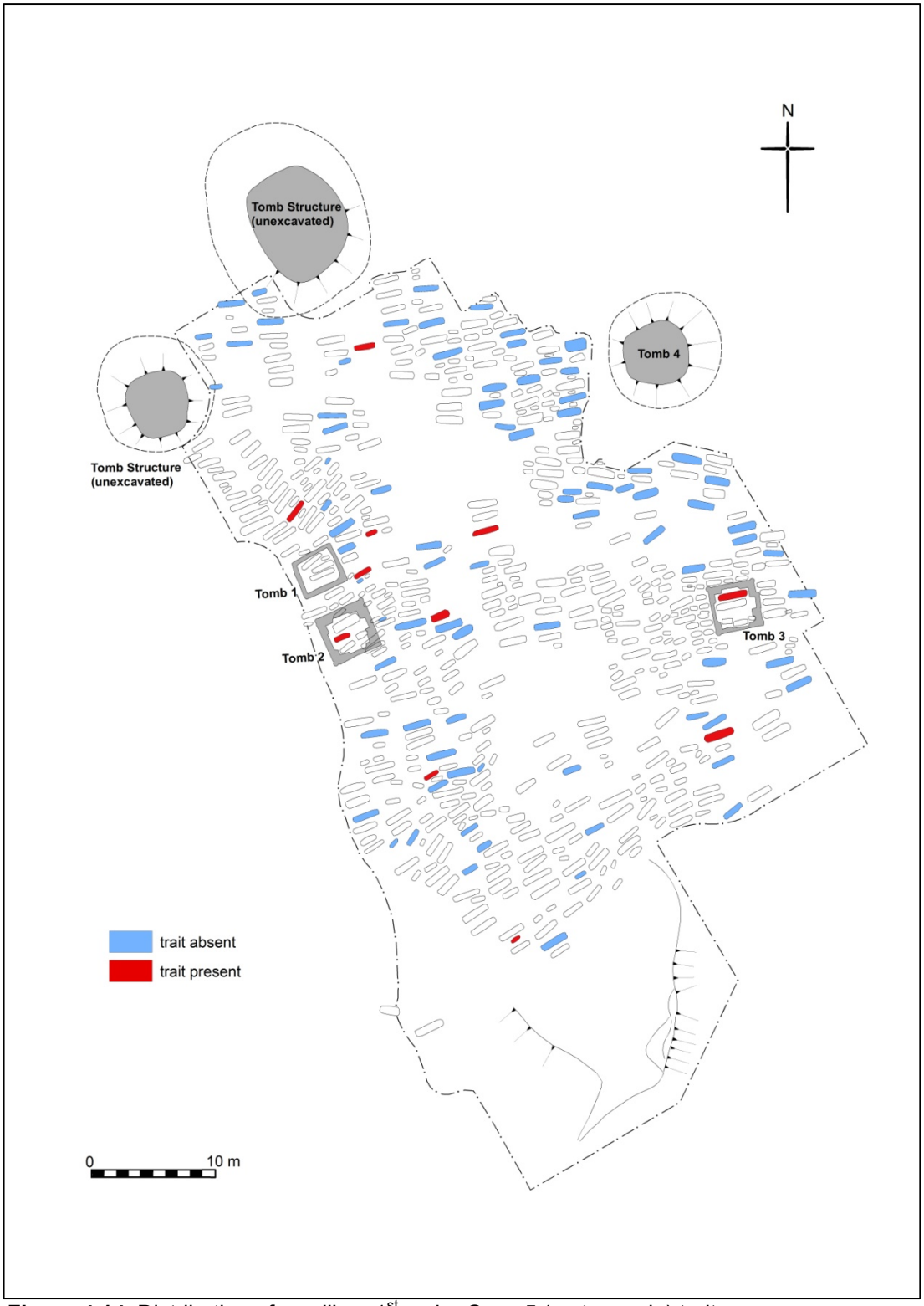


Figure 4.14. Distribution of maxillary 1st molar Cusp 5 (metaconule) trait.

Table 4.4. List of 20 traits used in MMD analysis and their breakpoints.

	Trait	Breakpoint
1	Shovelling UI1	ASU 2–6
2	Interruption Groove IU2	ASU +
3	Tuberculum Dentale UI2	ASU 2–6
4	Mesial Ridge UC	ASU 1–3
5	Distal Accessory Ridge UC	ASU 2–5
6	Hypocone UM2	ASU 3–5
7	Cusp 5 UM1	ASU 2–5
8	Carabelli's Cusp UM1	ASU 2–7
9	Enamel Extensions UM1	ASU 1–3
10	Root # UP3	ASU 2+
11	Root # UM2	ASU 3+
12	Peg-reduced UI2	ASU=+
13	Congenital Absence UM3	ASU=0
14	Lingual Cusp LP4	ASU 2–9
15	Y-Groove LM2	ASU Y
16	Cusp# LM2	ASU 5+
17	Protostylid LM1	ASU 1–6
18	Cusp 7 LM1	ASU 2–4
19	Tome's Root LP3	ASU 3–5
20	Root # LM2	ASU 2+

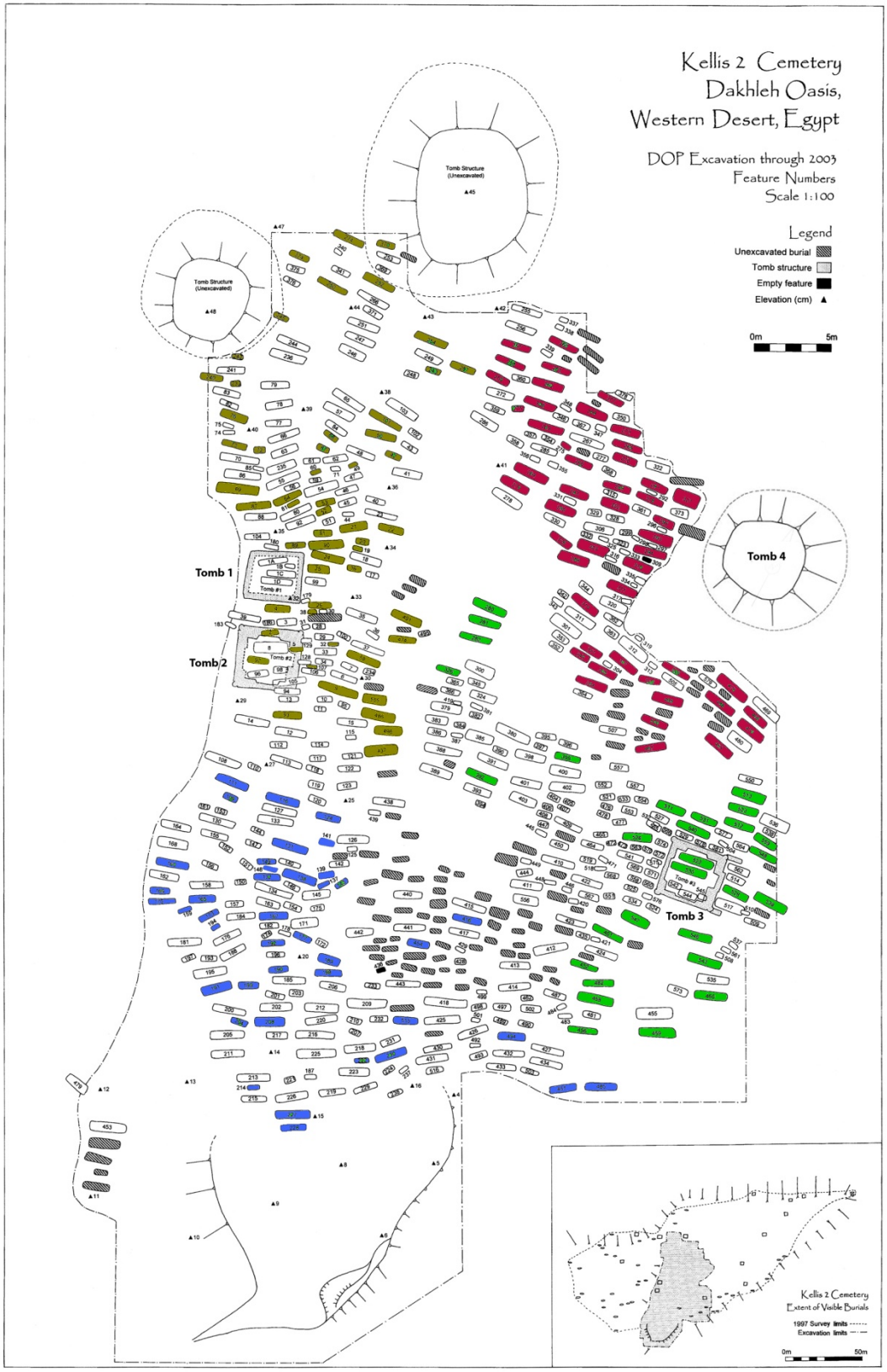


Figure 4.15. Map of Kellis 2 cemetery showing four burial subgroups (red=North group; green=East group; blue=South Group; brown=West group).

Table 4.5. MMD proximity matrix for Kellis 2 cemetery subgroups

GROUP	EAST (GREEN)	WEST (BROWN)	NORTH (RED)	SOUTH (BLUE)
EAST (GREEN)	0.000			
WEST (BROWN)	0.000	0.000		
NORTH (RED)	0.012	0.025	0.000	
SOUTH (BLUE)	0.073	0.031	0.032	0.000

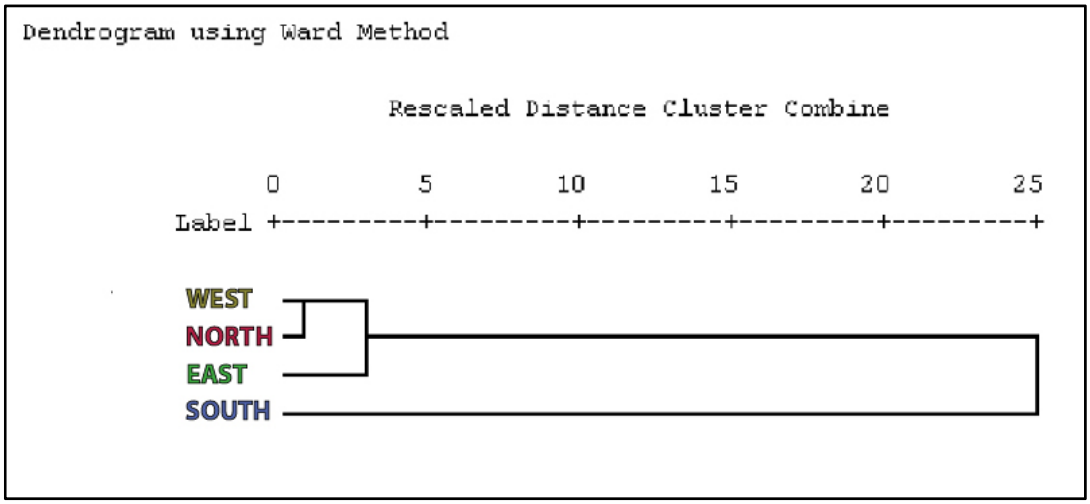


Figure 4.16. Hierarchical cluster analysis (using Ward's method) of Kellis 2 cemetery subgroup dental traits based on MMD values.

Table 4.6. Frequencies of commonly observed dental traits and sample sizes for Kellis and regional populations [comparative data taken from Scott and Turner (1997)]

	Population											
Tooth Trait	**Kellis 2**		**Western Europe**		**North Africa**		**West Africa**		**South Africa**		**Khoisan (Africa)**	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**
Shovelling UI1	91	2%	186	3%	194	8%	41	7%	220	9%	155	13%
Interruption Grooves UI2	108	19%	224	42%	241	32%	48	10%	301	12%	83	16%
Hypocone reduction UM2	108	17%	308	25%	446	11%	83	4%	531	7%	86	6%
Carabelli's UM1	82	43%	249	27%	200	20%	61	21%	246	11%	155	17%
Cusp 5 UM1	105	31%	238	12%	357	19%	48	63%	439	22%	66	35%
2-rooted UP3	126	50%	317	41%	468	57%	87	67%	386	61%	15	20%
4 -cusped LM1	107	6%	217	8%	250	10%	47	0%	346	1%	133	1%
4 -cusped LM2	108	85%	284	71%	381	66%	75	12%	370	30%	88	7%
Cusp 6 LM1	106	16%	217	8%	352	8%	47	45%	362	19%	85	5%
Cusp 7 LM1	110	9%	291	5%	414	9%	71	44%	385	27%	87	26%
Y-groove LM2	106	12%	257	27%	402	31%	67	33%	392	46%	89	72%
3-rooted LM1	99	1%	357	1%	337	1%	92	8%	240	0%	15	0%
1-rooted LM2	80	7%	318	28%	333	12%	82	9%	225	4%	15	29%

SITE	KEL	BAD	NAQ	HRK	ABY	THE	QUR	HES	KHA	TAR	SAQ	LIS	GIZ	GEG	HAW	GRM	KAW	KER	SOL	AGR	CGR	PHA	MER	XGR	CHR	KUS	ALG	BED	CAR	CHA	KAB	KEN	ETH	CNG	NIC	GHA	GAB	TOD
KEL	0.000																																					
BAD	*0.073*	0.000																																				
NAQ	*0.078*	0.000	0.000																																			
HRK	*0.073*	0.011	0.000	0.000																																		
ABY	*0.051*	0.004	0.013	0.003	0.000																																	
THE	*0.062*	0.000	0.013	0.023	0.000	0.000																																
QUR	*0.137*	0.015	*0.068*	*0.082*	*0.103*	0.023	0.000																															
HES	*0.154*	*0.055*	*0.124*	*0.092*	0.050	*0.064*	*0.091*	0.000																														
KHA	0.040	0.000	0.027	0.010	0.054	0.000	0.000	0.041	0.000																													
TAR	*0.126*	0.008	0.040	*0.062*	*0.066*	0.030	0.030	*0.101*	0.000	0.000																												
SAQ	*0.197*	0.067	*0.125*	0.091	*0.091*	0.000	0.024	*0.114*	0.000	0.055	0.000																											
LIS	*0.103*	0.054	0.041	0.026	*0.109*	*0.072*	*0.069*	*0.114*	0.000	*0.082*	*0.096*	0.000																										
GIZ	*0.085*	0.000	0.031	*0.047*	0.013	0.006	0.008	*0.081*	0.000	0.007	0.068	*0.066*	0.000																									
GEG	*0.200*	*0.099*	*0.153*	*0.153*	*0.211*	*0.130*	*0.070*	*0.129*	0.000	*0.132*	*0.115*	*0.114*	*0.099*	0.000																								
HAW	*0.082*	0.000	0.016	*0.038*	0.060	0.024	0.006	*0.064*	0.000	0.043	0.052	0.044	0.032	*0.135*	0.000																							
GRM	*0.248*	*0.107*	*0.119*	*0.085*	0.040	*0.126*	*0.207*	*0.147*	*0.184*	*0.146*	*0.177*	*0.206*	*0.139*	*0.293*	*0.162*	0.000																						
KAW	*0.128*	0.034	0.053	*0.045*	0.039	*0.054*	*0.115*	*0.104*	0.076	*0.091*	*0.095*	*0.085*	*0.114*	*0.198*	*0.084*	0.036	0.000																					
KER	*0.130*	0.028	0.016	*0.071*	0.032	0.037	*0.137*	*0.138*	*0.093*	*0.065*	*0.211*	*0.160*	*0.075*	*0.327*	*0.078*	*0.159*	*0.138*	0.000																				
SOL	*0.162*	0.033	0.072	*0.082*	*0.125*	*0.101*	*0.092*	0.053	0.000	*0.081*	*0.209*	0.000	0.057	*0.199*	0.055	*0.204*	*0.112*	0.076	0.000																			
AGR	*0.128*	0.008	0.018	*0.074*	0.032	*0.051*	*0.104*	*0.178*	*0.086*	0.032	*0.181*	*0.174*	0.039	*0.252*	*0.049*	*0.129*	0.104	0.007	0.119	0.000																		
CGR	*0.132*	*0.072*	0.042	*0.046*	*0.063*	0.036	*0.149*	*0.109*	0.073	*0.096*	*0.125*	*0.059*	*0.138*	*0.280*	*0.068*	*0.108*	0.014	*0.063*	0.057	*0.106*	0.000																	
PHA	*0.055*	0.000	0.015	0.020	0.010	0.011	*0.049*	*0.048*	0.000	0.027	*0.086*	0.005	0.009	*0.173*	0.000	*0.121*	0.035	0.038	0.000	0.027	0.020	0.000																
MER	*0.081*	*0.081*	*0.092*	*0.059*	0.002	*0.112*	*0.203*	*0.072*	*0.082*	*0.146*	*0.228*	*0.119*	*0.114*	*0.264*	*0.117*	*0.157*	*0.134*	*0.122*	*0.130*	*0.172*	*0.142*	*0.067*	0.000															
XGR	*0.128*	0.019	0.015	0.036	0.002	*0.053*	*0.171*	*0.069*	0.087	*0.112*	*0.147*	*0.117*	*0.098*	*0.282*	0.047	*0.145*	*0.123*	0.033	*0.119*	*0.106*	*0.059*	0.051	0.020	0.000														
CHR	*0.085*	*0.074*	0.062	*0.045*	0.006	0.030	*0.152*	*0.129*	0.058	*0.081*	*0.140*	*0.088*	*0.086*	*0.326*	*0.062*	*0.167*	*0.096*	0.005	0.071	0.044	0.036	0.013	0.047	0.021	0.000													
KUS	*0.126*	0.042	0.027	*0.036*	0.000	*0.081*	*0.133*	*0.051*	*0.118*	*0.120*	*0.222*	*0.121*	*0.096*	*0.243*	*0.052*	0.030	0.038	0.049	*0.086*	*0.067*	*0.045*	0.044	*0.053*	0.035	*0.074*	0.000												
ALG	*0.060*	0.022	0.013	0.018	0.045	0.030	*0.065*	0.023	0.002	0.038	*0.112*	0.031	0.056	*0.151*	0.000	*0.173*	*0.126*	0.053	0.030	0.056	0.025	0.000	*0.064*	0.000	0.031	0.028	0.000										
BED	*0.100*	0.026	0.040	0.021	0.055	*0.051*	*0.060*	0.015	0.003	*0.060*	*0.107*	0.000	0.042	*0.133*	0.000	*0.088*	0.055	*0.102*	0.000	*0.114*	0.022	0.000	*0.084*	*0.056*	*0.087*	0.014	0.000	0.000									
CAR	*0.155*	0.009	*0.114*	*0.108*	0.112	0.056	0.040	0.000	0.002	*0.071*	*0.147*	*0.086*	0.019	*0.105*	0.046	*0.224*	*0.133*	*0.096*	0.000	*0.098*	*0.116*	0.000	*0.179*	*0.147*	*0.139*	*0.109*	0.026	0.013	0.000								
CHA	*0.176*	*0.136*	*0.162*	*0.170*	*0.145*	*0.246*	*0.223*	*0.207*	*0.171*	*0.118*	*0.432*	*0.233*	*0.187*	*0.410*	*0.151*	*0.160*	*0.148*	*0.096*	*0.136*	*0.099*	*0.176*	*0.116*	*0.131*	*0.189*	*0.114*	0.054	*0.144*	0.137	*0.227*	0.000							
KAB	0.029	0.000	0.026	0.015	0.000	0.045	0.052	0.010	0.000	0.016	0.115	0.027	0.022	*0.137*	0.000	*0.081*	0.001	*0.094*	0.026	0.059	0.032	0.000	0.017	0.029	0.058	0.000	0.000	0.000	0.044	0.019	0.000						
KEN	*0.207*	*0.152*	*0.143*	*0.143*	*0.128*	*0.159*	*0.198*	*0.217*	*0.204*	*0.137*	*0.280*	*0.164*	*0.177*	*0.441*	*0.117*	*0.121*	*0.088*	*0.093*	*0.085*	*0.082*	*0.074*	*0.076*	*0.228*	*0.204*	*0.084*	*0.077*	*0.129*	*0.091*	*0.177*	0.033	*0.077*	0.000					
ETH	*0.295*	0.001	*0.088*	*0.083*	0.024	0.056	*0.079*	0.040	*0.108*	0.064	*0.150*	*0.158*	0.018	*0.230*	0.026	0.069	0.058	*0.072*	0.029	0.005	*0.081*	0.002	*0.147*	*0.105*	*0.092*	0.020	0.044	0.023	0.000	*0.112*	0.003	0.038	0.000				
CNG	*0.155*	*0.199*	*0.175*	*0.179*	*0.173*	*0.256*	*0.282*	*0.309*	*0.294*	*0.208*	*0.359*	*0.286*	*0.292*	*0.551*	*0.156*	*0.111*	*0.153*	*0.140*	*0.271*	*0.135*	*0.126*	*0.178*	*0.275*	*0.206*	*0.201*	0.066	*0.171*	*0.163*	*0.353*	0.027	*0.116*	0.015	*0.131*	0.000			
NIC	*0.295*	*0.165*	*0.157*	*0.171*	*0.095*	*0.243*	*0.334*	*0.222*	*0.312*	*0.234*	*0.450*	*0.329*	*0.244*	*0.537*	*0.217*	*0.093*	*0.193*	*0.078*	*0.201*	*0.121*	*0.153*	*0.159*	*0.171*	*0.141*	*0.173*	0.015	*0.184*	*0.175*	*0.247*	0.055	*0.142*	*0.107*	0.069	0.019	0.000		
GHA	*0.209*	*0.173*	*0.117*	*0.150*	*0.102*	*0.212*	*0.325*	*0.283*	*0.325*	*0.246*	*0.467*	*0.325*	*0.260*	*0.558*	*0.219*	*0.145*	*0.163*	0.065	*0.256*	*0.125*	*0.132*	*0.176*	*0.159*	*0.137*	*0.127*	0.040	*0.182*	*0.205*	*0.313*	0.059	*0.150*	*0.139*	*0.155*	0.074	0.000	0.000	
GAB	*0.224*	*0.108*	*0.112*	*0.121*	0.069	*0.171*	*0.184*	*0.232*	*0.227*	*0.124*	*0.246*	*0.230*	*0.172*	*0.466*	*0.108*	0.054	0.049	*0.118*	*0.218*	0.063	*0.116*	*0.099*	*0.188*	*0.149*	*0.124*	0.040	*0.146*	*0.127*	*0.283*	0.015	0.029	0.003	0.067	0.000	0.070	*0.077*	0.000	
TOD	*0.348*	*0.224*	*0.194*	*0.208*	*0.138*	*0.278*	*0.390*	*0.335*	*0.409*	*0.327*	*0.493*	*0.427*	0.339	*0.645*	*0.294*	*0.144*	*0.209*	*0.080*	*0.335*	*0.167*	*0.236*	*0.257*	*0.225*	*0.187*	*0.173*	0.080	*0.306*	*0.305*	*0.381*	*0.117*	*0.267*	*0.166*	*0.196*	0.076	0.000	0.000	*0.091*	0.000

Table 4.7. Twenty trait MMD distance matrix for Kellis and comparative groups (see Table 3.1 for site codes). Values in red represent statistically significant differences between population pairs.

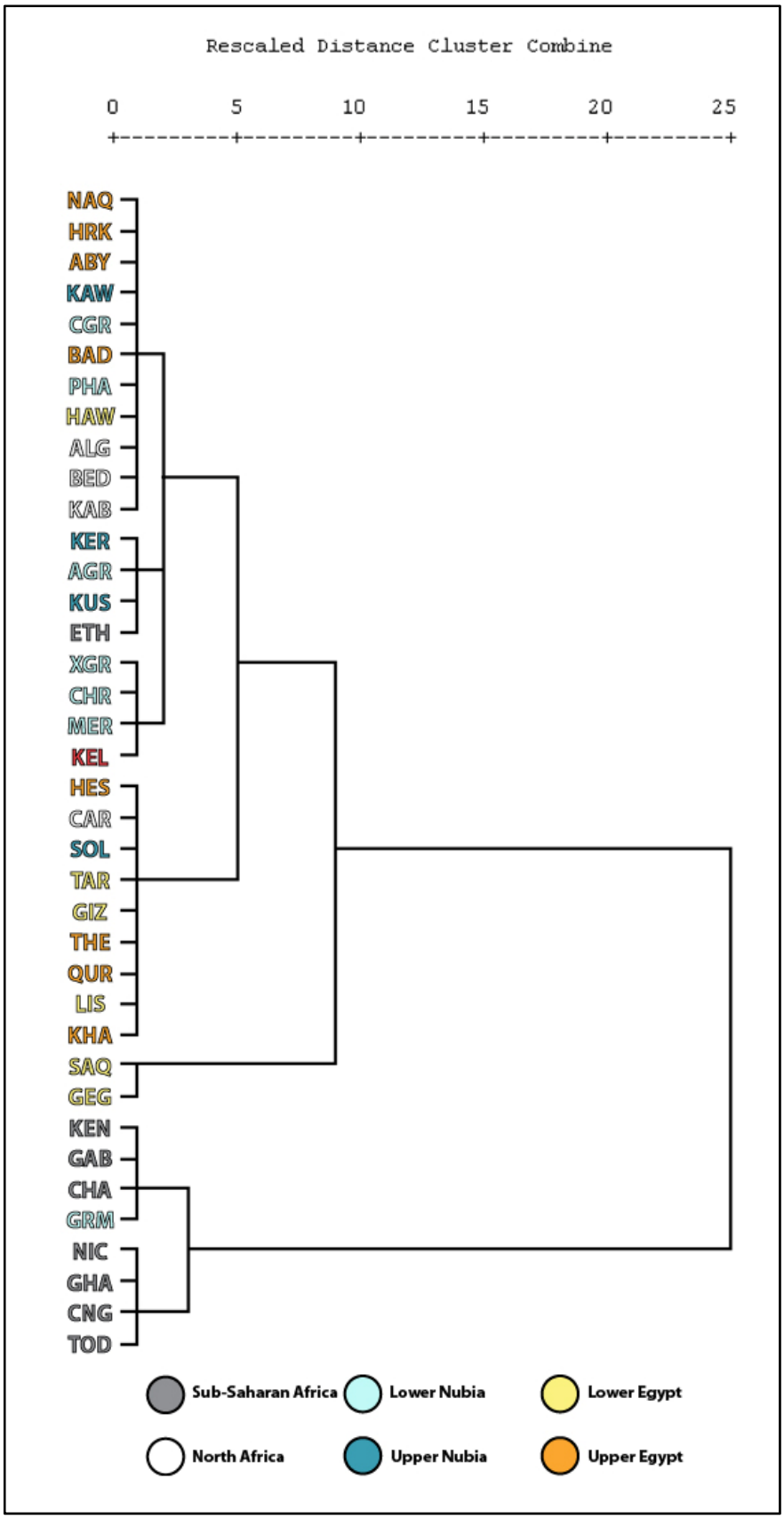


Figure 4.17. Hierarchical cluster analysis (using Ward's method) of Kellis (KEL) and comparative groups (see Table 3.1 for site codes) based on 20 trait MMD values (see Table 4.3 for list of traits used).

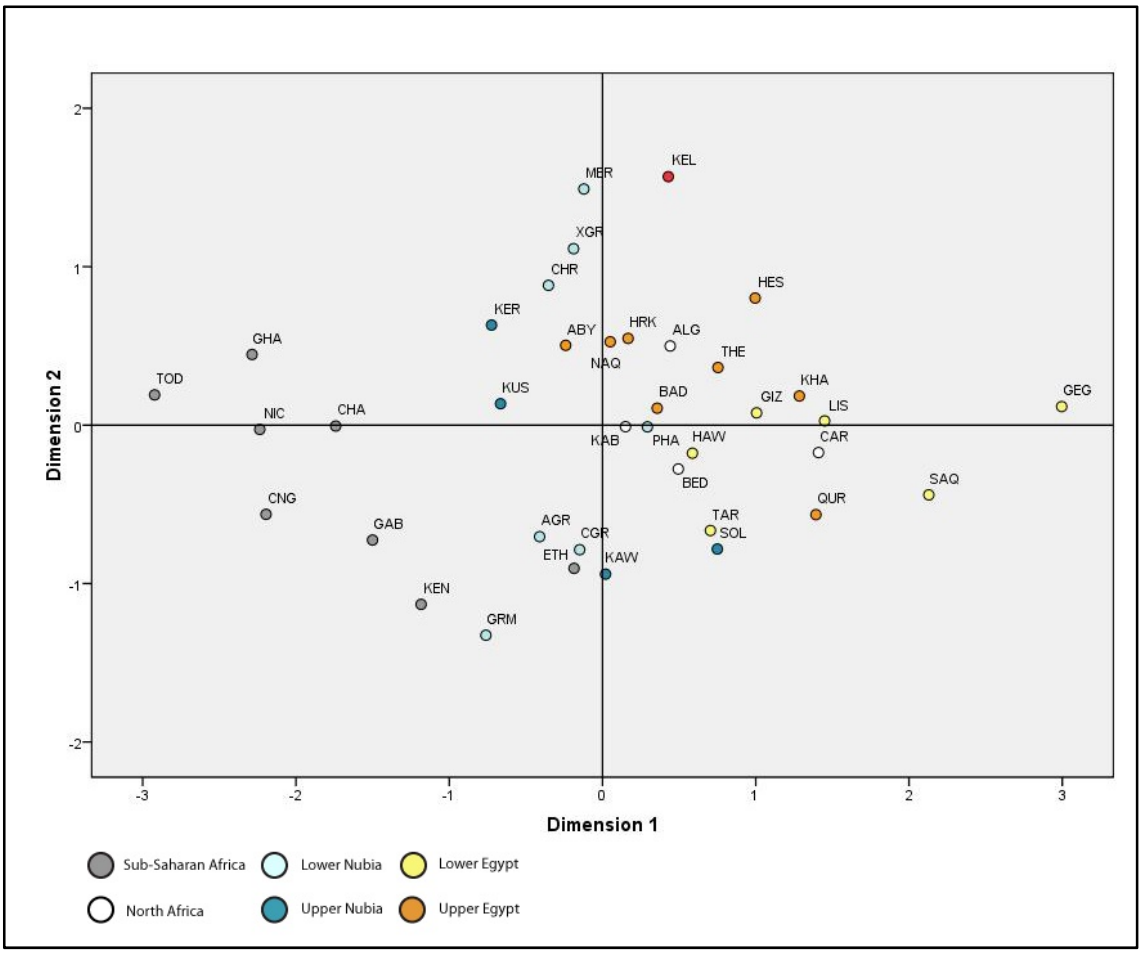


Figure 4.18. Multidimensional Scaling (MDS) plot in three dimensions for Kellis (KEL) and comparative groups (see Table 3.1 for site codes) based on 20 trait MMD values (see Table 4.3 for list of traits used).

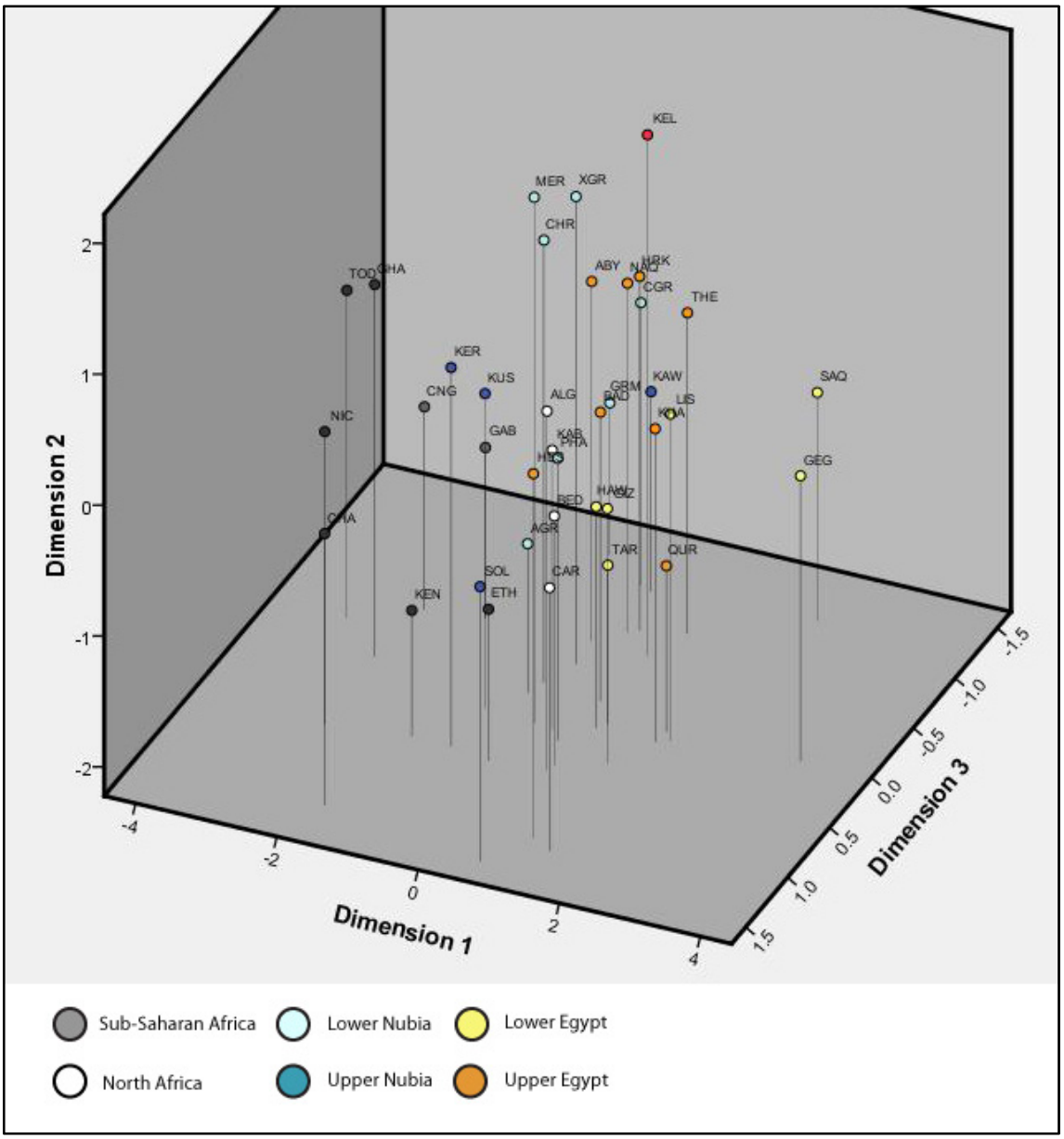


Figure 4.19. Multidimensional Scaling (MDS) plot in three dimensions for Kellis (KEL) and comparative groups (see Table 3.1 for site codes) based on 20 trait MMD values (see Table 4.3 for list of traits used).

Table 4.8. MMD distance matrix for Kellis 2 and regional population (based on 13 traits).

	Kellis	Western Europe	North Africa	West Africa	South Africa	Khoisan (Africa)
KEL	0.000					
WE	*0.086*	0.000				
NAF	*0.066*	0.040	0.000			
WAF	*0.373*	*0.490*	*0.329*	0.000		
SAF	*0.233*	*0.243*	*0.118*	*0.124*	0.000	
KHO	*0.086*	*0.341*	*0.281*	*0.228*	*0.148*	0.000

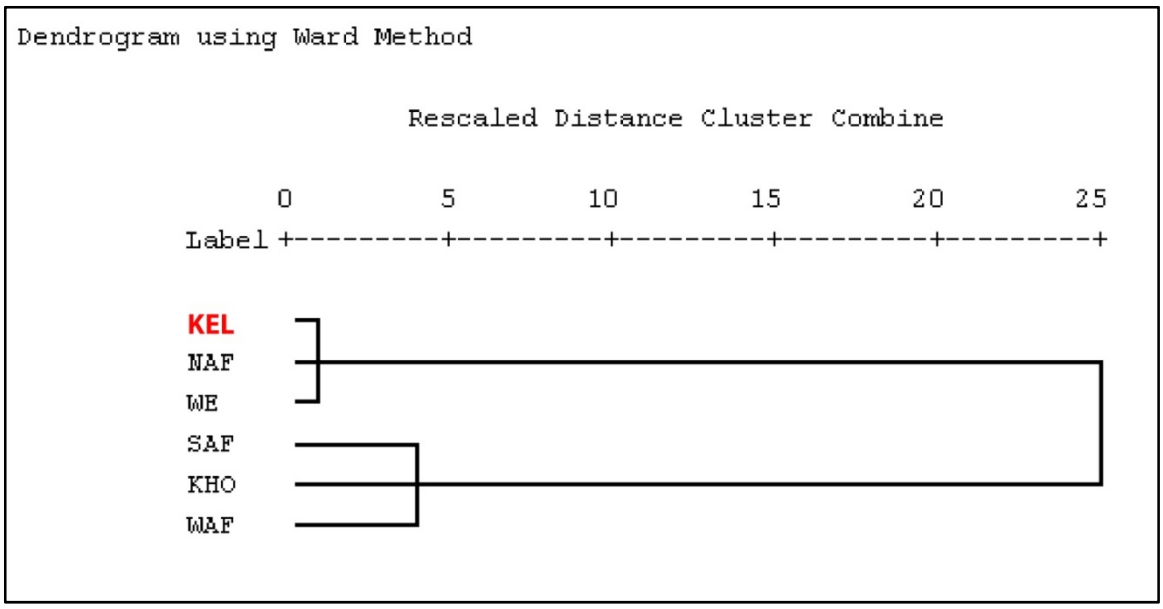


Figure 4.20. Hierarchical cluster analysis (using Ward's Method) of Kellis and regional populations based on 13 trait MMD values.

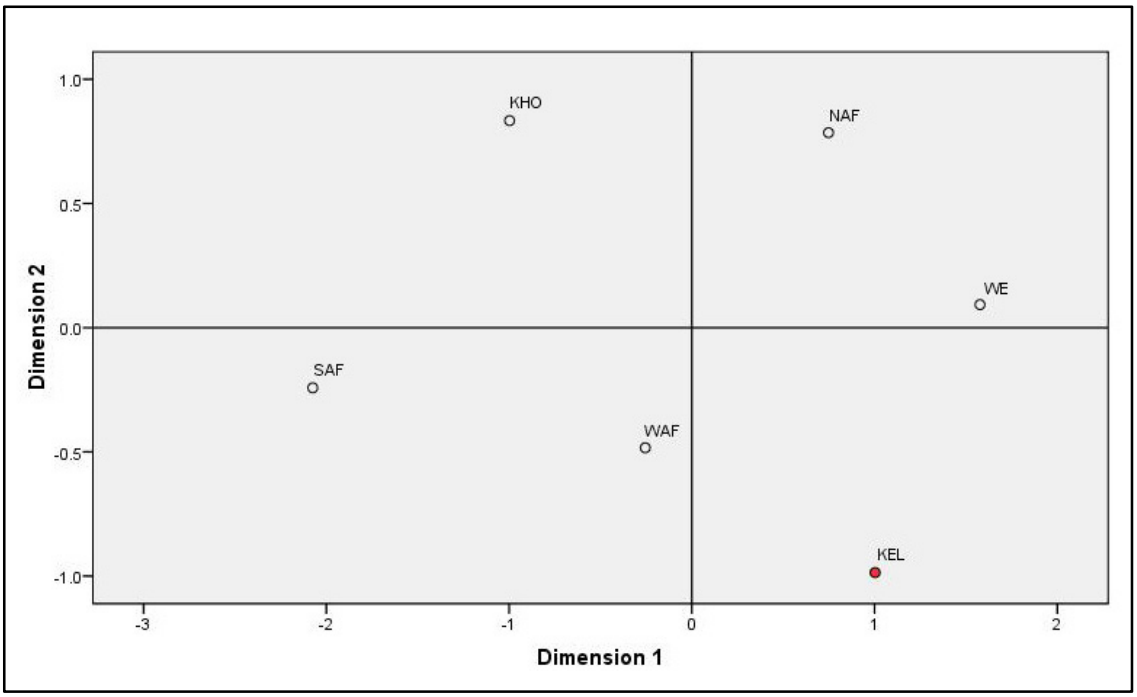


Figure 4.21. Multidimensional Scaling (MDS) plot in two dimensions of Kellis and regional populations based on 13 trait MMD values.

Chapter 5

Interpretation of Results and Discussion

5.1 Intra-cemetery trait analysis

The results of the intra-cemetery trait analysis presented in Chapter 4 allow us to address the first two hypotheses of the present study:

1. *Phenotypic variability between Kellis males and females will indicate post-marital residence status, whereby one sex is more mobile (marrying into the community from elsewhere) and the other stationary (resident to the community from birth).*

As patrilocal residency in Roman era Egypt was the norm (Bagnall and Frier 1994), we would expect that females would be more phenotypically variable than resident males as they would be marrying into the community from elsewhere. Through the use of the MMD statistic, chi-square and Fisher's Exact tests, however, it has been shown that there are few significant differences between Kellis males and females in terms of trait expression. Pairwise MMD values for males and females using all 29 traits and the reduced subset of 20 traits equal 0.000 in both instances. In the chi-square analysis only one trait, mandibular third molar congenital absence (P=0.049) showed a statistically significant difference between the sexes, while several others approached the significance threshold. Low levels of inter-sex trait variation are typical in dental morphological studies (Irish 1997, 2006; Johnson and Lovell 1994; Scott and Turner 1997; Ullinger 2005). Based on these results, the null hypothesis that Kellis males and females are drawn

from the same population cannot be rejected. Consequently, this could imply that the population of the oasis as a whole was largely homogenous, but until there are comparative data from other sites, no definitive statements can be made at this time.

Alternatively, marriage partners may have been sought from within the Kellis community (endogamous marriage); this could be a likely explanation for the low levels of variability seen between males and females. There is ample evidence to support this interpretation, not just in terms of affinal endogamy, but especially of lineage endogamy (also known as consanguineous marriage); even today in Egypt, marriages often take place between members of an extended family, typically in the form of patrilateral cousin marriage, whereby first cousins on the father's side are wed (Hafez *et al.* 1983; Weinreb 2008). The practice of consanguineous marriage has the effect of maintaining kin-group solidarity and averting potential disputes over the breakup of familial estates through inheritance. Consanguineous marriages are common throughout the Middle East, although many scholars believe it is not strictly a product of Islamic culture but rather predates it, as in the case of Coptic and other Middle Eastern Christian sects in which the practice also occurs (Weinreb 2008). Certainly there is ample evidence from ancient Egypt, especially during the Greco-Roman period, that such marriages occurred with great frequency (Hopkins 1980; Lewis 1983; Middleton 1962), even extending to brother-sister marriages (Remijsen and Clarysse 2008; Rowlandson and Takahashi 2009; Scheidel 1996a,b, 1997).

Regardless of its nature, some form of endogamy at Kellis remains an attractive explanation for the low levels of inter-sex trait variability.

Additional support for the interpretation of lineal endogamy comes from previous analyses of skeletal non-metric traits in the Kellis population. Scheidel (1996b) has shown that the offspring of closely related parents are prone to genetic (autosomal recessive) disorders a as result of increased homozygosity. Molto has argued for high levels of inbreeding at Kellis based on the re-occurrence of several rare genetic skeletal traits such as *spina bifida occulta*, precondylar tubercles of the occipital, infraorbital sutures and mylohyoid bridging in the mandible (Molto 2001; Molto *et al.* 2003). Interestingly, Hussien *et al.* (2009:623) report elevated levels (62.33%) of *spina bifida occulta* in a Greco-Roman skeletal assemblage from Bahariya Oasis which they also attribute to inbreeding as a result of geographic isolation. While rare dental morphological traits in the Kellis assemblage such as talon cusps, twinned incisors and odontomes are not observable, the unusually high rates of cusp and tubercle forms of Carabelli's cusp (42.7%) and deflecting wrinkle expression (62.5%), along with low expressions of second molar Y-groove pattern (11.5%) may be the result of consanguinity.

While the present and previous studies of biological variation in the Dakhleh Oasis characterize the population as largely homogenous and possibly inbred, Parr's (2002) analysis of a subset (N=13) of Kellis 2 mitochondrial DNA suggests a relatively high level of maternal genetic diversity. Such diversity could be interpreted as evidence for patrilocal forms of postmarital

residence, whereby unrelated females are marrying into the Kellis community from elsewhere. We cannot be certain however, until the corresponding analysis of Y-chromosome DNA from Kellis males allows us to compare maternal versus paternal levels of genetic diversity. Despite this uncertainty, and the contradictory results generated by the morphological and molecular studies of biological variation at Kellis, I do not necessarily see a conflict between the two approaches. Ancient DNA studies obviously provide a much higher resolution of analysis when compared to morphological studies, and as dental trait frequencies cannot be reduced to gene frequencies, the results cannot be directly compared. At any rate, until the DNA sequencing of the entire assemblage is complete, Parr's results must be treated with caution.

2. *Burials located closer together will share more dental traits than those located further apart. Such clustering of dental traits will represent kin group burial areas within the Kellis 2 cemetery.*

As seen in the individual trait maps in Chapter 4, there does appear to be some spatial variability in terms of trait expression within the Kellis 2 cemetery. Some traits tend to occur at different rates within particular areas of the cemetery; for example, the individuals within the eastern group of burials have a complete absence of Cusp 6 on the lower first molars, as well as an absence of 4-cusped lower first molars and incisor interruption grooves. The eastern area also contains individuals with the lowest occurrence of the upper first molar metaconule, while the highest

occurrences are among individuals within the western and southern areas of the cemetery. Cusp 6 expression is also highest within the western and southern burials. It is difficult to say whether the apparently non-random distribution of some traits represents groups of closely related individuals as they do not cluster tightly together among directly adjacent graves in most cases; the exception is congenitally absent mandibular fourth premolars, which occur in two adjacent males (B.240 and B.242) . Thus, while it is not entirely possible to identify small groups of burials which share the same trait, it may be possible to define larger areas within the cemetery that contain phenetically similar individuals.

Despite these apparent patterns, the results of this portion of the intracemetery analysis are not entirely convincing. This does not necessarily mean that kin-group burial clusters do not exist in the Kellis 2 cemetery; indeed, it is highly likely that they do exist given previous skeletal trait studies (Kron 2007; Molto 2002) and what is known about ancient Egyptian burial practices. It does imply, however, that mapping individual dental trait frequencies, as employed in the present study, may not be an effective means of detecting intracemetery kin-groups. Missing data for specific dental traits is one of the main problems in attempting this type of analysis. This is largely due to antemortem tooth loss, and dental wear. For specific traits, there simply were not enough observable cases among individuals to properly visualize their spatial distribution. Comparing multiple traits proved even more difficult because while several individuals may be observable for a particular trait, the same individuals may not be observable for additional

traits. The most important concern, however, is that the traits employed in the present study are not well-suited for the identification of closely-related individuals as they are not considered rare or genetically anomalous (Stojanowski and Schillaci 2006).

Despite the problems with identifying spatial patterns for specific traits between individuals, when the Kellis 2 burials are divided into four sex-combined groups (North, South, East and West) on the basis of location, some degree of biological variation within the cemetery becomes apparent. As seen in Chapter 4, there is a distinct, albeit insignificant, difference between the South and East groups in terms of MMD values (0.073). The East, North and West groups all share low MMD values. In addition, the East and West groups are more similar than they are to any of the other groups (MMD=0.000). These results are corroborated by the hierarchical cluster analysis which shows the West and North groups as closely related, while the South group diverges from the other three at a high level on the dendrogram.

Chi-square and Fisher's Exact tests of inter-group trait frequencies also reveals some interesting differences. Four traits: maxillary central incisor shovelling, maxillary second molar root number, mandibular canine root number and maxillary first molar Cusp 5, have P values which approach the significance threshold. Shovelling of the maxillary central incisors occurs at a rate of 8% and 9% for the West and East groups, respectively, while the South and North groups have an expression rate of 35% and 30%,

respectively. Three-rooted maxillary second molars occur in 100% of the East group burials, while the occurrence rate for the South, West and North groups are 86%, 77% and 67% respectively. The North group has a much higher expression rate (16%) for two-rooted mandibular canines when compared to the South (3%), West (3%) and East (4%) groups. Finally, Cusp 5 occurs in 21% of West group individuals, 18% of East group individuals and 10% of South group individuals, while there is no occurrence of Cusp 5 among the North group.

While morphological differences between the sexes are not observable in the combined Kellis townsite and cemetery assemblages, when inter-sex differences within the four cemetery spatial groups are analyzed, some interesting observations emerge. While no significant differences emerge, Fisher's Exact tests of several traits do approach the significance threshold within certain areas of the cemetery. The southern group of burials has the highest level of inter-sex variability; the maxillary central incisor (UI1) has a P value of 0.131, while two traits on the maxillary lateral incisor (UI2), interruption grooves and shovelling have P values of 0.131 and 0.132, respectively. Maxillary second molar Carabelli's cusp also has a P value of 0.154. Females have higher rates of occurrence than males for all of these traits. For the northern area of the cemetery, mandibular third premolar Tome's root (P=0.138) shows the greatest levels of inter-sex variability, with males having a higher rate of expression for the trait. The western and eastern groups show the lowest levels of inter-sex variation.

While the results are far from definitive, and the small sample sizes are statistically problematic, the southern area seems to be comprised of a morphologically distinctive subset of burials within the Kellis 2 cemetery based on the sex-combined MMD, chi-square and Fisher's Exact tests, as well as the inter-sex intra-group analysis. The question becomes whether or not this group represents a genetically related cluster of individuals (i.e. a kin-group burial area) distinctive from other groups, or perhaps an area reserved for individuals who were not native to Kellis. The higher levels of inter-sex morphological variation within this group of individuals suggest that only this particular area of the Kellis 2 cemetery shows any evidence for exogamy. Interestingly, one of the male burials belonging to this group, B.116, has previously been identified as non-native to the oasis on the basis of oxygen and nitrogen isotope analysis and may have originated from a less arid environment such as the Nile Valley or Nubia (Dupras and Schwarcz 2001). This individual suffered from leprosy, and may have been exiled from elsewhere in Egypt to the oasis. References to social and political outcasts being exiled to the oases during the Greco-Roman period can be found in many ancient texts (e.g. Nestorius). An analysis of the mitochondrial DNA of B.116 also supports the non-native ancestry of this individual by demonstrating a lack of shared maternal genetic characteristics with any of the 13 other Kellis 2 individuals analyzed (Parr *et al.* 1998). Additionally, in an earlier study of diet using carbon and nitrogen isotopes, Dupras (1999) highlighted seven out of 116 individuals with δN^{15} levels one standard deviation below the mean and one individual (B.116) with δN^{15} levels two standard deviations below the mean for the Kellis 2 cemetery. These

individuals have also been interpreted as having arrived in the oasis from a less arid environment. Of these eight individuals, five are adult males, two are adult females and one is a child. Three of the males (B.111, B.116 and B.132) and one female (B.165) are from the southern group of burials, again suggesting that this area of the cemetery is distinctive. Unfortunately, it is not possible to determine with any precision the geographic origins of these individuals.

Perhaps, then, it is males who are the more mobile sex within the Kellis assemblage. While papyrological evidence suggests regular contact with the Nile Valley, with oasis males often travelling to and residing in the valley for the purposes of trade, females were less likely to attempt the arduous journey across the desert (Gardner *et al.* 1999; Worp 1995). It seems that the transfer of people between the two regions was primarily unidirectional, as there would be more opportunity for underemployed Kellis males to earn a living in the bustling cities of Middle Egypt, whereas fewer Nile Valley residents would find life in the remote oasis region appealing. Indeed, little has changed in modern Egypt, where urban centres continue to act as a magnet for rural inhabitants seeking new opportunities. However, if people from the Nile Valley or further abroad were to travel to the oasis, it does seems more likely that they would be male than female. This analysis must be pursued further.

An alternative explanation is that the South group represents a temporally distinct area of the cemetery, in which case, genetic drift may account for the

differences observed between groups. The lack of reconciliation between the radiocarbon dates (50-450 AD) and the archaeological evidence (4th century AD only) for the dating of the cemetery exacerbates this question. If the radiocarbon dates based on human bone collagen are accurate – and they appear to be, given the number of samples tested (see discussion on page 30) - the temporal explanation becomes feasible, although it does not necessarily discount the kin-group/non-native hypothesis either. If the archaeologically-based time span for the cemetery is accepted however, the kin-group explanation becomes more likely, as there would not be enough time for genetic drift to affect trait frequencies. For the moment, the differences between the South group and the other three groups cannot easily be explained until a better handle on the chronology of the Kellis cemetery is achieved and further comparative groups are found from within the oasis.

5.2 Inter-regional trait comparisons

Based on the results of the inter-regional analysis of dental trait frequencies, the final two hypotheses of the present study can be addressed.

3. *The Dakhleh Oasis (Kellis) assemblage will share genotypic/phenotypic features with Nile Valley groups as a result of cultural, political and economic ties between the two regions beginning in the Neolithic period.*

As shown in Chapter 4, the Kellis assemblage shares some degree of phenetic similarity with the Egyptian comparative groups, although the only

Egyptian group that shares a statistically insignificant Mean Measure of Divergence value with Kellis is the Kharga Oasis assemblage (MMD=0.040). Other Egyptian groups which share low MMD values with Kellis are the Early Dynastic Abydos, Middle Kingdom Thebes and Predynastic Hierakonpolis, Badari and Naqada groups. As seen in the hierarchical cluster dendrogram, the Kellis assemblage forms part of a series of sub-clusters which include the Egyptian Naqada, Hierakonpolis, Abydos, Badari and Hawara groups, along with the Nubian and North African groups. When all of the comparative groups are plotted with the Kellis assemblage using multidimensional scaling, the closest Egyptian groups are the El Hesa, Abydos, Hierakonpolis, Naqada and Thebes groups. In both plot types, however, the Kellis assemblage is more closely linked with the later Nubian groups than with the Egyptian groups.

Thus, Hypothesis 3 cannot be refuted: the Kellis sample does share phenotypic characteristics with some Nile Valley groups. Given the textual and archaeological evidence for political, cultural and economic ties between the Dakhleh Oasis and the Nile Valley throughout the Pharaonic period, this should come as no surprise. The similarities with the Upper Egyptian Predynastic and Early Dynastic groups may indicate a common ancestry; this is supported by recent archaeological evidence which suggests that Neolithic cultures from the Western Desert made substantial contributions to the emergence of state level society in the Nile Valley, especially in Upper Egypt (Hassan 1986, 1988; Hendrickx and Vermeersch 2000; Kobusiewicz

et al. 2004; Kuper 2002; McDonald 1998; Midant-Reynes 2000; Wendorf and Schild 2002).

Despite certain shared characteristics however, it is clear from the multidimensional scaling plots that the Kellis assemblage remains relatively distinct from most of the Egyptian groups, which tend to cluster centrally. This is likely due to the isolated nature of the Dakhleh Oasis itself, separated from the Nile Valley by an inhospitable stretch of desert. While contact between the valley and the oasis has occurred for thousands of years, there is little evidence for large scale gene flow between the two regions. The arrival of Pharaonic Egyptians to Dakhleh in the Late Old Kingdom need not have required large numbers of newcomers, and there is no evidence that the indigenous population was replaced. Unlike Kharga Oasis, which is known to have had several Roman-era military outposts (Giddy 1987), the Dakhleh Oasis had less strategic importance to the State, and there is little to suggest the large-scale transfer of troops or administrators. Indeed, while non-Egyptian administrators and other representatives of the Roman Empire were certainly present in the major Egyptian centres, they were probably not a substantial presence (Peacock 2000); in rural areas, local elites typically acted as intermediaries between the State and its subjects (Bagnall 2003). Recently, however, archaeological evidence for the existence of a Roman *castrum* (fort) has been discovered beneath Qasr, a town in the Dakhleh Oasis; this fort is also alluded to on an ostrakon recovered from the nearby site of Amheida (ancient “Trimithis”) (Bagnall and Ruffini 2012). This almost certainly means that individuals from outside the oasis were present, but in

what number and for how long we cannot be certain. Despite this finding, however, the phenetic similarities between the Kellis assemblage and the earliest Egyptian groups suggest that the late Neolithic may have been the most significant period for population movement between the two regions and, based on the archaeological evidence, this movement was primarily from west to east, i.e. from the desert to the valley, as a result of the increasing aridification of the Sahara (Hassan 1986, 1988; Midant-Reynes 2000; Wendorf and Schild 1980). Since then, the oasis population, as characterized by the Kellis assemblage, appears to have diverged from Nile Valley groups as a result of genetic drift. The results of the present and previous intracemetery analyses suggesting a high level of homogeneity and inbreeding within the Dakhleh Oasis may also explain the phenetic distinctiveness of the Kellis assemblage in relation to Nile Valley groups.

While ample comparative data for the Nile Valley and Nubia exist, there are as yet no dental morphological trait data available for ancient Libyan (i.e. Meshwesh/Berber) populations. The presence of Libyans in the oasis is first alluded to by depictions in 18th Dynasty Nile Valley tombs of the inhabitants of the southern oases as foreigners paying tribute (Winnicki 2009:30). Later, during the 25th Dynasty, inscriptions on the smaller Dakhleh stela in the possession of the Ashmolean Museum make specific reference to Libyan tribes residing in the oasis (Janssen 1968). In addition, the authors of a compilation of personal names found in Greco-Roman texts from Kharga and Dakhleh suggest that some names may derive from Berber or other non-Egyptian/Greek languages (Salomons and Worp 2009). Because of the

Dakhleh Oasis' proximity and links, both ethnically and economically, to Libya, especially with Kufra Oasis (Förster 2007; Giddy 1987; Kuper 2001), it is highly likely that the Kellis population would share at least some genotypical/phenotypical relationships with these groups. In lieu of ancient dental morphological trait data for Western Saharan populations, frequencies for several recent North African groups from Morocco, Algeria, Tunisia, Libya and Chad as well as from ancient Carthage have been used in order to test this relationship. Of all the comparative groups used in the present study, the Kellis assemblage shares the lowest MMD value with the Kabyle Berber group (MMD=0.029), and the fifth-lowest MMD value with the Algerian Shawia Berber group (MMD=0.060). While it is tempting to see this as confirmation of the presence of Libyans in the Dakhleh oasis, the Kabyle and Algerian Berber groups share a high degree of phenetic similarity with the majority of Egyptian and Nubian groups. The Bedouin Arab group, and the Carthaginian group to a lesser extent, also shares a degree of phenetic similarity with the Egyptian groups. This, instead, points to the overall phenetic similarities between post-Pleistocene Egyptian, Nubian and Western Saharan populations observed by Irish, which he characterizes as a "North African Dental Trait Complex" (Irish 1998c,d, 2000). The Chad group is highly divergent from the Kellis, Egyptian and Nubian groups, having instead more phenetic similarities with the Sub-Saharan African groups, and to a lesser extent the Kabyle Berber and Bedouin Arab groups. When the Kellis assemblage is plotted with all of the comparative groups using hierarchical clustering and multidimensional scaling, it becomes clear that the North African groups have more in common with the Egyptian groups

than they do with Kellis. Again, inbreeding and limited gene flow are potential explanations for the distinctiveness of the Kellis assemblage.

4. *The Kellis sample will contain a Nubian/Sub-Saharan phenotypic component as a result of north-south gene flow.*

Despite claims by Dzierżykray-Rogalski (1980:72) that the southern oases of Egypt were inhabited by “Negroid” populations, the multivariate analyses of comparative trait frequencies have shown that there is no phenotypic similarity between Kellis and the Sub-Saharan comparative groups used in the present study. This is reflected in Mean Measure of Divergence values which are highest between Kellis and the Sub-Saharan groups (in addition to the Neolithic Nubian Gebel Ramlah assemblage). While Dzierżykray-Rogalski characterizes the Late and Ptolemaic Period skeletal remains found at Qila’ el-Dabbeh as belonging to a “Europoid” typology (1980:72), or to a “*race blanche orientale*” (1983:53), he interprets this as evidence for the presence of a ruling elite coming from northern Egypt, rather than accept the possibility that these remains might be representative of the oasis population as a whole. These results, however, should not be taken as definitive proof of a lack of Sub-Saharan genetic input in the Dakhleh Oasis, only that no link could be established using the current comparative data sets. Genetic studies have demonstrated shared characteristics between Egyptian and East African populations (e.g. Fox 1997; Keita 2005; Manni *et al.* 2002), while a number of previous biological distance studies have noted a Sub-

Saharan African component in Predynastic Upper Egyptian skeletal assemblages (e.g. Hillson 1978; Keita 1990; Strouhal 1971).

As discussed previously (Chapter 2), however, it is not the aim of this study to place the population of the Dakhleh Oasis within a “Caucasoid” or “Negroid” typology. Such broad-based, essentialist categorizations are no longer considered a valid approach to the study of human variation (Ousley *et al.* 2009; Relethford 2009) and are insufficient for understanding and reconstructing the complicated history of population movements between Egypt, North and Sub-Saharan Africa and the Near East. In addition, there is sufficiently large enough phenotypic variation within Sub-Saharan African and Western Eurasian populations as to render terms such as “Negroid”, “Europoid” and “Caucasoid” entirely meaningless.

While there are no apparent affinities with the Sub-Saharan African groups used in the present study, there is evidence for phenetic similarities between the Kellis assemblage and several Nubian groups. Despite statistically significant differences in MMD values for Kellis and the Nubian groups, when the values are plotted using hierarchical clustering and multidimensional scaling, the Kellis assemblage is consistently linked with the most recent Nubian assemblages: Meroitic, X-Group and Christian. In the hierarchical cluster plot, Kellis and these three groups form a separate sub-cluster within the larger cluster containing Upper Egyptians, North Africans and Nubians. The phenetic similarities between Kellis and these groups are also reflected by their spatial proximity in the multidimensional scaling plots. Thus, only the

first part of Hypothesis 4 cannot be refuted: the existence of phenetic similarities between the Kellis assemblage and roughly contemporaneous Nubian groups.

There does appear to be an arbitrary divide in the minds of some researchers that Egypt and Nubia represent two distinct entities, both culturally and biologically, with the two regions often treated separately in scholarly works. Certainly there have been periods throughout the history (and prehistory) of the Nile Valley region where Egyptian and Nubian cultures have diverged, but there is equal evidence for cultural exchange and co-evolution, especially during the Predynastic period, as well as the New Kingdom and Third Intermediate Period (Bianchi 2004; O'Connor 1993; Smith 1998; Taylor 2000; Wilkinson 1999). From a bioarchaeological perspective, studies of strontium, oxygen and carbon isotopes in a New Kingdom skeletal assemblage from Tombos in Lower Nubia have provided evidence of ethnic Egyptian and Nubian peoples living together peacefully (Buzon *et al.* 2007; Buzon and Bowen 2010). In terms of population structure, numerous biological distance studies of ancient Egyptian and Nubian skeletal remains have demonstrated a clear phenetic overlap between the two groups (Berry and Berry 1972; Billy 1977; Brace *et al*. 1993; Buzon 2006; Godde 2009; Irish 1993). DNA evidence also supports this interpretation (Hassan *et al.* 2008; Krings *et al.* 1999; Lucotte and Mercier 2003). This overlap is best described in terms of a north-south clinal distribution, with the Nile Valley acting as a corridor for the exchange of genes in both directions (Brace *et al.* 1993; Krings *et al.* 1999). As such, it

should not come as a surprise that the Kellis assemblage shares phenetic similarities with both Egyptian and Nubian groups. However, while documentary evidence from Late Roman Kellis indicates strong economic ties with the Nile Valley, specifically Middle Egypt, there are fewer references to regions further south, and none at all to Nubia (Gardner *et al.* 1999; Worp 1995). As such, the nature of the phenetic associations with Nubia remains unclear. Although Nubians may have trickled into the southern oasis regions over thousands of years, the closer level of association with the latest Nubian groups, i.e. Meroitic, X-Group and Christian, implies that gene flow between the two regions was higher in the Late Dynastic and Greco-Roman periods than in earlier times. Such findings are in accordance with Roe's (2005) suggestion that contact between the southern oases and Nubia via the Darb el-Arbein occurred more often during the 4th century AD than in previous periods when travel along the Nile predominated.

In Aleš Hrdlička's (1912) study of the modern inhabitants of Kharga oasis, he describes the population as relatively indistinguishable from contemporary Nile Valley populations. Sub-Saharan African admixture is noted but attributed to the Arab slave trade and thus deemed to be a relatively recent phenomenon. Comparisons of mitochondrial DNA from Roman era mummies and modern inhabitants appear to present a similar scenario for the Dakhleh oasis by demonstrating a post-Roman era increase in the frequency of Sub-Saharan genetic markers in the modern population (Graver *et al.* 2001). Based on observations of 2nd-5th century AD mummies from the necropolis at Bagawat, Hrdlička believed that, apart from recent Sub-Saharan admixture,

there was little difference between the ancient and modern peoples of Kharga oasis. He also speculates that the inhabitants of Kharga oasis may be descended from Libyan or Berber peoples (Hrdlička 1912:5), which implies the same could be true for the inhabitants of Dakhleh.

Average MMD values for the Kellis assemblage and separate regional groups provide another way of placing the Dakhleh Oasis population within a regional context. Seen from this perspective, the Kellis assemblage is most closely related to the Lower Nubian and Upper Egyptian groups, with low average MMD values of 0.101 and 0.102, respectively. This is followed by the North African groups, with an average MMD value of 0.104. The lack of phenetic similarities with the Sub-Saharan African groups is again demonstrated by an average MMD value of 0.247.

The results of the comparison of thirteen dental trait frequencies between the Kellis assemblage and Western European, North African and Sub-Saharan African groups also demonstrates the closest affinities to the North African (MMD=0.066) and, to a lesser extent, Western European group. The hierarchical cluster plot for these groups shows Kellis, North Africa and Western Europe forming a tightly grouped branch which diverges from the three Sub-Saharan African groups at a very high level on the dendrogram.

5.2.1 Isolation by distance

While the Kellis assemblage shares a statistically insignificant MMD value with the Kharga Oasis group, its closest neighbour in terms of geography

and time period, the two groups do not cluster together when the values are plotted. The Kharga assemblage shares even lower and insignificant MMD values with the majority of the North African groups and this may be due to small sample size. The Kellis assemblage also shares the lowest MMD value with the Kabyle Berber group, which diverges greatly in time and space from the Dakhleh Oasis group. It is clear from the MMD values that the Kellis assemblage's relationship with the regional comparative groups does not always fit a simple isolation-by-distance model. In such a model, where the temporal dimension is controlled, a positive correlation should exist for phenetic and geographic distances between populations (Konigsberg 1990; Wright 1943); i.e. populations that are geographically closer together should share more phenotypic characteristics than populations which are further apart. In the present study, the temporal dimension cannot easily be controlled due to the lack of sufficient contemporary comparative assemblages. In a craniometric study of archaeological skeletal material, Zakrzewski (2007) has also shown that an isolation-by-distance model is not appropriate for explaining biological affinities among ancient Egyptian populations. However, the results of a comparison of Y-chromosome variation between modern Egyptians, North Africans, Sub-Saharan Africans, Europeans and Middle Eastern populations suggest a high degree of genetic continuity between them and do support an isolation-by-distance model (Manni *et al.* 2002).

In the case of the Dakhleh Oasis, its geographically isolated nature - more akin to an island than part of a contiguous inhabited landscape - may also

render an isolation-by-distance model unsuitable in the present study. While the desert has certainly acted as a barrier to the large-scale movement of people between the oases and the Nile Valley - much as the sea would act as a barrier between an island and the mainland - textual and archaeological evidence make it abundantly clear that the Dakhleh Oasis was well-integrated into the Egyptian (and later Greco-Roman) cultural and economic sphere from a very early period. As well as ideas and items of trade, such integration would also have facilitated the exchange of people, and thus genes, although this may not have occurred on a large scale and is likely to have ebbed and flowed in accordance with the prevailing political and economic situation in the Nile Valley. Despite this, the Late Roman skeletal assemblage from Kellis, especially as characterized in the MDS plots, remain distinctive in comparison to skeletal assemblages from the Nile Valley and Nubia. In an “island model” of population genetics, high levels of gene flow should tend to make subpopulations more similar (Wright 1931), but this is clearly not the case with the assemblages from Dakhleh Oasis and the Nile Valley. At this stage, however, the effect over time of such genetic exchanges on the ancient population of Dakhleh cannot be gauged in the absence of pre-Greco-Roman comparative material from within the oasis.

Given the complicated nature of population movements throughout Egypt’s history, we should not expect an easy fit between simplified population genetics models and data derived from incomplete archaeological assemblages. As Konigsberg (1990) acknowledges, there are many problems associated with attempting to apply such models to ancient

populations; for example, we cannot determine effective population sizes or migration rates with any precision. Such models also do not take into account historical contingencies and the often non-rational choices made by human beings.

5.3 Conclusions

As represented by dental morphological traits, the skeletal assemblage from Late Roman Kellis can be characterized as phenotypically homogenous, with low overall levels of inter-sex trait variation. This is most likely due to endogamous mate selection, both affinal and lineal. Previous studies of skeletal nonmetric traits and unusually high frequencies for certain dental traits in the Kellis assemblage support this interpretation, although genetic founder effects must also be considered as a potential explanation. When trait variation is analyzed among spatially defined groups of individuals within the cemetery, however, significant differences between the sexes are observable, especially in the southern area. When the sex-combined trait frequencies for these four spatially defined areas of the cemetery are compared, the southern area of the cemetery again appears notably distinct from the rest of the site. The previous detection of several individuals in this area with non-native isotopic signatures may indicate that this region of the cemetery was reserved for outsiders to the community. Further analysis is required, however, before definitive conclusions can be made.

The results of the qualitative and quantitative dental trait frequency comparisons between Kellis and regional comparative groups lead to an

unequivocal conclusion: that the individuals interred at Kellis share more phenotypic characteristics with North African (and European) populations than with any of the Sub-Saharan groups used in the comparative analyses. It is unsurprising that the Kellis group should be most closely related to other North African populations, as Egypt is part of North Africa. Nubians are typically considered a North African population group as well, although they also share phenetic similarities with Sub-Saharan populations (Irish 1993, 1997, 2005). The Kellis assemblage's relatively close association with Europe is also not terribly surprising, given the long history of contact between North Africa and Europe via the Mediterranean and the Levant. Numerous biological distance and DNA studies have also demonstrated a close link between the two regions (e.g. Brace *et al.* 1993; Fadhlaoui-Zid *et al.* 2011; Irish and Guatelli-Steinberg 2003; Kujanová *et al.* 2009). The lack of discernible biological affinities with Sub-Saharan populations is interesting, given the location of the Dakhleh Oasis and its connections with other parts of the Sahara. Within northeast Africa, the Kellis assemblage has the closest affinities with the most recent Nubian groups, as well as the Predynastic and Early Dynastic Upper Egyptian groups. This suggests that gene flow between Egypt and the Dakhleh Oasis was higher in the Neolithic and Predynastic periods than in later periods, while gene flow between Dakhleh and Nubia has occurred more recently. Despite these phenetic similarities, the Kellis assemblage remains relatively distinct from the majority of the comparative groups. This is demonstrated by the high number of significantly different pair-wise MMD values and is especially clear in the multidimensional scaling plots, where Kellis appears as an outlier from the

central cluster of comparative groups. As other studies have demonstrated, founder effects and genetic drift within populations inhabiting isolated/peripheral areas appear to be the cause of such intraregional discontinuity (e.g. Hanihara *et al.* 2003).

5.4 Implications for Egyptology

The results of the intra-cemetery and inter-regional analyses of dental morphological trait variation have a number of implications for the study of the Dakhleh Oasis and its relations with Egypt and beyond. For the first time, it is possible to demonstrate that the Late Roman population of the oasis, while sharing phenetic similarities with other North African populations, remained relatively distinct from its neighbours as a result of its isolated location. The long and arduous nature of the journey between Dakhleh and the Nile Valley has likely inhibited gene-flow between the two regions. The close associations between the Kellis assemblage and Predynastic and Early Dynastic Upper Egyptian groups suggests that the greatest amount of gene-flow between the oasis and the Nile Valley probably occurred in the late Neolithic. Gene-flow between Dakhleh and Nubia, as reflected in similarities between the Meroitic, X-Group and Christian groups, however, appears to have occurred more recently.

Textual evidence demonstrates close ties between oasis residents and the cities of Middle Egypt during the Roman period, with males moving more freely between regions than females as a result of their involvement in the caravan trade. The presence of non-natives at Kellis is suggested by an area

within the Kellis 2 cemetery containing individuals with distinctive dental trait frequencies. However, this interpretation is tentative and must be treated with caution until more analysis is conducted. The presence of outsiders is almost guaranteed given the network of trade routes linking the Dakhleh Oasis and the wider region during the Greco-Roman period and the existence of a military garrison at Qasr; the number of outsiders, however, remains unknown, and their effect on the overall population structure is unclear.

5.5 Proposals for future work

In order to improve and expand on the work conducted in the present study, it would be greatly beneficial to obtain comparative dental samples, both synchronic and diachronic, from within the Dakhleh Oasis in order to compare them with the Kellis skeletal assemblage. At the moment, we cannot be certain that the skeletal assemblage from Kellis is typical of the larger Dakhleh Oasis population. There are numerous sites contemporary with Kellis - some larger, some smaller – which have yet to provide comparative skeletal data. For example, Amheida (ancient “Trimithis”), a particularly large site associated with a nearby Roman garrison, would be especially interesting to study as it is more likely than Kellis to have harboured a sizeable number of non-indigenous inhabitants. Contemporary (i.e. Roman-era) samples from within Dakhleh would permit a better understanding of the overall oasis population structure during this period, and whether or not the levels of phenotypic homogeneity observed at Kellis are representative. The addition of skeletal samples from pre-Roman periods

would also provide insight into the nature of the apparent population growth witnessed in the oasis during the Greco-Roman period, and to what extent this increase reflects an influx of newcomers to the region. A diachronic approach would also address the issue of *in situ* evolution versus gene flow between the Dakhleh Oasis and regions further afield.

The Kellis 2 cemetery is very large, and excavations to date have focused primarily on a single, localized area to the exclusion of other parts of the site. Further excavations, employing a proper sampling strategy, are required in order to obtain a more representative skeletal sample. This would also aim to cover the entire use-history of the cemetery, something that cannot be controlled for at the moment (i.e. we cannot be certain of the temporal dimension at Kellis, especially as the stratigraphy at Kellis is not vertical but horizontal – i.e. graves do not intercut one another). Although the issue of representativeness is a common problem in biological distance studies using archaeologically-derived material, it especially hampers the interpretation of intracemetery morphological variability, as well as influencing the results of inter-site comparisons.

Another avenue for biological distance research at Kellis is the use of Geographic Information Systems (GIS) to map the spatial distribution of dental and skeletal morphological traits within the Kellis 2 cemetery. GIS software such as ArcGIS and MapInfo, in combination with other programs like PASSaGE (Pattern Analysis, Spatial Statistics, and Geographic Exegesis*)*, can provide a much higher level of analytical detail than the

methods currently used. These programs however, especially GIS, require a great deal of training in order properly utilize them, and for this reason they were not employed in the present study.

Bibliography

Abrahams LC. 1949. Shovel-shaped incisors in the Cape Malays. Journal of the Dental Association of South Africa 4:7-13.

Alexandersen V. 1962. Root conditions in human lower canine with special regard to double-rooted canines. II. Occurrence of double-rooted lower canines in *Homo sapiens* and other primates. Saetryk af Tandlaegebladet 66:729-760.

Alexandersen V. 1963. Double-rooted human lower canine teeth. In: Brothwell DR, (ed.), Dental Anthropology. New York: Pergamon Press. p 235-244.

Alston, R. 1995. Soldier and Society in Roman Egypt: A Social History. London and New York: Routledge.

Alt KW, Brace CL, and Turp JC. 1998. The history of dental anthropology. In: Alt KW, Rösing FW, and Teschler-Nicola M (eds.), Dental Anthropology: Fundamentals, Limits, and Prospects. New York: Springer. p 15-39.

Alt KW, and Vach W. 1998. Kinship studies in skeletal remains. In: Alt KW, Rösing FW, and Teschler-Nicola M (eds.), Dental Anthropology: Fundamentals, Limits, and Prospects. New York: Springer. p 537-554.

Angel JL. 1972. Biological relations of Egyptian and eastern Mediterranean populations during Pre-Dynastic and Dynastic times. Journal of Human Evolution 1:307-313.

Anscombe FJ. 1948. The transformation of Poisson, binomial, and negative-binomial data. Biometrika 35:246-254.

Aufderheide AC, Cartmell LL, Zlonis M, and Sheldrick P. 2004. Mummification practices at Kellis site in Egypt's Dakhleh Oasis. Journal of the Society for the Study of Egyptian Antiquities 31:63-77.

Aufderheide AC, Zlonis M, Cartmell LL, Zimmerman MR, Sheldrick P, Cook M, and Molto JE. 1999. Human mummification practices at Ismant El-Kharab. Journal of Egyptian Archaeology 85:197-210.

Bagnall RS. 1997. The Kellis Agricultural Account Book. Oxford: Oxbow Books.

Bagnall RS. 2003. Later Roman Egypt: Society, Religion, Economy and Administration. Aldershot, Hampshire: Ashgate.

Bagnall RS. 2008. Economy and Ecology in the Kellis Agricultural Account Book. In: Wiseman MF, (ed.), The Oasis Papers 2: Proceedings of the Second International Conference of the Dakhleh Oasis Project.

Oxford: Oxbow. p 115-117.

Bagnall RS, and Frier BW. 1994. The Demography of Roman Egypt. Cambridge: Cambridge University Press.

Bagnall RS, and Ruffini GR. 2012. Amheida I: Ostraka from Trimithis Volume 1. New York: New York University Press.

Bang G, and Hasund A. 1972. Morphologic characteristics of the Alaskan Eskimo dentition. II. Carabelli's cusp. American Journal of Physical Anthropology 37(1):35-39.

Bass WM. 1995. Human Osteology: a Laboratory and Field Manual (4th edition). Missouri Archaeological Society Special Publication. 4th ed. Columbia, MO: Missouri Archaeological Society.

Bateson W. 1894. Materials for the Study of Variation. London: Methuen.

Batrawi AM. 1945. The racial history of Egypt and Nubia, Part I: craniology of Lower Nubia from Predynastic times to the Sixth Century A.D. Journal of the Royal Anthropological Institution 75:81-102.

Batrawi AM. 1946. The racial history of Egypt and Nubia, Part II: the racial relationships of the ancient and modern inhabitants of Egypt and Nubia. Journal of the Royal Anthropological Institution 76:131-156.

Bedrick EJ, Lapidus J, and Powell JF. 2000. Estimating the Mahalanobis distance from mixed continuous and discrete data. Biometrics 56(2):394-401.

Berry AC. 1976. The anthropological value of minor variants of the dental crown. American Journal of Physical Anthropology 45:257-268.

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

Berry AC, Berry RJ, and Ucko PJ. 1967. Genetical change in ancient Egypt. Man 2:551-568.

Berry RJ. 1968. The biology of non-metrical variation in mice and men. In: Brothwell DR, (ed.), The skeletal biology of earlier human populations. London: Pergamon Press. p 103-133.

Bevan ER. 1968. The house of Ptolemy: A History of Hellenistic Egypt Under the Ptolemaic Dynasty. Chicago: Ares.

Bianchi RS. 2004. Daily Life of the Nubians. Westport CT: Greenwood Press.

Billy G. 1977. Population changes in Egypt and Nubia. Journal of Human Evolution 6:697-704.

Billy GI, and Chamla M. 1981. Les restes humains des necropoles Pharaoniques de Soleb (Nubie Soudanaise). L'Anthropologie 85:59-90.

Birrell M. 1999. Excavations in the cemeteries of Ismant el-Kharab. In: Hope CA, and Mills AJ (eds.), Dakhleh Oasis Project: Preliminary Reports on the 1992-1993 and 1993-1994 Field Seasons. Oxford: Oxbow. p 29-42.

Bowen GE. 2002. The fourth-century churches at Ismant el-Kharab. In: Hope CA, and Bowen GE (eds.), Dakhleh Oasis Project: Preliminary Reports on the 1994-1995 to 1998-1999 Field Seasons. Oxford: Oxbow. p 65-85.

Bowen GE. 2003. Some observations on Christian burial practices at Kellis. In: Bowen GE, and Hope CA (eds.), The Oasis Papers 3: Proceedings of the Third International Conference of the Dakhleh Oasis Project. Oxford: Oxbow. p 167-182.

Bowman AK. 1986. Egypt After the Pharaohs 332 B.C. - A.D. 642: From Alexander to the Arab Conquest. Berkeley: University of California Press.

Brace CL, Tracer DP, Yaroch LA, Robb J, Brandt K, and Nelson AR. 1993. Clines and clusters versus race - a test in Ancient Egypt and the case of a death on the Nile. Yearbook of Physical Anthropology 36:1-31.

Brooks S and Suchey JM. 1990. Skeletal age determination based on the *os pubis*: A comparison of the Acsádi-Nemeskéri and Suchey-Brooks methods. Human Evolution 5:227-238.

Brothwell DR (editor), 1963. Dental Anthropology. Oxford: Pergamon.

Brothwell DR. 1963. The macroscopic dental pathology of some earlier human populations. In: Brothwell DR (ed.), Dental Anthropology. Oxford: Pergamon. p 271-288.

Brues AM. 1977. Peoples and Races. New York: Macmillan.

Buikstra JE, Frankenberg SR, and Konigsberg LW. 1990. Skeletal biological distance studies in American physical anthropology: recent trends. American Journal of Physical Anthropology 82:1-7.

Bulliet, RW. 1975. The Camel and the Wheel. Cambridge, MA: Harvard University Press.

Buzon MR, 2006. The relationship between biological and ethnic identity in

New Kingdom Nubia. Current Anthropology 47:683-695.

Buzon MR, Simonetti A, and Creaser, RA. 2007. Migration in the Nile Valley during the New Kingdom period: a preliminary strontium isotope study. Journal of Archaeological Science 9:1391-1401.

Buzon, MR, and Bowen, GJ. 2010. Oxygen isotope analysis of migration in the Nile Valley. Archaeometry 52:855-868.

Campbell TD. 1925. Dentition and Palate of the Australian Aboriginal. Adelaide: University of Adelaide.

Carbonell VM. 1963. Variation in the frequency of shovel-shaped incisors in different populations. In: Brothwell DR (ed.), Dental Anthropology. Oxford: Pergamon. p 211-234.

Chappel HG. 1927. Jaws and teeth of ancient Hawaiians. Memoirs of the Bernice P Bishop Museum 9:249-268.

Churcher CS. 1999. Holocene faunas of the Dakhleh Oasis. In: Churcher CS, and Mills AJ (eds.), Reports from the Survey of Dakhleh Oasis 1977-1987. Oxford: Oxbow. p 133-151.

Close AE, and Wendorf F. 1992. The beginnings of food production in the Eastern Sahara. In: Gebauer AB, and Price TD (eds.), Transitions to Agriculture in Prehistory. Madison, Wisconsin: Prehistory Press. p 63-72.

Cook M, Molto E, and Anderson C. 1988. Possible case of hyperparathyroidism in a Roman Period skeleton from the Dakhleh-Oasis, Egypt, diagnosed using bone histomorphometry. American Journal of Physical Anthropology 75(1):23-30.

Corruccini RS, and Shimada I. 2002. Dental relatedness corresponding to mortuary patterning at Huaca Loro, Peru. American Journal of Physical Anthropology 117:118-121.

Dahlberg AA. 1945. The changing dentition of man. Journal of the American Dental Association 32:676-690.

Dahlberg AA. 1945. The paramolar tubercle (Bolk). American Journal of Physical Anthropology(3):97-103.

Dahlberg AA. 1950. The evolutionary significance of the protostylid. American Journal of Physical Anthropology 8(1):15-26.

Dahlberg AA. 1951. The physical anthropology of the American Indian. In: Laughlin WS (ed.), Physical Anthropology of the American Indian. New York: Viking Fund. p 138-176.

Dahlberg AA. 1956. Materials for the establishment of standards for classification of tooth characteristics, attributes, and techniques in morphological studies of the dentition. Chicago: University of Chicago Press.

Dahlberg AA. 1963. Dental evolution and culture. American Journal of Physical Anthropology 35:237-249.

Dahlberg AA. 1991. Historical perspectives of dental anthropology. In: Kelly MA, and Larsen CS (eds.), Advances in Dental Anthropology. New York: Wiley-Liss. p 7-11.

Darnell JC. 2002. Opening the Narrow Doors of the Desert: Discoveries of the Theban Desert Road Survey. In: Friedman R (ed.), Egypt and Nubia: Gifts of the Desert. London: British Museum Press. p 132-155.

Davies PL. 1967. Agenesis of teeth: a sex-limited trait. Journal of Dental Research(46):1309.

De Souza P, and Houghton P. 1977. The Mean Measure of Divergence and the use of non-metric data in the estimation of biological distances. Journal of Archaeological Science 4:163-169.

Derry DE. 1956. The dynastic race in Egypt. Journal of Egyptian Archaeology 42:80-85.

Drennan RD. 2009. Statistics for Archaeologists, 2nd Edition. New York: Springer.

Dupras TL. 1999. Dining in the Dakhleh Oasis, Egypt: Determination of Diet Using Documents and Stable Isotope Analysis [PhD Thesis]. Hamilton: McMaster University.

Dupras T, and Tocheri M. 2003. Preliminary analysis of the human skeletal remains from North Tombs 1 and 2. In: Bowen GE, and Hope CA (eds.), The Oasis Papers 3: Proceedings of the Third International Conference of the Dakhleh Oasis Project. Oxford: Oxbow. p 183-196.

Dupras TL, and Schwarcz HP. 2001. Strangers in a strange land: stable isotope evidence for human migration in the Dakhleh Oasis, Egypt. Journal of Archaeological Science 28:1199-1208.

Dupras TL, Schwarcz HP, and Fairgrieve SI. 2001. Infant feeding and weaning practices in Roman Egypt. American Journal of Physical Anthropology 115(3):204-212.

Dupras TL, Schwarcz HP, and Fairgrieve SI. 2008. Dining in the Dakhleh Oasis: Determining Diet from Stable Isotopes. In: Wiseman MF (ed.), The Oasis Papers 2: Proceedings of the Second International Conference of the Dakhleh Oasis Project. Oxford: Oxbow. p 119-127.

Dupras TL, Tocheri MW, and Molto JE. 2001. Is eight enough? A comparison of eight aging methods on a juvenile skeletal sample from the Dakhleh Oasis, Egypt. American Journal of Physical Anthropology:60-61.

Dzierżykray-Rogalski T. 1978. Rapport sur les recherches anthropologiques menées dans l'oasis de Dakhleh en 1977 (IFAO-Balat). Bulletin de l'Institut Français d'Archéologie Orientale 78:141-145.

Dzierżykray-Rogalski T. 1979a. Paléopathologie des habitants de l'oasis de Dakhleh à l'époque ptolémaïque. Bulletin de l'Institut Français d'Archéologie Orientale 79:63-69.

Dzierżykray-Rogalski T. 1979b. Les ossements du gouverneur du mastaba V de Balat. Bulletin de l'Institut Français d'Archéologie Orientale 79:479-482.

Dzierżykray-Rogalski T. 1980. Paleopathology of the Ptolemaic inhabitants of Dakhleh Oasis (Egypt). Journal of Human Evolution 9:71-74.

Dzierżykray-Rogalski T. 1981. Sur la paléopathologie dans l'Oasis de Dakhleh à l'Ancien Empire. Bulletin de l'Institut Français d'Archéologie Orientale 81:219-221.

Dzierżykray-Rogalski T. 1983. Problèmes relatifs à la race et à la population de l'Oasis de Dakhleh. Bulletin de l'Institut Français d'Archéologie Orientale 83:313-316.

Dzierżykray-Rogalski T, and Szlatchetko K. 1980. Recherches sur la dentition du gouverneur de l'Oasis Medou-nefer (Dakhleh-Balat). Bulletin de l'Institut Français d'Archéologie Orientale 80:91-95.

Edgar HHJ. 2004. Dentitions, distance, and difficulty: a comparison of two statistical techniques for dental morphological data. Dental Anthropology 17(2):55-62.

Emery WB. 1961. Archaic Egypt. London: Penguin.

Enoki K, and Dahlberg AA. 1958. Rotated maxillary central incisors. Orthodontic Journal of Japan 17:157-169.

Fadhlaoui-Zid, F, Rodríguez-Botigué, L, Naoui,N, Benammar-Elgaaied, A, Calafell, F, and Comas, D. 2011. Mitochondrial DNA structure in North Africa reveals a genetic discontinuity in the Nile Valley. American Journal of Physical Anthropology 145:107-117.

Fairgrieve SI, and Molto JE. 2000. Cribra orbitalia in two temporally disjunct population samples from the Dakhleh Oasis, Egypt. American Journal of Physical Anthropology 111(3):319-331.

Fix AG. 1993. Kin-structured migration and isolation by distance. Human Biology 65:193-210.

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

Frey R. 1986. Dakhleh Oasis Project. Interim report on excavations at the 'Ein-Tirghi cemetery. Journal of the Society for the Study of Egyptian Antiquities 16:92-102.

Gardiner AH. 1933. The Dakhleh stela. Journal of Egyptian Archaeology 19:19-30.

Gardner I. 1996. Kellis Literary Texts, Volume 1. Oxford: Oxbow.

Gardner I, Alcock A, and Funk WP. 1999. Introduction. In: Gardner I, Alcock A, and Funk WP (eds.), Coptic Documentary Texts from Kellis Volume 1. Oxford: Oxbow Publishing. p 4-95.

Garn SM, Lewis AB, and Vicinus JH. 1962. Third molar agenesis and reduction in the number of other teeth. Journal of Dental Research(41):717.

Giddy LL. 1987. Egyptian Oases: Bahariya, Dakhla, Farafra and Kharga during Pharaonic Times. Wiltshire: Aris & Phillips Ltd.

Gill GW. 1998. Craniofacial criteria in forensic race identification. In: Reichs KJ (ed.), Forensic Osteology: Advances in the Identification of Human Remains, Second Edition. Springfield: Charles C. Thomas. p 293-318.

Godde K. 2009. An examination of Nubian and Egyptian biological distances: Support for biological diffusion or *in situ* development? Homo 60:389-404.

Graver, A., Molto, E., Parr, RL, Praymak, R., Walters, S. and Maki, J. 2001.Mitochondrial DNA research in the Dakhleh Oasis, Egypt: A preliminary report. Ancient Biomolecules 3, 239-253.

Greenberg JH, Turner CG, and Zegura S. 1985. Convergence of evidence for the peopling of the Americas. Collegium Antroplogicum 9:33-42.

Greenberg JH, Turner CG, and Zegura S. 1986. The settlement of the Americas: a comparison of the linguistic, dental and genetic evidence. Current Anthropology 24:477-497.

Greene DL. 1966. Dentition and the biological relationships of some Meroitic, X-Group and Christian populations from Wadi Halfa, Sudan. Kush 14:285-288.

Greene DL. 1972. Dental anthropology of early Egypt and Nubia. Journal of

Human Evolution 1:315-324.

Greene DL. 1982. Discrete dental variations and biological distances of Nubian populations. American Journal of Physical Anthropology 58(1):75-79.

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

Gregory WK. 1916. Studies on the evolution of the Primates. I. The Cope-Osborn 'theory of tritubercuIy' and the ancestral molar patterns of the Primates. Bulletin of the American Museum of Natural History 35:239-257.

Gregory WK. 1922. The Origin and Evolution of the Human Dentition. Baltimore: Williams and Wilkins.

Gregory WK, and Hellman M. 1926. The dentition of *dryopithecus* and the origin of man. American Museum of Natural History Anthropological Papers 28:1-117.

Grewal MS. 1962. The rate of genetic divergence in the C57BL strain of mice. Genetic Research 3:226-237.

Grüneberg H. 1952. Genetical studies on the skeleton of the mouse. IV. Quasi-continuous variations. Journal of Genetics 51, 95-114.

Guatelli-Steinberg D, Irish JD, and Lukacs JR. 2001. Canary islands-north African population affinities: measures of divergence based on dental morphology. Homo 52:173-188.

Hafez M, El-Tahan H, Awadalla M, El-Khayat H, Abdel-Gafar A, and Ghoneim M. 1983. Consanguineous matings in the Egyptian population. Journal of Medical Genetics 20:58-60.

Hallgrimsson B, Donnabhain BO, Walters GB, Cooper DML, Guobjartsson D, and Stefansson K. 2004. Composition of the Founding Population of Iceland: Biological Distance and Morphological Variation in Early Historic Atlantic Europe. American Journal of Physical Anthropology 124:257-274.

Hanihara K. 1963. Crown characters of the deciduous dentition of the Japanese-American hybrids. In: Brothwell DR (ed.), Dental Anthropology. New York: Pergamon. p 105-124.

Hanihara K, Masuda T, and Tanaka T. 1974. Affinities of dental characteristics in the Okinawa Islanders. JASN 82:75-82.

Hanihara K, and Minimidate T. 1965. *Tuberculum accessorium mediale*

internum in the deciduous lower second molars. JASN 73:9-19.

Hanihara T. 1998. Metric and Nonmetric Dental Variations of Major Human Populations. In: Lukacs JR (ed.), Human Dental Development, Morphology, and Pathology: A Tribute to Albert A Dahlberg. Eugene, OR: Department of Anthropology, University of Oregon. p 173-200.

Harris EF. 1977. Anthropologic and genetic aspects of the dental morphology of Solomon Islanders, Melanesia [PhD dissertation]: Arizona State University. 488 p.

Harris EF. 2008. Statistical applications in dental anthropology. In: Irish JD, and Nelson GC (eds.), Technique and application in dental anthropology. Cambridge: Cambridge University Press. p 35-67.

Harris EF, and Bailit HL. 1980. The metaconule: a morphologic and familial analysis of a molar cusp in humans. American Journal of Physical Anthropology 53(3):349-358.

Harris EF, and Sjøvold T. 2004. Calculation of Smith's Mean Measure of Divergence for Intergroup Comparisons Using Nonmetric Data. Dental Anthropology 17(3):83-93.

Hassan FA. 1986. Desert environment and origins of agriculture in Egypt. Norwegian Archaeological Review 19:63-76.

Hassan FA. 1988. The predynastic of Egypt. Journal of World Prehistory 2(2):135-185.

Hassan HY, Underhill PA, and Cavalli-Sforza LL. 2008. Y-chromosome variation among Sudanese: restricted gene flow, concordance with language, geography, and history. American Journal of Physical Anthropolgoy 137:316-323.

Hassanali J. 1982. Incidence of Carabelli's trait in Kenyan Africans and Asians. American Journal of Physical Anthropology 59(3):317-319.

Hellman M. 1928. Racial characters in human dentition. Proceedings of the American Philosophical Society 67:154-174.

Henderson M. 1993. A Craniometric Analysis of Samples from 'Ein Tirghi and Kellis 2, Dakhleh, Egypt [Unpublished Honours Thesis]. Thunder Bay: Lakehead University.

Hendrickx S, and Vermeersch P. 2000. Prehistory: from the Palaeolithic to the Badarian culture (c. 700,000-7000 BC). In: Shaw I (ed.), The Oxford History of Ancient Egypt. Oxford: Oxford University Press. p 17-43.

Hiernaux J. 1975. The People of Africa. New York: Charles Scribner's Sons.

Hillson S. 1978. Human biological variation in the Nile Valley, in relation to environmental factors [PhD Thesis] London: University of London.

Hillson S. 1996. Dental Anthropology. Cambridge: Cambridge University Press.

Hillson S. 2005. Teeth, 2nd edition. Cambridge: Cambridge University Press. 373 p.

Hope CA. 1980. Dakhleh Oasis Project: Report on the study of the pottery and kilns. Journal of the Society for the Study of Egyptian Antiquities 10:283-313.

Hope CA. 1995. Ismant el-Kharab (ancient Kellis) in the Dakhleh Oasis, Egypt. Mediterranean Archaeology 8:138-143.

Hope CA. 2001. Observations on the dating of the occupation at Ismant el-Kharab. In: Marlow CA, and Mills AJ (eds.), The Oasis Papers: Proceedings of the First International Symposium of the Dakhleh Oasis Project. Oxford: Oxbow. p 43-59.

Hope CA. 2002. Oases Amphorae of the New Kingdom. In: Friedman R (ed.), Egypt and Nubia: Gifts of the Desert. London: British Museum Press. p 95-131.

Hope CA. 2003. The excavations at Ismant el-Kharab from 2000 to 2002. In: Bowen GE, and Hope CA (eds.), The Oasis Papers 3: Proceedings of the Third International Conference of the Dakhleh Oasis Project. Oxford: Oxbow. p 207-289.

Hope CA, and McKenzie J. 1999. Interim report on the west tombs. In: Hope CA, and Mills AJ (eds.), Dakhleh Oasis Project: Preliminary Reports on the 1992-1993 and 1993-1994 Field Seasons (Dakhleh Oasis Project Monograph 8). Oxford: Oxbow. p 77-97.

Hope CA, and McKenzie J. 1999. Interim report on the West Tombs. In: Hope CA, and Mills AJ (eds.), Dakhleh Oasis Project: Preliminary Reports on the 1992-1993 and 1993-1994 Field Seasons. Oxford: Oxbow. p 53-68.

Hopkins K. 1980. Brother-sister marriage in Roman Egypt. Comparative Studies in Society and History 22:303-354.

Howell TL, and Kintigh KW. 1996. Archaeological Identification of Kin Groups Using Mortuary and biological data: an example from the American Southwest. American Antiquity 61(3):537-554.

Hrdlička A. 1911. Human dentition and teeth from the evolutionary and racial standpoint. Dominion Dental Journal 23:403-421.

Hrdlička A. 1912. The Natives of Kharga Oasis, Egypt. Washington D.C.: Smithsonian Institution. 135 p.

Hrdlička A. 1920. Shovel-shaped teeth. American Journal of Physical Anthropology 3:429-465.

Hrdlička A. 1924. New data on the teeth of early man and certain fossil European apes. American Journal of Physical Anthropology 7(1):109-132.

Huebner SR. 2007. 'Brother-sister' marriage in Roman Egypt: a curiosity of humankind or a widespread family strategy? Journal of Roman Studies 97:21-49.

Hussien FH, Sarry el-Din AM, Samie Kandeel WA and el Banna RAE-S. 2009. Spinal pathological findings in ancient Egyptians of the Greco Roman period living in Bahriyah Oasis. International Journal of Osteoarchaeology 19:613-627.

Irish JD. 1993. Biological Affinities of Late Pleistocene Through Modern African Aboriginal Populations: The Dental Evidence [PhD dissertation]. Tempe: Arizona State University.

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

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

Irish JD. 1998b. Dental morphological indications of population discontinuity and Egyptian gene flow in post-Paleolithic Nubia. In: Lukacs JR (ed.), Human Dental Development, Morphology and Paleopathology: A Tribute to Albert A Dahlberg. Eugene, Oregon: University of Oregon Press. p 156-172.

Irish JD. 1998c. Diachronic and synchronic dental trait affinities of Late and Post-Pleistocene peoples from North Africa. Homo 49(2):138-155.

Irish JD. 1998d. Dental morphological affinities of Late Pleistocene through recent sub-Saharan and North African peoples. Bulletins et Memoires de la Societé d'Anthropologie de Paris. Nouvelle Serie 10:237-272.

Irish JD. 2000. The Iberomaurusian enigma: North African progenitor or dead end? Journal of Human Evolution 39(4):393-410.

Irish JD. 2005. Population continuity vs. discontinuity revisited: Dental affinities among Late Palaeolithic through Christian-era Nubians. American Journal of Physical Anthropology 128:520-535.

Irish JD. 2006. Who were the ancient Egyptians? Dental affinities among Neolithic through postdynastic peoples. American Journal of Physical Anthropology 129:529-543.

Irish JD. 2010. The Mean Measure of Divergence: its utility in model-free and model-bound analyses relative to the Mahalanobis D^2 Distance for nonmetric traits. American Journal of Human Biology 22(3):378-395.

Irish JD, and Friedman R. 2010. Dental affinities of the C-group inhabitants of Hierakonpolis, Egypt: Nubian, Egyptian, or both? Homo 61:81-101.

Irish JD, and Hemphill BE. 2004. An odontometric investigation of Canary Islander origins. Dental Anthropology 17(1):8-17.

Irish JD, and Konigsberg LW. 2007. The ancient inhabitants of Jebel Moya redux: measures of population affinity based on dental morphology. International Journal of Osteoarchaeology 17:138-156.

Jamison PL, Meier RJ, and Thompson-Jacob D. 1989. Meaning of biodistance statistics: a test case using adult monozygotic twins. American Journal of Physical Anthropology 80:485-492.

Janssen JJ. 1968. The smaller Dakhla stela. Journal of Egyptian Archaeology 54:165-172.

Johnson AL, and Lovell NC. 1994. Biological differentiation at predynastic Naqada, Egypt: an analysis of dental morphological traits. American Journal of Physical Anthropology 93(4):427-433.

Johnson AL, and Lovell NC. 1995. Dental morphological evidence for biological continuity between the A-Group and C-Group periods in Lower Nubia. International Journal of Osteoarchaeology 5:368-376.

Julien C. 1970. History of North Africa. London: Routledge and Kegan Paul.

Keene HJ. 1996. On the classification of C6 (tuberculum sextum) of the mandibular molars. Human Evolution 9(3):231-247.

Keiser JA. 1990. Human Adult Odontometrics. Cambridge: Cambridge University Press.

Keita SOY. 1990. Studies of ancient crania from northern Africa. American Journal of Physical Anthropology 83(1):35-48.

Keita SOY. 1992. Further studies of crania from ancient northern Africa: an analysis of crania from first dynasty Egyptian tombs, using discriminant functions. American Journal of Physical Anthropology 87(3):245-254.

Keita SOY. 1993. Studies and comments on Ancient Egyptian biological relationships. History in Africa 20:129-154.

Keita, SOY. 2005. History in the interpretation of the pattern of p49a,f TaqI RFLP Y-chromosome variation in Egypt: A consideration of multiple lines of evidence. American Journal of Human Biology 17: 559-567.

Kemp BJ. 2006. Ancient Egypt: Anatomy of a Civilization, Second Edition. London and New York: Routledge.

Kitagawa Y. 2000. Nonmetric morphological characters of deciduous teeth in Japan: diachronic evidence of the past 4000 years. International Journal of Osteoarchaeology 10(4):242-253.

Kleindienst MR. 1999. Pleistocene archaeology and geoarchaeology of the Dakhleh Oasis: a status report. In: Churcher CS, and Mills AJ (eds.), Reports from the Survey of Dakhleh Oasis 1977-1987. Oxford: Oxbow. p 83-108.

Kleindienst MR, Churcher CS, McDonald MA, and Schwarcz HP. 1999. Geography, geology, geochronology and geoarchaeology of the Dakhleh Oasis region: an interim report. In: Churcher CS, and Mills AJ (eds.), Reports from the Survey of Dakhleh Oasis 1977-1987. Oxford: Oxbow. p 1-54.

Knudstad JE, and Frey RA. 1999. Kellis, the architectural survey of the Romano-Byzantine town at Ismant el-Kharab. In: Churcher CS, and Mills AJ (eds.), Reports from the Survey of Dakhleh Oasis 1977-1987. Oxford: Oxbow Books. p 189-214.

Kobusiewicz M, Kabaciński J, Schild R, Irish JD and Wendorf F. 2004. Discovery of the first Neolithic cemetery in Egypt's Western Desert. Antiquity 78:566–578.

Kolakowski D, Harris EF, and Bailit HL. 1980. Complex segregation analysis of Carabelli's trait in a Melanesian population. American Journal of Physical Anthropology 53(2):301-308.

Konigsberg LW. 1988. Migration models of prehistoric postmarital residence. American Journal of Physical Anthropology 77(4):471-482.

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

Konigsberg LW. 2006. A post-Neumann history of biological and genetic distance studies in bioarchaeology. In: Buikstra JE, and Beck LA (eds.), Bioarchaeology: The Contextual Analysis of Human Remains. New York: Academic Press. p 263-279.

Koritzer RT. 1973. An anthropological approach to the study of dental pathology. In: Dahlberg AA, and Graber TM (eds.), Orofacial Growth and Development. The Hague: Mouton. p 283-299.

Kraus BS, and Furr ML. 1953. Lower first premolars. Part 1. A definition and classification of discrete morphological traits. Journal of Dental Research 32:554-564.

Krings M, Salem AM, Bauer K, Geisert H, Malek AK, Chaix L, Simon C, Welsby D, Di Rienzo A, Utermann G and others. 1999. mtDNA analysis of Nile River Valley populations: a genetic corridor or a barrier to migration? American Journal of Human Genetics 64:1166-1176.

Krogman WM. 1927. Anthropological aspects of the human teeth and dentition. Journal of Dental Research 7:1-108.

Kron H. 2007. The Efficacy of GIS for Spatial Analysis of Mortuary Data based on Morphogenetic Traits in the Kellis 2 Cemetery, Dakhleh Oasis, Egypt [MA Thesis]. London: University of Western Ontario.

Kruskal JB, and Wish M. 1978. Multidimensional Scaling. Beverly Hills and London: Sage Publications.

Kujanová, M, Pereira, L, Fernandes,V, Pereira, JB, and Černy, J. 2009. Near Eastern Neolithic genetic input in a small oasis of the Egyptian Western Desert. American Journal of Physical Anthropology 140:336-346.

Kuper R. 2001. By Donkey Train to Kufra? How Mr Meri Went West (Egypt, Dakhla). Antiquity 75(290):801-802.

Kuper R. 2002. Routes and roots in Egypt's Western Desert: The early Holocene resettlement of the Eastern Sahara. In: Friedman R (ed.), Egypt and Nubia: Gifts of the Desert. London: British Museum Press. p 1-12.

Larsen CS. 1997. Bioarchaeology: Interpreting behavior from the human skeleton. Cambridge: Cambridge University Press.

Lasker GW. 1950. Genetic analysis of racial traits of the teeth. Cold Spring Harbor Symposia on Quantitative Biology 15:191-203.

Lebeuf AMD. 1959. Les Populations du Tchad. Paris: Presses Universitaires de France.

Leigh RW. 1928. Dental pathology of aboriginal California. University of California Publications in American Archaeology and Ethnology 23:399-440.

Leigh RW. 1929. Dental morphology and pathology of prehistoric Guam. Memoirs of the Bernice P Bishop Museum 2:451-479.

Lewis N. 1983. Life in Egypt Under Roman Rule. Oxford: Clarendon Press.

Lucotte G, and Mercier G. 2003. Brief communication: Y-chromosome haplotypes in Egypt. American Journal of Physical Anthropology 121(1):63-66.

Lukacs JR. 1983. Dental anthropology and the origins of two Iron Age populations from northern Pakistan. Homo 34:1-15.

Lukacs JR (ed.), 1984. The People of South Asia: The Biological Anthropology of India, Pakistan and Nepal. New York: Plenum Press.

Lukacs JR. 1987. Biological relationships derived from morphology of permanent teeth: recent evidence from prehistoric India. Anthropologischer Anzeiger 45:97-116.

Lukacs JR. 2007. Interpreting biological diversity in South Asian prehistory: Early Holocene population affinities and subsistence adaptations. In: Petraglia MD, and Allchin B (eds.), The Evolution and Population History of South Asia. New York: Springer. p 271-296.

Lukacs JR, and Hemphill BE. 1991. The dental anthropology of prehistoric Baluchistan: a morphometric approach to the peopling of south Asia. In: Kelly MA, and Larsen CS (eds.), Advances in Dental Anthropology. New York: Wiley-Liss. p 77-119.

Lukacs JR, and Walimbe SR. 1984. Deciduous dental morphology and the biological affinities of a late Chalcolithic skeletal series from western India. American Journal of Physical Anthropology 65(1):23-30.

Lumholtz AGS. 1902. Unknown Mexico. A Record of Five Years' Exploration Among the Tribes of the Western Sierra Madre; in the Terra Caliente of Tepic and Jalisco; and Among the Tarascos of Michoacan. Glorieta, New Mexico: The Rio Grande Press.

Mahalanobis PC. 1936. On the generalized distance in statistics. National Historic Institute of Science, India 2:49-55.

Manni F, Leonardi P, Barakat A-H, Rouba H, Heyer E, Klintschar M, McElreavey K and Quintana-Murci I. 2002. Y-chromosome analysis in Egypt suggests a genetic regional continuity in northeastern Africa. Human Biology 74: 645-658.

Mayhall JT. 2000. Dental morphology: techniques and strategies. In: Katzenberg MA, and Saunders SR (eds.), Biological Anthropology of the Human Skeleton. New York: Wiley-Liss. p 103-134.

McDonald MA. 1998. Early African pastoralism: view from Dakhleh Oasis (south central Egypt). Journal of Anthropological Archaeology 17:124-142.

McDonald MA. 1999. Neolithic cultural units and adaptations in the Dakhleh Oasis. In: Churcher CS, and Mills AJ (eds.), Reports from the Survey of Dakhleh Oasis 1977-1987. Oxford: Oxbow. p 117-132.

Meindl RS and Lovejoy CO. 1985. Ectocranial suture closure: A revised method for the determination of skeletal age at death based on the lateral-anterior sutures. American Journal of Physical Anthropology 68:57-66.

Midant-Reynes B. 2000. The Prehistory of Egypt: From the First Egyptians to the First Pharaohs. Malden, MA: Blackwell Publishing.

Middleton R. 1962. Brother-sister and father-daughter marriage in ancient Egypt. American Sociological Review 27(5):603-611.

Mills AJ. 1979. Dakhleh Oasis Project: report on the first season of survey, October-December 1978. Journal of the Society for the Study of Egyptian Antiquities 9(4):163-185.

Mills AJ. 1984. Research in the Dakhleh Oasis. In: Kryzaniak L, and Kobusiewicz M (eds.), Origins and Early Development of Food Producing Cultures in Northeastern Africa. Poznan: Poznan University Press. p 205-210.

Mills AJ. 1999. Pharaonic Egyptians in the Dakhleh Oasis. In: Churcher CS, and Mills AJ (eds.), Reports from the Survey of Dakhleh Oasis 1977-1987. Oxford: Oxbow Books. p 171-178.

Mills AJ. 2002. Another Old Kingdom site in the Dakhleh Oasis. In: Friedman R (ed.), Egypt and Nubia: Gifts of the Desert. London: British Museum Press. p 74-78.

Milner GR, and Larsen CS. 1991. Teeth as artifacts of human behavior: intentional mutilation and accidental modification. In: Kelley MA, and Larsen CS (eds.), Advances in Dental Anthropology. New York: Wiley-Liss. p 357-378.

Molto JE. 2000. Humerus varus deformity in Roman period burials from Kellis 2, Dakhleh, Egypt. American Journal of Physical Anthropology 113(1):103-109.

Molto JE. 2001. The comparative skeletal biology and paleoepidemiology of the people from Ein Tirghi and Kellis, Dakhleh, Egypt. In: Marlow CA, and Mills AJ (eds.), The Oasis Papers: Proceedings of the First International Symposium of the Dakhleh Oasis Project. Oxford: Oxbow Books. p 81-100.

Molto JE. 2002. Bioarchaeological research of Kellis 2: an overview. In: Hope CA, and Bowen GE (eds.), Dakhleh Oasis Project: Preliminary Reports on the 1994-1995 to 1998-1999 Field Seasons. Oxford: Oxbow. p 239-255.

Molto JE, Sheldrick P, Cerroni A, and Haddow S. 2003. Late Roman period human skeletal remains from Areas D/6 and D/7 and North Tomb 1 at Kellis. In: Bowen GE, and Hope CA (eds.), The Oasis Papers 3: Proceedings of the Third International Conference of the Dakhleh Oasis Project. Oxford: Oxbow. p 345-363.

Molto JE, Stewart JD, Reimer PJ, and Williams LJ. 2006. The dating of the Kellis 2 cemetery: an ongoing conundrum. Fifth International Conference of the Dakhleh Oasis Project. Cairo.

Montagu MFA. 1940. The significance of the variability of the upper lateral incisor teeth in man. Human Biology(12):323-358.

Morant GM. 1925. A study of Egyptian craniology from prehistoric to Roman times. Biometrika 17:1-53.

Morris DH. 1965. The Anthropological Utility of Dental Morphology [PhD Dissertation]. Tucson: University of Arizona.

Morris DH. 1970. On deflecting wrinkles and the Dryopithecus pattern in human mandibular molars. American Journal of Physical Anthropology 32(1):97-104.

Morris DH. 1975. Bushman maxillary canine polymorphism. South African Journal of Science 71:333-335.

Morris DH, Hughes SG, and Dahlberg AA. 1978. Uto-Aztecan Premolar: the Anthropology of a Dental Trait. In: Butler PM, and Joysey KA (eds.), Development, Function and Evolution of Teeth. London: Academic Press. p 69-79.

Morton SG. 1844. Crania Aegyptiaca: Or, Observations on Egyptian Ethnography, Derived from Anatomy, History and the Monuments. Philadephia: J. Pennington.

Nelson CT. 1938. The teeth of the Indians of Pecos Pueblo. American Journal of Physical Anthropology 23:261-293.

Nichol CR. 1990. Dental Genetics and Biological Relationships of the Pima Indians of Arizona [PhD Dissertation]. Tempe, AZ: Arizona State University.

Nichol CR, and Turner CG. 1986. Intra- and interobserver concordance in classifying dental morphology. American Journal of Physical

Anthropology 69(3):299-315.

Nichol CR, Turner CG, and Dahlberg AA. 1984. Variation in the convexity of the human maxillary incisor labial surface. American Journal of Physical Anthropology 63(4):361-370.

Nielsen OV. 1970. Human Remains: Metrical and Non-Metrical Anatomical Variations. Odense: The Scandinavian Joint Expedition to Sudanese Nubia.

O'Connor, D. 1993. Ancient Nubia: Egypt's Rival in Africa. Philadelphia: University of Philadelphia.

Osing J, Moursi M, Do. Arnold O, Neugebauer RA, Parker RA, Pingree D, and Nur el-Din MA (eds.), 1982. Denkmäler der Oase Dachla aus dem Nachlass von Ahmed Fakhry. Kairo: Deutsches Archäologisches Institut.

Ousley S, Jantz R, and Freid D. 2009. Understanding race and human variation: Why forensic anthropologists are good at identifying race. American Journal of Physical Anthropology 139:68-76.

Parr RL., Dupras TL., Walters S., Capricci J. and Molto E. 1998. A tale of two lepers from the Dakhleh Oasis, Egypt: A preliminary report on chemical and molecular analysis. Poster Presentation at the Palaeopathology Annual Meetings, Salt Lake City, Utah.

Parr RL. 2002. Mitochondrial DNA sequence analysis of skeletal remains from the Kellis 2 cemetery. In: Hope CA, and Bowen GE (eds.), Dakhleh Oasis Project: Preliminary Reports on the 1994-1995 to 1998-1999 Field Seasons. Oxford: Oxbow. p 257-261.

Peacock D. 2000. The Roman Period (30 BC-AD 395). In: Shaw I (ed.), The Oxford History of Ancient Egypt. Oxford: Oxford University Press. p 422-445.

Pedersen PO. 1949. The East Greenland Eskimo dentition. Meddelelser om Grønland 142:1-244.

Penrose LS. 1954. Distance, size, and shape. Annals of Eugenics 18:337-343.

Petrie WMF. 1920. Prehistoric Egypt. London: Bernard Quaritch.

Petrie WMF. 1939. The Making of Egypt. London: Sheldon Press.

Phenice TW. 1969. A newly developed visual method of sexing in the *os pubis*. American Journal of Physical Anthropology 30:297-301.

Promińska E. 1981. La stature des habitants de l'oasis de Dakhleh sous la

XXVIe dynastie et à l'époque ptolémaïque. Bulletins et Mémoires de la Société d'Anthropologie de Paris 8(3):275-280.

Prowse TL, and Lovell NC. 1996. Concordance of cranial and dental morphological traits and evidence for endogamy in ancient Egypt. American Journal of Physical Anthropology 101(2):237-246.

Reid C, van Reenen JF, and Groeneveld HT. 1991. Tooth size and the Carabelli trait. American Journal of Physical Anthropology 84(4):427-432.

Relethford, JH. 2009. Race and global patterns of phenotypic variation. American Journal of Physical Anthropology 139:16.22.

Relethford JH, and Lees FC. 1982. The use of quantitative traits in the study of human population structure. Yearbook of Physical Anthropology 25:153-168.

Remijsen S, and Clarysse W. 2008. Incest or adoption? Brother-sister marriage in Roman Egypt revisited. Journal of Roman Studies 98:53-61.

Ricaut FX, and Waelkens M. 2008. Cranial discrete traits in a Byzantine population and Eastern Mediterranean population movements. Human Biology 80:535-564.

Robinson JT. 1956. The Dentition of the *Australopithecinae*. Pretoria: Transvaal Museum.

Roe, A. 2005/2006. The Old "Darb al Arbein" caravan route and Kharga Oasis in Antiquity. Journal of the American Research Center in Egypt 42:119-129.

Rowlandson J, and Takahashi R. 2009. Brother-sister marriage and inheritance strategies in Greco-Roman Egypt. Journal of Roman Studies 99:104-139.

Rowley-Conwy P. 1988. The camel in the Nile Valley: New radiocarbon accelerator (AMS) dates from Qaṣr Ibrîm. Journal of Egyptian Archaeology 74:245-248.

Salomons RP and Worp KA. 2009. Onomasticon Oasiticum: An Onomasticon of Personal Names found in Documentary Texts from the Theban Oasis in Graeco-Roman Times. Published online at: http://media.leidenuniv.nl/legacy/onomas_final.pdf

Scheidel W. 1996a. Brother-sister and parent-child marriage outside royal families in ancient Egypt and Iran: A challenge to the sociobiological view of incest avoidance? Ethology and Sociobiology 17(5):319-340.

Scheidel W. 1996b. Measuring Sex, Age and Death in the Roman Empire. Ann Arbor, MI: Journal of Roman Archaeology.

Scheidel W. 1997. Brother-sister marriage in Roman Egypt. Journal of Biosocial Science 29:361-371.

Scheuer JL, Musgrave JH and Evans SP. 1980. The estimation of late fetal and perinatal age from limb bone length by linear and logarithmic regression. Annals of Human Biology 7, 257-265.

Schild R. 1987. Unchanging contrast? The Late Pleistocene Nile and Eastern Sahara. In: Close AE (ed.), Prehistory of Arid North Africa: Essays in Honor of Fred Wendorf. Dallas: Southern Methodist University Press. p 12-27.

Schild R, and Wendorf F. 1977. The prehistory of Dakhla Oasis and adjacent desert. Wroclaw: zaklad narodowy imienia Ossolinskich Wydnawnictwo Polskiej Akademii.

Schillaci MA, Irish JD, and Wood CCE. 2009. Further analysis of the population history of ancient Egyptians. American Journal of Physical Anthropology.

Schillaci MA, and Stojanowski CM. 2003. Postmarital residence and biological variation at Pueblo Bonito. American Journal of Physical Anthropology 120(1):1-15.

Schwartz JH. 1995. Skeleton Keys: An Introduction to Human Skeletal Morphology, Development, and Analysis. Oxford: Oxford University Press.

Sciulli PW, Doyle WJ, Kelly C, Siegel P, and Siegel MI. 1979. The interaction of stressors in the induction of increased levels of fluctuating asymmetry in the laboratory rat. American Journal of Physical Anthropology 50:279-284.

Scott GR. 1973. Dental Morphology: A Genetic Study of American White Families and Variation in Living Southwest Indians [PhD Dissertation]. Tempe: Arizona State University.

Scott GR. 1977. Classification, sex dimorphism, association, and population variation of the canine distal accessory ridge. Human Biology 49(3):453-469.

Scott GR. 1979. Association between the hypocone and Carabelli's trait of the maxillary molars. Journal of Dental Research 58:1403-1404.

Scott GR. 1980. Population variation of Carabelli's Trait. Human Biology 52(1):63-78.

Scott GR. 2008. Dental Morphology. In: Katzenberg MA, and Saunders SR (eds.), Biological Anthropology of the Human Skeleton, Second Edition. 2nd ed. New York: Wiley-Liss. p 265-298.

Scott GR, and Dahlberg AA. 1982. Microdifferentiation in tooth crown morphology among indians of the American Southwest. In: Kurten B (ed.), Teeth: Form, Function and Evolution. New York: Columbia University Press.

Scott GR, Potter RH, Noss JF, Dahlberg AA, and Dahlberg T. 1983. The dental morphology of Pima Indians. American Journal of Physical Anthropology 61(1):13-31.

Scott GR, and Turner CG. 1997. The Anthropology of Modern Human Teeth. Cambridge: Cambridge University Press.

Shaw BD. 1992. Explaining incest: Brother-sister marriage in Graeco-Roman Egypt. Man *New Series* 27(2):267-299.

Shaw JCM. 1931. The Teeth, the Bony Palate, and the Mandible in Bantu Races of South Africa. London: J. Bale and Sons.

Sjøvold T. 1973. The occurrence of minor non-metrical variants in the skeleton and their quantitative treatment for population comparisons. Homo 24:204-233.

Sjøvold T. 1977. Non-metrical divergence between skeletal populations: the theoretical foundation and biological importance of C.A.B. Smith's Mean Measure of Divergences. Ossa 4:1-33.

Sjøvold T. 1984. A report on the heritability of some cranial measurements and non-metric traits. In: van Vark GN, and Howells WW (eds.), Multivariate Statistical Methods in Physical Anthropology. Dordrecht: Reidel. p 223-246.

Smith CAB. 1977. A note on genetic distance. Annals of Human Genetics 40:463-479.

Smith GE. 1915. The influence of racial admixture in Egypt. The Eugenics Review 7(3):163-183.

Smith GE. 1923. The Ancient Egyptians and the Origin of Civilization. Piscatawy NJ: Gorgias Press.

Smith GE, and Wood Jones F. 1910. Report on the Human Remains (The Archaeological Survey of Nubia Report for 1907-08. Vol. 2). Cairo.

Smith ST. 1998. Nubia and Egypt: Interaction, acculturation and secondary state formation from the third to first millennium BC. In: Cusick J (ed.), Studies in Culture Contact: Interaction, Culture Change, and

Archaeology. Carbondale: Southern Illinois University. p 256-287.

Sofaer JA, MacLean CJ, and Bailit HL. 1972. Heredity and morphological variation in early and late developing teeth of the same morphological class. Archives of Oral Biology 17:811-816.

Staley RN, and Green LJ. 1971. Bilateral asymmetry in tooth cusp occurrence in human monozygotic twins, dizygotic twins and non-twins. Journal of Dental Research 50:83-89.

Stewart JD, Molto JE, and Reimer PJ. 2003. The Chronology of Kellis 2: The Interpretative Significance of Radiocarbon Dating of Human Remains. In: Bowen GE, and Hope CA (eds.), The Oasis Papers 3: Proceedings of the Third International Conference of the Dakhleh Oasis Project. Oxford: Oxbow. p 373-378.

Strouhal E. 1971. Evidence of the early penetration of negroes into prehistoric Egypt. Journal of African History 12:1-9.

Strouhal E, and Jungwirth J. 1979. Paleogenetics of the Late Roman-Early Byzantine Cemeteries at Sayala, Egyptian Nubia. Journal of Human Evolution 8:699-703.

Sutter R, and Mertz L. 2004. Nonmetric cranial trait variation and prehistoric biocultural change in the Azapa Valley, Chile. American Journal of Physical Anthropology 123:130-145.

Suzuki M, and Sakai T. 1964. Shovel-shaped incisors among the living Polynesians. American Journal of Physical Anthropology 22:65-72.

Swindler DR. 1976. Dentition of Living Primates. London: Academic Press.

Taylor J. 2000. The Third Intermediate Period (1069-664 BC). In: Shaw I (ed.), The Oxford History of Ancient Egypt. Oxford: Oxford University Press. p 324-363.

Thanheiser U, Walter J, and Hope CA. 2002. Roman agriculture and gardening in Egypt as seen from Kellis. In: Hope CA, and Bowen GE (eds.), Dakhleh Oasis Project: Preliminary Reports on the 1994-1995 to 1998-1999 Field Seasons. Oxford: Oxbow. p 299-310.

Thompson JL. 2008. Neolithic dental remains from Sheikh Muftah, Dakhleh Oasis: a preliminary report. In: Wiseman MF (ed.), The Oasis Papers 2: Proceedings of the Second International Conference of the Dakhleh Oasis Project. Oxford: Oxbow Books.

Thompson JL, and Madden GD. 2003. Health and disease of Neolithic remains from Sheikh Muftah, Dakhleh Oasis. In: Bowen GE, and Hope CA (eds.), The Oasis Papers 3: Proceedings of the Third International Conference of the Dakhleh Oasis Project. Oxford:

Oxbow. p 71-76.

Thompson JL, and Madden GD. 2006. Skeletal biology of Neolithic human remains from Dakhleh Oasis, Egypt. In: Chlodnicki M, Kobusiewicz M, and Kroeper K (eds.), Archaeology of Early Northeastern Africa: In Memory of Lech Krzyzaniak. Poznan: Poznan Museum of Archaeology. p 527-538.

Tocheri MW, Dupras TL, Sheldrick P, and Molto JE. 2005. Roman period fetal skeletons from the East Cemetery (Kellis 2) of Kellis, Egypt. International Journal of Osteoarchaeology 15:326-341.

Tocheri MW, and Molto JE. 2002. Aging fetal and juvenile skeletons from Roman period Egypt using basiocciput osteometrics. International Journal of Osteoarchaeology 12(5):356-363.

Tomczak PD, and Powell JF. 2003. Postmarital residence practices in the Windover population: sex-based dental variation as an indicator of patrilocality. American Antiquity 68:93-108.

Tomes CS. 1889. A Manual of Dental Anatomy: Human and Comparative. London: J. & A. Churchill.

Townsend GC, and Martin NG. 1992. Fitting genetic models to Carabelli trait data in South Australian twins. Journal of Dental Research 71:403-409.

Townsend GC, Richards LC, Brown T, Burgess VB, Travan GR, and Rogers JR. 1992. Genetic studies of dental morphology in South Australian twins. In: Smith P, and Tchernov E (eds.), Structure, Function and Evolution of Teeth. London: Freund Publishing House Ltd. p 501-518.

Trigger BG. 1983. The rise of Egyptian civilization. In: Trigger BG, Kemp BJ, O'Connor D, and Lloyd AB (eds.), Ancient Egypt: A Social History. Cambridge: Cambridge University Press. p 1-70.

Trotter, M, and Gleser, GC 1952. Estimation of stature from long bones of American whites and negroes. American Journal of Physical Anthropology 10(4):463-514.

Trotter, M, and Gleser, GC 1958. Re-evaluation of estimation of stature taken during life and of long bones after death. American Journal of Physical Anthropology 16(1):79-123.

Turner CG. 1967. The Dentition of Arctic Peoples [PhD thesis]. Madison: University of Wisconsin.

Turner CG. 1969. Microevolutionary interpretations from the dentition. American Journal of Physical Anthropology 30(3):421-426.

Turner CG. 1971. Three-rooted mandibular first permanent molars and the question of American Indian origins. American Journal of Physical Anthropology 34(2):229-241.

Turner CG. 1983. Dental evidence for the peopling of the Americas. In: Shutler Jr. R (ed.), Early Man in the New World. Beverly Hills CA: Sage Publications. p 145-157.

Turner CG. 1984. Advances in the dental search for native American origins. Acta Anthropogenetica 8:23-78.

Turner CG, and Hawkey DE. 1998. Whose teeth are these?: Carabelli's Trait. In: Lukacs JR (ed.), Human Dental Development, Morphology, and Pathology: a Tribute to Albert A Dahlberg. Eugene: University of Oregon Press. p 41-50.

Turner CG, Nichol CR, and Scott GR. 1991. Scoring procedures for key morphological traits of the permanent dentition: the Arizona State University Dental Anthropology System. In: Kelly MA, and Larsen CS (eds.), Advances in Dental Anthropology. New York: Wiley-Liss. p 13-31.

Turner CG, and Scott GR. 1977. Dentition of Easter Islanders. In: Dahlberg AA, and Graber TM (eds.), Orofacial Growth and Development. Mouton: The Hague. p 229-249.

Ubelaker DH (1989) Human Skeletal Remains: Excavation, Analysis and Interpretation (2nd Edition). Washington DC: Taraxacum.

Ullinger JM, Sheridan SG, Hawkey DE, Turner CG, and Cooley R. 2005. Bioarchaeological analysis of cultural transition in the southern Levant using dental nonmetric traits. American Journal of Physical Anthropology 128(2):466-476.

Valloggia M, and Henein NH. 1986. Balat I. Le mastaba de Medou-Nefer. Fouilles de l'Institut Français d'Archaéologie Orientale 31:1-239.

Van Gerven DP, Armelagos GJ, and Rohr A. 1977. Continuity and change in cranial morphology of three Nubian archaeological populations. Man 12:270-277.

Van Valen L. 1962a. Growth fields in the dentition *Peromyscus*. Evolution 16:272-277.

Van Valen L. 1962b. A study of fluctuating asymmetry. Evolution 16:125-142.

Wagner G. 1987. Les Oasis d'Égypte à l'Époque Grecque, Romaine et Byzantine, d'après les Documents Grecs. Cairo: Institut Français d'Archéologie Orientale.

Ward JH. 1963. Hierarchical grouping to optimize an objective function. Journal of the American Statistical Association 58:236-244.

Weidenreich F. 1937. The Dentition of *Sinathropus pekinensis*: A Comparative Odontography of the Hominids. Peking: Paleontologica Sinica, New Series D, No. 1 (Whole Series No. 101).

Weinreb AA. 2008. Characteristics of women in consanguineous marriages in Egypt, 1988–2000. European Journal of Population 24(2):185-210.

Wendorf F, and Schild R. 1980. Prehistory of the Eastern Sahara. New York: Academic Press.

Wendorf F, and Schild R. 2002. Implications of incipient social complexity in the Late Neolithic in the Egyptian Sahara. In: Friedman R (ed.), Egypt and Nubia: Gifts of the Desert. London: British Museum Press. p 13–20.

Wheeler SM. 2012. Nutritional and disease stress of juveniles from the Dakhleh Oasis, Egypt. International Journal of Osteoarchaeology 22:219-234.

White TD, and Folkens PA. 2005. The Human Bone Manual. Amsterdam: Elsevier Academic Press Publishing.

Wilkinson TAH. 1999. Early Dynastic Egypt. London: Routledge.

Williams LJ. 2008. Investigating Seasonality of Death at Kellis 2 Cemetery Using Solar Alignment and Isotopic Analysis of Mummified Tissues [PhD Thesis]. London: University of Western Ontario.

Winnicki JK. 2009. Late Egypt and Her Neighbours: Foreign Population in Egypt in the First Millennium BC. Warsaw: Journal of Juristic Papyrology.

Wiseman MF. 1999. Late Pleistocene prehistory in the Dakhleh Oasis. In: Churcher CS, and Mills AJ (eds.), Reports from the Survey of Dakhleh Oasis 1977-1987. Oxford: Oxbow. p 109-116.

Worp KW. 1995. Greek Papyri from Kellis: I. Oxford: Oxbow.

Wright HB. 1941. A frequent variation of the maxillary central incisors with some observations on dental caries among the Jivaro (Shuara) Indians of Ecuador. American Journal of Orthodontics 27:249-254.

Wright S. 1931. Evolution in Mendelian populations. Genetics 16:97-159.

Wright S. 1943. Isolation by distance. Genetics 28:114-138.

Wysner GM. 1945. The Kabyle People. New York: Privately Published.

Zakrzewski SR. 2007. Population continuity or population change: formation of the ancient Egyptian state. American Journal of Physical Anthropology 132:201-209.

Appendix I: Kellis 2 (K2) vs Kellis Townsite Burials (TS) dental trait frequencies

Premolar Lingual Cusp LP4 * Location

Crosstab

			Location		
			K2	TS	Total
PMLC LP4	0	Count	10	4	14
		Expected Count	12.2	1.8	14.0
	1	Count	30	2	32
		Expected Count	27.8	4.2	32.0
	Total	Count	40	6	46
		Expected Count	40.0	6.0	46.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	4.278[a]	1	.039		
Continuity Correction[b]	2.537	1	.111		
Likelihood Ratio	3.909	1	.048		
Fisher's Exact Test				.060	.060
N of Valid Cases	46				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.83.

b. Computed only for a 2x2 table

Molar Groove Pattern UM2 * Location

Crosstab

			Location		
			K2	TS	Total
MGP UM2	0	Count	85	8	93
		Expected Count	84.2	8.8	93.0
	1	Count	11	2	13
		Expected Count	11.8	1.2	13.0
	Total	Count	96	10	106
		Expected Count	96.0	10.0	106.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.614[a]	1	.433		
Continuity Correction[b]	.077	1	.782		
Likelihood Ratio	.538	1	.463		
Fisher's Exact Test				.354	.354
N of Valid Cases	106				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 1.23.

b. Computed only for a 2x2 table

Molar Cusp # UM2 * Location

Crosstab

			Location		
			K2	TS	Total
MC# UM2	0	Count	83	9	92
		Expected Count	84.3	7.7	92.0
	1	Count	16	0	16
		Expected Count	14.7	1.3	16.0
	Total	Count	99	9	108
		Expected Count	99.0	9.0	108.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.708[a]	1	.191		
Continuity Correction[b]	.667	1	.414		
Likelihood Ratio	3.025	1	.082		
Fisher's Exact Test				.350	.222
N of Valid Cases	108				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 1.33.

b. Computed only for a 2x2 table

Protostylid UM1 * Location

Crosstab

			Location		
			K2	TS	Total
Protostylid UM1	0	Count	44	5	49
		Expected Count	43.3	5.7	49.0
	1	Count	32	5	37
		Expected Count	32.7	4.3	37.0
	Total	Count	76	10	86
		Expected Count	76.0	10.0	86.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.225[a]	1	.635		
Continuity Correction[b]	.018	1	.893		
Likelihood Ratio	.223	1	.637		
Fisher's Exact Test				.739	.442
N of Valid Cases	86				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 4.30.

b. Computed only for a 2x2 table

Cusp 7 UM1 * Location

Crosstab

			Location		
			K2	TS	Total
C7 UM1	0	Count	91	9	100
		Expected Count	90.9	9.1	100.0
	1	Count	9	1	10
		Expected Count	9.1	.9	10.0
	Total	Count	100	10	110
		Expected Count	100.0	10.0	110.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.011[a]	1	.916		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.011	1	.918		
Fisher's Exact Test				1.000	.631
N of Valid Cases	110				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is .91.

b. Computed only for a 2x2 table

Tome's Root LP3 * Location

Crosstab

			Location		
			K2	TS	Total
TR LP3	0	Count	110	7	117
		Expected Count	110.2	6.8	117.0
	1	Count	19	1	20
		Expected Count	18.8	1.2	20.0
	Total	Count	129	8	137
		Expected Count	129.0	8.0	137.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.030[a]	1	.862		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.031	1	.860		
Fisher's Exact Test				1.000	.670
N of Valid Cases	137				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 1.17.

b. Computed only for a 2x2 table

Molar Root # LM2 * Location

Crosstab

			Location		
			K2	TS	Total
MR# LM2	0	Count	4	1	5
		Expected Count	4.9	.1	5.0
	1	Count	75	0	75
		Expected Count	74.1	.9	75.0
	Total	Count	79	1	80
		Expected Count	79.0	1.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	15.190[a]	1	.000		
Continuity Correction[b]	3.308	1	.069		
Likelihood Ratio	5.747	1	.017		
Fisher's Exact Test				.062	.062
N of Valid Cases	80				

a. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .06.

b. Computed only for a 2x2 table

Shovelling UI1 * Location

Crosstab

			Location		
			K2	TS	Total
shovel UI1	0	Count	67	6	73
		Expected Count	68.2	4.8	73.0
	1	Count	18	0	18
		Expected Count	16.8	1.2	18.0
	Total	Count	85	6	91
		Expected Count	85.0	6.0	91.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.584[a]	1	.208		
Continuity Correction[b]	.530	1	.466		
Likelihood Ratio	2.747	1	.097		
Fisher's Exact Test				.594	.255
N of Valid Cases	91				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.19.

b. Computed only for a 2x2 table

Interruption Groove UI2 * Location

Crosstab

			Location		
			K2	TS	Total
IG UI2	0	Count	84	3	87
		Expected Count	80.6	6.4	87.0
	1	Count	17	5	22
		Expected Count	20.4	1.6	22.0
	Total	Count	101	8	109
		Expected Count	101.0	8.0	109.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	9.597[a]	1	.002		
Continuity Correction[b]	6.971	1	.008		
Likelihood Ratio	7.507	1	.006		
Fisher's Exact Test				.008	.008
N of Valid Cases	109				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 1.61.

b. Computed only for a 2x2 table

Tuberculum dentale UI2 * Location

Crosstab

			Location		
			K2	TS	Total
TD UI2	0	Count	75	6	81
		Expected Count	74.8	6.2	81.0
	1	Count	10	1	11
		Expected Count	10.2	.8	11.0
	Total	Count	85	7	92
		Expected Count	85.0	7.0	92.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.039[a]	1	.843		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.037	1	.847		
Fisher's Exact Test				1.000	.603
N of Valid Cases	92				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is .84.

b. Computed only for a 2x2 table

Mesial Ridge UC * Location

Crosstab

			Location		
			K2	TS	Total
M. Ridge UC	0	Count	70	7	77
		Expected Count	70.1	6.9	77.0
	1	Count	1	0	1
		Expected Count	.9	.1	1.0
	Total	Count	71	7	78
		Expected Count	71.0	7.0	78.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.100[a]	1	.752		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.189	1	.663		
Fisher's Exact Test				1.000	.910
N of Valid Cases	78				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .09.

b. Computed only for a 2x2 table

Distal Accessory Ridge UC * Location

Crosstab

			Location		
			K2	TS	Total
DAR UC	0	Count	22	4	26
		Expected Count	22.6	3.4	26.0
	1	Count	11	1	12
		Expected Count	10.4	1.6	12.0
	Total	Count	33	5	38
		Expected Count	33.0	5.0	38.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.357[a]	1	.550		
Continuity Correction[b]	.007	1	.935		
Likelihood Ratio	.384	1	.536		
Fisher's Exact Test				1.000	.488
N of Valid Cases	38				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.58.

b. Computed only for a 2x2 table

Hypocone UM2 * Location

Crosstab

			Location		
			K2	TS	Total
Hypocone UM2	0	Count	25	2	27
		Expected Count	23.5	3.5	27.0
	1	Count	69	12	81
		Expected Count	70.5	10.5	81.0
	Total	Count	94	14	108
		Expected Count	94.0	14.0	108.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.985[a]	1	.321		
Continuity Correction[b]	.438	1	.508		
Likelihood Ratio	1.092	1	.296		
Fisher's Exact Test				.510	.263
N of Valid Cases	108				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 3.50.

b. Computed only for a 2x2 table

Cusp 5 UM1 * Location

Crosstab

			Location		
			K2	TS	Total
cusp 5 UM1	0	Count	85	7	92
		Expected Count	84.1	7.9	92.0
	1	Count	11	2	13
		Expected Count	11.9	1.1	13.0
	Total	Count	96	9	105
		Expected Count	96.0	9.0	105.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.879[a]	1	.349		
Continuity Correction[b]	.167	1	.683		
Likelihood Ratio	.749	1	.387		
Fisher's Exact Test				.308	.308
N of Valid Cases	105				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 1.11.

b. Computed only for a 2x2 table

Carabelli's Cusp UM1 * Location

Crosstab

			Location		
			K2	TS	Total
Carabelli UM1	0	Count	6	7	13
		Expected Count	11.3	1.7	13.0
	1	Count	65	4	69
		Expected Count	59.7	9.3	69.0
	Total	Count	71	11	82
		Expected Count	71.0	11.0	82.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	21.743[a]	1	.000		
Continuity Correction[b]	17.803	1	.000		
Likelihood Ratio	16.157	1	.000		
Fisher's Exact Test				.000	.000
N of Valid Cases	82				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 1.74.

b. Computed only for a 2x2 table

Enamel Extensions UM1 * Location

Crosstab

			Location		
			K2	TS	Total
EE UM1	0	Count	102	12	114
		Expected Count	102.6	11.4	114.0
	1	Count	6	0	6
		Expected Count	5.4	.6	6.0
	Total	Count	108	12	120
		Expected Count	108.0	12.0	120.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.702[a]	1	.402		
Continuity Correction[b]	.019	1	.889		
Likelihood Ratio	1.299	1	.254		
Fisher's Exact Test				1.000	.524
N of Valid Cases	120				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is .60.

b. Computed only for a 2x2 table

Premolar Root # UP3 * Location

Crosstab

			Location		
			K2	TS	Total
PMR# UP3	0	Count	58	5	63
		Expected Count	59.5	3.5	63.0
	1	Count	61	2	63
		Expected Count	59.5	3.5	63.0
	Total	Count	119	7	126
		Expected Count	119.0	7.0	126.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.361[a]	1	.243		
Continuity Correction[b]	.605	1	.437		
Likelihood Ratio	1.404	1	.236		
Fisher's Exact Test				.440	.220
N of Valid Cases	126				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.50.

b. Computed only for a 2x2 table

Molar Root # UM2 * Location

Crosstab

			Location		
			K2	TS	Total
MR# UM2	0	Count	21	1	22
		Expected Count	21.3	.7	22.0
	1	Count	75	2	77
		Expected Count	74.7	2.3	77.0
	Total	Count	96	3	99
		Expected Count	96.0	3.0	99.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.221[a]	1	.638		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.201	1	.654		
Fisher's Exact Test				.534	.534
N of Valid Cases	99				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .67.

b. Computed only for a 2x2 table

Peg-shaped Molar UM3 * Location

Crosstab

			Location		
			K2	TS	Total
Peg.Mol. UM3	0	Count	69	11	80
		Expected Count	69.5	10.5	80.0
	1	Count	4	0	4
		Expected Count	3.5	.5	4.0
	Total	Count	73	11	84
		Expected Count	73.0	11.0	84.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.633[a]	1	.426		
Continuity Correction[b]	.001	1	.971		
Likelihood Ratio	1.153	1	.283		
Fisher's Exact Test				1.000	.564
N of Valid Cases	84				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .52.

b. Computed only for a 2x2 table

Congenital Absence UM3 * Location

Crosstab

			Location		
			K2	TS	Total
CA UM3	0	Count	98	12	110
		Expected Count	98.6	11.4	110.0
	1	Count	6	0	6
		Expected Count	5.4	.6	6.0
	Total	Count	104	12	116
		Expected Count	104.0	12.0	116.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.730[a]	1	.393		
Continuity Correction[b]	.028	1	.868		
Likelihood Ratio	1.348	1	.246		
Fisher's Exact Test				1.000	.511
N of Valid Cases	116				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is .62.

b. Computed only for a 2x2 table

Appendix II: Combined (K2 + TS) Kellis male vs female dichotomized trait frequencies with Chi-Square analysis

Shovelling LI1 * Sex

Crosstab

			Sex		
			F	M	Total
Shovelling_LI1	0	Count	40	36	76
		Expected Count	40.5	35.5	76.0
	1	Count	1	0	1
		Expected Count	.5	.5	1.0
	Total	Count	41	36	77
		Expected Count	41.0	36.0	77.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.890[a]	1	.346		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.272	1	.259		
Fisher's Exact Test				1.000	.532
N of Valid Cases	77				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .47.

b. Computed only for a 2x2 table

Shovelling LI2 * Sex

Crosstab

			Sex		
			F	M	Total
Shovelling_LI2	0	Count	45	39	84
		Expected Count	45.5	38.5	84.0
	1	Count	1	0	1
		Expected Count	.5	.5	1.0
	Total	Count	46	39	85
		Expected Count	46.0	39.0	85.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.858[a]	1	.354		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.238	1	.266		
Fisher's Exact Test				1.000	.541
N of Valid Cases	85				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .46.

b. Computed only for a 2x2 table

Distal Accessory Ridge LC * Sex

Crosstab

			Sex		
			F	M	Total
DAR_LC	0	Count	17	16	33
		Expected Count	17.5	15.5	33.0
	1	Count	1	0	1
		Expected Count	.5	.5	1.0
	Total	Count	18	16	34
		Expected Count	18.0	16.0	34.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.916[a]	1	.339		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.299	1	.254		
Fisher's Exact Test				1.000	.529
N of Valid Cases	34				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .47.

b. Computed only for a 2x2 table

Lingual cusp LP3 * Sex

Crosstab

			Sex		
			F	M	Total
PMLC_LP3	0	Count	18	25	43
		Expected Count	17.5	25.5	43.0
	1	Count	4	7	11
		Expected Count	4.5	6.5	11.0
	Total	Count	22	32	54
		Expected Count	22.0	32.0	54.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.110[a]	1	.741		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.111	1	.739		
Fisher's Exact Test				1.000	.510
N of Valid Cases	54				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 4.48.

b. Computed only for a 2x2 table

Lingual cusp LP4 * Sex

Crosstab

			Sex		
			F	M	Total
PMLC_LP4	0	Count	3	8	11
		Expected Count	4.5	6.5	11.0
	1	Count	10	11	21
		Expected Count	8.5	12.5	21.0
	Total	Count	13	19	32
		Expected Count	13.0	19.0	32.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.239[a]	1	.266		
Continuity Correction[b]	.539	1	.463		
Likelihood Ratio	1.274	1	.259		
Fisher's Exact Test				.450	.233
N of Valid Cases	32				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 4.47.

b. Computed only for a 2x2 table

Anterior fovea LM1 * Sex

Crosstab

			Sex		
			F	M	Total
AF_LM1	0	Count	2	3	5
		Expected Count	2.5	2.5	5.0
	1	Count	1	0	1
		Expected Count	.5	.5	1.0
	Total	Count	3	3	6
		Expected Count	3.0	3.0	6.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.200[a]	1	.273		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.588	1	.208		
Fisher's Exact Test				1.000	.500
N of Valid Cases	6				

a. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .50.

b. Computed only for a 2x2 table

Y-groove LM1 * Sex

Crosstab

			Sex		
			F	M	Total
Ygroove_LM1	0	Count	4	5	9
		Expected Count	4.2	4.8	9.0
	1	Count	28	31	59
		Expected Count	27.8	31.2	59.0
	Total	Count	32	36	68
		Expected Count	32.0	36.0	68.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.028[a]	1	.866		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.029	1	.866		
Fisher's Exact Test				1.000	.577
N of Valid Cases	68				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 4.24.

b. Computed only for a 2x2 table

Y-groove LM2 * Sex

Crosstab

			Sex		
			F	M	Total
Ygroove_LM2	0	Count	38	37	75
		Expected Count	36.2	38.8	75.0
	1	Count	3	7	10
		Expected Count	4.8	5.2	10.0
	Total	Count	41	44	85
		Expected Count	41.0	44.0	85.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.509[a]	1	.219		
Continuity Correction[b]	.795	1	.373		
Likelihood Ratio	1.553	1	.213		
Fisher's Exact Test				.316	.187
N of Valid Cases	85				

a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 4.82.

b. Computed only for a 2x2 table

4-cusped LM1 * Sex

Crosstab

			Sex		
			F	M	Total
4 cusps_LM1	0	Count	32	34	66
		Expected Count	31.6	34.4	66.0
	1	Count	3	4	7
		Expected Count	3.4	3.6	7.0
	Total	Count	35	38	73
		Expected Count	35.0	38.0	73.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.080[a]	1	.777		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.081	1	.776		
Fisher's Exact Test				1.000	.547
N of Valid Cases	73				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.36.

b. Computed only for a 2x2 table

5 or more cusps LM2 * Sex

Crosstab

			Sex		
			F	M	Total
5 or more cusps_LM2	0	Count	39	36	75
		Expected Count	36.2	38.8	75.0
	1	Count	3	9	12
		Expected Count	5.8	6.2	12.0
	Total	Count	42	45	87
		Expected Count	42.0	45.0	87.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	3.020[a]	1	.082		
Continuity Correction[b]	2.036	1	.154		
Likelihood Ratio	3.156	1	.076		
Fisher's Exact Test				.120	.075
N of Valid Cases	87				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 5.79.

b. Computed only for a 2x2 table

Deflecting wrinkle LM1 * Sex

Crosstab

			Sex		
			F	M	Total
DW_LM1	0	Count	0	1	1
		Expected Count	.3	.8	1.0
	1	Count	1	2	3
		Expected Count	.8	2.3	3.0
	Total	Count	1	3	4
		Expected Count	1.0	3.0	4.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.444[a]	1	.505		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.680	1	.410		
Fisher's Exact Test				1.000	.750
N of Valid Cases	4				

a. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .25.

b. Computed only for a 2x2 table

Protostylid LM1 * Sex

Crosstab

			Sex		
			F	M	Total
Protostylid_LM1	0	Count	13	18	31
		Expected Count	13.5	17.5	31.0
	1	Count	11	13	24
		Expected Count	10.5	13.5	24.0
	Total	Count	24	31	55
		Expected Count	24.0	31.0	55.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.084[a]	1	.773		
Continuity Correction[b]	.000	1	.988		
Likelihood Ratio	.084	1	.773		
Fisher's Exact Test				.791	.493
N of Valid Cases	55				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 10.47.

b. Computed only for a 2x2 table

Protostylid LM2 * Sex

Crosstab

			Sex		
			F	M	Total
Protostylid_LM2	0	Count	21	25	46
		Expected Count	21.7	24.3	46.0
	1	Count	13	13	26
		Expected Count	12.3	13.7	26.0
	Total	Count	34	38	72
		Expected Count	34.0	38.0	72.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.126[a]	1	.723		
Continuity Correction[b]	.012	1	.913		
Likelihood Ratio	.126	1	.723		
Fisher's Exact Test				.808	.456
N of Valid Cases	72				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 12.28.

b. Computed only for a 2x2 table

Cusp 6 LM1 * Sex

Crosstab

			Sex		
			F	M	Total
C6_LM1	0	Count	31	32	63
		Expected Count	30.6	32.4	63.0
	1	Count	4	5	9
		Expected Count	4.4	4.6	9.0
	Total	Count	35	37	72
		Expected Count	35.0	37.0	72.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.071[a]	1	.789		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.072	1	.789		
Fisher's Exact Test				1.000	.536
N of Valid Cases	72				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 4.38.

b. Computed only for a 2x2 table

Cusp 6 LM2 * Sex

Crosstab

			Sex		
			F	M	Total
C6_LM2	0	Count	42	42	84
		Expected Count	41.0	43.0	84.0
	1	Count	0	2	2
		Expected Count	1.0	1.0	2.0
	Total	Count	42	44	86
		Expected Count	42.0	44.0	86.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.955[a]	1	.162		
Continuity Correction[b]	.466	1	.495		
Likelihood Ratio	2.726	1	.099		
Fisher's Exact Test				.494	.259
N of Valid Cases	86				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .98.

b. Computed only for a 2x2 table

Cusp 7 LM1 * Sex

Crosstab

			Sex		
			F	M	Total
C7_LM1	0	Count	34	34	68
		Expected Count	32.6	35.4	68.0
	1	Count	2	5	7
		Expected Count	3.4	3.6	7.0
	Total	Count	36	39	75
		Expected Count	36.0	39.0	75.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.168[a]	1	.280		
Continuity Correction[b]	.467	1	.494		
Likelihood Ratio	1.208	1	.272		
Fisher's Exact Test				.433	.250
N of Valid Cases	75				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.36.

b. Computed only for a 2x2 table

Cusp 7 LM2 * Sex

Crosstab

			Sex		
			F	M	Total
C7_LM2	0	Count	43	42	85
		Expected Count	42.0	43.0	85.0
	1	Count	0	2	2
		Expected Count	1.0	1.0	2.0
	Total	Count	43	44	87
		Expected Count	43.0	44.0	87.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	2.001[a]	1	.157		
Continuity Correction[b]	.489	1	.485		
Likelihood Ratio	2.773	1	.096		
Fisher's Exact Test				.494	.253
N of Valid Cases	87				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .99.

b. Computed only for a 2x2 table

2-rooted LC * Sex

Crosstab

			Sex		
			F	M	Total
2roots_LC	0	Count	65	44	109
		Expected Count	63.5	45.5	109.0
	1	Count	9	9	18
		Expected Count	10.5	7.5	18.0
	Total	Count	74	53	127
		Expected Count	74.0	53.0	127.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.590[a]	1	.443		
Continuity Correction[b]	.260	1	.610		
Likelihood Ratio	.583	1	.445		
Fisher's Exact Test				.452	.303
N of Valid Cases	127				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 7.51.

b. Computed only for a 2x2 table

Tome's root LP3 * Sex

Crosstab

			Sex		
			F	M	Total
TR_LP3	0	Count	59	42	101
		Expected Count	56.5	44.5	101.0
	1	Count	7	10	17
		Expected Count	9.5	7.5	17.0
	Total	Count	66	52	118
		Expected Count	66.0	52.0	118.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.754[a]	1	.185		
Continuity Correction[b]	1.125	1	.289		
Likelihood Ratio	1.742	1	.187		
Fisher's Exact Test				.199	.145
N of Valid Cases	118				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 7.49.

b. Computed only for a 2x2 table

3-rooted LM1 * Sex

Crosstab

			Sex		
			F	M	Total
3root_LM1	0	Count	36	37	73
		Expected Count	36.5	36.5	73.0
	1	Count	1	0	1
		Expected Count	.5	.5	1.0
	Total	Count	37	37	74
		Expected Count	37.0	37.0	74.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.014[a]	1	.314		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.400	1	.237		
Fisher's Exact Test				1.000	.500
N of Valid Cases	74				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .50.

b. Computed only for a 2x2 table

2-rooted LM2 * Sex

Crosstab

			Sex		
			F	M	Total
2root_LM2	0	Count	4	2	6
		Expected Count	2.8	3.2	6.0
	1	Count	27	33	60
		Expected Count	28.2	31.8	60.0
	Total	Count	31	35	66
		Expected Count	31.0	35.0	66.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.028[a]	1	.311		
Continuity Correction[b]	.342	1	.559		
Likelihood Ratio	1.038	1	.308		
Fisher's Exact Test				.408	.280
N of Valid Cases	66				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.82.

b. Computed only for a 2x2 table

Congenital absence LP4 * Sex

Crosstab

			Sex		
			F	M	Total
CA_LP4	0	Count	67	55	122
		Expected Count	65.9	56.1	122.0
	1	Count	0	2	2
		Expected Count	1.1	.9	2.0
	Total	Count	67	57	124
		Expected Count	67.0	57.0	124.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	2.389[a]	1	.122		
Continuity Correction[b]	.690	1	.406		
Likelihood Ratio	3.147	1	.076		
Fisher's Exact Test				.209	.209
N of Valid Cases	124				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .92.

b. Computed only for a 2x2 table

Congenital absence LM3 * Sex

Crosstab

			Sex		
			F	M	Total
CA_LM3	0	Count	42	50	92
		Expected Count	44.1	47.9	92.0
	1	Count	4	0	4
		Expected Count	1.9	2.1	4.0
	Total	Count	46	50	96
		Expected Count	46.0	50.0	96.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	4.537[a]	1	.033		
Continuity Correction[b]	2.620	1	.105		
Likelihood Ratio	6.075	1	.014		
Fisher's Exact Test				.049	.049
N of Valid Cases	96				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.92.

b. Computed only for a 2x2 table

Winging UI1 * Sex

Crosstab

			Sex		
			F	M	Total
Winging_UI1	0	Count	57	42	99
		Expected Count	57.8	41.2	99.0
	1	Count	2	0	2
		Expected Count	1.2	.8	2.0
	Total	Count	59	42	101
		Expected Count	59.0	42.0	101.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.452[a]	1	.228		
Continuity Correction[b]	.231	1	.631		
Likelihood Ratio	2.179	1	.140		
Fisher's Exact Test				.509	.339
N of Valid Cases	101				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .83.

b. Computed only for a 2x2 table

Shoveling UC * Sex

Crosstab

			Sex		
			F	M	Total
Shovel_UC	0	Count	32	30	62
		Expected Count	31.4	30.6	62.0
	1	Count	3	4	7
		Expected Count	3.6	3.4	7.0
	Total	Count	35	34	69
		Expected Count	35.0	34.0	69.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.193[a]	1	.660		
Continuity Correction[b]	.002	1	.968		
Likelihood Ratio	.193	1	.660		
Fisher's Exact Test				.710	.483
N of Valid Cases	69				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.45.

b. Computed only for a 2x2 table

Shoveling UI2 * Sex

Crosstab

			Sex		
			F	M	Total
Shovel_UI2	0	Count	21	24	45
		Expected Count	22.2	22.8	45.0
	1	Count	14	12	26
		Expected Count	12.8	13.2	26.0
	Total	Count	35	36	71
		Expected Count	35.0	36.0	71.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.340[a]	1	.560		
Continuity Correction[b]	.113	1	.736		
Likelihood Ratio	.340	1	.560		
Fisher's Exact Test				.627	.368
N of Valid Cases	71				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 12.82.

b. Computed only for a 2x2 table

Shoveling UI1 * Sex

Crosstab

			Sex		
			F	M	Total
Shovel_UI1	0	Count	27	26	53
		Expected Count	28.1	24.9	53.0
	1	Count	9	6	15
		Expected Count	7.9	7.1	15.0
	Total	Count	36	32	68
		Expected Count	36.0	32.0	68.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.385[a]	1	.535		
Continuity Correction[b]	.107	1	.743		
Likelihood Ratio	.388	1	.534		
Fisher's Exact Test				.573	.373
N of Valid Cases	68				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 7.06.

b. Computed only for a 2x2 table

Labial convexity UI2 * Sex

Crosstab

			Sex		
			F	M	Total
Lab.Co._UI2	0	Count	0	1	1
		Expected Count	.5	.5	1.0
	1	Count	45	38	83
		Expected Count	44.5	38.5	83.0
	Total	Count	45	39	84
		Expected Count	45.0	39.0	84.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.168[a]	1	.280		
Continuity Correction[b]	.005	1	.943		
Likelihood Ratio	1.548	1	.213		
Fisher's Exact Test				.464	.464
N of Valid Cases	84				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .46.

b. Computed only for a 2x2 table

Labial convexity UI1 * Sex

Crosstab

			Sex		
			F	M	Total
Lab.Co._UI1	0	Count	5	8	13
		Expected Count	7.5	5.5	13.0
	1	Count	42	27	69
		Expected Count	39.5	29.5	69.0
	Total	Count	47	35	82
		Expected Count	47.0	35.0	82.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	2.245[a]	1	.134		
Continuity Correction[b]	1.423	1	.233		
Likelihood Ratio	2.223	1	.136		
Fisher's Exact Test				.221	.117
N of Valid Cases	82				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 5.55.

b. Computed only for a 2x2 table

Double Shovelling UC * Sex

Crosstab

			Sex		
			F	M	Total
Dbl.Shov._UC	0	Count	49	39	88
		Expected Count	47.9	40.1	88.0
	1	Count	0	2	2
		Expected Count	1.1	.9	2.0
	Total	Count	49	41	90
		Expected Count	49.0	41.0	90.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	2.445[a]	1	.118		
Continuity Correction[b]	.715	1	.398		
Likelihood Ratio	3.199	1	.074		
Fisher's Exact Test				.205	.205
N of Valid Cases	90				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .91.

b. Computed only for a 2x2 table

Double Shovelling UI2 * Sex

Crosstab

			Sex		
			F	M	Total
Dbl.Shov._UI2	0	Count	44	39	83
		Expected Count	43.5	39.5	83.0
	1	Count	0	1	1
		Expected Count	.5	.5	1.0
	Total	Count	44	40	84
		Expected Count	44.0	40.0	84.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.113[a]	1	.291		
Continuity Correction[b]	.002	1	.962		
Likelihood Ratio	1.497	1	.221		
Fisher's Exact Test				.476	.476
N of Valid Cases	84				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .48.

b. Computed only for a 2x2 table

Interruption groove UI2 * Sex

Crosstab

			Sex		
			F	M	Total
IG_UI2	0	Count	40	33	73
		Expected Count	41.3	31.7	73.0
	1	Count	12	7	19
		Expected Count	10.7	8.3	19.0
	Total	Count	52	40	92
		Expected Count	52.0	40.0	92.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.429[a]	1	.512		
Continuity Correction[b]	.156	1	.693		
Likelihood Ratio	.434	1	.510		
Fisher's Exact Test				.608	.349
N of Valid Cases	92				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 8.26.

b. Computed only for a 2x2 table

Interruption groove UI1 * Sex

Crosstab

			Sex		
			F	M	Total
IG_UI1	0	Count	54	39	93
		Expected Count	53.3	39.7	93.0
	1	Count	1	2	3
		Expected Count	1.7	1.3	3.0
	Total	Count	55	41	96
		Expected Count	55.0	41.0	96.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.726[a]	1	.394		
Continuity Correction[b]	.067	1	.795		
Likelihood Ratio	.721	1	.396		
Fisher's Exact Test				.574	.390
N of Valid Cases	96				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.28.

b. Computed only for a 2x2 table

Tuberculum dentale UC * Sex

Crosstab

			Sex		
			F	M	Total
TD_UC	0	Count	29	21	50
		Expected Count	25.7	24.3	50.0
	1	Count	9	15	24
		Expected Count	12.3	11.7	24.0
	Total	Count	38	36	74
		Expected Count	38.0	36.0	74.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	2.728[a]	1	.099		
Continuity Correction[b]	1.969	1	.161		
Likelihood Ratio	2.747	1	.097		
Fisher's Exact Test				.137	.080
N of Valid Cases	74				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 11.68.

b. Computed only for a 2x2 table

Tuberculum dentale UI2 * Sex

Crosstab

			Sex		
			F	M	Total
TD_UI2	0	Count	35	31	66
		Expected Count	35.3	30.7	66.0
	1	Count	4	3	7
		Expected Count	3.7	3.3	7.0
	Total	Count	39	34	73
		Expected Count	39.0	34.0	73.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.043[a]	1	.836		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.043	1	.835		
Fisher's Exact Test				1.000	.578
N of Valid Cases	73				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.26.

b. Computed only for a 2x2 table

Tuberculum dentale UI1 * Sex

Crosstab

			Sex		
			F	M	Total
TD_UI1	0	Count	27	26	53
		Expected Count	27.6	25.4	53.0
	1	Count	10	8	18
		Expected Count	9.4	8.6	18.0
	Total	Count	37	34	71
		Expected Count	37.0	34.0	71.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.115[a]	1	.735		
Continuity Correction[b]	.004	1	.948		
Likelihood Ratio	.115	1	.735		
Fisher's Exact Test				.790	.475
N of Valid Cases	71				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 8.62.

b. Computed only for a 2x2 table

Mesial ridge UC * Sex

Crosstab

			Sex		
			F	M	Total
M.Ridge_UC	0	Count	31	29	60
		Expected Count	31.5	28.5	60.0
	1	Count	1	0	1
		Expected Count	.5	.5	1.0
	Total	Count	32	29	61
		Expected Count	32.0	29.0	61.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.921[a]	1	.337		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.305	1	.253		
Fisher's Exact Test				1.000	.525
N of Valid Cases	61				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .48.

b. Computed only for a 2x2 table

Distal accessory ridge UC * Sex

Crosstab

			Sex		
			F	M	Total
DAR_UC	0	Count	9	8	17
		Expected Count	8.5	8.5	17.0
	1	Count	3	4	7
		Expected Count	3.5	3.5	7.0
	Total	Count	12	12	24
		Expected Count	12.0	12.0	24.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.202[a]	1	.653		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.202	1	.653		
Fisher's Exact Test				1.000	.500
N of Valid Cases	24				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.50.

b. Computed only for a 2x2 table

Metacone UM2 * Sex

Crosstab

			Sex		
			F	M	Total
Metacone_UM2	0	Count	2	0	2
		Expected Count	1.1	.9	2.0
	1	Count	47	40	87
		Expected Count	47.9	39.1	87.0
	Total	Count	49	40	89
		Expected Count	49.0	40.0	89.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.670[a]	1	.196		
Continuity Correction[b]	.329	1	.566		
Likelihood Ratio	2.425	1	.119		
Fisher's Exact Test				.499	.300
N of Valid Cases	89				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .90.

b. Computed only for a 2x2 table

Hypocone UM2 * Sex

Crosstab

			Sex		
			F	M	Total
Hypocone_UM2	0	Count	12	8	20
		Expected Count	11.5	8.5	20.0
	1	Count	37	28	65
		Expected Count	37.5	27.5	65.0
	Total	Count	49	36	85
		Expected Count	49.0	36.0	85.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.059[a]	1	.808		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.060	1	.807		
Fisher's Exact Test				1.000	.509
N of Valid Cases	85				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 8.47.

b. Computed only for a 2x2 table

Cusp 5 (metaconule) UM2 * Sex

Crosstab

			Sex		
			F	M	Total
Cusp5_UM2	0	Count	37	30	67
		Expected Count	37.0	30.0	67.0
	1	Count	5	4	9
		Expected Count	5.0	4.0	9.0
	Total	Count	42	34	76
		Expected Count	42.0	34.0	76.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.000[a]	1	.985		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.000	1	.985		
Fisher's Exact Test				1.000	.635
N of Valid Cases	76				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 4.03.

b. Computed only for a 2x2 table

Cusp 5 (metaconule) UM1 * Sex

Crosstab

			Sex		
			F	M	Total
Cusp5_UM1	0	Count	37	25	62
		Expected Count	36.8	25.2	62.0
	1	Count	4	3	7
		Expected Count	4.2	2.8	7.0
	Total	Count	41	28	69
		Expected Count	41.0	28.0	69.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.017[a]	1	.897		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.017	1	.897		
Fisher's Exact Test				1.000	.600
N of Valid Cases	69				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.84.

b. Computed only for a 2x2 table

Carabelli's cusp UM2 * Sex

Crosstab

			Sex		
			F	M	Total
Carabelli_UM2	0	Count	39	29	68
		Expected Count	40.1	27.9	68.0
	1	Count	4	1	5
		Expected Count	2.9	2.1	5.0
	Total	Count	43	30	73
		Expected Count	43.0	30.0	73.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.987[a]	1	.321		
Continuity Correction[b]	.273	1	.601		
Likelihood Ratio	1.076	1	.300		
Fisher's Exact Test				.643	.311
N of Valid Cases	73				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.05.

b. Computed only for a 2x2 table

Carabelli's cusp UM1 * Sex

Crosstab

			Sex		
			F	M	Total
Carabelli_UM1	0	Count	2	6	8
		Expected Count	3.8	4.2	8.0
	1	Count	21	20	41
		Expected Count	19.2	21.8	41.0
	Total	Count	23	26	49
		Expected Count	23.0	26.0	49.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.848[a]	1	.174		
Continuity Correction[b]	.945	1	.331		
Likelihood Ratio	1.934	1	.164		
Fisher's Exact Test				.254	.166
N of Valid Cases	49				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.76.

b. Computed only for a 2x2 table

Parastyle UM3 * Sex

Crosstab

			Sex		
			F	M	Total
Parastyle_UM3	0	Count	37	27	64
		Expected Count	37.4	26.6	64.0
	1	Count	1	0	1
		Expected Count	.6	.4	1.0
	Total	Count	38	27	65
		Expected Count	38.0	27.0	65.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.722[a]	1	.396		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.085	1	.298		
Fisher's Exact Test				1.000	.585
N of Valid Cases	65				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .42.

b. Computed only for a 2x2 table

Parastyle UM2 * Sex

Crosstab

			Sex		
			F	M	Total
Parastyle_UM2	0	Count	45	35	80
		Expected Count	44.4	35.6	80.0
	1	Count	0	1	1
		Expected Count	.6	.4	1.0
	Total	Count	45	36	81
		Expected Count	45.0	36.0	81.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.266[a]	1	.261		
Continuity Correction[b]	.013	1	.910		
Likelihood Ratio	1.638	1	.201		
Fisher's Exact Test				.444	.444
N of Valid Cases	81				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .44.

b. Computed only for a 2x2 table

Parastyle UM1 * Sex

Crosstab

			Sex		
			F	M	Total
Parastyle_UM1	0	Count	41	34	75
		Expected Count	41.4	33.6	75.0
	1	Count	1	0	1
		Expected Count	.6	.4	1.0
	Total	Count	42	34	76
		Expected Count	42.0	34.0	76.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.820[a]	1	.365		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.197	1	.274		
Fisher's Exact Test				1.000	.553
N of Valid Cases	76				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .45.

b. Computed only for a 2x2 table

Enamel extensions UM3 * Sex

Crosstab

			Sex		
			F	M	Total
EE_UM3	0	Count	32	27	59
		Expected Count	32.3	26.7	59.0
	1	Count	3	2	5
		Expected Count	2.7	2.3	5.0
	Total	Count	35	29	64
		Expected Count	35.0	29.0	64.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.062[a]	1	.804		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.062	1	.803		
Fisher's Exact Test				1.000	.590
N of Valid Cases	64				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.27.

b. Computed only for a 2x2 table

Enamel extensions UM2 * Sex

Crosstab

			Sex		
			F	M	Total
EE_UM2	0	Count	41	35	76
		Expected Count	42.8	33.3	76.0
	1	Count	4	0	4
		Expected Count	2.3	1.8	4.0
	Total	Count	45	35	80
		Expected Count	45.0	35.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	3.275[a]	1	.070		
Continuity Correction[b]	1.671	1	.196		
Likelihood Ratio	4.766	1	.029		
Fisher's Exact Test				.127	.094
N of Valid Cases	80				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.75.

b. Computed only for a 2x2 table

Enamel extensions UM1 * Sex

Crosstab

			Sex		
			F	M	Total
EE_UM1	0	Count	49	35	84
		Expected Count	50.0	34.0	84.0
	1	Count	4	1	5
		Expected Count	3.0	2.0	5.0
	Total	Count	53	36	89
		Expected Count	53.0	36.0	89.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.920[a]	1	.338		
Continuity Correction[b]	.240	1	.624		
Likelihood Ratio	1.004	1	.316		
Fisher's Exact Test				.644	.323
N of Valid Cases	89				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.02.

b. Computed only for a 2x2 table

Enamel extensions UP3 * Sex

Crosstab

			Sex		
			F	M	Total
EE_UP3	0	Count	52	46	98
		Expected Count	52.5	45.5	98.0
	1	Count	1	0	1
		Expected Count	.5	.5	1.0
	Total	Count	53	46	99
		Expected Count	53.0	46.0	99.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.877[a]	1	.349		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.259	1	.262		
Fisher's Exact Test				1.000	.535
N of Valid Cases	99				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .46.

b. Computed only for a 2x2 table

2-rooted UP4 * Sex

Crosstab

			Sex		
			F	M	Total
2root_UP4	0	Count	55	41	96
		Expected Count	53.3	42.7	96.0
	1	Count	5	7	12
		Expected Count	6.7	5.3	12.0
	Total	Count	60	48	108
		Expected Count	60.0	48.0	108.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.055[a]	1	.304		
Continuity Correction[b]	.517	1	.472		
Likelihood Ratio	1.048	1	.306		
Fisher's Exact Test				.364	.235
N of Valid Cases	108				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 5.33.

b. Computed only for a 2x2 table

2-rooted UP3 * Sex

Crosstab

			Sex		
			F	M	Total
2root_UP1	0	Count	34	19	53
		Expected Count	29.2	23.8	53.0
	1	Count	26	30	56
		Expected Count	30.8	25.2	56.0
	Total	Count	60	49	109
		Expected Count	60.0	49.0	109.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	3.456[a]	1	.063		
Continuity Correction[b]	2.777	1	.096		
Likelihood Ratio	3.478	1	.062		
Fisher's Exact Test				.083	.048
N of Valid Cases	109				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 23.83.

b. Computed only for a 2x2 table

3-rooted UM2 * Sex

Crosstab

			Sex		
			F	M	Total
3root_UM2	0	Count	12	6	18
		Expected Count	9.8	8.2	18.0
	1	Count	35	33	68
		Expected Count	37.2	30.8	68.0
	Total	Count	47	39	86
		Expected Count	47.0	39.0	86.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.326[a]	1	.249		
Continuity Correction[b]	.784	1	.376		
Likelihood Ratio	1.352	1	.245		
Fisher's Exact Test				.295	.189
N of Valid Cases	86				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 8.16.

b. Computed only for a 2x2 table

3-rooted UM1 * Sex

Crosstab

			Sex		
			F	M	Total
3root_UM1	0	Count	4	2	6
		Expected Count	3.4	2.6	6.0
	1	Count	54	43	97
		Expected Count	54.6	42.4	97.0
	Total	Count	58	45	103
		Expected Count	58.0	45.0	103.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.278[a]	1	.598		
Continuity Correction[b]	.011	1	.918		
Likelihood Ratio	.285	1	.594		
Fisher's Exact Test				.694	.466
N of Valid Cases	103				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.62.

b. Computed only for a 2x2 table

Peg-shaped UM3 * Sex

Crosstab

			Sex		
			F	M	Total
Peg_UM3	0	Count	39	32	71
		Expected Count	38.8	32.2	71.0
	1	Count	2	2	4
		Expected Count	2.2	1.8	4.0
	Total	Count	41	34	75
		Expected Count	41.0	34.0	75.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.037[a]	1	.847		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.037	1	.848		
Fisher's Exact Test				1.000	.618
N of Valid Cases	75				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.81.

b. Computed only for a 2x2 table

Congenital absence UM3 * Sex

Crosstab

			Sex		
			F	M	Total
CA_UM3	0	Count	51	46	97
		Expected Count	52.3	44.7	97.0
	1	Count	4	1	5
		Expected Count	2.7	2.3	5.0
	Total	Count	55	47	102
		Expected Count	55.0	47.0	102.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.439[a]	1	.230		
Continuity Correction[b]	.547	1	.460		
Likelihood Ratio	1.557	1	.212		
Fisher's Exact Test				.370	.234
N of Valid Cases	102				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.30.

b. Computed only for a 2x2 table

Congenital absence UP4 * Sex

Crosstab

			Sex		
			F	M	Total
CA_UP4	0	Count	72	57	129
		Expected Count	71.9	57.1	129.0
	1	Count	1	1	2
		Expected Count	1.1	.9	2.0
	Total	Count	73	58	131
		Expected Count	73.0	58.0	131.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.027[a]	1	.870		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.027	1	.870		
Fisher's Exact Test				1.000	.691
N of Valid Cases	131				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .89.

b. Computed only for a 2x2 table

Congenital absence UI2 * Sex

Crosstab

			Sex		
			F	M	Total
CA_UI2	0	Count	73	59	132
		Expected Count	73.4	58.6	132.0
	1	Count	1	0	1
		Expected Count	.6	.4	1.0
	Total	Count	74	59	133
		Expected Count	74.0	59.0	133.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.803[a]	1	.370		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	1.179	1	.278		
Fisher's Exact Test				1.000	.556
N of Valid Cases	133				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .44.

b. Computed only for a 2x2 table

Appendix III: Kellis 2 cemetery groups dichotomized trait frequencies with Chi-Square analysis

Shovelling LI1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Shovelling_LI1	0	Count	19	26	15	28	88
		Expected Count	18.8	25.7	14.8	28.7	88.0
	1	Count	0	0	0	1	1
		Expected Count	.2	.3	.2	.3	1.0
	Total	Count	19	26	15	29	89
		Expected Count	19.0	26.0	15.0	29.0	89.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.092[a]	3	.553
Likelihood Ratio	2.266	3	.519
N of Valid Cases	89		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .17.

Shovelling LI2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Shovelling_LI2	0	Count	23	27	15	29	94
		Expected Count	22.8	26.7	14.8	29.7	94.0
	1	Count	0	0	0	1	1
		Expected Count	.2	.3	.2	.3	1.0
	Total	Count	23	27	15	30	95
		Expected Count	23.0	27.0	15.0	30.0	95.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.190[a]	3	.534
Likelihood Ratio	2.329	3	.507
N of Valid Cases	95		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .16.

Distal accessory ridge LC * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
DAR_LC	0	Count	13	10	6	10	39
		Expected Count	13.0	10.2	5.6	10.2	39.0
	1	Count	1	1	0	1	3
		Expected Count	1.0	.8	.4	.8	3.0
	Total	Count	14	11	6	11	42
		Expected Count	14.0	11.0	6.0	11.0	42.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	.587[a]	3	.899
Likelihood Ratio	1.006	3	.800
N of Valid Cases	42		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .43.

Lingual cusp LP3 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
PMLC_LP3	0	Count	15	14	8	9	46
		Expected Count	15.1	13.5	6.3	11.1	46.0
	1	Count	4	3	0	5	12
		Expected Count	3.9	3.5	1.7	2.9	12.0
	Total	Count	19	17	8	14	58
		Expected Count	19.0	17.0	8.0	14.0	58.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.110[a]	3	.250
Likelihood Ratio	5.489	3	.139
N of Valid Cases	58		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.66.

Lingual cusp LP4 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
PMLC_LP4	0	Count	6	2	0	2	10
		Expected Count	3.5	3.3	1.0	2.3	10.0
	1	Count	8	11	4	7	30
		Expected Count	10.5	9.8	3.0	6.8	30.0
	Total	Count	14	13	4	9	40
		Expected Count	14.0	13.0	4.0	9.0	40.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.392[a]	3	.222
Likelihood Ratio	5.168	3	.160
N of Valid Cases	40		

a. 5 cells (62.5%) have expected count less than 5. The minimum expected count is 1.00.

Anterior fovea LM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
AF_LM1	0	Count	4	5	1	3	13
		Expected Count	4.5	4.0	.9	3.6	13.0
	1	Count	6	4	1	5	16
		Expected Count	5.5	5.0	1.1	4.4	16.0
	Total	Count	10	9	2	8	29
		Expected Count	10.0	9.0	2.0	8.0	29.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	.708[a]	3	.871
Likelihood Ratio	.708	3	.871
N of Valid Cases	29		

a. 7 cells (87.5%) have expected count less than 5. The minimum expected count is .90.

Y-groove LM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Ygroove_LM1	0	Count	6	2	1	2	11
		Expected Count	3.1	2.9	1.3	3.6	11.0
	1	Count	20	22	10	28	80
		Expected Count	22.9	21.1	9.7	26.4	80.0
	Total	Count	26	24	11	30	91
		Expected Count	26.0	24.0	11.0	30.0	91.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.196[a]	3	.241
Likelihood Ratio	3.842	3	.279
N of Valid Cases	91		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.33.

Y-groove LM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Ygroove_LM2	0	Count	21	19	17	26	83
		Expected Count	22.1	19.4	15.0	26.5	83.0
	1	Count	4	3	0	4	11
		Expected Count	2.9	2.6	2.0	3.5	11.0
	Total	Count	25	22	17	30	94
		Expected Count	25.0	22.0	17.0	30.0	94.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.857[a]	3	.414
Likelihood Ratio	4.789	3	.188
N of Valid Cases	94		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.99.

4 cusped LM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
4 cusps_LM1	0	Count	24	23	12	30	89
		Expected Count	23.4	24.4	11.2	30.0	89.0
	1	Count	1	3	0	2	6
		Expected Count	1.6	1.6	.8	2.0	6.0
	Total	Count	25	26	12	32	95
		Expected Count	25.0	26.0	12.0	32.0	95.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.234[a]	3	.525
Likelihood Ratio	2.802	3	.423
N of Valid Cases	95		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .76.

5 or more cusps LM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
5 or more cusps_LM2	0	Count	22	19	15	25	81
		Expected Count	20.9	17.5	15.9	26.7	81.0
	1	Count	3	2	4	7	16
		Expected Count	4.1	3.5	3.1	5.3	16.0
	Total	Count	25	21	19	32	97
		Expected Count	25.0	21.0	19.0	32.0	97.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.067[a]	3	.559
Likelihood Ratio	2.138	3	.544
N of Valid Cases	97		

a. 3 cells (37.5%) have expected count less than 5. The minimum expected count is 3.13.

Deflecting wrinkle LM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
DW_LM1	0	Count	1	4	1	2	8
		Expected Count	2.8	2.4	.3	2.4	8.0
	1	Count	7	3	0	5	15
		Expected Count	5.2	4.6	.7	4.6	15.0
	Total	Count	8	7	1	7	23
		Expected Count	8.0	7.0	1.0	7.0	23.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	5.288[a]	3	.152
Likelihood Ratio	5.755	3	.124
N of Valid Cases	23		

a. 7 cells (87.5%) have expected count less than 5. The minimum expected count is .35.

Protostylid LM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Protostylid_LM1	0	Count	16	9	4	13	42
		Expected Count	13.6	11.4	4.0	13.1	42.0
	1	Count	8	11	3	10	32
		Expected Count	10.4	8.6	3.0	9.9	32.0
	Total	Count	24	20	7	23	74
		Expected Count	24.0	20.0	7.0	23.0	74.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.088[a]	3	.554
Likelihood Ratio	2.099	3	.552
N of Valid Cases	74		

a. 2 cells (25.0%) have expected count less than 5. The minimum expected count is 3.03.

Protostylid LM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Protostylid_LM2	0	Count	14	11	9	16	50
		Expected Count	13.3	11.4	9.5	15.8	50.0
	1	Count	7	7	6	9	29
		Expected Count	7.7	6.6	5.5	9.2	29.0
	Total	Count	21	18	15	25	79
		Expected Count	21.0	18.0	15.0	25.0	79.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	.215[a]	3	.975
Likelihood Ratio	.216	3	.975
N of Valid Cases	79		

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 5.51.

Cusp 6 LM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
C6_LM1	0	Count	21	23	10	28	82
		Expected Count	23.3	21.6	10.4	26.8	82.0
	1	Count	6	2	2	3	13
		Expected Count	3.7	3.4	1.6	4.2	13.0
	Total	Count	27	25	12	31	95
		Expected Count	27.0	25.0	12.0	31.0	95.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.862[a]	3	.413
Likelihood Ratio	2.778	3	.427
N of Valid Cases	95		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.64.

Cusp 6 LM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
C6_LM2	0	Count	24	20	19	31	94
		Expected Count	24.2	20.4	18.4	31.0	94.0
	1	Count	1	1	0	1	3
		Expected Count	.8	.6	.6	1.0	3.0
	Total	Count	25	21	19	32	97
		Expected Count	25.0	21.0	19.0	32.0	97.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	.870[a]	3	.833
Likelihood Ratio	1.425	3	.700
N of Valid Cases	97		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .59.

Cusp 7 LM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
C7_LM1	0	Count	23	24	11	30	88
		Expected Count	24.5	24.5	10.9	28.1	88.0
	1	Count	4	3	1	1	9
		Expected Count	2.5	2.5	1.1	2.9	9.0
	Total	Count	27	27	12	31	97
		Expected Count	27.0	27.0	12.0	31.0	97.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.453[a]	3	.484
Likelihood Ratio	2.724	3	.436
N of Valid Cases	97		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.11.

Cusp 7 LM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
C7_LM2	0	Count	24	21	19	31	95
		Expected Count	24.7	20.8	18.8	30.7	95.0
	1	Count	1	0	0	0	1
		Expected Count	.3	.2	.2	.3	1.0
	Total	Count	25	21	19	31	96
		Expected Count	25.0	21.0	19.0	31.0	96.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.870[a]	3	.412
Likelihood Ratio	2.721	3	.437
N of Valid Cases	96		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .20.

2-rooted LC * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
2roots_LC	0	Count	29	37	25	32	123
		Expected Count	28.0	35.4	24.2	35.4	123.0
	1	Count	1	1	1	6	9
		Expected Count	2.0	2.6	1.8	2.6	9.0
	Total	Count	30	38	26	38	132
		Expected Count	30.0	38.0	26.0	38.0	132.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	6.797[a]	3	.079
Likelihood Ratio	6.069	3	.108
N of Valid Cases	132		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.77.

Tome's root LP3 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
TR_LP3	0	Count	28	27	21	31	107
		Expected Count	25.5	28.9	21.2	31.4	107.0
	1	Count	2	7	4	6	19
		Expected Count	4.5	5.1	3.8	5.6	19.0
	Total	Count	30	34	25	37	126
		Expected Count	30.0	34.0	25.0	37.0	126.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.518[a]	3	.472
Likelihood Ratio	2.816	3	.421
N of Valid Cases	126		

a. 2 cells (25.0%) have expected count less than 5. The minimum expected count is 3.77.

3-rooted LM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
3root_LM1	0	Count	24	25	11	32	92
		Expected Count	23.7	25.7	10.9	31.7	92.0
	1	Count	0	1	0	0	1
		Expected Count	.3	.3	.1	.3	1.0
	Total	Count	24	26	11	32	93
		Expected Count	24.0	26.0	11.0	32.0	93.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.605[a]	3	.457
Likelihood Ratio	2.577	3	.462
N of Valid Cases	93		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .12.

2-rooted LM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
2root_LM2	0	Count	2	0	0	3	5
		Expected Count	1.2	1.2	.8	1.9	5.0
	1	Count	16	18	12	27	73
		Expected Count	16.8	16.8	11.2	28.1	73.0
	Total	Count	18	18	12	30	78
		Expected Count	18.0	18.0	12.0	30.0	78.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.362[a]	3	.339
Likelihood Ratio	5.082	3	.166
N of Valid Cases	78		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .77.

Congenital absence LP4 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
CA_LP4	0	Count	27	35	25	37	124
		Expected Count	26.6	36.4	24.6	36.4	124.0
	1	Count	0	2	0	0	2
		Expected Count	.4	.6	.4	.6	2.0
	Total	Count	27	37	25	37	126
		Expected Count	27.0	37.0	25.0	37.0	126.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.888[a]	3	.180
Likelihood Ratio	4.980	3	.173
N of Valid Cases	126		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .40.

Congenital absence LM3 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
CA_LM3	0	Count	22	26	23	28	99
		Expected Count	22.3	25.2	23.3	28.1	99.0
	1	Count	1	0	1	1	3
		Expected Count	.7	.8	.7	.9	3.0
	Total	Count	23	26	24	29	102
		Expected Count	23.0	26.0	24.0	29.0	102.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	1.100[a]	3	.777
Likelihood Ratio	1.829	3	.609
N of Valid Cases	102		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .68.

Winging UI1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Winging_UI1	0	Count	18	28	21	39	106
		Expected Count	17.7	27.5	21.6	39.3	106.0
	1	Count	0	0	1	1	2
		Expected Count	.3	.5	.4	.7	2.0
	Total	Count	18	28	22	40	108
		Expected Count	18.0	28.0	22.0	40.0	108.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	1.839[a]	3	.607
Likelihood Ratio	2.430	3	.488
N of Valid Cases	108		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .33.

Shovelling UC * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Shovel_UC	0	Count	13	26	10	19	68
		Expected Count	13.2	28.3	8.8	17.7	68.0
	1	Count	2	6	0	1	9
		Expected Count	1.8	3.7	1.2	2.3	9.0
	Total	Count	15	32	10	20	77
		Expected Count	15.0	32.0	10.0	20.0	77.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.776[a]	3	.287
Likelihood Ratio	4.937	3	.176
N of Valid Cases	77		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.17.

Shovelling UI2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Shovel_UI2	0	Count	10	17	7	19	53
		Expected Count	11.6	14.9	7.8	18.7	53.0
	1	Count	8	6	5	10	29
		Expected Count	6.4	8.1	4.2	10.3	29.0
	Total	Count	18	23	12	29	82
		Expected Count	18.0	23.0	12.0	29.0	82.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	1.734[a]	3	.629
Likelihood Ratio	1.751	3	.626
N of Valid Cases	82		

a. 1 cells (12.5%) have expected count less than 5. The minimum expected count is 4.24.

Shovelling UI1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Shovel_UI1	0	Count	13	24	10	19	66
		Expected Count	15.7	20.4	8.6	21.2	66.0
	1	Count	7	2	1	8	18
		Expected Count	4.3	5.6	2.4	5.8	18.0
	Total	Count	20	26	11	27	84
		Expected Count	20.0	26.0	11.0	27.0	84.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	7.175[a]	3	.067
Likelihood Ratio	7.772	3	.051
N of Valid Cases	84		

a. 2 cells (25.0%) have expected count less than 5. The minimum expected count is 2.36.

Labial Convexity UI2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Lab.Co._UI2	0	Count	1	0	0	0	1
		Expected Count	.2	.3	.2	.4	1.0
	1	Count	19	23	16	32	90
		Expected Count	19.8	22.7	15.8	31.6	90.0
	Total	Count	20	23	16	32	91
		Expected Count	20.0	23.0	16.0	32.0	91.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.589[a]	3	.309
Likelihood Ratio	3.070	3	.381
N of Valid Cases	91		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .18.

Labial convexity UI1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Lab.Co._UI1	0	Count	6	1	1	3	11
		Expected Count	2.5	2.9	2.0	3.6	11.0
	1	Count	15	24	16	28	83
		Expected Count	18.5	22.1	15.0	27.4	83.0
	Total	Count	21	25	17	31	94
		Expected Count	21.0	25.0	17.0	31.0	94.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	7.899[a]	3	.048
Likelihood Ratio	7.015	3	.071
N of Valid Cases	94		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.99.

Double Shovelling UC * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Dbl.Shov._UC	0	Count	21	32	12	29	94
		Expected Count	21.3	32.9	11.6	28.1	94.0
	1	Count	1	2	0	0	3
		Expected Count	.7	1.1	.4	.9	3.0
	Total	Count	22	34	12	29	97
		Expected Count	22.0	34.0	12.0	29.0	97.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.346[a]	3	.504
Likelihood Ratio	3.414	3	.332
N of Valid Cases	97		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .37.

Double Shovelling UI2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Dbl.Shov._UI2	0	Count	19	24	16	32	91
		Expected Count	19.8	23.7	15.8	31.7	91.0
	1	Count	1	0	0	0	1
		Expected Count	.2	.3	.2	.3	1.0
	Total	Count	20	24	16	32	92
		Expected Count	20.0	24.0	16.0	32.0	92.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.640[a]	3	.303
Likelihood Ratio	3.092	3	.378
N of Valid Cases	92		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .17.

Interruption groove UI2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
IG_UI2	0	Count	13	20	18	32	83
		Expected Count	15.8	20.8	16.6	29.9	83.0
	1	Count	6	5	2	4	17
		Expected Count	3.2	4.3	3.4	6.1	17.0
	Total	Count	19	25	20	36	100
		Expected Count	19.0	25.0	20.0	36.0	100.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.601[a]	3	.203
Likelihood Ratio	4.339	3	.227
N of Valid Cases	100		

a. 3 cells (37.5%) have expected count less than 5. The minimum expected count is 3.23.

Interruption groove UI1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
IG_UI1	0	Count	18	28	22	36	104
		Expected Count	20.0	27.7	21.0	35.3	104.0
	1	Count	3	1	0	1	5
		Expected Count	1.0	1.3	1.0	1.7	5.0
	Total	Count	21	29	22	37	109
		Expected Count	21.0	29.0	22.0	37.0	109.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	5.957[a]	3	.114
Likelihood Ratio	5.467	3	.141
N of Valid Cases	109		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .96.

Tuberculum dentale UC * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
TD_UC	0	Count	13	21	11	9	54
		Expected Count	10.7	20.7	8.0	14.7	54.0
	1	Count	3	10	1	13	27
		Expected Count	5.3	10.3	4.0	7.3	27.0
	Total	Count	16	31	12	22	81
		Expected Count	16.0	31.0	12.0	22.0	81.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	11.491[a]	3	.009
Likelihood Ratio	12.036	3	.007
N of Valid Cases	81		

a. 1 cells (12.5%) have expected count less than 5. The minimum expected count is 4.00.

Tuberculum dentale UI2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
TD_UI2	0	Count	15	21	14	24	74
		Expected Count	15.9	21.1	12.3	24.7	74.0
	1	Count	3	3	0	4	10
		Expected Count	2.1	2.9	1.7	3.3	10.0
	Total	Count	18	24	14	28	84
		Expected Count	18.0	24.0	14.0	28.0	84.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.441[a]	3	.486
Likelihood Ratio	4.052	3	.256
N of Valid Cases	84		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.67.

Tuberculum dentale UI1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
TD_UI1	0	Count	12	15	13	17	57
		Expected Count	11.5	15.6	10.2	19.7	57.0
	1	Count	5	8	2	12	27
		Expected Count	5.5	7.4	4.8	9.3	27.0
	Total	Count	17	23	15	29	84
		Expected Count	17.0	23.0	15.0	29.0	84.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.699[a]	3	.296
Likelihood Ratio	4.061	3	.255
N of Valid Cases	84		

a. 1 cells (12.5%) have expected count less than 5. The minimum expected count is 4.82.

Canine Mesial Ridge UC * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
M.Ridge_UC	0	Count	16	20	9	24	69
		Expected Count	15.8	20.7	8.9	23.7	69.0
	1	Count	0	1	0	0	1
		Expected Count	.2	.3	.1	.3	1.0
	Total	Count	16	21	9	24	70
		Expected Count	16.0	21.0	9.0	24.0	70.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.367[a]	3	.500
Likelihood Ratio	2.442	3	.486
N of Valid Cases	70		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .13.

Distal Accessory Ridge UC * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
DAR_UC	0	Count	5	7	3	7	22
		Expected Count	6.7	7.3	2.0	6.0	22.0
	1	Count	5	4	0	2	11
		Expected Count	3.3	3.7	1.0	3.0	11.0
	Total	Count	10	11	3	9	33
		Expected Count	10.0	11.0	3.0	9.0	33.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.295[a]	3	.348
Likelihood Ratio	4.192	3	.241
N of Valid Cases	33		

a. 5 cells (62.5%) have expected count less than 5. The minimum expected count is 1.00.

Metacone UM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Metacone_UM2	0	Count	1	0	1	2	4
		Expected Count	.9	1.3	.7	1.2	4.0
	1	Count	20	30	15	27	92
		Expected Count	20.1	28.8	15.3	27.8	92.0
	Total	Count	21	30	16	29	96
		Expected Count	21.0	30.0	16.0	29.0	96.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.038[a]	3	.565
Likelihood Ratio	3.178	3	.365
N of Valid Cases	96		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .67.

Hypocone UM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Hypocone_UM2	0	Count	7	9	3	5	24
		Expected Count	5.5	7.3	3.9	7.3	24.0
	1	Count	14	19	12	23	68
		Expected Count	15.5	20.7	11.1	20.7	68.0
	Total	Count	21	28	15	28	92
		Expected Count	21.0	28.0	15.0	28.0	92.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.376[a]	3	.498
Likelihood Ratio	2.423	3	.489
N of Valid Cases	92		

a. 1 cells (12.5%) have expected count less than 5. The minimum expected count is 3.91.

Cusp 5 (metaconule) UM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Cusp5_UM2	0	Count	18	24	13	21	76
		Expected Count	18.8	23.2	11.6	22.4	76.0
	1	Count	3	2	0	4	9
		Expected Count	2.2	2.8	1.4	2.6	9.0
	Total	Count	21	26	13	25	85
		Expected Count	21.0	26.0	13.0	25.0	85.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.846[a]	3	.416
Likelihood Ratio	4.119	3	.249
N of Valid Cases	85		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.38.

Cusp 5 (metaconule) UM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Cusp5_UM1	0	Count	18	23	14	28	83
		Expected Count	17.7	25.6	15.0	24.7	83.0
	1	Count	2	6	3	0	11
		Expected Count	2.3	3.4	2.0	3.3	11.0
	Total	Count	20	29	17	28	94
		Expected Count	20.0	29.0	17.0	28.0	94.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	6.615[a]	3	.085
Likelihood Ratio	9.442	3	.024
N of Valid Cases	94		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.99.

Carabelli's cusp UM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Carabelli_UM2	0	Count	18	25	12	20	75
		Expected Count	18.5	24.1	11.1	21.3	75.0
	1	Count	2	1	0	3	6
		Expected Count	1.5	1.9	.9	1.7	6.0
	Total	Count	20	26	12	23	81
		Expected Count	20.0	26.0	12.0	23.0	81.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.702[a]	3	.440
Likelihood Ratio	3.484	3	.323
N of Valid Cases	81		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .89.

Carabelli's cusp UM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Carabelli_UM1	0	Count	3	1	1	1	6
		Expected Count	1.1	1.9	1.3	1.7	6.0
	1	Count	10	21	14	19	64
		Expected Count	11.9	20.1	13.7	18.3	64.0
	Total	Count	13	22	15	20	70
		Expected Count	13.0	22.0	15.0	20.0	70.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.340[a]	3	.227
Likelihood Ratio	3.481	3	.323
N of Valid Cases	70		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.11.

Parastyle UM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Parastyle_UM2	0	Count	21	27	13	22	83
		Expected Count	20.5	28.3	12.7	21.5	83.0
	1	Count	0	2	0	0	2
		Expected Count	.5	.7	.3	.5	2.0
	Total	Count	21	29	13	22	85
		Expected Count	21.0	29.0	13.0	22.0	85.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.955[a]	3	.266
Likelihood Ratio	4.395	3	.222
N of Valid Cases	85		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .31.

Parastyle UM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Parastyle_UM1	0	Count	22	30	19	24	95
		Expected Count	21.8	30.7	18.8	23.8	95.0
	1	Count	0	1	0	0	1
		Expected Count	.2	.3	.2	.3	1.0
	Total	Count	22	31	19	24	96
		Expected Count	22.0	31.0	19.0	24.0	96.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.119[a]	3	.548
Likelihood Ratio	2.283	3	.516
N of Valid Cases	96		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .20.

Enamel extensions UM3 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
EE_UM3	0	Count	9	12	11	19	51
		Expected Count	9.1	11.8	11.8	18.2	51.0
	1	Count	1	1	2	1	5
		Expected Count	.9	1.2	1.2	1.8	5.0
	Total	Count	10	13	13	20	56
		Expected Count	10.0	13.0	13.0	20.0	56.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	1.085[a]	3	.781
Likelihood Ratio	1.043	3	.791
N of Valid Cases	56		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .89.

Enamel extensions UM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
EE_UM2	0	Count	19	23	13	25	80
		Expected Count	17.9	24.5	13.2	24.5	80.0
	1	Count	0	3	1	1	5
		Expected Count	1.1	1.5	.8	1.5	5.0
	Total	Count	19	26	14	26	85
		Expected Count	19.0	26.0	14.0	26.0	85.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.925[a]	3	.403
Likelihood Ratio	3.753	3	.289
N of Valid Cases	85		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .82.

Enamel extensions UM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
EE_UM1	0	Count	23	27	21	30	101
		Expected Count	22.7	27.4	20.8	30.2	101.0
	1	Count	1	2	1	2	6
		Expected Count	1.3	1.6	1.2	1.8	6.0
	Total	Count	24	29	22	32	107
		Expected Count	24.0	29.0	22.0	32.0	107.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	.257[a]	3	.968
Likelihood Ratio	.262	3	.967
N of Valid Cases	107		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.23.

Enamel extensions UP4 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
EE_UP4	0	Count	20	28	19	33	100
		Expected Count	19.8	28.7	18.8	32.7	100.0
	1	Count	0	1	0	0	1
		Expected Count	.2	.3	.2	.3	1.0
	Total	Count	20	29	19	33	101
		Expected Count	20.0	29.0	19.0	33.0	101.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.508[a]	3	.474
Likelihood Ratio	2.521	3	.472
N of Valid Cases	101		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .19.

Enamel extensions UP3 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
EE_UP3	0	Count	23	29	17	33	102
		Expected Count	22.6	29.4	17.7	32.4	102.0
	1	Count	0	1	1	0	2
		Expected Count	.4	.6	.3	.6	2.0
	Total	Count	23	30	18	33	104
		Expected Count	23.0	30.0	18.0	33.0	104.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.674[a]	3	.445
Likelihood Ratio	3.273	3	.351
N of Valid Cases	104		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .35.

2-rooted UP4 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
2root_UP4	0	Count	24	29	19	27	99
		Expected Count	22.3	31.2	17.8	27.6	99.0
	1	Count	1	6	1	4	12
		Expected Count	2.7	3.8	2.2	3.4	12.0
	Total	Count	25	35	20	31	111
		Expected Count	25.0	35.0	20.0	31.0	111.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.499[a]	3	.321
Likelihood Ratio	3.795	3	.285
N of Valid Cases	111		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 2.16.

2-rooted UP3 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
2root_UP3	0	Count	13	12	14	17	56
		Expected Count	13.4	15.8	10.5	16.3	56.0
	1	Count	15	21	8	17	61
		Expected Count	14.6	17.2	11.5	17.7	61.0
	Total	Count	28	33	22	34	117
		Expected Count	28.0	33.0	22.0	34.0	117.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.027[a]	3	.259
Likelihood Ratio	4.072	3	.254
N of Valid Cases	117		

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 10.53.

3-rooted UM2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
3root_UM2	0	Count	3	7	0	10	20
		Expected Count	4.4	6.5	2.7	6.3	20.0
	1	Count	18	24	13	20	75
		Expected Count	16.6	24.5	10.3	23.7	75.0
	Total	Count	21	31	13	30	95
		Expected Count	21.0	31.0	13.0	30.0	95.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	6.811[a]	3	.078
Likelihood Ratio	9.250	3	.026
N of Valid Cases	95		

a. 2 cells (25.0%) have expected count less than 5. The minimum expected count is 2.74.

3-rooted UM1 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
3root_UM1	0	Count	3	4	0	2	9
		Expected Count	2.2	2.9	1.5	2.5	9.0
	1	Count	27	35	20	32	114
		Expected Count	27.8	36.1	18.5	31.5	114.0
	Total	Count	30	39	20	34	123
		Expected Count	30.0	39.0	20.0	34.0	123.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.497[a]	3	.476
Likelihood Ratio	3.883	3	.274
N of Valid Cases	123		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.46.

Peg-shaped UM3 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
Peg_UM3	0	Count	12	14	14	28	68
		Expected Count	11.3	15.1	14.2	27.4	68.0
	1	Count	0	2	1	1	4
		Expected Count	.7	.9	.8	1.6	4.0
	Total	Count	12	16	15	29	72
		Expected Count	12.0	16.0	15.0	29.0	72.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.457[a]	3	.483
Likelihood Ratio	2.792	3	.425
N of Valid Cases	72		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .67.

Congenital absence UM3 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
CA_UM3	0	Count	18	28	17	34	97
		Expected Count	18.8	28.3	17.0	33.0	97.0
	1	Count	2	2	1	1	6
		Expected Count	1.2	1.7	1.0	2.0	6.0
	Total	Count	20	30	18	35	103
		Expected Count	20.0	30.0	18.0	35.0	103.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	1.239[a]	3	.744
Likelihood Ratio	1.254	3	.740
N of Valid Cases	103		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.05.

Congenital absence UP4 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
CA_UP4	0	Count	29	42	24	40	135
		Expected Count	28.8	41.7	24.8	39.7	135.0
	1	Count	0	0	1	0	1
		Expected Count	.2	.3	.2	.3	1.0
	Total	Count	29	42	25	40	136
		Expected Count	29.0	42.0	25.0	40.0	136.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.473[a]	3	.215
Likelihood Ratio	3.421	3	.331
N of Valid Cases	136		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .18.

Congenital absence UI2 * GROUP

Crosstab

			GROUP				
			South	West	East	North	Total
CA_UI2	0	Count	32	45	26	43	146
		Expected Count	32.8	44.7	25.8	42.7	146.0
	1	Count	1	0	0	0	1
		Expected Count	.2	.3	.2	.3	1.0
	Total	Count	33	45	26	43	147
		Expected Count	33.0	45.0	26.0	43.0	147.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.478[a]	3	.324
Likelihood Ratio	3.012	3	.390
N of Valid Cases	147		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .18.

Appendix IV: Kellis 2 males and females by group with Chi-square analysis

Shovelling LI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Shovelling_LI1	0	Count	8	8	16
			Expected Count	8.0	8.0	16.0
		Total	Count	8	8	16
			Expected Count	8.0	8.0	16.0
West	Shovelling_LI1	0	Count	10	10	20
			Expected Count	10.0	10.0	20.0
		Total	Count	10	10	20
			Expected Count	10.0	10.0	20.0
East	Shovelling_LI1	0	Count	9	4	13
			Expected Count	9.0	4.0	13.0
		Total	Count	9	4	13
			Expected Count	9.0	4.0	13.0
North	Shovelling_LI1	0	Count	10	9	19
			Expected Count	10.5	8.5	19.0
		1	Count	1	0	1
			Expected Count	.6	.5	1.0
		Total	Count	11	9	20
			Expected Count	11.0	9.0	20.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	16				
West	Pearson Chi-Square	.[a]				
	N of Valid Cases	20				
East	Pearson Chi-Square	.[a]				
	N of Valid Cases	13				
North	Pearson Chi-Square	.861[b]	1	.353		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	1.239	1	.266		
	Fisher's Exact Test				1.000	.550
	N of Valid Cases	20				

a. No statistics are computed because Shovelling_LI1 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .45.

c. Computed only for a 2x2 table

Shovelling LI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Shovelling_LI2	0	Count	9	9	18
			Expected Count	9.0	9.0	18.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	Shovelling_LI2	0	Count	11	11	22
			Expected Count	11.0	11.0	22.0
		Total	Count	11	11	22
			Expected Count	11.0	11.0	22.0
East	Shovelling_LI2	0	Count	10	4	14
			Expected Count	10.0	4.0	14.0
		Total	Count	10	4	14
			Expected Count	10.0	4.0	14.0
North	Shovelling_LI2	0	Count	11	9	20
			Expected Count	11.4	8.6	20.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	12	9	21
			Expected Count	12.0	9.0	21.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	18				
West	Pearson Chi-Square	.[a]				
	N of Valid Cases	22				
East	Pearson Chi-Square	.[a]				
	N of Valid Cases	14				
North	Pearson Chi-Square	.788[b]	1	.375		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	1.157	1	.282		
	Fisher's Exact Test				1.000	.571
	N of Valid Cases	21				

a. No statistics are computed because Shovelling_LI2 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .43.

c. Computed only for a 2x2 table

Double Shovelling LI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	dbl shovel_LI1	0	Count	9	11	20
			Expected Count	9.0	11.0	20.0
		Total	Count	9	11	20
			Expected Count	9.0	11.0	20.0
West	dbl shovel_LI1	0	Count	11	10	21
			Expected Count	11.0	10.0	21.0
		Total	Count	11	10	21
			Expected Count	11.0	10.0	21.0
East	dbl shovel_LI1	0	Count	9	4	13
			Expected Count	9.0	4.0	13.0
		Total	Count	9	4	13
			Expected Count	9.0	4.0	13.0
North	dbl shovel_LI1	0	Count	11	9	20
			Expected Count	11.0	9.0	20.0
		Total	Count	11	9	20
			Expected Count	11.0	9.0	20.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	20
West	Pearson Chi-Square	.[a]
	N of Valid Cases	21
East	Pearson Chi-Square	.[a]
	N of Valid Cases	13
North	Pearson Chi-Square	.[a]
	N of Valid Cases	20

a. No statistics are computed because dbl shovel_LI1 is a constant.

Double Shovelling LI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	dbl shovel_LI2	0	Count	9	9	18
			Expected Count	9.0	9.0	18.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	dbl shovel_LI2	0	Count	13	12	25
			Expected Count	13.0	12.0	25.0
		Total	Count	13	12	25
			Expected Count	13.0	12.0	25.0
East	dbl shovel_LI2	0	Count	10	4	14
			Expected Count	10.0	4.0	14.0
		Total	Count	10	4	14
			Expected Count	10.0	4.0	14.0
North	dbl shovel_LI2	0	Count	12	8	20
			Expected Count	12.0	8.0	20.0
		Total	Count	12	8	20
			Expected Count	12.0	8.0	20.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	18
West	Pearson Chi-Square	.[a]
	N of Valid Cases	25
East	Pearson Chi-Square	.[a]
	N of Valid Cases	14
North	Pearson Chi-Square	.[a]
	N of Valid Cases	20

a. No statistics are computed because dbl shovel_LI2 is a constant.

Distal accessory ridge LC * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	DAR_LC	0	Count	5	6	11
			Expected Count	5.5	5.5	11.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	6	6	12
			Expected Count	6.0	6.0	12.0
West	DAR_LC	0	Count	3	4	7
			Expected Count	3.0	4.0	7.0
		Total	Count	3	4	7
			Expected Count	3.0	4.0	7.0
East	DAR_LC	0	Count	4	1	5
			Expected Count	4.0	1.0	5.0
		Total	Count	4	1	5
			Expected Count	4.0	1.0	5.0
North	DAR_LC	0	Count	3	3	6
			Expected Count	3.0	3.0	6.0
		Total	Count	3	3	6
			Expected Count	3.0	3.0	6.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.091[a]	1	.296		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.477	1	.224		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	12				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	7				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	5				
North	Pearson Chi-Square	.[c]				
	N of Valid Cases	6				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .50.

b. Computed only for a 2x2 table

c. No statistics are computed because DAR_LC is a constant.

Lingual cusp LP3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	PMLC_LP3	0	Count	6	7	13
			Expected Count	5.7	7.3	13.0
		1	Count	1	2	3
			Expected Count	1.3	1.7	3.0
		Total	Count	7	9	16
			Expected Count	7.0	9.0	16.0
West	PMLC_LP3	0	Count	4	7	11
			Expected Count	3.9	7.1	11.0
		1	Count	1	2	3
			Expected Count	1.1	1.9	3.0
		Total	Count	5	9	14
			Expected Count	5.0	9.0	14.0
East	PMLC_LP3	0	Count	4	3	7
			Expected Count	4.0	3.0	7.0
		Total	Count	4	3	7
			Expected Count	4.0	3.0	7.0
North	PMLC_LP3	0	Count	1	3	4
			Expected Count	1.1	2.9	4.0
		1	Count	1	2	3
			Expected Count	.9	2.1	3.0
		Total	Count	2	5	7
			Expected Count	2.0	5.0	7.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.163[a]	1	.687		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.166	1	.684		
	Fisher's Exact Test				1.000	.600
	N of Valid Cases	16				
West	Pearson Chi-Square	.009[c]	1	.923		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.009	1	.922		
	Fisher's Exact Test				1.000	.725
	N of Valid Cases	14				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	7				
North	Pearson Chi-Square	.058[e]	1	.809		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.058	1	.810		
	Fisher's Exact Test				1.000	.714
	N of Valid Cases	7				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.31.

b. Computed only for a 2x2 table

c. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 1.07.

d. No statistics are computed because PMLC_LP3 is a constant.

e. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .86.

Lingual cusp LP4 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	PMLC_LP4	0	Count	2	4	6
			Expected Count	3.0	3.0	6.0
		1	Count	4	2	6
			Expected Count	3.0	3.0	6.0
		Total	Count	6	6	12
			Expected Count	6.0	6.0	12.0
West	PMLC_LP4	0	Count	0	1	1
			Expected Count	.3	.7	1.0
		1	Count	3	5	8
			Expected Count	2.7	5.3	8.0
		Total	Count	3	6	9
			Expected Count	3.0	6.0	9.0
East	PMLC_LP4	1	Count	2	1	3
			Expected Count	2.0	1.0	3.0
		Total	Count	2	1	3
			Expected Count	2.0	1.0	3.0
North	PMLC_LP4	1	Count	1	1	2
			Expected Count	1.0	1.0	2.0
		Total	Count	1	1	2
			Expected Count	1.0	1.0	2.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.333[a]	1	.248		
	Continuity Correction[b]	.333	1	.564		
	Likelihood Ratio	1.359	1	.244		
	Fisher's Exact Test				.567	.284
	N of Valid Cases	12				
West	Pearson Chi-Square	.563[c]	1	.453		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.872	1	.350		
	Fisher's Exact Test				1.000	.667
	N of Valid Cases	9				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	3				
North	Pearson Chi-Square	.[d]				
	N of Valid Cases	2				

a. 4 cells (100.0%) have expected count less than 5. The minimum expected count is 3.00.

b. Computed only for a 2x2 table

c. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .33.

d. No statistics are computed because PMLC_LP4 is a constant.

Anterior fovea LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	AF_LM1	0	Count	1	2	3
			Expected Count	1.5	1.5	3.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	2	2	4
			Expected Count	2.0	2.0	4.0
West	AF_LM1	0	Count	1		1
			Expected Count	1.0		1.0
		Total	Count	1		1
			Expected Count	1.0		1.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.333[a]	1	.248		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.726	1	.189		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	4				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	1				

a. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .50.

b. Computed only for a 2x2 table

c. No statistics are computed because AF_LM1 and Sex are constants.

Y-groove LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Ygroove_LM1	0	Count	3	3	6
			Expected Count	2.7	3.3	6.0
		1	Count	6	8	14
			Expected Count	6.3	7.7	14.0
		Total	Count	9	11	20
			Expected Count	9.0	11.0	20.0
West	Ygroove_LM1	0	Count	0	1	1
			Expected Count	.4	.6	1.0
		1	Count	6	7	13
			Expected Count	5.6	7.4	13.0
		Total	Count	6	8	14
			Expected Count	6.0	8.0	14.0
East	Ygroove_LM1	1	Count	6	2	8
			Expected Count	6.0	2.0	8.0
		Total	Count	6	2	8
			Expected Count	6.0	2.0	8.0
North	Ygroove_LM1	1	Count	7	11	18
			Expected Count	7.0	11.0	18.0
		Total	Count	7	11	18
			Expected Count	7.0	11.0	18.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.087[a]	1	.769		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.086	1	.769		
	Fisher's Exact Test				1.000	.574
	N of Valid Cases	20				
West	Pearson Chi-Square	.808[c]	1	.369		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.177	1	.278		
	Fisher's Exact Test				1.000	.571
	N of Valid Cases	14				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	8				
North	Pearson Chi-Square	.[d]				
	N of Valid Cases	18				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.70.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .43.

d. No statistics are computed because Ygroove_LM1 is a constant.

Y-groove LM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Ygroove_LM2	0	Count	8	11	19
			Expected Count	7.8	11.2	19.0
		1	Count	1	2	3
			Expected Count	1.2	1.8	3.0
		Total	Count	9	13	22
			Expected Count	9.0	13.0	22.0
West	Ygroove_LM2	0	Count	7	7	14
			Expected Count	6.6	7.4	14.0
		1	Count	1	2	3
			Expected Count	1.4	1.6	3.0
		Total	Count	8	9	17
			Expected Count	8.0	9.0	17.0
East	Ygroove_LM2	0	Count	10	5	15
			Expected Count	10.0	5.0	15.0
		Total	Count	10	5	15
			Expected Count	10.0	5.0	15.0
North	Ygroove_LM2	0	Count	11	9	20
			Expected Count	10.0	10.0	20.0
		1	Count	0	2	2
			Expected Count	1.0	1.0	2.0
		Total	Count	11	11	22
			Expected Count	11.0	11.0	22.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.082[a]	1	.774		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.084	1	.772		
	Fisher's Exact Test				1.000	.642
	N of Valid Cases	22				
West	Pearson Chi-Square	.275[c]	1	.600		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.281	1	.596		
	Fisher's Exact Test				1.000	.547
	N of Valid Cases	17				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	15				
North	Pearson Chi-Square	2.200[e]	1	.138		
	Continuity Correction[b]	.550	1	.458		
	Likelihood Ratio	2.973	1	.085		
	Fisher's Exact Test				.476	.238
	N of Valid Cases	22				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.23.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.41.

d. No statistics are computed because Ygroove_LM2 is a constant.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.00.

4 cusped LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	4 cusps_LM1	0	Count	8	10	18
			Expected Count	8.5	9.5	18.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	9	10	19
			Expected Count	9.0	10.0	19.0
West	4 cusps_LM1	0	Count	5	8	13
			Expected Count	4.9	8.1	13.0
		1	Count	1	2	3
			Expected Count	1.1	1.9	3.0
		Total	Count	6	10	16
			Expected Count	6.0	10.0	16.0
East	4 cusps_LM1	0	Count	7	2	9
			Expected Count	7.0	2.0	9.0
		Total	Count	7	2	9
			Expected Count	7.0	2.0	9.0
North	4 cusps_LM1	0	Count	8	10	18
			Expected Count	8.1	9.9	18.0
		1	Count	1	1	2
			Expected Count	.9	1.1	2.0
		Total	Count	9	11	20
			Expected Count	9.0	11.0	20.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.173[a]	1	.279		
	Continuity Correction[b]	.003	1	.957		
	Likelihood Ratio	1.556	1	.212		
	Fisher's Exact Test				.474	.474
	N of Valid Cases	19				
West	Pearson Chi-Square	.027[c]	1	.869		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.028	1	.868		
	Fisher's Exact Test				1.000	.696
	N of Valid Cases	16				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	9				
North	Pearson Chi-Square	.022[e]	1	.881		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.022	1	.881		
	Fisher's Exact Test				1.000	.711
	N of Valid Cases	20				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .47.

b. Computed only for a 2x2 table

c. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 1.13.

d. No statistics are computed because 4 cusps_LM1 is a constant.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .90.

5 or more cusps LM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	5 or more cusps_LM2	0	Count	9	10	19
			Expected Count	7.8	11.2	19.0
		1	Count	0	3	3
			Expected Count	1.2	1.8	3.0
		Total	Count	9	13	22
			Expected Count	9.0	13.0	22.0
West	5 or more cusps_LM2	0	Count	6	8	14
			Expected Count	6.1	7.9	14.0
		1	Count	1	1	2
			Expected Count	.9	1.1	2.0
		Total	Count	7	9	16
			Expected Count	7.0	9.0	16.0
East	5 or more cusps_LM2	0	Count	10	4	14
			Expected Count	9.1	4.9	14.0
		1	Count	1	2	3
			Expected Count	1.9	1.1	3.0
		Total	Count	11	6	17
			Expected Count	11.0	6.0	17.0
North	5 or more cusps_LM2	0	Count	11	8	19
			Expected Count	9.9	9.1	19.0
		1	Count	1	3	4
			Expected Count	2.1	1.9	4.0
		Total	Count	12	11	23
			Expected Count	12.0	11.0	23.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	2.405[a]	1	.121		
	Continuity Correction[b]	.845	1	.358		
	Likelihood Ratio	3.480	1	.062		
	Fisher's Exact Test				.240	.186
	N of Valid Cases	22				
West	Pearson Chi-Square	.036[c]	1	.849		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.036	1	.849		
	Fisher's Exact Test				1.000	.700
	N of Valid Cases	16				
East	Pearson Chi-Square	1.570[d]	1	.210		
	Continuity Correction[b]	.345	1	.557		
	Likelihood Ratio	1.504	1	.220		
	Fisher's Exact Test				.515	.272
	N of Valid Cases	17				
North	Pearson Chi-Square	1.433[e]	1	.231		
	Continuity Correction[b]	.418	1	.518		
	Likelihood Ratio	1.479	1	.224		
	Fisher's Exact Test				.317	.261
	N of Valid Cases	23				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.23.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .88.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 1.06.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.91.

Deflecting wrinkle LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	DW_LM1	1	Count		2	2
			Expected Count		2.0	2.0
		Total	Count		2	2
			Expected Count		2.0	2.0
North	DW_LM1	1	Count	1		1
			Expected Count	1.0		1.0
		Total	Count	1		1
			Expected Count	1.0		1.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	2
North	Pearson Chi-Square	.[a]
	N of Valid Cases	1

a. No statistics are computed because DW_LM1 and Sex are constants.

Protostylid LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Protostylid_LM1	0	Count	4	9	13
			Expected Count	5.1	7.9	13.0
		1	Count	3	2	5
			Expected Count	1.9	3.1	5.0
		Total	Count	7	11	18
			Expected Count	7.0	11.0	18.0
West	Protostylid_LM1	0	Count	3	2	5
			Expected Count	2.5	2.5	5.0
		1	Count	3	4	7
			Expected Count	3.5	3.5	7.0
		Total	Count	6	6	12
			Expected Count	6.0	6.0	12.0
East	Protostylid_LM1	0	Count	2	0	2
			Expected Count	1.5	.5	2.0
		1	Count	1	1	2
			Expected Count	1.5	.5	2.0
		Total	Count	3	1	4
			Expected Count	3.0	1.0	4.0
North	Protostylid_LM1	0	Count	2	5	7
			Expected Count	2.3	4.7	7.0
		1	Count	2	3	5
			Expected Count	1.7	3.3	5.0
		Total	Count	4	8	12
			Expected Count	4.0	8.0	12.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.298[a]	1	.255		
	Continuity Correction[b]	.360	1	.549		
	Likelihood Ratio	1.279	1	.258		
	Fisher's Exact Test				.326	.272
	N of Valid Cases	18				
West	Pearson Chi-Square	.343[c]	1	.558		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.345	1	.557		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	12				
East	Pearson Chi-Square	1.333[d]	1	.248		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.726	1	.189		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	4				
North	Pearson Chi-Square	.171[e]	1	.679		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.170	1	.680		
	Fisher's Exact Test				1.000	.576
	N of Valid Cases	12				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.94.

b. Computed only for a 2x2 table

c. 4 cells (100.0%) have expected count less than 5. The minimum expected count is 2.50.

d. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .50.

e. 4 cells (100.0%) have expected count less than 5. The minimum expected count is 1.67.

Protostylid LM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Protostylid_LM2	0	Count	6	7	13
			Expected Count	5.5	7.5	13.0
		1	Count	2	4	6
			Expected Count	2.5	3.5	6.0
		Total	Count	8	11	19
			Expected Count	8.0	11.0	19.0
West	Protostylid_LM2	0	Count	3	6	9
			Expected Count	3.2	5.8	9.0
		1	Count	2	3	5
			Expected Count	1.8	3.2	5.0
		Total	Count	5	9	14
			Expected Count	5.0	9.0	14.0
East	Protostylid_LM2	0	Count	4	4	8
			Expected Count	4.9	3.1	8.0
		1	Count	4	1	5
			Expected Count	3.1	1.9	5.0
		Total	Count	8	5	13
			Expected Count	8.0	5.0	13.0
North	Protostylid_LM2	0	Count	6	4	10
			Expected Count	5.9	4.1	10.0
		1	Count	4	3	7
			Expected Count	4.1	2.9	7.0
		Total	Count	10	7	17
			Expected Count	10.0	7.0	17.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.277[a]	1	.599		
	Continuity Correction[b]	.001	1	.979		
	Likelihood Ratio	.281	1	.596		
	Fisher's Exact Test				1.000	.494
	N of Valid Cases	19				
West	Pearson Chi-Square	.062[c]	1	.803		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.062	1	.804		
	Fisher's Exact Test				1.000	.622
	N of Valid Cases	14				
East	Pearson Chi-Square	1.170[d]	1	.279		
	Continuity Correction[b]	.246	1	.620		
	Likelihood Ratio	1.229	1	.268		
	Fisher's Exact Test				.565	.315
	N of Valid Cases	13				
North	Pearson Chi-Square	.014[e]	1	.906		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.014	1	.906		
	Fisher's Exact Test				1.000	.646
	N of Valid Cases	17				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.53.

b. Computed only for a 2x2 table

c. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 1.79.

d. 4 cells (100.0%) have expected count less than 5. The minimum expected count is 1.92.

e. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 2.88.

Cusp 6 LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	C6_LM1	0	Count	8	8	16
			Expected Count	6.9	9.1	16.0
		1	Count	1	4	5
			Expected Count	2.1	2.9	5.0
		Total	Count	9	12	21
			Expected Count	9.0	12.0	21.0
West	C6_LM1	0	Count	6	8	14
			Expected Count	6.5	7.5	14.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	7	8	15
			Expected Count	7.0	8.0	15.0
East	C6_LM1	0	Count	5	2	7
			Expected Count	5.4	1.6	7.0
		1	Count	2	0	2
			Expected Count	1.6	.4	2.0
		Total	Count	7	2	9
			Expected Count	7.0	2.0	9.0
North	C6_LM1	0	Count	8	10	18
			Expected Count	7.6	10.4	18.0
		1	Count	0	1	1
			Expected Count	.4	.6	1.0
		Total	Count	8	11	19
			Expected Count	8.0	11.0	19.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.400[a]	1	.237		
	Continuity Correction[b]	.443	1	.506		
	Likelihood Ratio	1.497	1	.221		
	Fisher's Exact Test				.338	.258
	N of Valid Cases	21				
West	Pearson Chi-Square	1.224[c]	1	.268		
	Continuity Correction[b]	.005	1	.945		
	Likelihood Ratio	1.606	1	.205		
	Fisher's Exact Test				.467	.467
	N of Valid Cases	15				
East	Pearson Chi-Square	.735[d]	1	.391		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.159	1	.282		
	Fisher's Exact Test				1.000	.583
	N of Valid Cases	9				
North	Pearson Chi-Square	.768[e]	1	.381		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.133	1	.287		
	Fisher's Exact Test				1.000	.579
	N of Valid Cases	19				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.14.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .47.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .44.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .42.

Cusp 6 LM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	C6_LM2	0	Count	9	12	21
			Expected Count	8.6	12.4	21.0
		1	Count	0	1	1
			Expected Count	.4	.6	1.0
		Total	Count	9	13	22
			Expected Count	9.0	13.0	22.0
West	C6_LM2	0	Count	7	8	15
			Expected Count	6.6	8.4	15.0
		1	Count	0	1	1
			Expected Count	.4	.6	1.0
		Total	Count	7	9	16
			Expected Count	7.0	9.0	16.0
East	C6_LM2	0	Count	11	6	17
			Expected Count	11.0	6.0	17.0
		Total	Count	11	6	17
			Expected Count	11.0	6.0	17.0
North	C6_LM2	0	Count	12	11	23
			Expected Count	12.0	11.0	23.0
		Total	Count	12	11	23
			Expected Count	12.0	11.0	23.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.725[a]	1	.394		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.085	1	.298		
	Fisher's Exact Test				1.000	.591
	N of Valid Cases	22				
West	Pearson Chi-Square	.830[c]	1	.362		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.202	1	.273		
	Fisher's Exact Test				1.000	.563
	N of Valid Cases	16				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	17				
North	Pearson Chi-Square	.[d]				
	N of Valid Cases	23				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .41.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .44.

d. No statistics are computed because C6_LM2 is a constant.

Cusp 7 LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	C7_LM1	0	Count	8	10	18
			Expected Count	7.7	10.3	18.0
		1	Count	1	2	3
			Expected Count	1.3	1.7	3.0
		Total	Count	9	12	21
			Expected Count	9.0	12.0	21.0
West	C7_LM1	0	Count	8	8	16
			Expected Count	7.5	8.5	16.0
		1	Count	0	1	1
			Expected Count	.5	.5	1.0
		Total	Count	8	9	17
			Expected Count	8.0	9.0	17.0
East	C7_LM1	0	Count	7	2	9
			Expected Count	7.0	2.0	9.0
		Total	Count	7	2	9
			Expected Count	7.0	2.0	9.0
North	C7_LM1	0	Count	8	10	18
			Expected Count	7.6	10.4	18.0
		1	Count	0	1	1
			Expected Count	.4	.6	1.0
		Total	Count	8	11	19
			Expected Count	8.0	11.0	19.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.130[a]	1	.719		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.132	1	.716		
	Fisher's Exact Test				1.000	.612
	N of Valid Cases	21				
West	Pearson Chi-Square	.944[c]	1	.331		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.327	1	.249		
	Fisher's Exact Test				1.000	.529
	N of Valid Cases	17				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	9				
North	Pearson Chi-Square	.768[e]	1	.381		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.133	1	.287		
	Fisher's Exact Test				1.000	.579
	N of Valid Cases	19				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.29.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .47.

d. No statistics are computed because C7_LM1 is a constant.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .42.

Cusp 7 LM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	C7_LM2	0	Count	9	12	21
			Expected Count	8.6	12.4	21.0
		1	Count	0	1	1
			Expected Count	.4	.6	1.0
		Total	Count	9	13	22
			Expected Count	9.0	13.0	22.0
West	C7_LM2	0	Count	8	9	17
			Expected Count	8.0	9.0	17.0
		Total	Count	8	9	17
			Expected Count	8.0	9.0	17.0
East	C7_LM2	0	Count	11	6	17
			Expected Count	11.0	6.0	17.0
		Total	Count	11	6	17
			Expected Count	11.0	6.0	17.0
North	C7_LM2	0	Count	12	11	23
			Expected Count	12.0	11.0	23.0
		Total	Count	12	11	23
			Expected Count	12.0	11.0	23.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.725[a]	1	.394		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.085	1	.298		
	Fisher's Exact Test				1.000	.591
	N of Valid Cases	22				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	17				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	17				
North	Pearson Chi-Square	.[c]				
	N of Valid Cases	23				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .41.

b. Computed only for a 2x2 table

c. No statistics are computed because C7_LM2 is a constant.

2-rooted LC * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	2roots_LC	0	Count	15	12	27
			Expected Count	14.5	12.5	27.0
		1	Count	0	1	1
			Expected Count	.5	.5	1.0
		Total	Count	15	13	28
			Expected Count	15.0	13.0	28.0
West	2roots_LC	0	Count	18	14	32
			Expected Count	17.5	14.5	32.0
		1	Count	0	1	1
			Expected Count	.5	.5	1.0
		Total	Count	18	15	33
			Expected Count	18.0	15.0	33.0
East	2roots_LC	0	Count	16	8	24
			Expected Count	16.3	7.7	24.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	17	8	25
			Expected Count	17.0	8.0	25.0
North	2roots_LC	0	Count	16	10	26
			Expected Count	16.3	9.8	26.0
		1	Count	4	2	6
			Expected Count	3.8	2.3	6.0
		Total	Count	20	12	32
			Expected Count	20.0	12.0	32.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.197[a]	1	.274		
	Continuity Correction[b]	.005	1	.942		
	Likelihood Ratio	1.577	1	.209		
	Fisher's Exact Test				.464	.464
	N of Valid Cases	28				
West	Pearson Chi-Square	1.237[c]	1	.266		
	Continuity Correction[b]	.009	1	.926		
	Likelihood Ratio	1.615	1	.204		
	Fisher's Exact Test				.455	.455
	N of Valid Cases	33				
East	Pearson Chi-Square	.490[d]	1	.484		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.791	1	.374		
	Fisher's Exact Test				1.000	.680
	N of Valid Cases	25				
North	Pearson Chi-Square	.055[e]	1	.815		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.055	1	.814		
	Fisher's Exact Test				1.000	.601
	N of Valid Cases	32				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .46.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .45.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .32.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.25.

Tome's root LP3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	TR_LP3	0	Count	14	12	26
			Expected Count	14.4	11.6	26.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	15	12	27
			Expected Count	15.0	12.0	27.0
West	TR_LP3	0	Count	13	10	23
			Expected Count	11.5	11.5	23.0
		1	Count	2	5	7
			Expected Count	3.5	3.5	7.0
		Total	Count	15	15	30
			Expected Count	15.0	15.0	30.0
East	TR_LP3	0	Count	13	8	21
			Expected Count	14.0	7.0	21.0
		1	Count	3	0	3
			Expected Count	2.0	1.0	3.0
		Total	Count	16	8	24
			Expected Count	16.0	8.0	24.0
North	TR_LP3	0	Count	16	9	25
			Expected Count	14.2	10.8	25.0
		1	Count	1	4	5
			Expected Count	2.8	2.2	5.0
		Total	Count	17	13	30
			Expected Count	17.0	13.0	30.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.831[a]	1	.362		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.206	1	.272		
	Fisher's Exact Test				1.000	.556
	N of Valid Cases	27				
West	Pearson Chi-Square	1.677[c]	1	.195		
	Continuity Correction[b]	.745	1	.388		
	Likelihood Ratio	1.721	1	.190		
	Fisher's Exact Test				.390	.195
	N of Valid Cases	30				
East	Pearson Chi-Square	1.714[d]	1	.190		
	Continuity Correction[b]	.429	1	.513		
	Likelihood Ratio	2.642	1	.104		
	Fisher's Exact Test				.526	.277
	N of Valid Cases	24				
North	Pearson Chi-Square	3.285[e]	1	.070		
	Continuity Correction[b]	1.738	1	.187		
	Likelihood Ratio	3.379	1	.066		
	Fisher's Exact Test				.138	.094
	N of Valid Cases	30				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .44.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.50.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.00.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.17.

3-rooted LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	3root_LM1	0	Count	10	10	20
			Expected Count	10.0	10.0	20.0
		Total	Count	10	10	20
			Expected Count	10.0	10.0	20.0
West	3root_LM1	0	Count	7	11	18
			Expected Count	7.6	10.4	18.0
		1	Count	1	0	1
			Expected Count	.4	.6	1.0
		Total	Count	8	11	19
			Expected Count	8.0	11.0	19.0
East	3root_LM1	0	Count	6	3	9
			Expected Count	6.0	3.0	9.0
		Total	Count	6	3	9
			Expected Count	6.0	3.0	9.0
North	3root_LM1	0	Count	10	12	22
			Expected Count	10.0	12.0	22.0
		Total	Count	10	12	22
			Expected Count	10.0	12.0	22.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	20				
West	Pearson Chi-Square	1.451[b]	1	.228		
	Continuity Correction[c]	.027	1	.870		
	Likelihood Ratio	1.807	1	.179		
	Fisher's Exact Test				.421	.421
	N of Valid Cases	19				
East	Pearson Chi-Square	.[a]				
	N of Valid Cases	9				
North	Pearson Chi-Square	.[a]				
	N of Valid Cases	22				

a. No statistics are computed because 3root_LM1 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .42.

c. Computed only for a 2x2 table

2-rooted LM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	2root_LM2	0	Count	1	1	2
			Expected Count	1.0	1.0	2.0
		1	Count	7	7	14
			Expected Count	7.0	7.0	14.0
		Total	Count	8	8	16
			Expected Count	8.0	8.0	16.0
West	2root_LM2	1	Count	6	11	17
			Expected Count	6.0	11.0	17.0
		Total	Count	6	11	17
			Expected Count	6.0	11.0	17.0
East	2root_LM2	1	Count	6	4	10
			Expected Count	6.0	4.0	10.0
		Total	Count	6	4	10
			Expected Count	6.0	4.0	10.0
North	2root_LM2	0	Count	2	1	3
			Expected Count	1.4	1.6	3.0
		1	Count	8	11	19
			Expected Count	8.6	10.4	19.0
		Total	Count	10	12	22
			Expected Count	10.0	12.0	22.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.000[a]	1	1.000		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.000	1	1.000		
	Fisher's Exact Test				1.000	.767
	N of Valid Cases	16				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	17				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	10				
North	Pearson Chi-Square	.630[d]	1	.427		
	Continuity Correction[b]	.029	1	.865		
	Likelihood Ratio	.633	1	.426		
	Fisher's Exact Test				.571	.429
	N of Valid Cases	22				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.00.

b. Computed only for a 2x2 table

c. No statistics are computed because 2root_LM2 is a constant.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.36.

Congenital absence LI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_LI1	0	Count	16	14	30
			Expected Count	16.0	14.0	30.0
		Total	Count	16	14	30
			Expected Count	16.0	14.0	30.0
West	CA_LI1	0	Count	18	17	35
			Expected Count	18.0	17.0	35.0
		Total	Count	18	17	35
			Expected Count	18.0	17.0	35.0
East	CA_LI1	0	Count	17	8	25
			Expected Count	17.0	8.0	25.0
		Total	Count	17	8	25
			Expected Count	17.0	8.0	25.0
North	CA_LI1	0	Count	19	13	32
			Expected Count	19.0	13.0	32.0
		Total	Count	19	13	32
			Expected Count	19.0	13.0	32.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	30
West	Pearson Chi-Square	.[a]
	N of Valid Cases	35
East	Pearson Chi-Square	.[a]
	N of Valid Cases	25
North	Pearson Chi-Square	.[a]
	N of Valid Cases	32

a. No statistics are computed because CA_LI1 is a constant.

Congenital absence LI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_LI2	0	Count	16	13	29
			Expected Count	16.0	13.0	29.0
		Total	Count	16	13	29
			Expected Count	16.0	13.0	29.0
West	CA_LI2	0	Count	18	17	35
			Expected Count	18.0	17.0	35.0
		Total	Count	18	17	35
			Expected Count	18.0	17.0	35.0
East	CA_LI2	0	Count	17	8	25
			Expected Count	17.0	8.0	25.0
		Total	Count	17	8	25
			Expected Count	17.0	8.0	25.0
North	CA_LI2	0	Count	19	13	32
			Expected Count	19.0	13.0	32.0
		Total	Count	19	13	32
			Expected Count	19.0	13.0	32.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	29
West	Pearson Chi-Square	.[a]
	N of Valid Cases	35
East	Pearson Chi-Square	.[a]
	N of Valid Cases	25
North	Pearson Chi-Square	.[a]
	N of Valid Cases	32

a. No statistics are computed because CA_LI2 is a constant.

Congenital absence LC * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_LC	0	Count	16	13	29
			Expected Count	16.0	13.0	29.0
		Total	Count	16	13	29
			Expected Count	16.0	13.0	29.0
West	CA_LC	0	Count	19	17	36
			Expected Count	19.0	17.0	36.0
		Total	Count	19	17	36
			Expected Count	19.0	17.0	36.0
East	CA_LC	0	Count	17	8	25
			Expected Count	17.0	8.0	25.0
		Total	Count	17	8	25
			Expected Count	17.0	8.0	25.0
North	CA_LC	0	Count	19	13	32
			Expected Count	19.0	13.0	32.0
		Total	Count	19	13	32
			Expected Count	19.0	13.0	32.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	29
West	Pearson Chi-Square	.[a]
	N of Valid Cases	36
East	Pearson Chi-Square	.[a]
	N of Valid Cases	25
North	Pearson Chi-Square	.[a]
	N of Valid Cases	32

a. No statistics are computed because CA_LC is a constant.

Congenital absence LP3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_LP3	0	Count	16	13	29
			Expected Count	16.0	13.0	29.0
		Total	Count	16	13	29
			Expected Count	16.0	13.0	29.0
West	CA_LP3	0	Count	19	17	36
			Expected Count	19.0	17.0	36.0
		Total	Count	19	17	36
			Expected Count	19.0	17.0	36.0
East	CA_LP3	0	Count	17	8	25
			Expected Count	17.0	8.0	25.0
		Total	Count	17	8	25
			Expected Count	17.0	8.0	25.0
North	CA_LP3	0	Count	18	13	31
			Expected Count	18.0	13.0	31.0
		Total	Count	18	13	31
			Expected Count	18.0	13.0	31.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	29
West	Pearson Chi-Square	.[a]
	N of Valid Cases	36
East	Pearson Chi-Square	.[a]
	N of Valid Cases	25
North	Pearson Chi-Square	.[a]
	N of Valid Cases	31

a. No statistics are computed because CA_LP1 is a constant.

Congenital absence LP4 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_LP4	0	Count	12	13	25
			Expected Count	12.0	13.0	25.0
		Total	Count	12	13	25
			Expected Count	12.0	13.0	25.0
West	CA_LP4	0	Count	16	15	31
			Expected Count	15.0	16.0	31.0
		1	Count	0	2	2
			Expected Count	1.0	1.0	2.0
		Total	Count	16	17	33
			Expected Count	16.0	17.0	33.0
East	CA_LP4	0	Count	16	8	24
			Expected Count	16.0	8.0	24.0
		Total	Count	16	8	24
			Expected Count	16.0	8.0	24.0
North	CA_LP4	0	Count	17	13	30
			Expected Count	17.0	13.0	30.0
		Total	Count	17	13	30
			Expected Count	17.0	13.0	30.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	25				
West	Pearson Chi-Square	2.004[b]	1	.157		
	Continuity Correction[c]	.470	1	.493		
	Likelihood Ratio	2.775	1	.096		
	Fisher's Exact Test				.485	.258
	N of Valid Cases	33				
East	Pearson Chi-Square	.[a]				
	N of Valid Cases	24				
North	Pearson Chi-Square	.[a]				
	N of Valid Cases	30				

a. No statistics are computed because CA_LP2 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .97.

c. Computed only for a 2x2 table

Congenital absence LM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_LM1	0	Count	13	14	27
			Expected Count	13.0	14.0	27.0
		Total	Count	13	14	27
			Expected Count	13.0	14.0	27.0
West	CA_LM1	0	Count	15	15	30
			Expected Count	15.0	15.0	30.0
		Total	Count	15	15	30
			Expected Count	15.0	15.0	30.0
East	CA_LM1	0	Count	14	7	21
			Expected Count	14.0	7.0	21.0
		Total	Count	14	7	21
			Expected Count	14.0	7.0	21.0
North	CA_LM1	0	Count	14	13	27
			Expected Count	14.0	13.0	27.0
		Total	Count	14	13	27
			Expected Count	14.0	13.0	27.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	27
West	Pearson Chi-Square	.[a]
	N of Valid Cases	30
East	Pearson Chi-Square	.[a]
	N of Valid Cases	21
North	Pearson Chi-Square	.[a]
	N of Valid Cases	27

a. No statistics are computed because CA_LM1 is a constant.

Congenital absence LM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_LM2	0	Count	13	13	26
			Expected Count	13.0	13.0	26.0
		Total	Count	13	13	26
			Expected Count	13.0	13.0	26.0
West	CA_LM2	0	Count	14	15	29
			Expected Count	14.0	15.0	29.0
		Total	Count	14	15	29
			Expected Count	14.0	15.0	29.0
East	CA_LM2	0	Count	13	7	20
			Expected Count	13.0	7.0	20.0
		Total	Count	13	7	20
			Expected Count	13.0	7.0	20.0
North	CA_LM2	0	Count	13	13	26
			Expected Count	13.0	13.0	26.0
		Total	Count	13	13	26
			Expected Count	13.0	13.0	26.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	26
West	Pearson Chi-Square	.[a]
	N of Valid Cases	29
East	Pearson Chi-Square	.[a]
	N of Valid Cases	20
North	Pearson Chi-Square	.[a]
	N of Valid Cases	26

a. No statistics are computed because CA_LM2 is a constant.

Congenital absence LM3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_LM3	0	Count	9	11	20
			Expected Count	9.5	10.5	20.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	10	11	21
			Expected Count	10.0	11.0	21.0
West	CA_LM3	0	Count	8	15	23
			Expected Count	8.0	15.0	23.0
		Total	Count	8	15	23
			Expected Count	8.0	15.0	23.0
East	CA_LM3	0	Count	13	8	21
			Expected Count	13.4	7.6	21.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	14	8	22
			Expected Count	14.0	8.0	22.0
North	CA_LM3	0	Count	10	11	21
			Expected Count	10.5	10.5	21.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	11	11	22
			Expected Count	11.0	11.0	22.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.155[a]	1	.283		
	Continuity Correction[b]	.002	1	.961		
	Likelihood Ratio	1.539	1	.215		
	Fisher's Exact Test				.476	.476
	N of Valid Cases	21				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	23				
East	Pearson Chi-Square	.599[d]	1	.439		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.931	1	.335		
	Fisher's Exact Test				1.000	.636
	N of Valid Cases	22				
North	Pearson Chi-Square	1.048[e]	1	.306		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.434	1	.231		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	22				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .48.

b. Computed only for a 2x2 table

c. No statistics are computed because CA_LM3 is a constant.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .36.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .50.

Winging UI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Winging_UI1	0	Count	8	8	16
			Expected Count	8.0	8.0	16.0
		Total	Count	8	8	16
			Expected Count	8.0	8.0	16.0
West	Winging_UI1	0	Count	15	8	23
			Expected Count	15.0	8.0	23.0
		Total	Count	15	8	23
			Expected Count	15.0	8.0	23.0
East	Winging_UI1	0	Count	13	7	20
			Expected Count	13.3	6.7	20.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	14	7	21
			Expected Count	14.0	7.0	21.0
North	Winging_UI1	0	Count	17	13	30
			Expected Count	17.4	12.6	30.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	18	13	31
			Expected Count	18.0	13.0	31.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	16				
West	Pearson Chi-Square	.[a]				
	N of Valid Cases	23				
East	Pearson Chi-Square	.525[b]	1	.469		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	.836	1	.361		
	Fisher's Exact Test				1.000	.667
	N of Valid Cases	21				
North	Pearson Chi-Square	.746[d]	1	.388		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	1.111	1	.292		
	Fisher's Exact Test				1.000	.581
	N of Valid Cases	31				

a. No statistics are computed because Winging_UI1 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .33.

c. Computed only for a 2x2 table

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .42.

Shovelling UC * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Shovel_UC	0	Count	5	6	11
			Expected Count	5.9	5.1	11.0
		1	Count	2	0	2
			Expected Count	1.1	.9	2.0
		Total	Count	7	6	13
			Expected Count	7.0	6.0	13.0
West	Shovel_UC	0	Count	14	9	23
			Expected Count	12.8	10.2	23.0
		1	Count	1	3	4
			Expected Count	2.2	1.8	4.0
		Total	Count	15	12	27
			Expected Count	15.0	12.0	27.0
East	Shovel_UC	0	Count	6	3	9
			Expected Count	6.0	3.0	9.0
		Total	Count	6	3	9
			Expected Count	6.0	3.0	9.0
North	Shovel_UC	0	Count	5	7	12
			Expected Count	4.6	7.4	12.0
		1	Count	0	1	1
			Expected Count	.4	.6	1.0
		Total	Count	5	8	13
			Expected Count	5.0	8.0	13.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	2.026[a]	1	.155		
	Continuity Correction[b]	.426	1	.514		
	Likelihood Ratio	2.787	1	.095		
	Fisher's Exact Test				.462	.269
	N of Valid Cases	13				
West	Pearson Chi-Square	1.776[c]	1	.183		
	Continuity Correction[b]	.620	1	.431		
	Likelihood Ratio	1.808	1	.179		
	Fisher's Exact Test				.294	.216
	N of Valid Cases	27				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	9				
North	Pearson Chi-Square	.677[e]	1	.411		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.023	1	.312		
	Fisher's Exact Test				1.000	.615
	N of Valid Cases	13				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .92.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.78.

d. No statistics are computed because Shovel_UC is a constant.

e. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .38.

Shovelling UI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Shovel_UI2	0	Count	2	6	8
			Expected Count	4.0	4.0	8.0
		1	Count	6	2	8
			Expected Count	4.0	4.0	8.0
		Total	Count	8	8	16
			Expected Count	8.0	8.0	16.0
West	Shovel_UI2	0	Count	8	6	14
			Expected Count	7.0	7.0	14.0
		1	Count	1	3	4
			Expected Count	2.0	2.0	4.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
East	Shovel_UI2	0	Count	4	2	6
			Expected Count	3.8	2.2	6.0
		1	Count	3	2	5
			Expected Count	3.2	1.8	5.0
		Total	Count	7	4	11
			Expected Count	7.0	4.0	11.0
North	Shovel_UI2	0	Count	7	5	12
			Expected Count	6.6	5.4	12.0
		1	Count	4	4	8
			Expected Count	4.4	3.6	8.0
		Total	Count	11	9	20
			Expected Count	11.0	9.0	20.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	4.000[a]	1	.046		
	Continuity Correction[b]	2.250	1	.134		
	Likelihood Ratio	4.186	1	.041		
	Fisher's Exact Test				.132	.066
	N of Valid Cases	16				
West	Pearson Chi-Square	1.286[c]	1	.257		
	Continuity Correction[b]	.321	1	.571		
	Likelihood Ratio	1.333	1	.248		
	Fisher's Exact Test				.576	.288
	N of Valid Cases	18				
East	Pearson Chi-Square	.052[d]	1	.819		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.052	1	.819		
	Fisher's Exact Test				1.000	.652
	N of Valid Cases	11				
North	Pearson Chi-Square	.135[e]	1	.714		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.135	1	.714		
	Fisher's Exact Test				1.000	.535
	N of Valid Cases	20				

a. 4 cells (100.0%) have expected count less than 5. The minimum expected count is 4.00.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.00.

d. 4 cells (100.0%) have expected count less than 5. The minimum expected count is 1.82.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.60.

Shovelling UI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Shovel_UI1	0	Count	4	7	11
			Expected Count	5.8	5.2	11.0
		1	Count	5	1	6
			Expected Count	3.2	2.8	6.0
		Total	Count	9	8	17
			Expected Count	9.0	8.0	17.0
West	Shovel_UI1	0	Count	10	6	16
			Expected Count	10.7	5.3	16.0
		1	Count	2	0	2
			Expected Count	1.3	.7	2.0
		Total	Count	12	6	18
			Expected Count	12.0	6.0	18.0
East	Shovel_UI1	0	Count	5	4	9
			Expected Count	4.5	4.5	9.0
		1	Count	0	1	1
			Expected Count	.5	.5	1.0
		Total	Count	5	5	10
			Expected Count	5.0	5.0	10.0
North	Shovel_UI1	0	Count	8	4	12
			Expected Count	6.7	5.3	12.0
		1	Count	2	4	6
			Expected Count	3.3	2.7	6.0
		Total	Count	10	8	18
			Expected Count	10.0	8.0	18.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	3.438[a]	1	.064		
	Continuity Correction[b]	1.811	1	.178		
	Likelihood Ratio	3.681	1	.055		
	Fisher's Exact Test				.131	.088
	N of Valid Cases	17				
West	Pearson Chi-Square	1.125[c]	1	.289		
	Continuity Correction[b]	.070	1	.791		
	Likelihood Ratio	1.744	1	.187		
	Fisher's Exact Test				.529	.431
	N of Valid Cases	18				
East	Pearson Chi-Square	1.111[d]	1	.292		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.498	1	.221		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	10				
North	Pearson Chi-Square	1.800[e]	1	.180		
	Continuity Correction[b]	.703	1	.402		
	Likelihood Ratio	1.816	1	.178		
	Fisher's Exact Test				.321	.201
	N of Valid Cases	18				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.82.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .67.

d. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .50.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.67.

Labial convexity UI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Lab.Co._UI2	0	Count	0	1	1
			Expected Count	.5	.5	1.0
		1	Count	9	8	17
			Expected Count	8.5	8.5	17.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	Lab.Co._UI2	1	Count	11	9	20
			Expected Count	11.0	9.0	20.0
		Total	Count	11	9	20
			Expected Count	11.0	9.0	20.0
East	Lab.Co._UI2	1	Count	11	4	15
			Expected Count	11.0	4.0	15.0
		Total	Count	11	4	15
			Expected Count	11.0	4.0	15.0
North	Lab.Co._UI2	1	Count	12	11	23
			Expected Count	12.0	11.0	23.0
		Total	Count	12	11	23
			Expected Count	12.0	11.0	23.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.059[a]	1	.303		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.445	1	.229		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	18				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	20				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	15				
North	Pearson Chi-Square	.[c]				
	N of Valid Cases	23				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .50.

b. Computed only for a 2x2 table

c. No statistics are computed because Lab.Co._UI2 is a constant.

Labial convexity UI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Lab.Co._UI1	0	Count	4	1	5
			Expected Count	2.5	2.5	5.0
		1	Count	5	8	13
			Expected Count	6.5	6.5	13.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	Lab.Co._UI1	1	Count	12	7	19
			Expected Count	12.0	7.0	19.0
		Total	Count	12	7	19
			Expected Count	12.0	7.0	19.0
East	Lab.Co._UI1	0	Count	0	1	1
			Expected Count	.7	.3	1.0
		1	Count	11	4	15
			Expected Count	10.3	4.7	15.0
		Total	Count	11	5	16
			Expected Count	11.0	5.0	16.0
North	Lab.Co._UI1	0	Count	1	2	3
			Expected Count	1.8	1.2	3.0
		1	Count	12	7	19
			Expected Count	11.2	7.8	19.0
		Total	Count	13	9	22
			Expected Count	13.0	9.0	22.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	2.492[a]	1	.114		
	Continuity Correction[b]	1.108	1	.293		
	Likelihood Ratio	2.626	1	.105		
	Fisher's Exact Test				.294	.147
	N of Valid Cases	18				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	19				
East	Pearson Chi-Square	2.347[d]	1	.126		
	Continuity Correction[b]	.175	1	.676		
	Likelihood Ratio	2.477	1	.115		
	Fisher's Exact Test				.313	.313
	N of Valid Cases	16				
North	Pearson Chi-Square	.953[e]	1	.329		
	Continuity Correction[b]	.119	1	.730		
	Likelihood Ratio	.940	1	.332		
	Fisher's Exact Test				.544	.358
	N of Valid Cases	22				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.50.

b. Computed only for a 2x2 table

c. No statistics are computed because Lab.Co._UI1 is a constant.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .31.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.23.

Double Shovelling UC * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Dbl.Shov._UC	0	Count	11	8	19
			Expected Count	10.5	8.5	19.0
		1	Count	0	1	1
			Expected Count	.6	.5	1.0
		Total	Count	11	9	20
			Expected Count	11.0	9.0	20.0
West	Dbl.Shov._UC	0	Count	17	11	28
			Expected Count	16.4	11.6	28.0
		1	Count	0	1	1
			Expected Count	.6	.4	1.0
		Total	Count	17	12	29
			Expected Count	17.0	12.0	29.0
East	Dbl.Shov._UC	0	Count	8	3	11
			Expected Count	8.0	3.0	11.0
		Total	Count	8	3	11
			Expected Count	8.0	3.0	11.0
North	Dbl.Shov._UC	0	Count	10	12	22
			Expected Count	10.0	12.0	22.0
		Total	Count	10	12	22
			Expected Count	10.0	12.0	22.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.287[a]	1	.257		
	Continuity Correction[b]	.011	1	.918		
	Likelihood Ratio	1.662	1	.197		
	Fisher's Exact Test				.450	.450
	N of Valid Cases	20				
West	Pearson Chi-Square	1.467[c]	1	.226		
	Continuity Correction[b]	.032	1	.859		
	Likelihood Ratio	1.816	1	.178		
	Fisher's Exact Test				.414	.414
	N of Valid Cases	29				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	11				
North	Pearson Chi-Square	.[d]				
	N of Valid Cases	22				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .45.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .41.

d. No statistics are computed because Dbl.Shov._UC is a constant.

Double Shovelling UI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Dbl.Shov._UI2	0	Count	9	8	17
			Expected Count	8.5	8.5	17.0
		1	Count	0	1	1
			Expected Count	.5	.5	1.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	Dbl.Shov._UI2	0	Count	11	9	20
			Expected Count	11.0	9.0	20.0
		Total	Count	11	9	20
			Expected Count	11.0	9.0	20.0
East	Dbl.Shov._UI2	0	Count	10	5	15
			Expected Count	10.0	5.0	15.0
		Total	Count	10	5	15
			Expected Count	10.0	5.0	15.0
North	Dbl.Shov._UI2	0	Count	12	11	23
			Expected Count	12.0	11.0	23.0
		Total	Count	12	11	23
			Expected Count	12.0	11.0	23.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.059[a]	1	.303		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.445	1	.229		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	18				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	20				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	15				
North	Pearson Chi-Square	.[c]				
	N of Valid Cases	23				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .50.

b. Computed only for a 2x2 table

c. No statistics are computed because Dbl.Shov._UI2 is a constant.

Double Shovelling UI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Dbl.Shov._UI1	0	Count	9	9	18
			Expected Count	9.0	9.0	18.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	Dbl.Shov._UI1	0	Count	13	7	20
			Expected Count	13.0	7.0	20.0
		Total	Count	13	7	20
			Expected Count	13.0	7.0	20.0
East	Dbl.Shov._UI1	0	Count	9	5	14
			Expected Count	9.0	5.0	14.0
		Total	Count	9	5	14
			Expected Count	9.0	5.0	14.0
North	Dbl.Shov._UI1	0	Count	13	8	21
			Expected Count	13.0	8.0	21.0
		Total	Count	13	8	21
			Expected Count	13.0	8.0	21.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	18
West	Pearson Chi-Square	.[a]
	N of Valid Cases	20
East	Pearson Chi-Square	.[a]
	N of Valid Cases	14
North	Pearson Chi-Square	.[a]
	N of Valid Cases	21

a. No statistics are computed because Dbl.Shov._UI1 is a constant.

Interruption groove UI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	IG_UI2	0	Count	4	8	12
			Expected Count	6.0	6.0	12.0
		1	Count	5	1	6
			Expected Count	3.0	3.0	6.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	IG_UI2	0	Count	9	8	17
			Expected Count	9.7	7.3	17.0
		1	Count	3	1	4
			Expected Count	2.3	1.7	4.0
		Total	Count	12	9	21
			Expected Count	12.0	9.0	21.0
East	IG_UI2	0	Count	12	5	17
			Expected Count	12.5	4.5	17.0
		1	Count	2	0	2
			Expected Count	1.5	.5	2.0
		Total	Count	14	5	19
			Expected Count	14.0	5.0	19.0
North	IG_UI2	0	Count	14	10	24
			Expected Count	13.3	10.7	24.0
		1	Count	1	2	3
			Expected Count	1.7	1.3	3.0
		Total	Count	15	12	27
			Expected Count	15.0	12.0	27.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	4.000[a]	1	.046		
	Continuity Correction[b]	2.250	1	.134		
	Likelihood Ratio	4.270	1	.039		
	Fisher's Exact Test				.131	.066
	N of Valid Cases	18				
West	Pearson Chi-Square	.643[c]	1	.422		
	Continuity Correction[b]	.058	1	.810		
	Likelihood Ratio	.675	1	.411		
	Fisher's Exact Test				.603	.414
	N of Valid Cases	21				
East	Pearson Chi-Square	.798[d]	1	.372		
	Continuity Correction[b]	.002	1	.964		
	Likelihood Ratio	1.304	1	.254		
	Fisher's Exact Test				1.000	.532
	N of Valid Cases	19				
North	Pearson Chi-Square	.675[e]	1	.411		
	Continuity Correction[b]	.042	1	.837		
	Likelihood Ratio	.676	1	.411		
	Fisher's Exact Test				.569	.414
	N of Valid Cases	27				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.00.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.71.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .53.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.33.

Interruption groove UI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	IG_UI1	0	Count	8	7	15
			Expected Count	7.5	7.5	15.0
		1	Count	1	2	3
			Expected Count	1.5	1.5	3.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	IG_UI1	0	Count	15	8	23
			Expected Count	15.0	8.0	23.0
		Total	Count	15	8	23
			Expected Count	15.0	8.0	23.0
East	IG_UI1	0	Count	14	7	21
			Expected Count	14.0	7.0	21.0
		Total	Count	14	7	21
			Expected Count	14.0	7.0	21.0
North	IG_UI1	0	Count	16	12	28
			Expected Count	16.0	12.0	28.0
		Total	Count	16	12	28
			Expected Count	16.0	12.0	28.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.400[a]	1	.527		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.407	1	.524		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	18				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	23				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	21				
North	Pearson Chi-Square	.[c]				
	N of Valid Cases	28				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.50.

b. Computed only for a 2x2 table

c. No statistics are computed because IG_UI1 is a constant.

Tuberculum dentale UC * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	TD_UC	0	Count	4	7	11
			Expected Count	4.7	6.3	11.0
		1	Count	2	1	3
			Expected Count	1.3	1.7	3.0
		Total	Count	6	8	14
			Expected Count	6.0	8.0	14.0
West	TD_UC	0	Count	12	7	19
			Expected Count	11.0	8.0	19.0
		1	Count	3	4	7
			Expected Count	4.0	3.0	7.0
		Total	Count	15	11	26
			Expected Count	15.0	11.0	26.0
East	TD_UC	0	Count	7	3	10
			Expected Count	7.3	2.7	10.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	8	3	11
			Expected Count	8.0	3.0	11.0
North	TD_UC	0	Count	4	2	6
			Expected Count	2.6	3.4	6.0
		1	Count	3	7	10
			Expected Count	4.4	5.6	10.0
		Total	Count	7	9	16
			Expected Count	7.0	9.0	16.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.884[a]	1	.347		
	Continuity Correction[b]	.080	1	.778		
	Likelihood Ratio	.882	1	.348		
	Fisher's Exact Test				.538	.385
	N of Valid Cases	14				
West	Pearson Chi-Square	.864[c]	1	.353		
	Continuity Correction[b]	.232	1	.630		
	Likelihood Ratio	.857	1	.355		
	Fisher's Exact Test				.407	.313
	N of Valid Cases	26				
East	Pearson Chi-Square	.413[d]	1	.521		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.674	1	.412		
	Fisher's Exact Test				1.000	.727
	N of Valid Cases	11				
North	Pearson Chi-Square	2.049[e]	1	.152		
	Continuity Correction[b]	.830	1	.362		
	Likelihood Ratio	2.075	1	.150		
	Fisher's Exact Test				.302	.182
	N of Valid Cases	16				

a. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 1.29.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.96.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .27.

e. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 2.63.

Tuberculum dentale UI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	TD_UI2	0	Count	6	7	13
			Expected Count	6.5	6.5	13.0
		1	Count	2	1	3
			Expected Count	1.5	1.5	3.0
		Total	Count	8	8	16
			Expected Count	8.0	8.0	16.0
West	TD_UI2	0	Count	10	8	18
			Expected Count	10.4	7.6	18.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	11	8	19
			Expected Count	11.0	8.0	19.0
East	TD_UI2	0	Count	9	4	13
			Expected Count	9.0	4.0	13.0
		Total	Count	9	4	13
			Expected Count	9.0	4.0	13.0
North	TD_UI2	0	Count	9	8	17
			Expected Count	8.9	8.1	17.0
		1	Count	1	1	2
			Expected Count	1.1	.9	2.0
		Total	Count	10	9	19
			Expected Count	10.0	9.0	19.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.410[a]	1	.522		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.417	1	.519		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	16				
West	Pearson Chi-Square	.768[c]	1	.381		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.133	1	.287		
	Fisher's Exact Test				1.000	.579
	N of Valid Cases	19				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	13				
North	Pearson Chi-Square	.006[e]	1	.937		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.006	1	.937		
	Fisher's Exact Test				1.000	.737
	N of Valid Cases	19				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.50.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .42.

d. No statistics are computed because TD_UI2 is a constant.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .95.

Tuberculum dentale UI1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	TD_UI1	0	Count	4	6	10
			Expected Count	5.0	5.0	10.0
		1	Count	3	1	4
			Expected Count	2.0	2.0	4.0
		Total	Count	7	7	14
			Expected Count	7.0	7.0	14.0
West	TD_UI1	0	Count	10	4	14
			Expected Count	9.1	4.9	14.0
		1	Count	1	2	3
			Expected Count	1.9	1.1	3.0
		Total	Count	11	6	17
			Expected Count	11.0	6.0	17.0
East	TD_UI1	0	Count	7	5	12
			Expected Count	6.9	5.1	12.0
		1	Count	1	1	2
			Expected Count	1.1	.9	2.0
		Total	Count	8	6	14
			Expected Count	8.0	6.0	14.0
North	TD_UI1	0	Count	6	6	12
			Expected Count	6.6	5.4	12.0
		1	Count	5	3	8
			Expected Count	4.4	3.6	8.0
		Total	Count	11	9	20
			Expected Count	11.0	9.0	20.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.400[a]	1	.237		
	Continuity Correction[b]	.350	1	.554		
	Likelihood Ratio	1.449	1	.229		
	Fisher's Exact Test				.559	.280
	N of Valid Cases	14				
West	Pearson Chi-Square	1.570[c]	1	.210		
	Continuity Correction[b]	.345	1	.557		
	Likelihood Ratio	1.504	1	.220		
	Fisher's Exact Test				.515	.272
	N of Valid Cases	17				
East	Pearson Chi-Square	.049[d]	1	.825		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.048	1	.826		
	Fisher's Exact Test				1.000	.692
	N of Valid Cases	14				
North	Pearson Chi-Square	.303[e]	1	.582		
	Continuity Correction[b]	.008	1	.927		
	Likelihood Ratio	.305	1	.581		
	Fisher's Exact Test				.670	.465
	N of Valid Cases	20				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.00.

b. Computed only for a 2x2 table

c. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 1.06.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .86.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 3.60.

Mesial ridge UC * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	M.Ridge_UC	0	Count	9	5	14
			Expected Count	9.0	5.0	14.0
		Total	Count	9	5	14
			Expected Count	9.0	5.0	14.0
West	M.Ridge_UC	0	Count	8	7	15
			Expected Count	8.4	6.6	15.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	9	7	16
			Expected Count	9.0	7.0	16.0
East	M.Ridge_UC	0	Count	5	3	8
			Expected Count	5.0	3.0	8.0
		Total	Count	5	3	8
			Expected Count	5.0	3.0	8.0
North	M.Ridge_UC	0	Count	8	9	17
			Expected Count	8.0	9.0	17.0
		Total	Count	8	9	17
			Expected Count	8.0	9.0	17.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	14				
West	Pearson Chi-Square	.830[b]	1	.362		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	1.202	1	.273		
	Fisher's Exact Test				1.000	.563
	N of Valid Cases	16				
East	Pearson Chi-Square	.[a]				
	N of Valid Cases	8				
North	Pearson Chi-Square	.[a]				
	N of Valid Cases	17				

a. No statistics are computed because M.Ridge_UC is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .44.

c. Computed only for a 2x2 table

Distal accessory ridge UC * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	DAR_UC	0	Count	3	2	5
			Expected Count	3.1	1.9	5.0
		1	Count	2	1	3
			Expected Count	1.9	1.1	3.0
		Total	Count	5	3	8
			Expected Count	5.0	3.0	8.0
West	DAR_UC	0	Count	3	1	4
			Expected Count	2.7	1.3	4.0
		1	Count	1	1	2
			Expected Count	1.3	.7	2.0
		Total	Count	4	2	6
			Expected Count	4.0	2.0	6.0
East	DAR_UC	0	Count	1	1	2
			Expected Count	1.0	1.0	2.0
		Total	Count	1	1	2
			Expected Count	1.0	1.0	2.0
North	DAR_UC	0	Count	1	1	2
			Expected Count	.7	1.3	2.0
		1	Count	0	1	1
			Expected Count	.3	.7	1.0
		Total	Count	1	2	3
			Expected Count	1.0	2.0	3.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.036[a]	1	.850		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.036	1	.850		
	Fisher's Exact Test				1.000	.714
	N of Valid Cases	8				
West	Pearson Chi-Square	.375[c]	1	.540		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.367	1	.545		
	Fisher's Exact Test				1.000	.600
	N of Valid Cases	6				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	2				
North	Pearson Chi-Square	.750[e]	1	.386		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.046	1	.306		
	Fisher's Exact Test				1.000	.667
	N of Valid Cases	3				

a. 4 cells (100.0%) have expected count less than 5. The minimum expected count is 1.13.

b. Computed only for a 2x2 table

c. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .67.

d. No statistics are computed because DAR_UC is a constant.

e. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .33.

Metacone UM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Metacone_UM2	1	Count	7	11	18
			Expected Count	7.0	11.0	18.0
		Total	Count	7	11	18
			Expected Count	7.0	11.0	18.0
West	Metacone_UM2	1	Count	15	9	24
			Expected Count	15.0	9.0	24.0
		Total	Count	15	9	24
			Expected Count	15.0	9.0	24.0
East	Metacone_UM2	0	Count	1	0	1
			Expected Count	.7	.3	1.0
		1	Count	9	5	14
			Expected Count	9.3	4.7	14.0
		Total	Count	10	5	15
			Expected Count	10.0	5.0	15.0
North	Metacone_UM2	0	Count	1	0	1
			Expected Count	.6	.5	1.0
		1	Count	10	9	19
			Expected Count	10.5	8.5	19.0
		Total	Count	11	9	20
			Expected Count	11.0	9.0	20.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	18				
West	Pearson Chi-Square	.[a]				
	N of Valid Cases	24				
East	Pearson Chi-Square	.536[b]	1	.464		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	.846	1	.358		
	Fisher's Exact Test				1.000	.667
	N of Valid Cases	15				
North	Pearson Chi-Square	.861[d]	1	.353		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	1.239	1	.266		
	Fisher's Exact Test				1.000	.550
	N of Valid Cases	20				

a. No statistics are computed because Metacone_UM2 is a constant.

b. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .33.

c. Computed only for a 2x2 table

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .45.

Metacone UM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Metacone_UM1	1	Count	9	10	19
			Expected Count	9.0	10.0	19.0
		Total	Count	9	10	19
			Expected Count	9.0	10.0	19.0
West	Metacone_UM1	1	Count	11	11	22
			Expected Count	11.0	11.0	22.0
		Total	Count	11	11	22
			Expected Count	11.0	11.0	22.0
East	Metacone_UM1	1	Count	14	6	20
			Expected Count	14.0	6.0	20.0
		Total	Count	14	6	20
			Expected Count	14.0	6.0	20.0
North	Metacone_UM1	1	Count	18	7	25
			Expected Count	18.0	7.0	25.0
		Total	Count	18	7	25
			Expected Count	18.0	7.0	25.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	19
West	Pearson Chi-Square	.[a]
	N of Valid Cases	22
East	Pearson Chi-Square	.[a]
	N of Valid Cases	20
North	Pearson Chi-Square	.[a]
	N of Valid Cases	25

a. No statistics are computed because Metacone_UM1 is a constant.

Hypocone UM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Hypocone_UM2	0	Count	2	4	6
			Expected Count	2.3	3.7	6.0
		1	Count	5	7	12
			Expected Count	4.7	7.3	12.0
		Total	Count	7	11	18
			Expected Count	7.0	11.0	18.0
West	Hypocone_UM2	0	Count	4	3	7
			Expected Count	4.8	2.2	7.0
		1	Count	11	4	15
			Expected Count	10.2	4.8	15.0
		Total	Count	15	7	22
			Expected Count	15.0	7.0	22.0
East	Hypocone_UM2	0	Count	2	0	2
			Expected Count	1.4	.6	2.0
		1	Count	8	4	12
			Expected Count	8.6	3.4	12.0
		Total	Count	10	4	14
			Expected Count	10.0	4.0	14.0
North	Hypocone_UM2	0	Count	2	1	3
			Expected Count	1.7	1.3	3.0
		1	Count	9	7	16
			Expected Count	9.3	6.7	16.0
		Total	Count	11	8	19
			Expected Count	11.0	8.0	19.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.117[a]	1	.732		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.118	1	.731		
	Fisher's Exact Test				1.000	.572
	N of Valid Cases	18				
West	Pearson Chi-Square	.577[c]	1	.448		
	Continuity Correction[b]	.072	1	.789		
	Likelihood Ratio	.563	1	.453		
	Fisher's Exact Test				.630	.387
	N of Valid Cases	22				
East	Pearson Chi-Square	.933[d]	1	.334		
	Continuity Correction[b]	.015	1	.904		
	Likelihood Ratio	1.475	1	.225		
	Fisher's Exact Test				1.000	.495
	N of Valid Cases	14				
North	Pearson Chi-Square	.112[e]	1	.737		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.115	1	.735		
	Fisher's Exact Test				1.000	.624
	N of Valid Cases	19				

a. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 2.33.

b. Computed only for a 2x2 table

c. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 2.23.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .57.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.26.

Hypocone UM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Hypocone_UM1	1	Count	9	10	19
			Expected Count	9.0	10.0	19.0
		Total	Count	9	10	19
			Expected Count	9.0	10.0	19.0
West	Hypocone_UM1	1	Count	11	11	22
			Expected Count	11.0	11.0	22.0
		Total	Count	11	11	22
			Expected Count	11.0	11.0	22.0
East	Hypocone_UM1	1	Count	13	6	19
			Expected Count	13.0	6.0	19.0
		Total	Count	13	6	19
			Expected Count	13.0	6.0	19.0
North	Hypocone_UM1	1	Count	18	6	24
			Expected Count	18.0	6.0	24.0
		Total	Count	18	6	24
			Expected Count	18.0	6.0	24.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	19
West	Pearson Chi-Square	.[a]
	N of Valid Cases	22
East	Pearson Chi-Square	.[a]
	N of Valid Cases	19
North	Pearson Chi-Square	.[a]
	N of Valid Cases	24

a. No statistics are computed because Hypocone_UM1 is a constant.

Cusp 5 (metaconule) UM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Cusp5_UM2	0	Count	6	9	15
			Expected Count	5.8	9.2	15.0
		1	Count	1	2	3
			Expected Count	1.2	1.8	3.0
		Total	Count	7	11	18
			Expected Count	7.0	11.0	18.0
West	Cusp5_UM2	0	Count	11	8	19
			Expected Count	11.4	7.6	19.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	12	8	20
			Expected Count	12.0	8.0	20.0
East	Cusp5_UM2	0	Count	8	4	12
			Expected Count	8.0	4.0	12.0
		Total	Count	8	4	12
			Expected Count	8.0	4.0	12.0
North	Cusp5_UM2	0	Count	8	6	14
			Expected Count	8.8	5.3	14.0
		1	Count	2	0	2
			Expected Count	1.3	.8	2.0
		Total	Count	10	6	16
			Expected Count	10.0	6.0	16.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.047[a]	1	.829		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.048	1	.827		
	Fisher's Exact Test				1.000	.674
	N of Valid Cases	18				
West	Pearson Chi-Square	.702[c]	1	.402		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.057	1	.304		
	Fisher's Exact Test				1.000	.600
	N of Valid Cases	20				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	12				
North	Pearson Chi-Square	1.371[e]	1	.242		
	Continuity Correction[b]	.152	1	.696		
	Likelihood Ratio	2.049	1	.152		
	Fisher's Exact Test				.500	.375
	N of Valid Cases	16				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.17.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .40.

d. No statistics are computed because Cusp5_UM2 is a constant.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .75.

Cusp 5 (metaconule) UM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Cusp5_UM1	0	Count	4	10	14
			Expected Count	4.7	9.3	14.0
		1	Count	1	0	1
			Expected Count	.3	.7	1.0
		Total	Count	5	10	15
			Expected Count	5.0	10.0	15.0
West	Cusp5_UM1	0	Count	7	7	14
			Expected Count	7.0	7.0	14.0
		1	Count	1	1	2
			Expected Count	1.0	1.0	2.0
		Total	Count	8	8	16
			Expected Count	8.0	8.0	16.0
East	Cusp5_UM1	0	Count	8	4	12
			Expected Count	8.0	4.0	12.0
		1	Count	2	1	3
			Expected Count	2.0	1.0	3.0
		Total	Count	10	5	15
			Expected Count	10.0	5.0	15.0
North	Cusp5_UM1	0	Count	14	2	16
			Expected Count	14.0	2.0	16.0
		Total	Count	14	2	16
			Expected Count	14.0	2.0	16.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	2.143[a]	1	.143		
	Continuity Correction[b]	.134	1	.714		
	Likelihood Ratio	2.344	1	.126		
	Fisher's Exact Test				.333	.333
	N of Valid Cases	15				
West	Pearson Chi-Square	.000[c]	1	1.000		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.000	1	1.000		
	Fisher's Exact Test				1.000	.767
	N of Valid Cases	16				
East	Pearson Chi-Square	.000[d]	1	1.000		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.000	1	1.000		
	Fisher's Exact Test				1.000	.758
	N of Valid Cases	15				
North	Pearson Chi-Square	.[e]				
	N of Valid Cases	16				

a. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .33.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.00.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is 1.00.

e. No statistics are computed because Cusp5_UM1 is a constant.

Carabelli's cusp UM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Carabelli_UM2	0	Count	5	10	15
			Expected Count	6.2	8.8	15.0
		1	Count	2	0	2
			Expected Count	.8	1.2	2.0
		Total	Count	7	10	17
			Expected Count	7.0	10.0	17.0
West	Carabelli_UM2	0	Count	14	6	20
			Expected Count	14.0	6.0	20.0
		Total	Count	14	6	20
			Expected Count	14.0	6.0	20.0
East	Carabelli_UM2	0	Count	8	3	11
			Expected Count	8.0	3.0	11.0
		Total	Count	8	3	11
			Expected Count	8.0	3.0	11.0
North	Carabelli_UM2	0	Count	8	4	12
			Expected Count	7.7	4.3	12.0
		1	Count	1	1	2
			Expected Count	1.3	.7	2.0
		Total	Count	9	5	14
			Expected Count	9.0	5.0	14.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	3.238[a]	1	.072		
	Continuity Correction[b]	1.071	1	.301		
	Likelihood Ratio	3.939	1	.047		
	Fisher's Exact Test				.154	.154
	N of Valid Cases	17				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	20				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	11				
North	Pearson Chi-Square	.207[d]	1	.649		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.200	1	.655		
	Fisher's Exact Test				1.000	.604
	N of Valid Cases	14				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .82.

b. Computed only for a 2x2 table

c. No statistics are computed because Carabelli_UM2 is a constant.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .71.

Carabelli's cusp UM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Carabelli_UM1	0	Count	0	2	2
			Expected Count	.5	1.5	2.0
		1	Count	2	4	6
			Expected Count	1.5	4.5	6.0
		Total	Count	2	6	8
			Expected Count	2.0	6.0	8.0
West	Carabelli_UM1	1	Count	4	6	10
			Expected Count	4.0	6.0	10.0
		Total	Count	4	6	10
			Expected Count	4.0	6.0	10.0
East	Carabelli_UM1	1	Count	8	5	13
			Expected Count	8.0	5.0	13.0
		Total	Count	8	5	13
			Expected Count	8.0	5.0	13.0
North	Carabelli_UM1	1	Count	6	3	9
			Expected Count	6.0	3.0	9.0
		Total	Count	6	3	9
			Expected Count	6.0	3.0	9.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.889[a]	1	.346		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.359	1	.244		
	Fisher's Exact Test				1.000	.536
	N of Valid Cases	8				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	10				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	13				
North	Pearson Chi-Square	.[c]				
	N of Valid Cases	9				

a. 4 cells (100.0%) have expected count less than 5. The minimum expected count is .50.

b. Computed only for a 2x2 table

c. No statistics are computed because Carabelli_UM1 is a constant.

Parastyle UM3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Parastyle_UM3	0	Count	4	6	10
			Expected Count	4.0	6.0	10.0
		Total	Count	4	6	10
			Expected Count	4.0	6.0	10.0
West	Parastyle_UM3	0	Count	11	3	14
			Expected Count	11.0	3.0	14.0
		Total	Count	11	3	14
			Expected Count	11.0	3.0	14.0
East	Parastyle_UM3	0	Count	9	3	12
			Expected Count	9.0	3.0	12.0
		Total	Count	9	3	12
			Expected Count	9.0	3.0	12.0
North	Parastyle_UM3	0	Count	10	9	19
			Expected Count	10.0	9.0	19.0
		Total	Count	10	9	19
			Expected Count	10.0	9.0	19.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	10
West	Pearson Chi-Square	.[a]
	N of Valid Cases	14
East	Pearson Chi-Square	.[a]
	N of Valid Cases	12
North	Pearson Chi-Square	.[a]
	N of Valid Cases	19

a. No statistics are computed because Parastyle_UM3 is a constant.

Parastyle UM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Parastyle_UM2	0	Count	7	11	18
			Expected Count	7.0	11.0	18.0
		Total	Count	7	11	18
			Expected Count	7.0	11.0	18.0
West	Parastyle_UM2	0	Count	15	8	23
			Expected Count	14.4	8.6	23.0
		1	Count	0	1	1
			Expected Count	.6	.4	1.0
		Total	Count	15	9	24
			Expected Count	15.0	9.0	24.0
East	Parastyle_UM2	0	Count	8	4	12
			Expected Count	8.0	4.0	12.0
		Total	Count	8	4	12
			Expected Count	8.0	4.0	12.0
North	Parastyle_UM2	0	Count	9	6	15
			Expected Count	9.0	6.0	15.0
		Total	Count	9	6	15
			Expected Count	9.0	6.0	15.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	18				
West	Pearson Chi-Square	1.739[b]	1	.187		
	Continuity Correction[c]	.070	1	.792		
	Likelihood Ratio	2.035	1	.154		
	Fisher's Exact Test				.375	.375
	N of Valid Cases	24				
East	Pearson Chi-Square	.[a]				
	N of Valid Cases	12				
North	Pearson Chi-Square	.[a]				
	N of Valid Cases	15				

a. No statistics are computed because Parastyle_UM2 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .38.

c. Computed only for a 2x2 table

Parastyle UM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Parastyle_UM1	0	Count	7	10	17
			Expected Count	7.0	10.0	17.0
		Total	Count	7	10	17
			Expected Count	7.0	10.0	17.0
West	Parastyle_UM1	0	Count	8	10	18
			Expected Count	8.5	9.5	18.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	9	10	19
			Expected Count	9.0	10.0	19.0
East	Parastyle_UM1	0	Count	12	5	17
			Expected Count	12.0	5.0	17.0
		Total	Count	12	5	17
			Expected Count	12.0	5.0	17.0
North	Parastyle_UM1	0	Count	11	3	14
			Expected Count	11.0	3.0	14.0
		Total	Count	11	3	14
			Expected Count	11.0	3.0	14.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	17				
West	Pearson Chi-Square	1.173[b]	1	.279		
	Continuity Correction[c]	.003	1	.957		
	Likelihood Ratio	1.556	1	.212		
	Fisher's Exact Test				.474	.474
	N of Valid Cases	19				
East	Pearson Chi-Square	.[a]				
	N of Valid Cases	17				
North	Pearson Chi-Square	.[a]				
	N of Valid Cases	14				

a. No statistics are computed because Parastyle_UM1 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .47.

c. Computed only for a 2x2 table

Enamel extensions UM3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	EE_UM3	0	Count	4	5	9
			Expected Count	3.6	5.4	9.0
		1	Count	0	1	1
			Expected Count	.4	.6	1.0
		Total	Count	4	6	10
			Expected Count	4.0	6.0	10.0
West	EE_UM3	0	Count	8	4	12
			Expected Count	8.3	3.7	12.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	9	4	13
			Expected Count	9.0	4.0	13.0
East	EE_UM3	0	Count	8	3	11
			Expected Count	7.6	3.4	11.0
		1	Count	1	1	2
			Expected Count	1.4	.6	2.0
		Total	Count	9	4	13
			Expected Count	9.0	4.0	13.0
North	EE_UM3	0	Count	9	10	19
			Expected Count	9.5	9.5	19.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	10	10	20
			Expected Count	10.0	10.0	20.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.741[a]	1	.389		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.095	1	.295		
	Fisher's Exact Test				1.000	.600
	N of Valid Cases	10				
West	Pearson Chi-Square	.481[c]	1	.488		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.772	1	.380		
	Fisher's Exact Test				1.000	.692
	N of Valid Cases	13				
East	Pearson Chi-Square	.410[d]	1	.522		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.385	1	.535		
	Fisher's Exact Test				1.000	.538
	N of Valid Cases	13				
North	Pearson Chi-Square	1.053[e]	1	.305		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.439	1	.230		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	20				

a. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .40.

b. Computed only for a 2x2 table

c. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .31.

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .62.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .50.

Enamel extensions UM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	EE_UM2	0	Count	7	10	17
			Expected Count	7.0	10.0	17.0
		Total	Count	7	10	17
			Expected Count	7.0	10.0	17.0
West	EE_UM2	0	Count	11	7	18
			Expected Count	12.0	6.0	18.0
		1	Count	3	0	3
			Expected Count	2.0	1.0	3.0
		Total	Count	14	7	21
			Expected Count	14.0	7.0	21.0
East	EE_UM2	0	Count	8	4	12
			Expected Count	8.3	3.7	12.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	9	4	13
			Expected Count	9.0	4.0	13.0
North	EE_UM2	0	Count	11	8	19
			Expected Count	11.0	8.0	19.0
		Total	Count	11	8	19
			Expected Count	11.0	8.0	19.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	17				
West	Pearson Chi-Square	1.750[b]	1	.186		
	Continuity Correction[c]	.438	1	.508		
	Likelihood Ratio	2.677	1	.102		
	Fisher's Exact Test				.521	.274
	N of Valid Cases	21				
East	Pearson Chi-Square	.481[d]	1	.488		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	.772	1	.380		
	Fisher's Exact Test				1.000	.692
	N of Valid Cases	13				
North	Pearson Chi-Square	.[a]				
	N of Valid Cases	19				

a. No statistics are computed because EE_UM2 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.00.

c. Computed only for a 2x2 table

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .31.

Enamel extensions UM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	EE_UM1	0	Count	10	8	18
			Expected Count	9.5	8.5	18.0
		1	Count	0	1	1
			Expected Count	.5	.5	1.0
		Total	Count	10	9	19
			Expected Count	10.0	9.0	19.0
West	EE_UM1	0	Count	7	9	16
			Expected Count	8.0	8.0	16.0
		1	Count	2	0	2
			Expected Count	1.0	1.0	2.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
East	EE_UM1	0	Count	13	6	19
			Expected Count	13.3	5.7	19.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	14	6	20
			Expected Count	14.0	6.0	20.0
North	EE_UM1	0	Count	15	6	21
			Expected Count	15.3	5.7	21.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	16	6	22
			Expected Count	16.0	6.0	22.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.173[a]	1	.279		
	Continuity Correction[b]	.003	1	.957		
	Likelihood Ratio	1.556	1	.212		
	Fisher's Exact Test				.474	.474
	N of Valid Cases	19				
West	Pearson Chi-Square	2.250[c]	1	.134		
	Continuity Correction[b]	.563	1	.453		
	Likelihood Ratio	3.023	1	.082		
	Fisher's Exact Test				.471	.235
	N of Valid Cases	18				
East	Pearson Chi-Square	.451[d]	1	.502		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.736	1	.391		
	Fisher's Exact Test				1.000	.700
	N of Valid Cases	20				
North	Pearson Chi-Square	.393[e]	1	.531		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.655	1	.418		
	Fisher's Exact Test				1.000	.727
	N of Valid Cases	22				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .47.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.00.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .30.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .27.

Enamel extensions UP4 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	EE_UP4	0	Count	9	9	18
			Expected Count	9.0	9.0	18.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	EE_UP4	0	Count	13	12	25
			Expected Count	13.0	12.0	25.0
		Total	Count	13	12	25
			Expected Count	13.0	12.0	25.0
East	EE_UP4	0	Count	12	6	18
			Expected Count	12.0	6.0	18.0
		Total	Count	12	6	18
			Expected Count	12.0	6.0	18.0
North	EE_UP4	0	Count	15	12	27
			Expected Count	15.0	12.0	27.0
		Total	Count	15	12	27
			Expected Count	15.0	12.0	27.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	18
West	Pearson Chi-Square	.[a]
	N of Valid Cases	25
East	Pearson Chi-Square	.[a]
	N of Valid Cases	18
North	Pearson Chi-Square	.[a]
	N of Valid Cases	27

a. No statistics are computed because EE_UP2 is a constant.

Enamel extension UP3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	EE_UP3	0	Count	9	11	20
			Expected Count	9.0	11.0	20.0
		Total	Count	9	11	20
			Expected Count	9.0	11.0	20.0
West	EE_UP3	0	Count	15	10	25
			Expected Count	15.0	10.0	25.0
		Total	Count	15	10	25
			Expected Count	15.0	10.0	25.0
East	EE_UP3	0	Count	11	6	17
			Expected Count	11.3	5.7	17.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	12	6	18
			Expected Count	12.0	6.0	18.0
North	EE_UP3	0	Count	12	13	25
			Expected Count	12.0	13.0	25.0
		Total	Count	12	13	25
			Expected Count	12.0	13.0	25.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	20				
West	Pearson Chi-Square	.[a]				
	N of Valid Cases	25				
East	Pearson Chi-Square	.529[b]	1	.467		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	.840	1	.359		
	Fisher's Exact Test				1.000	.667
	N of Valid Cases	18				
North	Pearson Chi-Square	.[a]				
	N of Valid Cases	25				

a. No statistics are computed because EE_UP1 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .33.

c. Computed only for a 2x2 table

2-rooted UP4 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	2root_UP4	0	Count	12	10	22
			Expected Count	11.5	10.5	22.0
		1	Count	0	1	1
			Expected Count	.5	.5	1.0
		Total	Count	12	11	23
			Expected Count	12.0	11.0	23.0
West	2root_UP4	0	Count	15	11	26
			Expected Count	13.8	12.2	26.0
		1	Count	2	4	6
			Expected Count	3.2	2.8	6.0
		Total	Count	17	15	32
			Expected Count	17.0	15.0	32.0
East	2root_UP4	0	Count	12	6	18
			Expected Count	12.3	5.7	18.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	13	6	19
			Expected Count	13.0	6.0	19.0
North	2root_UP4	0	Count	13	10	23
			Expected Count	13.3	9.7	23.0
		1	Count	2	1	3
			Expected Count	1.7	1.3	3.0
		Total	Count	15	11	26
			Expected Count	15.0	11.0	26.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.140[a]	1	.286		
	Continuity Correction[b]	.002	1	.965		
	Likelihood Ratio	1.525	1	.217		
	Fisher's Exact Test				.478	.478
	N of Valid Cases	23				
West	Pearson Chi-Square	1.162[c]	1	.281		
	Continuity Correction[b]	.389	1	.533		
	Likelihood Ratio	1.172	1	.279		
	Fisher's Exact Test				.383	.267
	N of Valid Cases	32				
East	Pearson Chi-Square	.487[d]	1	.485		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.784	1	.376		
	Fisher's Exact Test				1.000	.684
	N of Valid Cases	19				
North	Pearson Chi-Square	.112[e]	1	.738		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.114	1	.735		
	Fisher's Exact Test				1.000	.619
	N of Valid Cases	26				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .48.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.81.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .32.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.27.

2-rooted UP3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	2root_UP3	0	Count	7	5	12
			Expected Count	5.8	6.2	12.0
		1	Count	5	8	13
			Expected Count	6.2	6.8	13.0
		Total	Count	12	13	25
			Expected Count	12.0	13.0	25.0
West	2root_UP3	0	Count	7	3	10
			Expected Count	5.2	4.8	10.0
		1	Count	8	11	19
			Expected Count	9.8	9.2	19.0
		Total	Count	15	14	29
			Expected Count	15.0	14.0	29.0
East	2root_UP3	0	Count	10	3	13
			Expected Count	9.3	3.7	13.0
		1	Count	5	3	8
			Expected Count	5.7	2.3	8.0
		Total	Count	15	6	21
			Expected Count	15.0	6.0	21.0
North	2root_UP3	0	Count	8	6	14
			Expected Count	7.5	6.5	14.0
		1	Count	7	7	14
			Expected Count	7.5	6.5	14.0
		Total	Count	15	13	28
			Expected Count	15.0	13.0	28.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.987[a]	1	.320		
	Continuity Correction[b]	.352	1	.553		
	Likelihood Ratio	.993	1	.319		
	Fisher's Exact Test				.434	.277
	N of Valid Cases	25				
West	Pearson Chi-Square	2.042[c]	1	.153		
	Continuity Correction[b]	1.077	1	.299		
	Likelihood Ratio	2.087	1	.149		
	Fisher's Exact Test				.245	.150
	N of Valid Cases	29				
East	Pearson Chi-Square	.505[d]	1	.477		
	Continuity Correction[b]	.045	1	.831		
	Likelihood Ratio	.497	1	.481		
	Fisher's Exact Test				.631	.410
	N of Valid Cases	21				
North	Pearson Chi-Square	.144[e]	1	.705		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.144	1	.705		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	28				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 5.76.

b. Computed only for a 2x2 table

c. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 4.83.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.29.

e. 0 cells (.0%) have expected count less than 5. The minimum expected count is 6.50.

3-rooted UM2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	3root_UM2	0	Count	1	2	3
			Expected Count	1.4	1.6	3.0
		1	Count	8	8	16
			Expected Count	7.6	8.4	16.0
		Total	Count	9	10	19
			Expected Count	9.0	10.0	19.0
West	3root_UM2	0	Count	4	1	5
			Expected Count	2.8	2.2	5.0
		1	Count	11	11	22
			Expected Count	12.2	9.8	22.0
		Total	Count	15	12	27
			Expected Count	15.0	12.0	27.0
East	3root_UM2	1	Count	9	4	13
			Expected Count	9.0	4.0	13.0
		Total	Count	9	4	13
			Expected Count	9.0	4.0	13.0
North	3root_UM2	0	Count	6	3	9
			Expected Count	4.5	4.5	9.0
		1	Count	6	9	15
			Expected Count	7.5	7.5	15.0
		Total	Count	12	12	24
			Expected Count	12.0	12.0	24.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.281[a]	1	.596		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.287	1	.592		
	Fisher's Exact Test				1.000	.542
	N of Valid Cases	19				
West	Pearson Chi-Square	1.485[c]	1	.223		
	Continuity Correction[b]	.519	1	.471		
	Likelihood Ratio	1.593	1	.207		
	Fisher's Exact Test				.342	.240
	N of Valid Cases	27				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	13				
North	Pearson Chi-Square	1.600[e]	1	.206		
	Continuity Correction[b]	.711	1	.399		
	Likelihood Ratio	1.623	1	.203		
	Fisher's Exact Test				.400	.200
	N of Valid Cases	24				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.42.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.22.

d. No statistics are computed because 3root_UM2 is a constant.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 4.50.

3-rooted UM1 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	3root_UM1	0	Count	1	1	2
			Expected Count	1.0	1.0	2.0
		1	Count	11	12	23
			Expected Count	11.0	12.0	23.0
		Total	Count	12	13	25
			Expected Count	12.0	13.0	25.0
West	3root_UM1	0	Count	1	0	1
			Expected Count	.5	.5	1.0
		1	Count	14	13	27
			Expected Count	14.5	12.5	27.0
		Total	Count	15	13	28
			Expected Count	15.0	13.0	28.0
East	3root_UM1	1	Count	12	8	20
			Expected Count	12.0	8.0	20.0
		Total	Count	12	8	20
			Expected Count	12.0	8.0	20.0
North	3root_UM1	0	Count	1	1	2
			Expected Count	1.2	.8	2.0
		1	Count	15	10	25
			Expected Count	14.8	10.2	25.0
		Total	Count	16	11	27
			Expected Count	16.0	11.0	27.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.003[a]	1	.953		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.003	1	.953		
	Fisher's Exact Test				1.000	.740
	N of Valid Cases	25				
West	Pearson Chi-Square	.899[c]	1	.343		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.280	1	.258		
	Fisher's Exact Test				1.000	.536
	N of Valid Cases	28				
East	Pearson Chi-Square	.[d]				
	N of Valid Cases	20				
North	Pearson Chi-Square	.077[e]	1	.782		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.075	1	.784		
	Fisher's Exact Test				1.000	.658
	N of Valid Cases	27				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .96.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .46.

d. No statistics are computed because 3root_UM1 is a constant.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .81.

Peg-shaped UI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Peg_UI2	0	Count	9	9	18
			Expected Count	9.0	9.0	18.0
		Total	Count	9	9	18
			Expected Count	9.0	9.0	18.0
West	Peg_UI2	0	Count	14	9	23
			Expected Count	14.0	9.0	23.0
		Total	Count	14	9	23
			Expected Count	14.0	9.0	23.0
East	Peg_UI2	0	Count	15	5	20
			Expected Count	15.0	5.0	20.0
		Total	Count	15	5	20
			Expected Count	15.0	5.0	20.0
North	Peg_UI2	0	Count	16	13	29
			Expected Count	16.0	13.0	29.0
		Total	Count	16	13	29
			Expected Count	16.0	13.0	29.0

Chi-Square Tests

GROUP		Value
South	Pearson Chi-Square	.[a]
	N of Valid Cases	18
West	Pearson Chi-Square	.[a]
	N of Valid Cases	23
East	Pearson Chi-Square	.[a]
	N of Valid Cases	20
North	Pearson Chi-Square	.[a]
	N of Valid Cases	29

a. No statistics are computed because Peg_UI2 is a constant.

Peg-shaped UM3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	Peg_UM3	0	Count	4	6	10
			Expected Count	4.0	6.0	10.0
		Total	Count	4	6	10
			Expected Count	4.0	6.0	10.0
West	Peg_UM3	0	Count	10	4	14
			Expected Count	9.6	4.4	14.0
		1	Count	1	1	2
			Expected Count	1.4	.6	2.0
		Total	Count	11	5	16
			Expected Count	11.0	5.0	16.0
East	Peg_UM3	0	Count	10	4	14
			Expected Count	9.3	4.7	14.0
		1	Count	0	1	1
			Expected Count	.7	.3	1.0
		Total	Count	10	5	15
			Expected Count	10.0	5.0	15.0
North	Peg_UM3	0	Count	11	12	23
			Expected Count	11.5	11.5	23.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	12	12	24
			Expected Count	12.0	12.0	24.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	10				
West	Pearson Chi-Square	.374[b]	1	.541		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	.351	1	.554		
	Fisher's Exact Test				1.000	.542
	N of Valid Cases	16				
East	Pearson Chi-Square	2.143[d]	1	.143		
	Continuity Correction[c]	.134	1	.714		
	Likelihood Ratio	2.344	1	.126		
	Fisher's Exact Test				.333	.333
	N of Valid Cases	15				
North	Pearson Chi-Square	1.043[e]	1	.307		
	Continuity Correction[c]	.000	1	1.000		
	Likelihood Ratio	1.430	1	.232		
	Fisher's Exact Test				1.000	.500
	N of Valid Cases	24				

a. No statistics are computed because Peg_UM3 is a constant.

b. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .63.

c. Computed only for a 2x2 table

d. 3 cells (75.0%) have expected count less than 5. The minimum expected count is .33.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .50.

Congenital absence UM3 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_UM3	0	Count	5	11	16
			Expected Count	5.3	10.7	16.0
		1	Count	1	1	2
			Expected Count	.7	1.3	2.0
		Total	Count	6	12	18
			Expected Count	6.0	12.0	18.0
West	CA_UM3	0	Count	16	11	27
			Expected Count	16.4	10.6	27.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	17	11	28
			Expected Count	17.0	11.0	28.0
East	CA_UM3	0	Count	11	6	17
			Expected Count	11.3	5.7	17.0
		1	Count	1	0	1
			Expected Count	.7	.3	1.0
		Total	Count	12	6	18
			Expected Count	12.0	6.0	18.0
North	CA_UM3	0	Count	14	12	26
			Expected Count	14.4	11.6	26.0
		1	Count	1	0	1
			Expected Count	.6	.4	1.0
		Total	Count	15	12	27
			Expected Count	15.0	12.0	27.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.281[a]	1	.596		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.267	1	.605		
	Fisher's Exact Test				1.000	.569
	N of Valid Cases	18				
West	Pearson Chi-Square	.671[c]	1	.413		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.022	1	.312		
	Fisher's Exact Test				1.000	.607
	N of Valid Cases	28				
East	Pearson Chi-Square	.529[d]	1	.467		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.840	1	.359		
	Fisher's Exact Test				1.000	.667
	N of Valid Cases	18				
North	Pearson Chi-Square	.831[e]	1	.362		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	1.206	1	.272		
	Fisher's Exact Test				1.000	.556
	N of Valid Cases	27				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .67.

b. Computed only for a 2x2 table

c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .39.

d. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .33.

e. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .44.

Congenital absence UP4 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_UP4	0	Count	13	14	27
			Expected Count	13.0	14.0	27.0
		Total	Count	13	14	27
			Expected Count	13.0	14.0	27.0
West	CA_UP4	0	Count	20	16	36
			Expected Count	20.0	16.0	36.0
		Total	Count	20	16	36
			Expected Count	20.0	16.0	36.0
East	CA_UP4	0	Count	15	8	23
			Expected Count	14.4	8.6	23.0
		1	Count	0	1	1
			Expected Count	.6	.4	1.0
		Total	Count	15	9	24
			Expected Count	15.0	9.0	24.0
North	CA_UP4	0	Count	19	13	32
			Expected Count	19.0	13.0	32.0
		Total	Count	19	13	32
			Expected Count	19.0	13.0	32.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	.[a]				
	N of Valid Cases	27				
West	Pearson Chi-Square	.[a]				
	N of Valid Cases	36				
East	Pearson Chi-Square	1.739[b]	1	.187		
	Continuity Correction[c]	.070	1	.792		
	Likelihood Ratio	2.035	1	.154		
	Fisher's Exact Test				.375	.375
	N of Valid Cases	24				
North	Pearson Chi-Square	.[a]				
	N of Valid Cases	32				

a. No statistics are computed because CA_UP4 is a constant.

b. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .38.

c. Computed only for a 2x2 table

Congenital absence UI2 * Sex * GROUP

Crosstab

GROUP				Sex		
				F	M	Total
South	CA_UI2	0	Count	13	15	28
			Expected Count	13.5	14.5	28.0
		1	Count	1	0	1
			Expected Count	.5	.5	1.0
		Total	Count	14	15	29
			Expected Count	14.0	15.0	29.0
West	CA_UI2	0	Count	20	16	36
			Expected Count	20.0	16.0	36.0
		Total	Count	20	16	36
			Expected Count	20.0	16.0	36.0
East	CA_UI2	0	Count	15	9	24
			Expected Count	15.0	9.0	24.0
		Total	Count	15	9	24
			Expected Count	15.0	9.0	24.0
North	CA_UI2	0	Count	20	13	33
			Expected Count	20.0	13.0	33.0
		Total	Count	20	13	33
			Expected Count	20.0	13.0	33.0

Chi-Square Tests

GROUP		Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
South	Pearson Chi-Square	1.110[a]	1	.292		
	Continuity Correction[b]	.001	1	.972		
	Likelihood Ratio	1.495	1	.221		
	Fisher's Exact Test				.483	.483
	N of Valid Cases	29				
West	Pearson Chi-Square	.[c]				
	N of Valid Cases	36				
East	Pearson Chi-Square	.[c]				
	N of Valid Cases	24				
North	Pearson Chi-Square	.[c]				
	N of Valid Cases	33				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .48.

b. Computed only for a 2x2 table

c. No statistics are computed because CA_UI2 is a constant.