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## Chapter 6

# Dental anthropology from the Circle: non-metric traits of the posterior dentition and population relationships in the Neolithic Mediterranean

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### 6.1. Introduction

The ubiquity of human teeth within the Circle assemblage, combined with their innate durability, provides an excellent platform to explore how the dentition can illuminate our understanding of *who* the individuals and groups were that utilized the Circle for generations, or perhaps more importantly, *how* or indeed *if* they were connected. Many have wondered whether this burial place was the preserve of certain families, kinship groups, or 'classes' of individuals, organized in some manner by status, kinship or occupation (Stoddart & Malone 2008, 27; Stoddart & Malone 2015). However, before this volume, no studies have sought to analyse biological indications of proximity or distance among the hundreds of people interred and commingled in this space for hundreds of years, nor how they related to other groups around the Mediterranean region.

Research conducted as part of this project has investigated genetic relationships between the people deposited in the Circle and mid-Holocene agricultural populations from the Northern Mediterranean and Europe (Chapter 11). These analyses were based on aDNA extracted from the remains of nine individuals and provide a preliminary and, by necessity of conservation, partial evaluation of the genetic affinities of the people of the Circle. The results show similarities between the late Neolithic populations of Malta and the Neolithic peoples of central Europe. While genetic analyses provide unparalleled insights into broader population relationships, they are by nature destructive and must be supplemented by broader non-destructive bioarchaeological analyses in order to understand variation better. With its focus on inferring genetic pathways through non-destructive statistical analyses of tooth morphology and size, the discipline of

dental anthropology offers ideal means to approach the critically important questions of population affinities within the large assemblage from the Circle.

Dental anthropology provides a range of useful interpretations in archaeological research, particularly among fragmentary and commingled funerary assemblages, as discussed elsewhere in this volume (Chapters 4 & 5), because of the strength and resilience of teeth even under the most unfavourable depositional environments (Hillson 2005, 158). Additionally, once formed in childhood, the shape of teeth is unchanged throughout adult life, provided they can withstand the impacts of wear and decay through diet and disease (Hillson 2005, 257; Chapter 10). Scholars have been interested in exploring the utility of the dentition as a means to provide insights into human variation and behaviour since the early 20th century (Scott & Turner 2008, 11). The observation and quantification of non-metric traits of the dentition is a useful approach for the study of microevolutionary patterns within and between populations, including genetic drift, mutation, gene flow and, to a lesser extent, natural selection (Turner 1969, 1986a). While it is not generally possible to differentiate these processes based on dental traits alone, the study of variation is useful for biological distance estimates or affinity assessment, in which genetic relationships are estimated by similarities observed in phenetic expression within and between groups. Observed differences are the result of one or more of the four evolutionary processes listed above. In this respect, greater observed differences generally suggest a greater influence of these processes, and hence a longer period of separation or divergence between groups.

The shape and morphological characteristics of teeth are under tight genetic control during development (Alvesalo & Tigerstedt 1974; Berry 1978; Garn *et*

*al.* 1965; Goose 1971; Harris & Bailit 1980; Nichol 1990; Scott & Turner 2008, 11; Townsend & Brown 1978), and can therefore provide valuable information for those wishing to trace relationships between and amongst groups of humans. As anatomical structures, the forms of teeth are primarily determined by the genotype, along with prevailing environments and behaviours (Hillson 2005, 257), for example, geographical isolation and reproductive strategies. In this way, certain dental characteristics and structures may be more common in some populations than others; equally, we may characterize groups according to the degree of observed variations (Hillson 2005, 257).

Morphological study of dentition involves the inspection of specific features of the crowns and roots of teeth. While it is beyond the scope and intention of the current work to summarize the history and vast achievements of dental anthropology as a sub-discipline (this has been achieved to great effect elsewhere; Scott & Turner 2008, 11), early investigations including those by Hrdlička (1920) and Hellman (1928) revealed that dental traits often vary in their frequency of occurrence and expression between populations. Furthermore, it was recognized that several of these discrete traits are characteristic of certain populations (for example, Carabelli's trait in Europeans; Kraus 1951), and thus not only aid in assessing biological relationships but also in estimating the amounts of genetic admixture between populations (Turner 1967). Many researchers have used suites of these dental features to describe a variety of human populations (Dahlberg 1971; Hanihara 1963; Kirveskari 1974; Moorrees 1957; Morris 1965; Pedersen 1949; Turner 1984, 1985a; Zubov 1979). Considering dental traits on a global scale, Turner (1984, 1985a) found that modern populations share enough dental similarities to support the interpretation of a recent common ancestral population, an interpretation that is supported by a wealth of other morphological and genetic evidence. Regionally, Lukacs and Walimbe (1984) demonstrated that the prehistoric people of India express variation in dental traits that are clinally distributed relative to European and Asian populations. On a local scale, similarities in non-metric traits have supported the hypothesis of common ancestry among some Southern African populations (Haeussler *et al.* 1989).

Dental non-metric traits with useful discriminatory power are found across tooth types. In the anterior dentition, incisor shovelling and winging have both demonstrated utility, while useful dental traits of the posterior dentition include maxillary and mandibular molar cusp number and size variation, mandibular molar groove pattern and deflecting wrinkle, and premolar and molar root number (Dahlberg 1963;

Kirveskari 1974; Lukacs 1985; Moorrees 1957; Pedersen 1949; Turner 1984, 1985a; Turner *et al.* 1991).

The purpose of this study is to compare non-metric traits of selected subsets of the posterior dentition of the Circle assemblage to test for the frequency of traits that may represent close genetic affinities within the population and to test for broader population affinities throughout the Mediterranean region. While it is beyond the scope of the current work to present a full analysis of dental non-metric traits across the entire dentition, the present study represents the first attempt to apply these methods to the Circle population or indeed *any* Maltese skeletal assemblage. We focus here on the non-metric traits of the permanent maxillary and mandibular molars (posterior dentition) from selected contexts within the Circle and compare the resulting trait frequencies to a range of populations from the circum-Mediterranean region to investigate population affinities. This study should therefore be considered only as a baseline analysis, and we anticipate developing this branch of research to include a broader range of traits and archaeological contexts in the near future.

## 6.2. Materials

As discussed in Chapter 2, a total of 11,706 teeth were isolated from their associated skeletal remains and inventoried according to context by the FRAGSUS Population History Workgroup across five laboratory seasons at the National Museum of Archaeology (NMA), Valletta, between November 2014 and May 2017. Of these, a total of 815 teeth (7.0% of isolated sample) of adult maxillary and mandibular molar types were studied by the first author (RKP) for the purposes of quantifying the non-metric traits among the population/s represented within the Circle. The posterior dentition (molars) were analysed in order to align with the broader archaeometric sampling strategy of the Population History Workgroup which focused on analyses of the posterior teeth. As noted previously and detailed in Table 6.1, the studied teeth are only a subsample of the overall assemblage, representing a proportion of 14 selected contexts as excavated thus far across the entire use-life of the Circle, from Early to Late use-phases dating to *c.* 2900–2350 BC. Further to this, it is critical to note that the site was not completely excavated, and it is known that further remains are preserved at the site to allow for work to continue at the hands of future generations of archaeologists. As mentioned, in accordance with the temporal and pecuniary parameters of the project, the contexts examined here were determined by the excavators to be of greatest cultural and temporal significance to the

**Table 6.1.** *Materials included in pathology study, including provenance and representation.*

Context	Location	Date	N teeth isolated	Σ teeth studied	% Context
595	East Cave	Early	123	123	100
833	West Cave: north niche	Early	18	2	11
951	West Cave: north niche	Early	2306	751	33
698	East Cave: southern pit	Early	13	3	23
1209	West Cave: shrine	Middle	4	4	100
1241	East Cave	Middle	170	170	100
433	East Cave: central	Late	35	6	17
436	East Cave: central	Late	32	32	100
715	East Cave	Late	56	54	96
738	East Cave	Late	17	15	88
790	Intermediate zone	Late	11	11	100
1206	West Cave: shrine	Late	642	508	79
960	West Cave: shrine	Latest	870	405	47
783	West Cave: display	Latest	2900	976	34
<b>Total</b>			7197	3060	43

overarching research questions, and thus included in whole or part here.

Comparative data were derived from thirteen dental assemblages from southern Europe, the Middle East, and northern Africa, all compiled and recorded by the senior author (JDI). These were used for qualitative and quantitative comparisons of non-metric traits with those recorded by the first author (RKP). These particular samples were selected based on their geographical and, in several instances, temporal proximity to the date of the Circle occupation to assess the presence (if any) and degree of genetic input to the Circle burial population. Summary data for these samples are provided in Table 6.2. Detailed descriptions are available in several prior publications (Dicke-Toupin 2012; Irish 1993, 1998a, 1998b, 2000, 2006; Irish *et al.* 2017).

### 6.3. Methods

#### 6.3.1. Data collection

For the dental non-metric study, selected permanent maxillary and mandibular molars of both left and right sides and articulation states (exfoliated or in occlusion) were examined individually within their context batches. Each tooth was apportioned a unique inventory code, that comprised the sample number, find context and tooth type according to the notation convention established by the *Fédération Dentaire Internationale* (ISO 3950). Each tooth was examined and scored according to trait expressions established by the *Arizona State University Dental Anthropology System* (ASUDAS; Scott & Irish 2016 Turner *et al.* 1991), for

permanent molars, including maxillary (Hypocone, Cusp 5 Metaconule, Carabelli's Trait, C2 Parastyle, Enamel Extensions, Enamel Pearls, Upper Molar Root Number, Peg-Shaped Molar, Congenital Absence) and mandibular (Anterior Fovea, Groove Pattern, Cusp Number, Distal Trigonid Crest, Protosylid, Cusp 5, Cusp 6, Cusp 7, Lower Molar Root Number and, where extant, Torsomolar Angle) traits. Radical Number and Deflecting Wrinkle traits were not recorded.

An additional trait, Buccal Fovea, was scored, though not used in the final analyses. This feature is described by van Beek (1983, 82) as the '*foramen caecum molarum*': a patent pit or hole located at the terminal aspect of the groove which runs between the lobes of the protoconid and hypoconid (or mesio- and distobuccal cusps) and was scored in this study as 0=present, 1=absent. Although this trait is not recognized by the ASUDAS, it was included within the study because of anecdotal observations of its frequency within the assemblage during the initial sorting process described in Chapter 2. We sought to quantify its incidence and prevalence rates within the selected sample to determine if it aligns with the estimated rates described by van Beek (approximately 60%; 1983, 82), or if any statistical correlations exist with the appearance of other traits.

In total, 39 traits were used for the present comparative study (refer to Table 6.3 for the full list). Tooth status and caries were also recorded for each tooth (following Turner *et al.* 1991, 26–7), along with notes describing any prevailing circumstances which may have impacted on the presence

**Table 6.2.** The 13 comparative dental samples. \*Institutions in which the samples are curated: MMLT = Museu Municipal Leonel Trindade - Torres Vedras; AMNH = American Museum of Natural History, New York; NHM = Natural History Museum, London; MH = Musée de l'Homme, Paris; UIM = University of Minnesota, Minneapolis; NMNH = National Museum of Natural History, Washington, DC; CAM = Cambridge University, UK.

	Sample	Geographical origin	Affiliation	Dates	n	Institution*
S. Europe/Middle East	Cova da Moura (CDM)	Estremadura, Portugal	Neolithic/Copper Age	3700–2300 BC	41	MMLT
	Greece (GRK)	Greece	Classic to Historic	475–300 BC to ~ AD 1800+	77	AMNH
	Italy (ITA)	Italy	Roman	30 BC – AD 395	35	NHM
	Italy (ITM)	Italy	Historic/Modern	AD 1800–1900s	55	NHM
	Pai Mogo I (PAI)	Estremadura, Portugal	Neolithic/Copper Age	3000–2600 BC	49	MMLT
	Palestine (PAL)	Lachish/Jericho, Palestine	Copper to Iron Age	1150–1047 BC	86	NHM
	Turkey (TRK)	Anatolia/Turkey and Cyprus	Classic to Ottoman	>300 BC to ~ AD 1300+	40	AMNH
North Africa	Bedouin (BED)	Morocco, Tunisia, Libya	Historic Arab	AD 1800–1900s	49	MH, UM
	Carthage (CAR)	Tunisia	Phoenician	751–146 BC	28	MH
	Kabyle (KAB)	Northern Algeria	Historic Berber	AD 1800–1900s	32	MH
	Lisht (LIS)	Lower Egypt	Middle Kingdom	1991–1783 BC	61	NMNH
	Shawia (SHA)	Southern Algeria	Historic Berber	AD 1800–1900s	26	MH
	Tarkhan (TAR)	Lower Egypt	Early Dynastic	~3000–2890 BC	51	CAM

or observable expression of each trait (for example, fractures, extreme wear, calculus, pathology including caries and enamel hypoplasia, eruption status, taphonomy/diagenesis, congenital variation). An inter-observer error study was carried out in 2016 at the NMA, based on traits scored by the first author and assessed by the senior author.

In addition to the above, all teeth (both left and right) examined for non-metric traits were also subject to metric analysis by Power. Following Hillson (2005, 261ff., Fig. 4.1), measurements were recorded in millimeters to 0.01 for the maximum mesiodistal (length between most mesial and distal points of the crown, often characterized by interproximal contact facets between the teeth; Hillson 2005, 260) and buccolingual (approximate right-angle to the mesiodistal line, length between the lip/cheek and tongue surfaces of the tooth; Hillson 2005, 260) diameters of both the crown and cementum enamel junctions using digital Mitutoyo calipers as standard Vernier for exfoliated teeth; needle-point for teeth still in occlusion. Data were recorded for all teeth in a Microsoft Excel spreadsheet to form a searchable digital database/inventory. The sample bags containing each tooth were marked once analysis was completed and curated within the NMA as part of the FRAGSUS Research Archive.

### 6.3.2. Quantitative analyses

All analyses were conducted by the senior author (JDI). First, the rank-scale ASUDAS traits were dichotomized into categories of present or absent, based on their appraised morphological thresholds (Nichol 1990; Scott 1973) following standard procedure (Irish

1993; Turner 1985b, 1987). Dichotomization simplifies tabulation of the trait frequencies for presentation and is necessary before these data can be compared using available distance statistics, including the mean measure of divergence (MMD) as used here (Berry & Berry 1967; Green & Suchey 1976; Harris & Sjøvold 2004; Irish 2010; Sjøvold 1973, 1977).

Next, the MMD was used to estimate among-sample phenetic affinities by calculating a dissimilarity measure between each sample pair; i.e., high values indicate divergence and *vice versa*. Beyond holding several advantages over other distance measures (Irish 2010) the MMD works well with pooled sample data, to address missing data common among archaeological remains and, importantly, the use of composite individuals for this study as necessitated by the commingled state of all human remains. However, it is important to edit these data prior to final quantitative analyses. Specifically, those traits that have little (i.e., invariant across samples) or no contributory information should be deleted (Harris & Sjøvold 2004). Those traits that are invariant can be recognized qualitatively, whereas traits that are the least, or conversely the most, likely to influence the inter-sample variation may be quantitatively identified; to do so, principal components analysis (PCA) was used in the present analysis (Irish 2016; Irish & Guatelli-Steinberg 2003). The MMD distances should also be based on as many traits as possible, though none should be highly inter-correlated – which could render inaccurate inter-sample results (Sjøvold 1977). To identify traits of this kind, the rank-scale data were submitted to Kendall's tau-*b* correlation coefficient.

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**Table 6.3.** Frequencies of the 39 dental traits by ASUDAS grade for the Circle sample and total present (%). \*Grade frequencies in bold indicate those considered 'present' and, when totalled, equal the % Present in the final column for each trait. See text for details.

Trait	Presence	n	Grade*									% Present	
			0	1	2	3	3.5	4	5	6	7		
Hypocone UM1	Grade=3+	133	0.000	0.000	0.038	0.278	0.000	<b>0.662</b>	<b>0.023</b>				<b>96.3</b>
Hypocone UM2	Grade=3+	98	0.112	0.153	0.173	<b>0.255</b>	<b>0.051</b>	<b>0.245</b>	0.010				<b>56.1</b>
Hypocone UM3	Grade=3+	67	0.239	0.358	0.134	<b>0.179</b>	<b>0.060</b>	<b>0.030</b>	<b>0.000</b>				<b>26.9</b>
Cusp 5 Metaconule UM1	Grade=2+	129	0.868	0.100	0.023	0.008		0.000	0.000				<b>3.1</b>
Cusp 5 Metaconule UM2	Grade=2+	100	0.710	0.130	<b>0.060</b>	<b>0.050</b>		0.030	0.020				<b>16.0</b>
Cusp 5 Metaconule UM3	Grade=2+	68	0.456	0.103	<b>0.103</b>	<b>0.161</b>		0.103	0.073				<b>44.0</b>
Carabelli's Trait UM1	Grade=5+	126	0.460	0.127	0.071	0.103		0.071	<b>0.095</b>	<b>0.048</b>	<b>0.024</b>		<b>16.7</b>
Carabelli's Trait UM2	Grade=5+	98	0.888	0.051	0.010	0.010		0.010	<b>0.030</b>	<b>0.000</b>	<b>0.000</b>		<b>3.0</b>
Carabelli's Trait UM3	Grade=5+	68	0.882	0.029	0.000	0.029		0.000	<b>0.044</b>	<b>0.000</b>	<b>0.015</b>		<b>5.9</b>
C2 Parastyle UM1	Grade=2+	128	1.000	0.000	<b>0.000</b>	<b>0.000</b>		0.000	0.000				<b>0.0</b>
C2 Parastyle UM2	Grade=2+	102	1.000	0.000	<b>0.000</b>	<b>0.000</b>		0.000	0.000				<b>0.0</b>
C2 Parastyle UM3	Grade=2+	68	1.000	0.000	<b>0.000</b>	0.000		0.000	0.000				<b>0.0</b>
Enamel Extensions UM1	Grade=2+	121	0.992	0.008	<b>0.000</b>	<b>0.000</b>							<b>0.0</b>
Enamel Extensions UM2	Grade=2+	97	0.918	0.062	0.021	0.000							<b>2.1</b>
Enamel Extensions UM3	Grade=2+	66	0.924	0.061	<b>0.015</b>	<b>0.000</b>							<b>1.5</b>
Root Number UM1	Grade=3+	70	0.000	0.000	0.043	<b>0.957</b>							<b>95.7</b>
Root Number UM2	Grade=3+	62	0.000	0.097	0.113	<b>0.774</b>		0.016					<b>79.0</b>
Root Number UM3	Grade=3+	50	0.000	0.420	0.280	<b>0.300</b>							<b>30.0</b>
Congenital Absence UM3	Grade=1	69	1.000	<b>0.000</b>									<b>0.0</b>
Anterior Fovea LM1	Grade=2+	190	0.279	0.232	<b>0.242</b>	<b>0.174</b>		0.073					<b>48.9</b>
Groove Pattern LM2	Grade=Y	156	<b>0.417</b>	0.288	0.295								<b>41.7</b>
Groove Pattern LM3	Grade=Y	101	<b>0.485</b>	0.079	0.436								<b>48.5</b>
Cusp Number LM1	Grade=6	212	0.000	0.000	0.005	0.000		0.024	0.892	<b>0.080</b>			<b>8.0</b>
Cusp Number LM2	Grade=5+	160	0.000	0.000	0.000	0.000		0.719	<b>0.275</b>	<b>0.006</b>			<b>28.1</b>
Cusp Number LM3	Grade=5+	113	0.000	0.000	0.000	0.053		0.336	<b>0.504</b>	<b>0.097</b>	<b>0.009</b>		<b>61.0</b>
Distal Trigonid Crest LM1	Grade=1	205	0.995	<b>0.005</b>									<b>0.5</b>
Distal Trigonid Crest LM2	Grade=1	156	1.000	<b>0.000</b>									<b>0.0</b>
Distal Trigonid Crest LM3	Grade=1	112	0.991	<b>0.009</b>									<b>0.9</b>
Protostylid LM1	Grade=3+	210	0.971	0.014	0.010	<b>0.000</b>		<b>0.000</b>	<b>0.000</b>	<b>0.005</b>	<b>0.000</b>		<b>0.5</b>
Protostylid LM2	Grade=3+	160	0.963	0.025	0.006	<b>0.000</b>		0.006	0.000	0.000	<b>0.000</b>		<b>0.0</b>
Protostylid LM3	Grade=3+	112	0.714	0.125	0.071	<b>0.000</b>		<b>0.036</b>	<b>0.027</b>	<b>0.000</b>	<b>0.027</b>		<b>9.0</b>
Cusp 7 LM1	Grade=2+	210	0.962	0.005	0.019	<b>0.000</b>	<b>0.000</b>	<b>0.014</b>					<b>1.4</b>
Cusp 7 LM2	Grade=2+	163	0.994	0.000	0.000	<b>0.006</b>	<b>0.000</b>	<b>0.000</b>					<b>0.6</b>
Cusp 7 LM3	Grade=2+	113	0.965	0.000	0.000	<b>0.018</b>	<b>0.000</b>	<b>0.018</b>					<b>3.6</b>
Root Number LM1	Grade=3+	100		0.000	1.000	<b>0.000</b>							<b>0.0</b>
Root Number LM2	Grade=2+	84		0.083	<b>0.893</b>	<b>0.000</b>		0.024					<b>91.7</b>
Root number LM3	Grade=2+	62		0.355	<b>0.581</b>	<b>0.065</b>							<b>64.6</b>
Torsomolar Angle LM3	Grade=1	44	0.901	<b>0.091</b>									<b>9.0</b>
Congenital Absence LM3	Grade=1	118	1.000	<b>0.000</b>									<b>0.0</b>

The MMD formula used here contains the Freeman and Tukey angular transformation to correct for low (<0.05) or high (>0.95) trait frequencies and small sample sizes (n>10) (Green & Suchey 1976;

Sjøvold 1973, 1977). To determine whether two samples differ significantly, the resultant MMD value is compared with its standard deviation (SD). If the MMD >2xSD, then the null hypothesis of P1=P2 (P=sample

population) is rejected at the 0.025 level. The MMD and standard deviation formulae, rationale for significance, and other details can be found elsewhere (Irish 2010; Sjøvold 1977). To visualize the MMD distance values among samples (i.e., the matrix), interval-level multi-dimensional scaling (MDS) (Kruskal & Wish 1978) in SPSS 24.0 Procedure Alscal was used to create 3D spatial representations of the sample variation to aid interpretation.

Finally, the correlation between MMD and geographical distances in kilometres between Xaghra and each comparative sample was calculated using a simple bivariate Pearson's correlation; both distances were then used as coordinates to plot pertinent sample pair relationships in 2D. These methods help explore if the Circle sample appears more similar to an extra-regional group than expected, under the assumption that genetic (and phenetic) relatedness among populations decreases exponentially as spatial distance increases (Relethford 2004). Gene flow, the causative agent with isolation-by-distance (Wright 1943), cannot pertain directly to those samples which differ in age from those from the Circle; still, some indication of potential northern African, southern European, and/or Middle Eastern influence may be obtained to help supplement the MMD results. The Geographical Distance Matrix Generator (vers. 1.2.3) (Ersts 2014) was used to calculate the inter-sample straight line distances. The latter rarely reflect reality on land, but in this instance are most appropriate concerning across-water movement, i.e., the most direct routes from surrounding mainland regions to the island location of Malta.

## 6.4. Results

The frequencies for each ASUDAS grade for all 39 traits recorded in the Circle sample are provided in Table 6.3, along with the total number scored and cumulative percent considered present based on standard ASUDAS dichotomization protocol (Scott & Irish 2017; Turner *et al.* 1991). These trait percentages are then carried over to Table 6.4, to contrast with the same traits for the 13 comparative samples. The sheer amount of data makes qualitative comparisons difficult, but it can be seen that several trait percentages are comparable by region. In particular, the data from the Circle share a number of similarities with, for example, the ancient Italians (ITA), Carthage (CAR), the Kabyle Berbers (KAB), and others. Specific frequencies and phenetic distances are provided in the tables and figures below. Similarities among comparative samples are also evident in particular geographical regions.

Next, trait editing was conducted as noted. First, patently invariant traits were deleted (Table 6.4); these included Hypocone UM1 (all fixed at or near 100% across samples), Parastyle UM1 (0% across samples), and Protostylid LM1 (at or near 0%). Further, traits with minimal variation across all samples, here defined as <10% (with exception), were dropped, including Carabelli's Trait UM2 and UM3, Parastyle UM2, and Cusp 7 LM2, among others, to reduce the trait number from 39 to 29. As mentioned, highly inter-correlated traits should also be dropped prior to using the MMD, here considered to as  $Tau \geq |0.5|$  based on prior research (for example, Irish 2006, 2010). Because only molar traits were recorded,

**Table 6.4.** Dental trait percentages (%) and number of individuals scored (n) for the Malta (the Circle) and comparative samples. See text for details. \*Malta = the Circle; BED = Bedouin, CAR = Carthage, CDM = Cova da Moura, GRK = Greece, ITA = Italy ancient, ITM = Italy historic/modern, KAB = Kabyle, LIS = Lisht, PAI = Pai Mogo I, PAL = Palestine, SHA = Shawia, TAR = Tarkhan, TRK = Anatolia/Turkey and Cyprus (see Table 6.2 and text for details).

Trait / presence		Malta*	BED	CAR	CDM	GRK	ITA	ITM	KAB	LIS	PAI	PAL	SHA	TAR	TRK
Hypocone UM1 (ASU Grade=3+)	% n	96.30 133	100.00 39	100.00 19	100.00 34	100.00 57	100.00 26	95.74 47	100.00 22	100.00 40	100.00 49	100.00 67	100.00 23	100.00 45	100.00 28
Hypocone UM2 (ASU Grade=3+)	% n	56.10 98	58.82 34	68.42 19	56.00 25	50.00 54	60.00 25	59.57 47	63.64 22	88.10 42	63.83 47	82.46 57	68.42 19	75.00 40	60.00 25
Hypocone UM3 (ASU Grade=3+)	% n	26.90 67	30.00 20	25.00 12	13.64 22	44.44 36	41.67 12	44.83 29	29.17 24	35.48 31	44.19 43	37.14 35	30.77 13	57.14 35	46.15 13
Cusp 5 Metaconule UM1 (ASU Grade=2+)	% n	3.10 129	8.82 34	8.33 12	8.70 23	5.66 53	5.00 20	23.26 43	11.76 17	15.38 26	17.02 47	21.43 42	10.00 20	0.00 23	4.55 22
Cusp 5 Metaconule UM2 (ASU Grade=2+)	% n	16.00 100	3.03 33	10.00 10	8.33 24	4.08 49	8.70 23	13.33 45	16.67 18	5.56 36	9.09 44	10.87 46	10.53 19	9.09 33	9.52 21
Cusp 5 Metaconule UM3 (ASU Grade=2+)	% n	44.00 68	25.00 20	30.00 10	19.05 21	22.86 35	20.00 10	28.57 28	10.53 19	23.33 30	23.08 39	25.00 32	30.77 13	33.33 33	0.00 12
Carabelli's Trait UM1 (ASU Grade=5+)	% n	16.70 126	18.18 33	25.00 16	29.63 27	16.67 48	10.53 19	25.58 43	26.32 19	26.09 23	26.53 49	31.71 41	11.11 18	35.71 28	19.05 21
Carabelli's Trait UM2 (ASU Grade=5+)	% n	3.00 98	0.00 33	0.00 17	0.00 20	0.00 48	0.00 25	2.17 46	0.00 23	2.78 36	0.00 45	1.79 56	0.00 19	2.63 38	0.00 22
Carabelli's Trait UM3 (ASU Grade=5+)	% n	5.90 68	5.00 20	0.00 13	0.00 22	0.00 34	0.00 13	7.69 26	0.00 22	6.90 29	0.00 38	0.00 35	0.00 13	0.00 34	0.00 13

Dental anthropology from the Circle

Table 6.4 (cont.).

Trait / presence		Malta*	BED	CAR	CDM	GRK	ITA	ITM	KAB	LIS	PAI	PAL	SHA	TAR	TRK
C2 Parastyle UM1 (ASU Grade=2+)	% n	0.00 128	0.00 39	0.00 19	0.00 26	0.00 54	0.00 25	0.00 46	0.00 23	0.00 40	0.00 49	0.00 64	0.00 22	0.00 42	0.00 27
C2 Parastyle UM2 (ASU Grade=2+)	% n	0.00 102	0.00 34	0.00 18	0.00 23	0.00 50	0.00 25	2.08 48	4.35 23	0.00 42	0.00 48	1.69 59	0.00 19	0.00 42	0.00 24
C2 Parastyle UM3 (ASU Grade=2+)	% n	0.00 68	0.00 20	0.00 14	0.00 22	0.00 33	0.00 13	0.00 28	0.00 22	0.00 32	4.76 42	5.56 36	7.69 13	2.63 38	0.00 13
Enamel Extensions UM1 (ASU Grade=2+)	% n	0.00 121	5.56 36	5.56 18	3.70 27	3.70 54	0.00 26	2.33 43	0.00 23	10.64 47	2.27 44	1.56 64	4.76 21	0.00 45	4.17 24
Enamel Extensions UM2 (ASU Grade=2+)	% n	2.10 97	12.90 31	5.56 18	18.75 16	16.67 48	3.85 26	6.38 47	8.70 23	18.60 43	19.44 36	4.92 61	11.11 18	9.76 41	22.73 22
Enamel Extensions UM3 (ASU Grade=2+)	% n	1.50 66	6.25 16	0.00 11	0.00 14	0.00 32	0.00 12	0.00 22	5.26 19	12.90 31	4.17 24	0.00 35	10.00 10	3.33 30	10.00 10
Upper Molar Root Number UM1 (ASU Grade=3+)	% n	95.70 70	97.37 38	100.00 16	95.45 22	97.50 40	94.12 17	90.91 22	100.00 19	97.73 44	100.00 24	95.00 20	100.00 22	100.00 24	100.00 25
Upper Molar Root Number UM2 (ASU Grade=3+)	% n	79.00 62	68.97 29	77.78 18	57.14 21	58.33 36	70.59 17	81.82 22	68.42 19	77.27 44	89.80 49	80.00 20	72.22 18	72.22 18	62.07 29
Upper Molar Root Number UM3 (ASU Grade=3+)	% n	30.00 50	26.32 19	40.00 15	58.82 17	30.00 30	38.46 13	40.00 15	57.14 14	34.38 32	41.94 31	22.73 22	61.54 13	66.67 21	11.11 18
Congenital Absence UM3 (ASU Grade=1)	% n	0.00 69	21.05 38	30.43 23	6.90 29	17.65 68	29.03 31	20.00 50	3.45 29	3.64 55	8.33 48	18.75 64	23.08 26	4.08 49	21.88 32
Anterior Fovea LM1 (ASU Grade=2+)	% n	48.90 190	37.50 24	20.00 10	58.82 17	36.36 11	20.00 5	56.67 30	60.00 10	37.50 8	80.56 36	40.00 20	29.41 17	0.00 2	40.00 10
Groove Pattern LM2 (ASU Grade=Y)	% n	41.70 156	46.88 32	38.46 13	32.50 40	43.48 23	22.22 18	27.91 43	27.78 18	37.50 24	52.08 48	34.29 70	36.84 19	30.56 36	5.88 17
Groove Pattern LM3 (ASU Grade=Y)	% n	48.50 101	40.91 22	22.22 9	36.11 36	22.73 22	8.33 12	25.00 32	30.77 13	35.29 17	23.81 21	18.18 44	29.41 17	22.22 27	36.36 11
Cusp Number LM1 (ASU Grade=6)	% n	8.00 212	12.50 32	0.00 11	2.50 40	0.00 19	0.00 13	2.63 38	31.25 16	5.56 18	9.09 44	3.70 54	9.52 21	5.00 20	0.00 19
Cusp Number LM2 (ASU Grade=5+)	% n	28.10 160	42.86 28	16.67 12	23.68 38	47.62 21	30.00 10	37.14 35	33.33 18	20.83 24	40.43 47	37.04 54	31.58 19	50.00 28	41.18 17
Cusp Number LM3 (ASU Grade=5+)	% n	61.00 113	62.50 24	44.44 9	70.27 37	60.00 20	60.00 10	63.33 30	50.00 14	44.44 18	66.67 21	51.22 41	58.82 17	76.00 25	80.00 10
Distal Trigonid Crest LM1 (ASU Grade=1)	% n	0.50 205	3.03 33	0.00 9	0.00 26	5.88 17	9.09 11	5.56 36	0.00 14	11.11 9	0.00 41	3.13 32	0.00 20	0.00 16	0.00 13
Distal Trigonid Crest LM2 (ASU Grade=1)	% n	0.00 156	3.13 32	0.00 12	0.00 40	0.00 21	0.00 16	0.00 42	0.00 18	0.00 20	2.08 48	0.00 67	0.00 20	5.56 36	0.00 17
Distal Trigonid Crest LM3 (ASU Grade=1)	% n	0.90 112	4.17 24	0.00 9	10.81 37	10.53 19	0.00 10	0.00 33	0.00 14	0.00 17	0.00 23	11.63 43	0.00 17	6.90 29	0.00 11
Protostylid LM1 (ASU Grade=3+)	% n	0.50 210	0.00 33	0.00 10	0.00 30	0.00 19	0.00 13	0.00 38	0.00 16	0.00 15	0.00 42	0.00 58	0.00 21	0.00 20	0.00 17
Protostylid LM2 (ASU Grade=3+)	% n	0.00 160	0.00 29	0.00 12	2.56 39	9.52 21	0.00 17	0.00 43	0.00 18	0.00 21	2.13 47	2.94 68	0.00 22	0.00 34	0.00 16
Protostylid LM3 (ASU Grade=3+)	% n	9.00 112	12.00 25	10.00 10	20.59 34	0.00 21	0.00 12	6.25 32	0.00 14	5.56 18	22.73 22	12.24 49	6.25 16	3.45 29	10.00 10
Cusp 7 LM1 (ASU Grade=2+)	% n	1.40 210	5.88 34	7.69 13	0.00 39	5.56 18	11.11 18	2.63 38	5.88 17	0.00 23	6.25 48	0.00 67	4.76 21	3.70 27	0.00 19
Cusp 7 LM2 (ASU Grade=2+)	% n	0.60 163	0.00 32	0.00 13	2.50 40	9.52 21	0.00 18	0.00 43	0.00 18	0.00 25	0.00 49	0.00 71	0.00 20	0.00 38	0.00 17
Cusp 7 LM3 (ASU Grade=2+)	% n	3.60 113	0.00 24	10.00 10	5.13 39	0.00 21	0.00 12	3.03 33	7.14 14	0.00 20	0.00 23	6.12 49	5.88 17	3.57 28	9.09 11
Root Number LM1 (ASU Grade=3+)	% n	0.00 100	0.00 33	0.00 11	0.00 36	0.00 22	0.00 18	0.00 25	0.00 17	0.00 29	0.00 30	3.03 33	0.00 22	0.00 33	5.26 19
Root Number LM2 (ASU Grade=2+)	% n	91.70 84	88.89 27	80.00 10	82.50 40	91.30 23	100.00 19	100.00 38	88.89 18	86.21 29	100.00 43	79.55 44	95.45 22	85.00 40	89.47 19
Root number LM3 (ASU Grade=2+)	% n	64.60 62	88.00 25	100.00 2	84.38 32	91.67 12	66.67 15	100.00 18	100.00 11	85.71 21	76.47 17	73.68 19	85.71 14	90.91 22	70.00 10
Torsomolar Angle LM3 (ASU Grade=1)	% n	9.01 44	20.00 25	10.00 10	8.82 34	13.04 23	12.50 16	18.52 27	21.43 14	30.77 26	5.56 36	14.29 56	23.53 17	5.56 36	31.25 16
Congenital Absence LM3 (ASU Grade=0)	% n	0.00 118	12.12 33	23.08 13	7.32 41	10.71 28	9.09 22	23.91 46	27.78 18	11.11 36	24.44 45	14.67 75	16.67 24	8.33 48	25.00 20

**Table 6.5.** Component loadings, eigenvalues, and variance explained for 22 traits in the Malta and 13 comparative samples. Values in boldface indicate strong loadings ( $\geq 0.5$ ). \*Denotes the 12 traits used in the MMD comparison, as detailed in text.

Trait	Comp 1	Comp 2	Comp 3
Hypocone UM2	.491	.368	.010
Cusp 5 UM1*	.226	<b>.542</b>	<b>.716</b>
Cusp 5 UM2	-.437	.400	.122
Carabelli's Trait UM1*	.118	<b>.707</b>	-.311
C2 Parastyle UM3	.041	.447	.007
Enamel Extensions UM1*	<b>.850</b>	-.124	.107
Enamel Extensions UM2*	<b>.696</b>	-.018	-.212
Enamel Extensions UM3*	<b>.804</b>	-.097	-.060
Root Number UM1*	.352	.088	<b>-.615</b>
Root Number UM2*	-.113	<b>.585</b>	<b>.513</b>
Root Number UM3	-.264	.313	-.445
Congenital Absence UM3	-.055	-.486	.329
Anterior Fovea LM1*	.056	<b>.509</b>	.427
Groove Pattern LM2	-.099	.381	.039
Cusp Number LM2	-.137	-.095	-.192
Distal Trigonid Crest LM1*	.208	-.453	<b>.531</b>
Protostylid LM3*	.160	<b>.609</b>	.030
Cusp 7 LM1	-.489	-.358	.089
Root Number LM2*	-.293	-.210	<b>.546</b>
Root number LM3	.095	.149	-.159
Torsomolar Angle LM3*	<b>.752</b>	-.345	.260
Congenital Absence LM3	.242	.240	.264
<b>Eigenvalue</b>	3.620	3.358	2.604
<b>% of Variance</b>	16.454	15.264	11.836
<b>Cumulative %</b>	16.454	31.719	43.555

inter-correlation was particularly problematic, relative to the field concept (Scott & Irish 2017; Turner *et al.* 1991). In this case, the 10 traits deleted because of minimal variation were also all highly correlated with many other molar traits (i.e., ranging from two to 13 total trait pairs). However, seven additional traits that are not invariant also had to be deleted on this basis (i.e.,  $\text{Tau} \geq 0.5$ ), including Hypocone UM3, Cusp Number LM1 and LM3, Cusp 7 LM3, and others, which further reduced the trait number to 22. Lastly, percentages of these traits were submitted to PCA in order to identify those which contribute little to among-sample variation (Table 6.5). The first three components were used for this purpose, as they contribute much, though certainly not all, of the total variance. Based on those loadings considered to be strong (i.e.,  $\geq 0.5$ ) in the table, 12 of the remaining 22 traits were retained for the MMD analysis: Cusp 5 UM1, Carabelli's UM1, Enamel Extensions UM1–UM3,

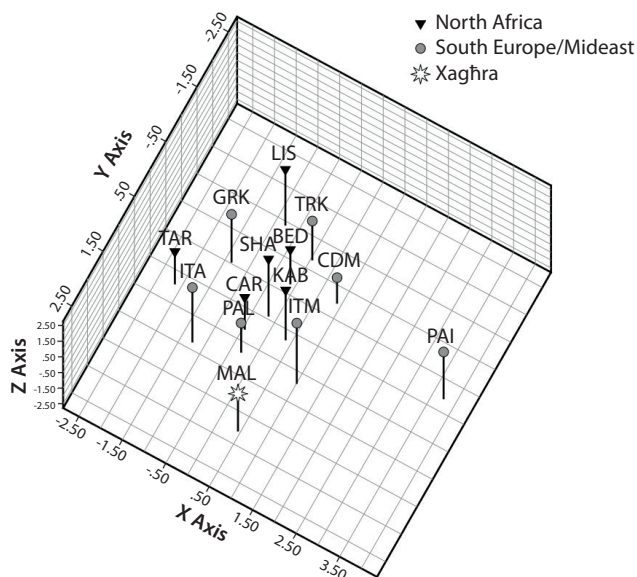
Root Number UM1–UM2, Anterior Fovea LM1, Distal Trigonid Crest LM1, Protostylid LM3, Root Number LM2, and Torsomolar Angle LM3. Again, detailed descriptions of these highly hereditary traits can be found elsewhere (Scott & Irish 2017; Turner *et al.* 1991).

The resulting MMD distances (and geographical distances, see below) between the Circle and the comparative samples are listed in Table 6.6. The full MMD distance matrix is not provided because: 1) relatedness among the comparative samples is not critical, given the focus of this chapter, and 2) these distances are available elsewhere—based on a full suite of 36 non-metric traits throughout the dentition (Dicke-Toupin 2012; Irish 1993, 1998a, 1998b, 2000, 2006; Irish *et al.* 2017). Based just on these 12 molar traits, it is evident that, with some exceptions (i.e., Egyptian Lisht (LIS), Portuguese Pai Mogo (PAI), and to a lesser extent, Greece (GRK)), the Circle sample does not differ significantly from most comparative samples. It is particularly close phenetically to the comparative samples from Carthage (CAR), Kabyle (KAB), ancient Italy (ITA), and Palestine (PAL), which may suggest evidence for more genetic input from these regions. This relatedness is visualized in the MDS plot of the full MMD matrix (Fig. 6.1). For example, except for Portuguese Pai Mogo (PAI) (Irish *et al.* 2017 for rationale), much sample homogeneity is evident, including the Circle. Moreover, this homogeneity may show some regional bias but overall it appears that, Mediterranean-wide, genetic contact among all populations was common.

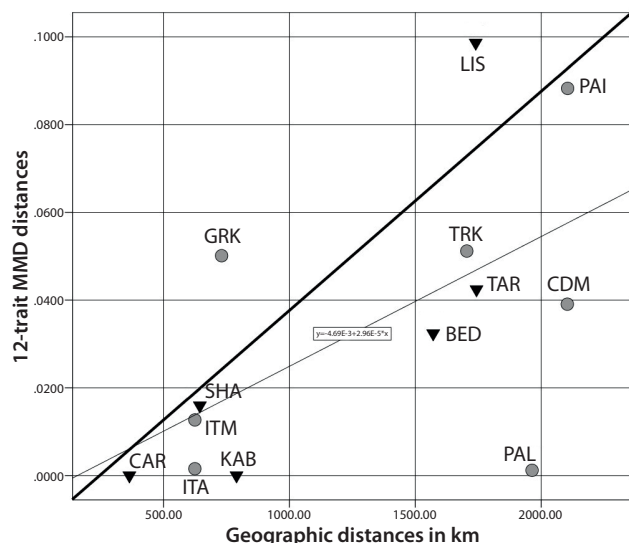
**Table 6.6.** Pairwise distances between Malta (the Circle) and the 13 comparative samples based on MMD for 12 dental traits and kilometers (KM). <sup>1</sup>Underlined MMD distances indicate significant difference at the 0.025 alpha level. <sup>2</sup>BED = Bedouin, CAR = Carthage, CDM = Cova da Moura, GRK = Greece, ITA = Italy ancient, ITM = Italy historic/modern, KAB = Kabyle, LIS = Lisht, PAI = Pai Mogo I, PAL = Palestine, SHA = Shawia, TAR = Tarkhan, TRK = Anatolia/Turkey and Cyprus.

	MMD <sup>1</sup>	KM
BED <sup>2</sup>	0.03239	1571.02
CAR	0.00000	364.60
CDM	0.03906	2103.64
GRK	0.05010	730.90
ITA	0.00155	624.69
ITM	0.01268	624.69
KAB	0.00000	790.00
LIS	0.09864	1739.79
PAI	0.08825	2104.81
PAL	0.00119	1963.46
SHA	0.01595	644.41
TAR	0.04242	1743.07
TRK	0.05117	1704.51





**Figure 6.1.** Three-dimensional MDS of 12-trait MMD distances between the Circle and the 13 comparative samples. The three-letter sample abbreviations are defined in Tables 6.2, 6.4 and 6.6 (see text for details).



**Figure 6.2.** Two-dimensional scatterplot of the Circle sample relative to the 13 comparative samples based on geographical (x-axis) vs. phenetic (y-axis) distances. The thick black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e.,  $y=0+1x$ , where  $y=a+bx$ ) is provided to illustrate where the other samples would be if a 1:1 correspondence existed between the distances. The actual regression coefficient is also provided as the line of best fit (thin black line) through the data cloud (with equation provided;  $r^2 = 0.348$ ). See text for details.

Lastly, the data from the Circle were plotted against the rest of the samples using pairwise geographical and MMD distances as co-ordinates on the x- and y-axes in Figure 6.2. A linear equation reference line (thick black) with a slope (b) of 1 and y-intercept (a) of 0 is provided (i.e.,  $y=0+1x$ , where  $y=a+bx$ ) to simply illustrate where the other samples would be located if a 1:1 correspondence existed between spatial and phenetic distances. The actual sample locations identify those which are phenetically closer to the Circle than expected (i.e., below the reference line), and vice versa (above the line), relative to the geographical separation.

For comparison purposes, the true regression coefficient is also provided as the line of best fit (thin black) through the data cloud of comparative samples. Assuming that phenetic affinity is a function of spatial separation, a coefficient of determination was calculated via the linear regression procedure in SPSS 24.0 ( $r^2 = 0.348$ ,  $r = 0.590$ ,  $p = 0.034$ ). Thus, 35% of the variability in MMD distances is associated with or explained by variability in the geographical distances.

## 6.5. Discussion and conclusions

This chapter has reported on the analysis of 39 non-metric traits of the posterior dentition (maxillary and mandibular molars) derived from selected archaeological contexts of the Circle. While the results provide interesting evidence for broad genetic affinities throughout the Mediterranean region, it is important to identify a number of limitations of the current analysis. Firstly, with over 11,000 isolated teeth in the Circle assemblage that provide a potential wealth of data on the population affinities and lifestyle of the Neolithic peoples of Malta, this analysis represents only the first step in consideration of the broader population affinities reflected in the dental morphology. We focused on the posterior dentition because of the wealth of observable non-metric traits with discriminatory power.

That said, the analyses presented here can be refined by the inclusion of data representing non-metric trait frequencies of the incisors, canines, and premolars. By focusing on the molars, and because of the absence of some traits (such as the Deflecting Wrinkle and Radical Number) among all populations, the discriminatory power of analyses was limited. Furthermore, the commingled nature of the site means that we were unable to analyse the complete dentition of intact individuals; although these data are available, articulated and undisturbed individuals represent only a small percentage of the total depositional population in the Circle (estimated at 2% in Malone & Stoddart 2009, 365–6). Recent research, however, has demonstrated

that even among such assemblages, dental non-metric traits provide useful data on regional population affinities (Irish *et al.* 2017). Additional complexities arise because our sampling strategy did not, by necessity, provide comprehensive coverage of the site, which is compounded by the likelihood of some tooth movement through stratigraphy related to diachronic cultural and natural commingling processes following *postmortem* exfoliation (Chapter 3 & Chapter 12).

With these caveats in mind, the results provide preliminary evidence of the population affinities of the Neolithic people interred in the Circle. In general, the populations of the northern, eastern and southern Mediterranean share a range of dental characteristics that suggest broad patterns of prehistoric gene flow throughout the region. The non-metric traits of the posterior dentition of the Maltese, however, show somewhat stronger affinities to the Ancient Italian, Carthaginian, and more distantly Kabyle Berber and Palestinian populations. While we cannot interpret this as direct evidence for ancestor-descendent relationships, the results suggest that Neolithic Malta was connected by population movements throughout the Mediterranean, albeit somewhat isolated as a genetic pool. One might predict, because of its relative distance, either a strong signature of genetic isolation, or particular affinities with only individual regions, such

as Italy, within the Mediterranean. The observation of affinities with populations of the north, south and more distant eastern Mediterranean regions suggest that the Neolithic Maltese population remained well-connected throughout the region. The results also suggest that future and more expansive genetic analyses should investigate links to populations in Northern Africa (see discussions on prospective cultural links to this region via dental modification analyses in Chapter 5).

These relationships can also be clarified by further dental non-metric trait analyses, as they have been demonstrated to be an excellent proxy for neutral genetic distances (Irish *et al.* 2020). Some of the patterns of variation observed in the present analyses are undoubtedly shaped by the limitations of data analysis from the posterior dentition only. Inclusion of traits from incisors, canines and pre-molars will improve the resolution of such analyses and clarify phenetic distances to the other Mediterranean populations. These results must be interpreted as a first step in this process, which nevertheless highlight both the interconnectedness of the Neolithic Maltese population within the Mediterranean cultural sphere, and the utility of dental non-metric approaches in the further exploration and understanding of these patterns of human movement and interaction in prehistory.