Bridging the Gap: Using Biological Data from Teeth to Comment on Social Identity of Archaeological Populations from Early Anglo-Saxon, England

ABSTRACT

Human teeth are storytellers, in that, through analysis of their size and shape osteoarchaeologists are able to 'talk' to the dead and translate biological data into social meaning. This concept has been explored in parts of the world through investigations of biological similarity and kinship, but few have focused in depth on early medieval populations who emphasised the importance of family and kinship. This paper presents the results from four early Anglo-Saxon cemeteries which highlight the utility of dental metrics in identifying biological similarity within the skeletal assemblages. 5988 mesiodistal and buccolingual measurements were recorded from the identifiable permanent dentition of adult individuals from early Anglo-Saxon cemeteries in the UK counties of Cambridgeshire and Kent. Results from statistical hierarchical cluster analysis of dental metric data revealed that it was possible to identify individuals within the cemetery sites that were more similar to one another according to their dental metrics. This similarity was not attributed statistically to biological sex or shared familial environment, as similarity between individuals could be found between males and females and few significant differences were found across the sites sampled. It was found that tooth metrics provided a meaningful biological dataset from which current theories regarding the identity of Anglo-Saxon individuals and families could be refined and improved. These types of data are useful as building blocks which help to bridge the gap between social constructs and human skeletal remains in order to substantiate interpretations about past populations in more significant ways. This work supports the need for multidisciplinary approaches to bioarchaeological investigations of past people while highlighting the utility of human dentition to enhance such areas of study.

Keywords: dentition, dental metrics, biological similarity, identity, Anglo-Saxon, bioarchaeology

1. INTRODUCTION

Being able to study and understand social identity in archaeological populations is a difficult task helped by the contribution of a variety of evidence types, such as anthropologic and historic sources. In many instances available evidence may be limited and the understanding of complex social phenomena requires researchers to make use of contextual, artefactual and biological data in order to piece together theories regarding social concepts. One such time period where the complexity in understanding social constructs is apparent, is the early Anglo-Saxon period (5th through 6th centuries AD); a time of migratory and political change across the European continent and United Kingdom (Williams, 2007). Research on this era has focused on discussing group identity, kinship, marriage and mobility, while successfully demonstrating that there are numerous evidence bases from which these discussions can be constructed. Examples of these evidence types include: using grave goods and furnishings (Härke, 2014; Huggett, 1996; Lucy, 2000), overall spatial patterning of cemeteries (Sayer, 2009; 2020; Stoodley, 2002), DNA (Schiffels et al., 2016) and the appearance of inherited traits on skeletal remains (Stewart and Sayer, *in prep*) in order to try to understand these various social constructs. Arguably, stronger theories related to cultural or social identity are derived from multidisciplinary investigations of past people. For example, for the early Anglo-Saxon period, Sayer (2020, 248) indicates that the creation and decoration of graves within each cemetery is the product of local communities communicating at a cultural level. The decisions related to grave goods and burial locations were meant to communicate a narrative, or community history, to participants which would change depending on the priorities of families at a local level (Sayer, 2020, 272). This work incorporates data from grave good analyses, spatial organisation, historical documentation and

biological data from skeletal remains highlighting the utility of incorporating various types of evidence into such discussions.

Biological research in archaeological investigations mainly relies on direct observations of skeletal material or data obtained from skeletal remains such as DNA (i.e. Deguilloux et al., 2014) or isotopes (i.e. Gregoricka, 2013). However, skeletal preservation overtime is negatively influenced by factors such as soil erosion, water, heat and time in general (Galloway et al., 1997). Teeth, in comparison, are more resilient to degradation and damage over time compared to the remainder of the skeleton due to the robust chemical structure of their enamel and dentine components (Bell et al., 1991). Teeth, once formed, do not remodel or change in size and shape (Hillson, 2005) and are therefore able to retain morphological traits over an individual's life. As such, human dentition provides a strong medium through which researchers can obtain useful biological data that relates to a person's identity on population, community, and individual levels (Hughes and Townsend, 2013; Irish, 1997).

While teeth have factored into discussions related to identity of past people (i.e. Alt et al., 1997), studies involving teeth have limited inclusions from other types of data beyond skeletal demography or DNA analyses (i.e Adachi et al., 2003). While not necessarily problematic to do so, as researchers in bioarchaeology have been advocating for a wider inclusion of multiple evidence types to help refine theories in order to improve the overall robusticity of conclusions within the field (Johnson and Paul, 2016; Johnson, 2019), teeth have the ability to provide an additional and important source of data alongside contextual and artefactual evidence. Furthermore, while the full understanding of tooth development from a genetic perspective is still progressing, studies have demonstrated that the size and shape of teeth can be strongly linked to the influence and interaction of various genes (i.e. Maeda et al. 2019; Sunohara et al. 2020). Tooth crown dimensions have been shown to reflect genetic inheritance through correlation analyses of tooth sizes across parent and offspring and sibling to sibling relationships (i.e. Townsend and Brown 1978a; 1978b). From this, the concept of dental phenomics has more recently been established to discuss the genetic influence on tooth size and shape. Moreno Uribe and Miller (2015) and Brook et al. (2014) discussed how crown dimensions account for size differences in teeth attributed to nonmetric inherited traits, such as accessory tubercles and cusps (i.e. Guatelli-Steinberg et al., 2013). These ideas can be applied to cases where families display metric and nonmetric dental traits that deviate from the normal ranges of expression in the rest of the population (i.e. Skrinjaric et al. 2016). Hlusko (2016) demonstrated that quantitative genetic approaches can be used to elicit information regarding the relationship between inherited genetic material and resultant dental phenotypes in offspring, helping to support the ideas mentioned above.

When looking at individuals who share strong biological connections, such as when investigating families by comparing parents to offspring or between siblings, correlations in tooth sizes do appear (i.e. Alt and Vach, 1995; Alt et al., 1997; Biggerstaff, 1970; Guatelli-Steinberg et al., 2013; Hughes and Townsend, 2013; Moreno Uribe and Miller, 2015; Stewart, *unpublished;* Townsend and Brown, 1978a; 1978b). Biological sex has also shown to influence tooth size with some (i.e. İşcan and Kedici, 2003; Garn et al., 1965; Townsend and Brown, 1978a; 1978b) suggesting that the influence of X and Y chromosomes leads to changes in tooth dimensions within a population, although, this does not appear to be a consistent trend found across all populations (i.e Stewart, *unpublished*). While there are other factors that contribute to the determination of final tooth size, such as biological sex, maternal environment, common family environment (Townsend et al. 2009), and random genetic mutations (Hughes and Townsend, 2013; Mossey, 1999), it does appear in the literature that shared genetics contributes most strongly to these observable metric traits (Biggerstaff, 1970; Boraas et al., 1988; Dempsey et al., 1995; Hughes et al., 2000; Townsend, 1980).

Biological similarity, or affinity, is a broad term that simply relates to the degree at which individuals demonstrate similarity in biodata; this study focuses on similarity in dental metrics. It is important to highlight that identifying individuals who share greater levels of similarity in their biodata is a biological observation only and does not necessarily equate to social connections. However, it is imperative that biological data is used when discussing such connections between people, because biological identity may be central to the way many societies construct their ideas of social relatedness. Moreover, the inclusion of new approaches that help to connect biological data to social meaning can help strengthen existing theories and discussion on such cultural aspects. It is the aim of this paper to highlight the usefulness of teeth in discovering biological similarity within archaeological populations. Applications of this type of data, in combination with contextual, artefactual, spatial and historical evidence will, in future, explore how dental biodata can add to a discussion around ideas of kinship, family identity in death and cemetery organisation in the early Anglo-Saxon period.

2. MATERIAL AND METHODS

Four early Anglo-Saxon cemeteries were chosen for investigation in this study, two were from Cambridgeshire and two from Kent, all located in South-East England. From Cambridgeshire, the cemeteries of Hatherdene (n=126) (Ladd et al., 2018), excavated in the village of Cherry Hinton and Oakington (n=128) (Mortimer et al., 2017), excavated in the village of Oakington are similarly dated to the early Anglo-Saxon period (5^{th} – 6^{th} c. AD) and were located approximately 10km apart, placing them within walking distance. From Kent, Polhill (n=182)(Philip, 2002), excavated near Sevenoaks and Eastry (n= ~300)(Welch et al., 2008) excavated near the village of Eastry, are dated later than Hatherdene and Oakington (6^{th} – 7^{th} c. AD), but still cover part of the early Anglo-Saxon period. The cemeteries from Kent are approximately 80km apart, and approximately 200km from the Cambridgeshire sites. Figure 1 is a map of the relative locations of these cemeteries in England, sites are numbered as: Hatherdene (1), Oakington (2), Polhill (3) and Eastry (4). The early Anglo-Saxon period spans 410-660 AD with the majority of settlements in England concentrated in the South-East area of the country. Cemeteries from the early Anglo-Saxon period make an interesting case study to investigate biological similarity due to the changing political and religious infrastructures across the 5^{th} and 6^{th} centuries AD (Williams, 2007). The material culture from these cemeteries has been plentiful, with gendered divisions among grave goods having been cited (i.e. Dickinson and Härke, 1992; Härke, 2014).

There are several crown and root measurements (see Hillson, 2005; Hillson et al., 2005) that could be taken but the mesiodistal and buccolingual diameters of the crown are the most commonly used metric indicators of genetic influence on tooth dimensions (Adachi et al., 2003; Alvesalo and Tigerstedt, 1974; Bernal, 2007; Boraas et al., 1988; Dempsey et al., 1995; Haeussler et al., 1989; Lavelle, 1968; Moorrees and Reed, 1964; Townsend and Brown, 1978a; 1978b). As such, the mesiodistal and buccolingual diameters were used within the present study. Figure 2 displays the approach to measuring the mesiodistal and buccolingual diameters of tooth crowns which was employed in this study for incisors, canines, premolars and molars (see Hillson, 2005; Hillson et al., 2005 for more detailed descriptions of measurements). The measurements were collected by the author using digital callipers, calibrated to 0.01mm, from identifiable permanent teeth (whether *in situ* or loose) from adult remains with reported estimated sex (sex estimated via standard anthropological assessment of skeletal remains, see Buikstra and Ubelaker, 1994). As biological sex has been shown to have some influence on tooth size (i.e. İşcan and Kedici 2003), it was important to account for it in statistical comparisons. Each crown measurement was taken three times and the average was recorded. Teeth with dental wear on the crown or pathologies (i.e. caries) preventing

reliable measurement were omitted from study. From the assemblages excavated from Hatherdene, Oakington, Polhill and Eastry, Table 1 provides an overview of individuals chosen for statistical analysis and the corresponding number of measurements collected from their dentition.

Figure 1 – Locations of Hatherdene (1), Oakington (2), Polhill (3) and Eastry (4) cemeteries within England. Rectangles indicate general areas of Cambridgeshire and Kent counties, with London indicated as a reference point. Approximate direct distance between Hatherdene and Oakington cemeteries is 10km. Approximate distance between Polhill and Eastry cemeteries is 80km. Approximate distance between Cambridgeshire (1 and 2) and Kent (3 and 4) cemeteries is 200km (Mapcustomizer.com 2020).

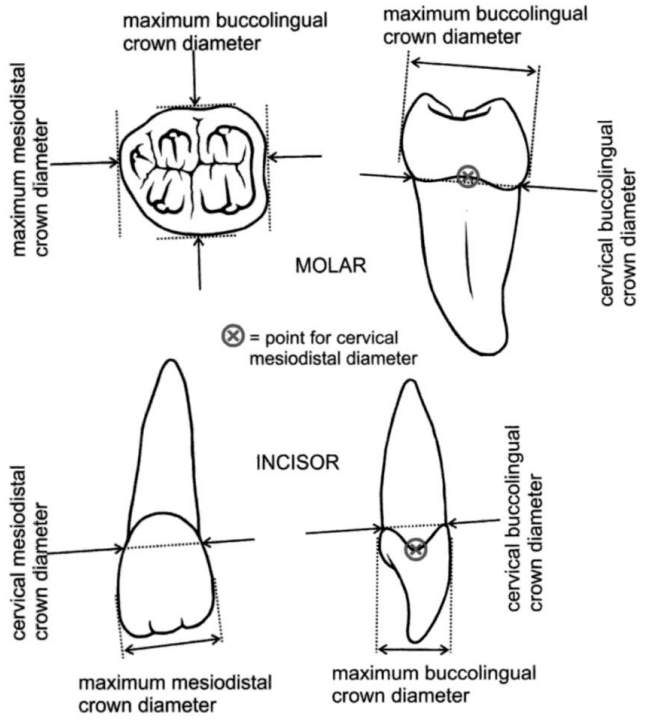

Figure 2 – Measuring points for mesiodistal and buccolingual crown diameters of incisors and molars used during data collection (Hillson 2005, Figure 4.1). This approach was similarly applied to premolars and canines.

Table 1 – Overview of number of skeletons divided by sex and cemetery, and subsequent number of measurements collected from their permanent dentition from Hatherdene, Oakington, Polhill and Eastry cemeteries. Mesiodistal (MD) and buccolingual (BL) recorded.

Sample	Total n	Number of Males (M) / Females (F)	Tooth	Measurement Recorded	Number of Measurements
Hatherdene	56	28 M / 28 F	Incisor	MD	271
				BL	271
			Canine	MD	176
				BL	176
			Premolar	MD	351
				BL	351
			Molar	MD	452
				BL	452
Oakington	48	21 M / 27 F	Incisor	MD	256
				BL	256
			Canine	MD	147
				BL	137
			Premolar	MD	312
				BL	312
			Molar	MD	365
				BL	365
Polhill	26	10 M / 16 F	Incisor	MD	108
				BL	108
			Canine	MD	75

				BL	75
			Premolar	MD	141
				BL	141
			Molar	MD	183
				BL	183
Eastry	15	6 M / 9 F	Incisor	MD	29
				BL	29
			Canine	MD	25
				BL	25
			Premolar	MD	45
				BL	45
			Molar	MD	58
				BL	58
TOTAL	**145**	**65 M / 80 F**			**5988**

Using SPSS (IBM Core 2016), descriptive statistics and normality of data were quantified for each of the 32 permanent teeth across the sample; complete overview of descriptive statistics for each cemetery sample are provided in Appendix A. These first statistical tests were used to better understand the spread of data within the entire sample. Following these tests, analysis of variance (ANOVA) tests were used to investigate the impact of biological sex and of common familial environment (cemetery site) on tooth size. Post-hoc Tukey tests were used to determine which sites, if any, contributed to the differences observed to help with subsequent analysis and interpretation. If teeth were identified to have significant differences in size between sexes or cemetery sites, those teeth were used for within group comparisons only as opposed to pooled sex or pooled cemetery comparisons. Following these analyses, additional statistical testing was used to cluster individuals based on similarity in tooth sizes to see if there were patterns present in relation to the individuals being grouped together. The teeth selected for hierarchical cluster analysis (HCA) for combined sex comparisons were limited to those that had normally distributed data, found not to be affected by common familial environment (those in Table 2) and not sexually dimorphic (those in Tables 3-4). For any comparisons involving separate sexes, the teeth presented in Tables 3-4 were included to allow the comparison of males or females within single sex groups.

For the clustering investigations, teeth were analysed and grouped using Ward's Linkage (Ward 1963) hierarchical cluster analysis (HCA), an agglomerative approach to separating data into clusters of similarity based on given data sets (Fraley and Raftery 1998; Grubesic and Murray 2001). Distances between clusters were recorded using squared Euclidean distances, with a maximum distance of 25. The clusters derived from HCA are difficult to quantify in terms of validity, as HCA will create clusters regardless of what data is entered, however, validation of patterns observed in the establishment of clusters can be done through repeated testing across data sets (Tee et al. 2013). In the context of this study, any clusters of individuals produced through HCA could indicate potential biological relationships, and this hypothesis would be stronger the more times these individuals were shown to cluster together across multiple teeth. It was possible to identify such instances using dendrogram outputs from the HCA as they made it easy and quick to visualise the individuals who had been clustered together. Any clusters that showed individuals grouped at a squared Euclidean distance of ≤5 were classed as sharing a high level of similarity in tooth size, distances of 6-15 were classed as sharing moderate levels of similarity in tooth size and distances of 16-25 were classed as sharing low levels of similarity in tooth size. Those that consistently clustered together at higher levels signified individuals displaying greater levels of biological similarity and therefore interpreted

as being more likely to share a genetic connection. In contrast, those that were repeatedly found to be grouped in low level clusters indicated lower levels of similarity and were interpreted as being less likely to share a genetic connection. Appendix B provides a worked-through example of the statistical approach to analysing tooth data in this study to demonstrate the process in full for reference.

3. RESULTS AND DISCUSSION

Overall, results from the ANOVA analyses regarding the effects of common familial environment and biological sex on tooth size showed that each of those factors had little influence on the crown measurements of the individuals interred within Hatherdene, Oakington, Polhill and Eastry. ANOVA results for the effect of common familial environment on tooth size only revealed two measurements that were significantly different between the four sites when sexes were pooled. When males were considered on their own, only one measurement was found to be significantly different. When females were considered separately six measurements were significantly different between the sites. Table 2 provides the details of these measurements and significance values associated with each. These results show that, overall, there are few significant differences in tooth sizes across all four samples used in this study. Post-hoc Tukey tests were used to identify the cemetery sample(s) responsible for the significant differences observed. In most cases these were attributable to Polhill and Eastry, which is not surprising given their smaller sample sizes compared to Hatherdene and Oakington (Table 1).

Table 2 - The significant results from the ANOVA testing for the effect of cemetery sample on tooth dimension between Hatherdene, Oakington, Polhill and Eastry cemeteries. Results are separated into combined sex and separate sex comparisons. Mesiodistal (MD) and buccolingual (BL) measurements were considered separately.

Group Comparison	**Significant Measurement (MD or BL)**	**Significance Value**
Pooled sex	MD right maxillary lateral incisor	Df=3, F = 2.989, p = 0.036
	MD left mandibular second molar	Df=3, F = 3.376, p = 0.021
Males only	MD left maxillary third molar	Df=3, F = 4.176, p = 0.017
Females only	MD right maxillary lateral incisor	Df=3, F = 3.723, p = 0.018
	MD left maxillary canine	Df=3, F = 3.034, p = 0.040
	MD left maxillary first molar	Df=3, F = 3.481, p = 0.023
	MD left mandibular second molar	Df=3, F = 3.542, p = 0.021
	BL right mandibular first premolar	Df=3, F = 3.528, p = 0.020
	MD right mandibular second premolar	Df=3, F = 3.006, p = 0.038

Data analysed through ANOVA testing in regard to the effect of biological sex on tooth size demonstrated there was not a purely bimodal expression in size between males and females. Additionally, the way in which biological sex influenced mesiodistal and buccolingual measurements separately was also not consistent. Of the 32 teeth that comprise the permanent dentition set, only nine from Hatherdene and five from Oakington were shown to have both tooth dimensions differ significantly between males and females. No teeth at Polhill and Eastry were shown to have both dimensions significantly different between males and females. The teeth that were found to differ consisted of maxillary and mandibular teeth, as well as including incisors, canines, premolars and molars. Tables 3 and 4 present the teeth that were found to differ between the two sexes at Hatherdene and Oakington and their associated significance values.

Table 3 – The significant results from the ANOVA testing for the effect of biological sex on tooth dimension size at Hatherdene cemetery. Nine teeth were found to be statistically significant in both dimensions. Results are separated into mesiodistal (MD) and buccolingual (BL) dimensions.

Tooth	**Measurement**	**Significance Value**
Right maxillary canine	MD	Df=1, F = 4.466, p = 0.041
	BL	Df=1, F = 6.205, p = 0.017
Left maxillary central incisor	MD	Df=1, F = 6.925, p = 0.014
	BL	p = 0.014*
Left maxillary canine	MD	Df=1, F = 7.789, p = 0.008
	BL	p = 0.025*
Left maxillary first molar	MD	Df=1, F = 4.189, p = 0.048
	BL	Df=1, F = 11.904, p = 0.001
Left mandibular third molar	MD	Df=1, F = 7.006, p = 0.012
	BL	Df=1, F = 8.652, p = 0.006
Left mandibular second molar	MD	Df=1, F = 10.149, p = 0.003
	BL	Df=1, F = 8.830, p = 0.005
Left mandibular canine	MD	Df=1, F = 10.092, p = 0.003
	BL	Df=1, F = 11.259, p = 0.002
Right mandibular canine	MD	Df=1, F = 10.143, p = 0.003
	BL	Df=1, F = 10.281, p = 0.003
Right mandibular second molar	MD	Df=1, F = 7.771, p = 0.008
	BL	Df=1, F = 7.930, p = 0.008

* The Kruskall-Wallis test for significance was used in these cases as raw data was not normally distributed.

Table 4 – The significant results from the ANOVA testing for the effect of biological sex on tooth dimension size at Oakington cemetery. Five teeth were found to be statistically significant in both dimensions. Results are separated into mesiodistal (MD) and buccolingual (BL) dimensions.

Tooth	**Measurement**	**Significance Value**
Right maxillary canine	MD	p = 0.042*
	BL	Df=1, F = 8.875, p = 0.005
Left mandibular second molar	MD	Df=1, F = 4.641, p = 0.038
	BL	Df=1, F = 7.925, p = 0.008
Left mandibular canine	MD	Df=1, F = 10.092, p = 0.003
	BL	Df=1, F = 11.259, p = 0.002
Right mandibular canine	MD	Df=1, F = 22.841, p <0.001
	BL	Df=1, F = 8.737, p = 0.006
Right mandibular second premolar	MD	Df=1, F = 5.583, p = 0.024

	BL	Df=1, F = 4.828, p = 0.034

* The Kruskall-Wallis test for significance was used in this case as raw data was not normally distributed.

According to Hughes and Townsend (2013) and Townsend et al. (2012), three of the main factors that influence tooth size are: environment (maternal and common familial), biological sex and genetics. While genetics is linked to biological sex, there are reportedly over 300 genes that can be inherited which affect tooth size and shape (Thesleff 2006). This means that the dental phenotype of parents based on the various contributions of those genes further dictates the size and shape of teeth in offspring. The above results in Tables 2-4 indicate that within this sample both common familial environment and biological sex were not major contributors to differences observed in tooth size, therefore the remaining variation in measurements must have been the result of additional biological inheritance patterns. As the majority of remaining variation was due to genetically inherited traits, the data was interpreted to mean that those individuals who were more similar in tooth size likely shared a closer biological relationship compared to others in the population. In order to better visualise this, a series of dendrograms produced through hierarchical cluster analyses presented the individuals within Hatherdene, Oakington, Polhill and Eastry in clusters based on level of similarity in tooth size.

The HCA dendrograms were a useful visual aid to help identify individuals who were found to share greater levels of similarity across multiple teeth. They were arranged to show how similar individuals were based on squared Euclidean distances. Those that were clustered together at smaller distances showed the most similarity in their tooth measurements while those that were separated at greater distances displayed less similarity. This can be seen in Figure 3, a dendrogram from Hatherdene, which highlights a strong degree of similarity between the tooth sizes of female individuals H1272, H956 and H300 being repeated across two separate teeth. Other individuals are shown to be close to this cluster (H325, H225 and H443) but not directly part of the same grouping, with some, like H493, showing very different tooth sizes.

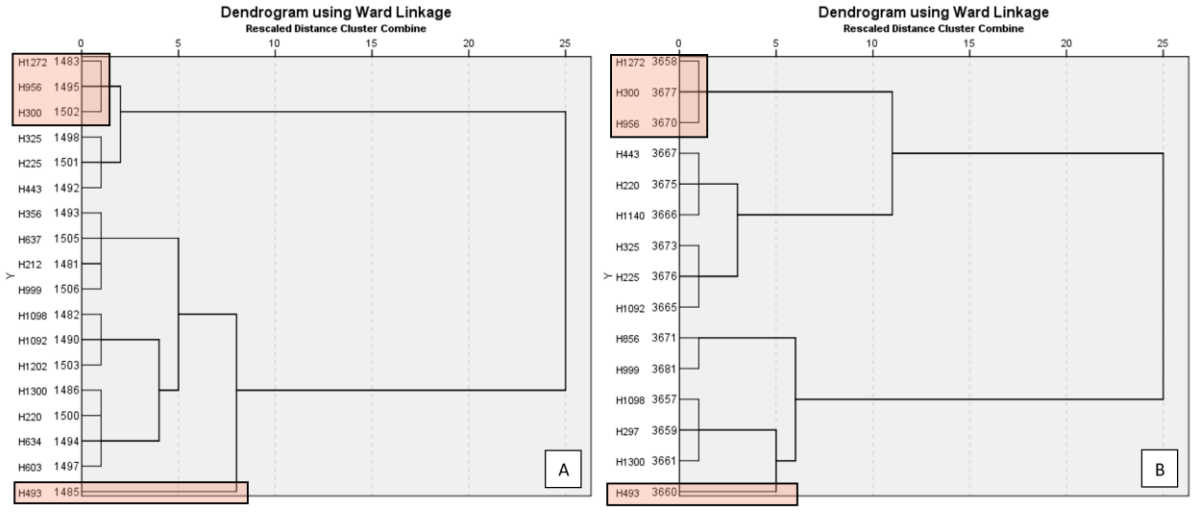

Figure 3 – HCA dendrogram outputs from hierarchical cluster analysis for the left maxillary canine (A) and the right mandibular lateral incisor (B) from the female only sample at Hatherdene. Highlighted sections show consistent higher levels of similarity between individuals H1272, H956 and H300 across both teeth as they are grouped together at a squared Euclidean distance of 1. H493 is shown to be less similar than the rest of the group as she has not been grouped in a cluster with any other individual at this distance.

To put these findings back in the context of this paper, the clustering indicated in Figure 3 would mean that there is likely a biological connection between females H1272, H300 and H956. In contrast, H493 is less likely to share a biological connection with the rest of the females of this group. It is advantageous to include as many teeth as possible for the HCA as not all teeth showed the same patterns regarding biological similarity. For example, individuals who appeared clustered together for one tooth would not always appear clustered together for another, despite being present in the comparative sample. Figure 4 presents an example of six males from Oakington that show inconsistent levels of similarity across two separate teeth.

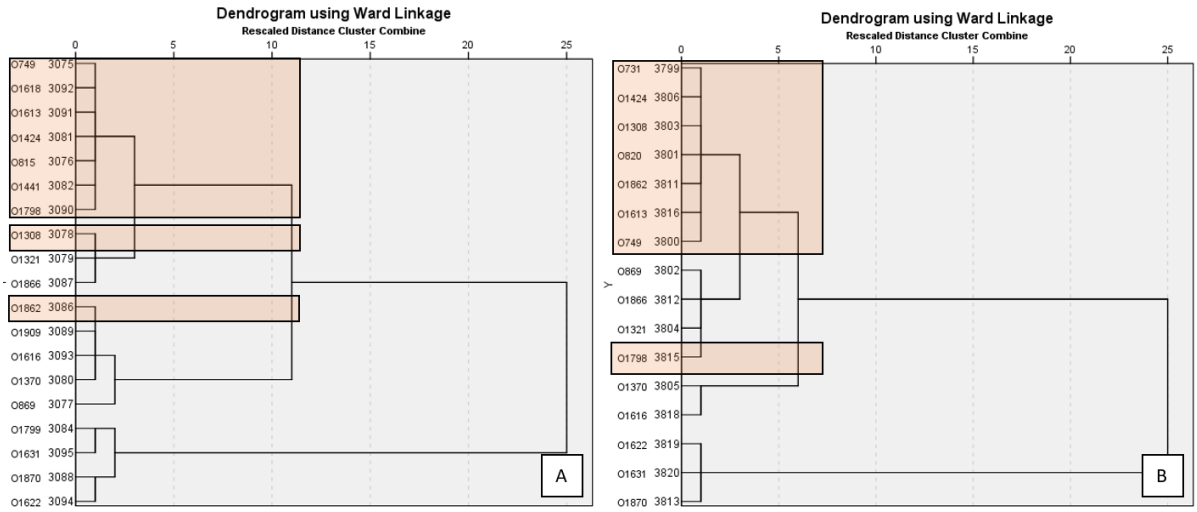

Figure 4 – HCA dendrogram outputs from hierarchical cluster analysis for the left mandibular canine (A) and the right mandibular canine (B) from the male only sample at Oakington. Highlighted sections show consistent high levels of similarity between individuals O749, O1424 and O1613. These individuals are clustered together across both teeth at a squared Euclidean distance of 1. In contrast O1308, O1798 and O1862 appear as part of this cluster in A, but not in B or *vice versa*.

When six other teeth were looked at, combinations of the individuals highlighted in Figure 4 appeared in clusters at the squared Euclidean distance of 1. Of the possible eight teeth available to compare across Oakington males, all of them showed that these six males displayed high levels of similarity within the assemblage. This group of males at Oakington are more likely to share close biological connections than other males present in the cemetery. If only the HCA output of the left and right mandibular canines were looked at, as in Figure 4, the true nature of the connections between these six individuals may have been missed or underestimated. Therefore, utilising multiple teeth is strongly advised.

The hierarchical cluster analyses identified interesting patterns between the male and female data across the four cemeteries. In the Oakington, Polhill and Eastry populations, the male individuals separated into fewer clusters of more individuals. In contrast, the female individuals were separated into more clusters with fewer individuals in each. This result indicates greater amounts of similarity in the male populations of Oakington, Polhill and Eastry compared to females. Interestingly, the Hatherdene results were the opposite. Here, females were found to have fewer clusters compared to males. Table 5 provides an overview of the average number of clusters at a squared Euclidean distance of 1, average size of largest clusters from comparisons of all teeth and the associated proportion these reflect in the overall group.

Table 5 – An overview of the average number of clusters at a squared Euclidean distance of 1, average size of largest cluster for all permanent teeth and the associated proportion this comprises of the comparative group. Male data overall shows greater levels of similarity compared to females with the exception of Hatherdene.

Comparative Group	Average Number of Clusters at sq. Euclidean Distance of 1	Average Size of Largest Cluster	Proportion of Population (%)
Oakington males	5.00	6.50	43.5
Oakington females	6.75	4.75	27.0
Hatherdene males	8.50	4.50	20.5
Hatherdene females	5.75	4.25	26.5
Polhill males	5.00	2.00	29.0
Polhill females	6.50	3.00	25.0
Eastry males	2.00	2.00	67.0
Eastry females	3.25	2.00	49.3

The results in Table 5 show that, overall on a population level, male and female tooth data present distinct patterns relative to the levels of biological similarity in their dental metrics. Males across the whole population appear to be more similar as they are being sorted into fewer groups compared to females. This indicates there are likely to be more shared biological connections among the males of these sites, while the females as a group are less likely to share biological connections among themselves. Research surrounding the residence and mobility patterns of males and females during the early Anglo-Saxon period has highlighted the presence of local settlements based on male lineages with females entering these groups from elsewhere for marriage (i.e. Sayer 2014; 2020). Patterns revealed using similarity in tooth metrics from this paper mirror these findings, as it was the males that were found to share higher levels of similarity whereas the females appeared more varied in their clustering, suggesting they are not as strongly connected biologically. These findings demonstrate that human dentition can add important biological support for such discussions which, in future, can help to corroborate aspects of social identity and kinship in more depth.

4. CONCLUSIONS

The aim of this paper was to ascertain whether human dentition could be used to identify biological similarity in large skeletal assemblages. Once common familial environment and biological sex had been accounted for in the dataset, hierarchical cluster analysis (HCA) proved a relatively simple way to quickly sort through large amounts of metric data from multiple teeth to locate individuals who share high levels of biological similarity across mesiodistal and buccolingual tooth dimensions. The results obtained from the HCA established a strong starting point for future discussions on connections between individuals both on a biological and social level. The biological connections discovered in this dataset have the potential to be explored both within and between the cemeteries of Hatherdene, Oakington, Polhill and Eastry. Thus, dental metrics can add to discussion of population, community and familial identity in early Anglo-Saxon culture and archaeological populations. However, to bridge the gap between biological data and social constructs a wider holistic approach that utilises archaeological data and biodata together will help to understand the dynamism of evidence within past populations (Johnson and Paul, 2016; Johnson, 2019; Sayer, 2020). Statistical analyses of tooth metrics, arguably, help to fill that gap and provide a way to begin a discussion of relatedness. The results presented here are a starting point and, while further

exploration will be required to fully explore kinship and social connectivity (Stewart, *unpublished*; Stewart, *in prep*), this paper was able to frame the results of comparative analysis within a socially derived context, situating the degree of male relatedness with culturally determined residence patterns. Results from these and future studies will further demonstrate the importance of including dental biodata in studies relating to the identity of past populations and approaching studies of kinship in a multi-disciplinary way.

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APPENDIX A

Table A.1 – Descriptive statistics from the pooled sample (n=145), not separated by sex.

Tooth	N	Minimum Value (mm)	Maximum Value (mm)	Mean	Standard Error	Standard Deviation	Variance	Confidence Interval (mm) (95%)
Right maxillary molar 3	MD = 69	6.42	10.78	8.43	0.101	0.839	0.704	8.22 – 8.63
	BL = 69	8.17	12.9	10.22	0.107	0.849	0.801	10.01 – 10.44
Right maxillary molar 2	MD = 92	7.03	10.66	9.07	0.071	0.680	0.462	8.93 – 9.21
	BL = 92	8.66	12.32	10.67	0.070	0.672	0.452	10.53 – 10.81
Right maxillary molar 1	MD = 87	8.12	11.25	9.97	0.059	0.549	0.301	9.85 – 10.09
	BL = 87	9.71	12.29	10.98	0.058	0.538	0.290	10.86 – 11.09
Right maxillary premolar 2	MD = 104	4.91	7.47	6.40	0.046	0.467	0.218	6.31- 6.49
	BL = 104	7.57	10.15	8.85	0.055	0.558	0.312	8.75 – 8.96
Right maxillary premolar 1	MD = 100	5.56	7.49	6.50	0.040	0.405	0.164	6.42 – 6.58
	BL = 100	7.37	10.25	8.73	0.059	0.594	0.353	8.61 – 8.85
Right maxillary canine	MD = 101	5.35	8.28	7.44	0.044	0.449	0.201	7.35 – 7.53
	BL = 101	6.92	9.83	8.16	0.050	0.499	0.249	8.06 – 8.26
Right maxillary lateral incisor	MD = 83	4.43	7.80	6.52	0.064	0.586	0.343	6.40 – 6.65
	BL = 83	4.56	7.72	6.37	0.057	0.521	0.271	6.26 – 6.49
Right maxillary central incisor	MD = 66	7.30	9.56	8.34	0.063	0.509	0.259	8.22 – 8.47
	BL = 66	5.90	8.30	7.05	0.052	0.426	0.182	6.94 – 7.15
Left maxillary central incisor	MD = 81	7.31	9.30	8.34	0.051	0.462	0.213	8.24 – 8.44
	BL = 81	6.00	8.83	7.14	0.051	0.457	0.209	7.04 – 7.24

Left maxillary lateral incisor	MD = 86	4.43	7.78	6.56	0.061	0.564	0.318	6.44 – 6.68
	BL = 86	5.01	7.46	6.23	0.054	0.497	0.247	6.13 – 6.34
Left maxillary canine	MD = 98	6.64	8.41	7.44	0.040	0.393	0.155	7.36 – 7.52
	BL = 98	6.67	9.94	8.14	0.048	0.480	0.230	8.04 – 8.24
Left maxillary premolar 1	MD = 94	5.60	7.33	6.49	0.042	0.404	0.163	6.41 – 6.57
	BL = 94	7.03	10.14	8.66	0.061	0.593	0.351	8.54 – 8.78
Left maxillary premolar 2	MD = 95	5.03	7.40	6.34	0.046	0.445	0.198	6.25 – 6.43
	BL = 95	7.66	10.23	8.88	0.058	0.565	0.319	8.77 – 9.00
Left maxillary molar 1	MD = 89	8.44	11.29	10.00	0.055	0.520	0.270	9.89 – 10.11
	BL = 89	9.54	12.30	10.96	0.058	0.549	0.301	10.84 – 11.07
Left maxillary molar 2	MD = 90	7.28	11.14	9.19	0.071	0.675	0.455	9.04 – 9.33
	BL = 90	9.09	12.08	10.62	0.070	0.667	0.445	10.48 = 10.76
Left maxillary molar 3	MD = 68	6.99	9.78	8.50	0.078	0.645	0.416	8.34 – 8.65
	BL = 68	7.67	11.61	10.04	0.099	0.819	0.671	9.85 – 10.24
Left mandibular molar 3	MD = 80	8.36	11.94	10.26	0.088	0.790	0.625	10.09 – 10.44
	BL = 80	8.08	11.20	9.57	0.072	0.648	0.420	9.42 – 9.71
Left mandibular molar 2	MD = 105	8.11	12.67	10.30	0.067	0.690	0.476	10.16 – 10.43
	BL = 105	8.28	11.35	9.85	0.054	0.551	0.303	9.74 – 9.95
Left mandibular molar 1	MD = 97	8.91	12.08	10.70	0.063	0.616	0.379	10.58 – 10.83
	BL = 97	8.79	11.52	10.29	0.051	0.499	0.249	10.19 – 10.39
Left mandibular premolar 2	MD = 116	5.44	10.57	6.71	0.055	0.595	0.355	6.60 – 6.82
	BL = 116	5.41	9.76	7.92	0.054	0.578	0.334	7.82 – 8.03
Left mandibular premolar 1	MD = 114	5.45	7.73	6.63	0.038	0.410	0.168	6.55 – 6.70
	BL = 114	6.44	8.75	7.48	0.044	0.467	0.219	7.40 – 7.57
Left mandibular canine	MD = 113	5.57	7.66	6.54	0.037	0.392	0.154	6.47 – 6.61
	BL = 113	6.25	8.90	7.54	0.049	0.526	0.276	7.44 – 7.64

Left mandibular lateral incisor	MD = 101	4.18	6.77	5.64	0.047	0.476	0.227	5.55 – 5.74
	BL = 101	5.27	7.30	6.31	0.040	0.404	0.163	6.23 – 6.39
Left mandibular central incisor	MD = 78	3.46	6.04	4.98	0.051	0.448	0.201	4.87 – 5.08
	BL = 78	5.38	6.88	5.92	0.037	0.328	0.108	5.84 – 5.99
Right mandibular central incisor	MD = 75	3.70	5.98	4.93	0.056	0.485	0.235	4.82 – 5.04
	BL = 75	5.34	7.00	5.93	0.041	0.357	0.127	5.84 – 6.01
Right mandibular lateral incisor	MD = 94	4.71	6.63	5.67	0.049	0.472	0.223	5.58 – 5.77
	BL = 94	5.05	7.39	6.26	0.044	0.430	0.185	6.18 – 6.35
Right mandibular canine	MD = 111	5.57	7.73	6.51	0.039	0.412	0.169	6.43 – 6.59
	BL = 111	6.41	9.43	7.54	0.051	0.541	0.292	7.44 – 7.65
Right mandibular premolar 1	MD = 117	5.56	7.61	6.66	0.038	0.408	0.166	6.56 – 6.73
	BL = 117	6.31	8.94	7.51	0.045	0.488	0.238	7.43 – 7.60
Right mandibular premolar 2	MD = 109	5.65	8.09	6.70	0.044	0.457	0.209	6.61 – 6.78
	BL = 109	6.36	9.23	7.91	0.053	0.549	0.301	7.80 – 8.01
Right mandibular molar 1	MD = 101	8.95	12.10	10.66	0.062	0.624	0.390	10.54 – 10.78
	BL = 101	8.57	11.41	10.30	0.047	0.468	0.219	10.21 – 10.39
Right mandibular molar 2	MD = 103	8.69	11.88	10.28	0.063	0.643	0.413	10.15 – 10.40
	BL = 103	8.19	11.20	9.77	0.054	0.547	0.299	9.66 – 9.88
Right mandibular molar 3	MD = 77	8.10	11.57	10.10	0.089	0.777	0.604	9.93 – 10.28
	BL = 77	7.90	10.62	9.41	0.071	0.625	0.390	9.26 – 9.55
Total N	**5988**							

Table A.2 – Descriptive statistics from Hatherdene (n= 56), pooled sex.

Tooth	N	Minimum Value (mm)	Maximum Value (mm)	Mean	Standard Error	Standard Deviation	Variance	Confidence Interval (mm) (95%)
Right maxillary molar 3	MD = 33	6.75	10.08	8.41	0.154	0.883	0.781	8.10 – 8.72
	BL = 33	8.17	12.90	10.18	0.182	1.042	1.088	9.81 – 10.55
Right maxillary molar 2	MD = 40	7.03	10.66	9.13	0.111	0.707	0.500	8.91 – 9.36
	BL = 40	9.47	12.32	10.73	0.115	0.728	0.530	10.50 – 10.96
Right maxillary molar 1	MD = 34	8.89	11.17	9.99	0.087	0.504	0.254	9.81 – 10.16
	BL = 34	9.74	12.28	11.01	0.096	0.558	0.311	10.82 – 11.20
Right maxillary premolar 2	MD = 43	4.91	7.47	6.41	0.077	0.508	0.258	6.26 – 6.57
	BL = 43	7.57	9.93	8.87	0.082	0.535	0.286	8.70 – 9.03
Right maxillary premolar 1	MD = 43	5.67	7.22	6.50	0.059	0.386	0.149	6.38 – 6.62
	BL = 43	7.43	10.24	8.75	0.085	0.558	0.311	8.58 – 8.92
Right maxillary canine	MD = 44	6.58	8.20	7.43	0.062	0.411	0.169	7.31 – 7.56
	BL = 44	7.27	9.83	8.16	0.078	0.513	0.263	8.00 – 8.31
Right maxillary lateral incisor	MD = 36	5.21	7.57	6.39	0.094	0.564	0.318	6.20 – 6.58
	BL = 36	5.51	7.60	6.42	0.085	0.508	0.258	6.25 – 6.59
Right maxillary central incisor	MD = 26	7.30	9.13	8.30	0.094	0.480	0.230	8.11 – 8.49
	BL = 26	6.38	7.68	6.97	0.076	0.386	0.149	6.82 – 7.13
Left maxillary central incisor	MD = 29	7.31	9.20	8.31	0.094	0.505	0.255	8.12 – 8.50
	BL = 29	6.45	8.83	7.13	0.090	0.485	0.236	6.95 – 7.32
Left maxillary lateral incisor	MD = 39	4.43	7.55	6.44	0.097	0.608	0.369	6.24 – 6.64
	BL = 39	5.01	7.46	6.14	0.079	0.493	0.243	5.98 – 6.30

Left maxillary canine	MD = 41	6.64	8.41	7.42	0.059	0.376	0.141	7.30 – 7.54
	BL = 41	7.31	9.94	8.19	0.075	0.477	0.228	8.04 – 8.34
Left maxillary premolar 1	MD = 41	5.80	7.28	6.50	0.057	0.365	0.133	6.38 – 6.61
	BL = 41	7.91	10.14	8.69	0.076	0.484	0.234	8.52 – 8.82
Left maxillary premolar 2	MD = 42	5.08	7.16	6.34	0.072	0.467	0.218	6.20 – 6.49
	BL = 42	7.87	10.15	8.91	0.083	0.535	0.287	8.75 – 9.08
Left maxillary molar 1	MD = 38	8.44	11.26	9.94	0.096	0.595	0.354	9.74 – 10.13
	BL = 38	9.54	12.26	10.99	0.091	0.563	0.316	10.80 – 11.17
Left maxillary molar 2	MD = 41	7.80	10.48	9.28	0.094	0.602	0.362	9.09 – 9.47
	BL = 41	9.20	12.08	10.68	0.112	0.718	0.516	10.45 – 10.91
Left maxillary molar 3	MD = 34	7.22	9.78	8.49	0.110	0.640	0.409	8.26 – 8.71
	BL = 34	7.91	11.61	10.02	0.163	0.953	0.907	9.69 – 10.35
Left mandibular molar 3	MD = 39	8.36	11.94	10.33	0.144	0.896	0.803	10.04 – 10.63
	BL = 39	8.36	11.20	9.55	0.116	0.727	0.528	9.31 – 9.78
Left mandibular molar 2	MD = 43	8.52	11.75	10.34	0.105	0.691	0.477	10.12 – 10.55
	BL = 43	8.32	11.35	9.92	0.094	0.614	0.378	9.73 – 10.11
Left mandibular molar 1	MD = 36	8.91	12.08	10.74	0.125	0.748	0.560	10.49 – 10.76
	BL = 36	8.79	11.41	10.31	0.092	0.555	0.308	10.12 – 10.49
Left mandibular premolar 2	MD = 47	5.44	10.57	6.76	0.116	0.795	0.632	6.53 – 7.00
	BL = 47	5.41	9.76	7.90	0.097	0.666	0.443	7.70 – 8.09
Left mandibular premolar 1	MD = 48	5.45	7.73	6.61	0.065	0.447	0.200	6.48 – 6.74
	BL = 48	6.62	8.53	7.47	0.065	0.451	0.203	7.34 – 7.60
Left mandibular canine	MD = 47	5.57	7.39	6.48	0.060	0.409	0.168	6.36 – 6.60
	BL = 47	6.38	8.75	7.55	0.075	0.514	0.264	7.40 – 7.70
	MD = 43	4.72	6.65	5.63	0.069	0.452	0.205	5.49 – 5.77

Left mandibular lateral incisor	BL = 43	5.38	7.07	6.31	0.066	0.430	0.185	6.17 – 6.44
Left mandibular central incisor	MD = 32	4.26	6.04	4.93	0.070	0.398	0.159	4.78 – 5.07
	BL = 32	5.39	6.75	5.92	0.061	0.345	0.119	5.79 – 6.04
Right mandibular central incisor	MD = 30	3.77	5.73	4.82	0.089	0.485	0.236	4.64 – 5.00
	BL = 30	5.43	6.68	5.94	0.058	0.317	0.101	5.82 – 6.06
Right mandibular lateral incisor	MD = 36	4.83	6.43	5.62	0.075	0.449	0.202	5.47 – 5.77
	BL = 36	5.56	7.39	6.28	0.074	0.444	0.197	6.13 – 6.43
Right mandibular canine	MD = 44	5.57	7.73	6.47	0.069	0.459	0.211	6.33 – 6.61
	BL = 44	6.46	9.43	7.58	0.085	0.561	0.315	7.41 – 7.75
Right mandibular premolar 1	MD = 44	5.56	7.61	6.62	0.070	0.463	0.214	6.48 – 6.76
	BL = 44	6.31	8.59	7.45	0.073	0.484	0.235	7.29 – 7.58
Right mandibular premolar 2	MD = 43	5.65	7.81	6.64	0.073	0.480	0.231	6.49 – 6.78
	BL = 43	6.36	9.23	7.87	0.083	0.546	0.299	7.70 – 8.04
Right mandibular molar 1	MD = 39	8.95	12.03	10.70	0.117	0.730	0.533	10.46 – 10.94
	BL = 39	8.57	11.41	10.31	0.081	0.503	0.253	10.15 – 10.48
Right mandibular molar 2	MD = 42	8.84	11.59	10.29	0.105	0.683	0.467	10.08 – 10.50
	BL = 42	8.19	11.04	9.84	0.091	0.590	0.349	9.66 – 10.03
Right mandibular molar 3	MD = 33	8.13	11.37	10.26	0.139	0.797	0.635	9.97 – 10.54
	BL = 33	8.08	10.62	9.48	0.119	0.681	0.464	9.24 – 9.72
Total N	**2500**							

Table A.3 – Descriptive statistics from Oakington (n= 48), pooled sex.

Tooth	N	Minimum Value (mm)	Maximum Value (mm)	Mean	Standard Error	Standard Deviation	Variance	Confidence Interval (mm) (95%)
Right maxillary molar 3	MD = 21	6.42	10.78	8.34	0.186	0.854	0.729	7.95 – 8.73
	BL = 21	8.89	11.60	10.15	0.144	0.661	0.437	9.85 – 10.46
Right maxillary molar 2	MD = 35	7.78	10.25	8.91	0.108	0.636	0.405	8.69 – 9.13
	BL = 35	8.66	11.95	10.50	0.113	0.670	0.449	10.27 – 10.73
Right maxillary molar 1	MD = 33	8.93	11.25	10.04	0.091	0.520	0.271	9.86 – 10.22
	BL = 33	9.71	12.29	10.89	0.101	0.582	0.338	10.68 – 11.09
Right maxillary premolar 2	MD = 40	5.42	7.38	6.35	0.066	0.420	0.177	6.21 – 6.48
	BL = 40	7.77	10.15	8.82	0.094	0.597	0.357	8.63 – 9.01
Right maxillary premolar 1	MD = 38	5.56	7.49	6.49	0.072	0.448	0.201	6.34 – 6.64
	BL = 38	7.37	10.25	8.71	0.102	0.631	0.398	8.50 – 8.91
Right maxillary canine	MD = 35	5.35	8.28	7.43	0.089	0.525	0.276	7.25 – 7.61
	BL = 25	6.92	9.60	8.16	0.099	0.585	0.342	7.96 – 8.37
Right maxillary lateral incisor	MD = 33	5.88	7.80	6.71	0.085	0.486	0.236	6.54 – 6.89
	BL = 33	5.74	7.72	6.40	0.091	0.522	0.273	6.21 – 6.58
Right maxillary central incisor	MD = 29	7.47	9.56	8.35	0.104	0.559	0.312	8.13 – 8.56
	BL = 29	5.90	8.30	7.05	0.086	0.463	0.214	6.88 – 7.23
Left maxillary central incisor	MD = 35	7.51	9.30	8.32	0.077	0.456	0.208	8.16 – 8.47
	BL = 35	6.00	8.43	7.12	0.080	0.471	0.222	6.95 – 7.27
Left maxillary lateral incisor	MD = 32	5.51	7.49	6.62	0.091	0.517	0.267	6.43 – 6.80
	BL = 32	5.57	7.46	6.34	0.081	0.457	0.209	6.17 – 6.50

Left maxillary canine	MD = 36	6.67	8.20	7.49	0.069	0.414	0.172	7.35 – 7.63
	BL = 36	6.67	9.18	8.12	0.090	0.541	0.292	7.93 – 8.30
Left maxillary premolar 1	MD = 36	5.79	7.32	6.44	0.066	0.398	0.158	6.30 – 6.57
	BL = 36	7.03	9.71	8.57	0.101	0.605	0.366	8.37 – 8.78
Left maxillary premolar 2	MD = 37	5.03	7.40	6.31	0.072	0.435	0.189	6.16 – 6.45
	BL = 37	7.66	10.23	8.84	0.092	0.558	0.311	8.65 – 9.03
Left maxillary molar 1	MD = 32	9.37	11.29	10.13	0.085	0.482	0.232	9.96 – 10.31
	BL = 32	9.72	12.30	10.93	0.104	0.588	0.345	10.72 – 11.14
Left maxillary molar 2	MD = 30	7.28	10.41	8.96	0.131	0.715	0.511	8.69 – 9.08
	BL = 30	9.09	11.98	10.54	0.120	0.660	0.435	10.30 – 10.79
Left maxillary molar 3	MD = 19	6.99	9.12	8.37	0.142	0.617	0.381	8.07 – 8.67
	BL = 19	7.67	11.20	10.08	0.189	0.822	0.676	9.68 – 10.47
Left mandibular molar 3	MD = 26	8.75	11.40	10.01	0.131	0.667	0.446	9.74 – 10.28
	BL = 26	8.08	10.36	9.54	0.130	0.661	0.437	9.27 – 9.81
Left mandibular molar 2	MD = 38	8.11	11.83	10.12	0.104	0.641	0.410	9.91 – 10.33
	BL = 38	8.28	11.15	9.80	0.087	0.536	0.288	9.63 – 9.98
Left mandibular molar 1	MD = 35	9.54	11.32	10.59	0.087	0.515	0.265	10.41 – 10.77
	BL = 35	9.49	11.37	10.25	0.081	0.477	0.228	10.08 – 10.41
Left mandibular premolar 2	MD = 42	5.80	7.76	6.65	0.069	0.449	0.201	6.51 – 6.79
	BL = 42	6.82	9.01	7.97	0.078	0.507	0.257	7.82 – 8.13
Left mandibular premolar 1	MD = 39	5.77	7.63	6.60	0.062	0.392	0.154	6.47 – 6.73
	BL = 39	6.44	8.23	7.46	0.075	0.468	0.219	7.30 – 7.61
Left mandibular canine	MD = 39	5.85	7.45	6.62	0.062	0.385	0.148	6.49 – 6.74
	BL = 39	6.25	8.85	7.52	0.090	0.060	0.313	7.33 – 7.70
	MD = 35	4.18	6.77	5.62	0.099	0.584	0.341	5.42 – 5.82

Left mandibular lateral incisor	BL = 35	5.27	7.30	6.30	0.066	0.393	0.155	6.17 – 6.44
Left mandibular central incisor	MD = 28	3.46	6.02	4.94	0.110	0.582	0.338	4.71 – 5.17
	BL = 28	5.38	6.88	5.89	0.068	0.362	0.131	5.75 – 6.03
Right mandibular central incisor	MD = 28	3.70	5.98	5.00	0.108	0.573	0.328	4.78 – 5.22
	BL = 28	5.34	7.00	5.93	0.082	0.432	0.187	5.77 – 6.10
Right mandibular lateral incisor	MD = 36	4.71	6.63	5.73	0.082	0.489	0.239	5.57 – 5.90
	BL = 36	5.35	7.08	6.26	0.063	0.379	0.144	6.13 – 6.38
Right mandibular canine	MD = 37	5.92	7.22	6.56	0.063	0.386	0.149	6.43 – 6.69
	BL = 37	6.70	8.83	7.56	0.090	0.545	0.297	7.38 – 7.74
Right mandibular premolar 1	MD = 42	6.04	7.42	6.67	0.054	0.351	0.124	6.56 – 6.78
	BL = 42	6.63	8.94	7.53	0.077	0.502	0.252	7.37 – 7.69
Right mandibular premolar 2	MD = 38	5.80	7.46	6.69	0.069	0.427	0.182	6.55 – 6.83
	BL = 38	6.66	9.10	7.96	0.094	0.583	0.340	7.77 – 8.16
Right mandibular molar 1	MD = 36	9.42	11.35	10.53	0.087	0.522	0.273	10.35 – 10.71
	BL = 36	9.45	11.23	10.24	0.084	0.506	0.256	10.07 – 10.71
Right mandibular molar 2	MD = 34	8.69	11.81	10.19	0.114	0.666	0.444	9.96 – 10.43
	BL = 34	8.38	11.20	9.76	0.098	0.572	0.328	9.56 – 9.96
Right mandibular molar 3	MD = 26	8.10	11.24	9.90	0.150	0.763	0.583	9.59 – 10.21
	BL = 26	7.90	10.39	9.42	0.126	0.642	0.412	9.16 – 9.67
Total N	**2150**							

Table A.4 – Descriptive statistics from Polhill (n= 26), pooled sex.

Tooth	N	Minimum Value (mm)	Maximum Value (mm)	Mean	Standard Error	Standard Deviation	Variance	Confidence Interval (mm) (95%)
Right maxillary molar 3	MD = 11	7.26	10.32	8.58	0.231	0.766	0.587	8.06 – 9.09
	BL = 11	9.00	11.87	10.30	0.273	0.907	0.823	9.69 – 10.91
Right maxillary molar 2	MD = 14	8.14	10.44	9.21	0.176	0.657	0.432	8.83 – 9.59
	BL = 14	9.80	11.52	10.87	0.132	0.493	0.243	10.59 – 11.16
Right maxillary molar 1	MD = 15	8.12	10.84	9.69	0.175	0.677	0.458	9.31 – 10.06
	BL = 15	10.33	11.66	11.16	0.090	0.348	0.121	10.97 – 11.36
Right maxillary premolar 2	MD = 18	5.66	7.18	6.50	0.102	0.432	0.186	6.29 – 6.72
	BL = 18	8.19	10.01	8.98	0.124	0.527	0.278	8.72 – 9.25
Right maxillary premolar 1	MD = 16	5.90	7.17	6.53	0.093	0.370	0.137	6.33 – 6.73
	BL = 16	7.70	9.81	8.72	0.163	0.652	0.426	8.37 – 9.06
Right maxillary canine	MD = 17	7.03	8.16	7.54	0.073	0.299	0.090	7.38 – 7.69
	BL = 17	7.60	8.61	8.15	0.074	0.304	0.092	8.00 – 8.31
Right maxillary lateral incisor	MD = 12	4.43	7.14	6.44	0.235	0.813	0.661	5.92 – 6.95
	BL = 12	4.56	6.76	6.23	0.176	0.608	0.370	5.85 – 6.62
Right maxillary central incisor	MD = 10	7.77	8.81	8.34	0.128	0.405	0.164	8.05 – 8.63
	BL = 10	6.59	7.74	7.17	0.132	0.416	0.173	6.87 – 7.47
Left maxillary central incisor	MD = 14	7.68	8.95	8.34	0.094	0.350	0.123	8.13 – 8.54
	BL = 14	6.48	7.75	7.18	0.114	0.428	0.183	6.93 – 7.43
Left maxillary lateral incisor	MD = 12	6.23	7.49	6.71	0.115	0.400	0.160	6.45 – 6.96
	BL = 12	5.15	7.45	6.32	0.178	0.618	0.382	5.93 – 6.71

Left maxillary canine	MD = 16	6.79	8.22	7.42	0.110	0.440	0.194	7.18 – 7.65
	BL = 16	7.57	8.82	8.09	0.093	0.371	0.138	7.89 – 8.29
Left maxillary premolar 1	MD = 13	5.60	7.33	6.60	0.160	0.577	0.333	6.25 – 6.94
	BL = 13	7.10	9.84	8.88	0.230	0.831	0.691	8.38 – 9.38
Left maxillary premolar 2	MD = 12	5.52	7.01	6.41	0.134	0.464	0.216	6.12 – 6.71
	BL = 12	7.76	9.79	9.05	0.191	0.661	0.437	8.63 – 9.47
Left maxillary molar 1	MD = 15	9.22	10.82	9.91	0.105	0.408	0.166	9.69 – 10.14
	BL = 15	10.23	11.53	11.08	0.081	0.315	0.099	10.91 – 11.26
Left maxillary molar 2	MD = 15	8.33	10.41	9.28	0.151	0.584	0.341	8.96 – 9.61
	BL = 15	9.58	11.20	10.62	0.117	0.454	0.206	10.37 – 10.88
Left maxillary molar 3	MD = 11	7.05	9.34	8.58	0.205	0.681	0.463	8.13 – 9.04
	BL = 11	9.26	10.97	9.98	0.134	0.444	0.197	9.68 – 10.28
Left mandibular molar 3	MD = 12	9.60	11.63	10.60	0.178	0.617	0.381	10.21 – 10.99
	BL = 12	8.99	10.30	9.69	0.121	0.419	0.175	9.42 – 9.96
Left mandibular molar 2	MD = 19	9.80	12.67	10.66	0.156	0.678	0.460	10.33 – 10.98
	BL = 19	8.86	10.72	9.82	0.103	0.449	0.202	9.61 – 10.04
Left mandibular molar 1	MD = 20	9.87	11.75	10.83	0.116	0.517	0.267	10.59 – 11.07
	BL = 20	9.78	11.52	10.39	0.097	0.435	0.189	10.18 – 10.59
Left mandibular premolar 2	MD = 21	5.89	7.41	6.75	0.082	0.376	0.141	6.58 – 6.92
	BL = 21	7.08	9.18	7.97	0.110	0.505	0.255	7.74 – 8.20
Left mandibular premolar 1	MD = 20	6.01	7.47	6.72	0.085	0.380	0.144	6.54 – 6.89
	BL = 20	6.56	8.75	7.58	0.119	0.531	0.282	7.33 – 7.83
Left mandibular canine	MD = 20	5.77	7.66	6.54	0.093	0.416	0.173	6.35 – 6.73
	BL = 20	6.63	8.90	7.56	0.125	0.560	0.314	7.30 – 7.82
	MD = 17	4.75	6.45	5.67	0.091	0.374	0.140	5.47 – 5.86

Left mandibular lateral incisor	BL = 17	5.67	7.14	6.34	0.096	0.397	0.158	6.14 – 6.54
Left mandibular central incisor	MD = 12	4.62	5.56	5.07	0.068	0.236	0.056	4.92 – 5.22
	BL = 12	5.54	6.38	5.97	0.072	0.251	0.063	5.81 – 6.13
Right mandibular central incisor	MD = 14	4.54	5.45	4.95	0.074	0.277	0.077	4.79 – 5.10
	BL = 14	5.34	6.34	5.86	0.080	0.300	0.090	5.68 – 6.03
Right mandibular lateral incisor	MD = 17	4.71	6.37	5.57	0.127	0.525	0.276	5.30 – 5.84
	BL = 17	5.05	7.13	6.25	0.130	0.535	0.287	5.97 – 6.52
Right mandibular canine	MD = 22	5.76	7.42	6.47	0.084	0.396	0.157	6.29 – 6.64
	BL = 22	6.41	8.95	7.43	0.115	0.541	0.293	7.19 – 7.67
Right mandibular premolar 1	MD = 23	5.83	7.51	6.67	0.087	0.417	0.174	6.48 – 6.85
	BL = 23	6.82	8.48	7.60	0.090	0.431	0.186	7.41 – 7.79
Right mandibular premolar 2	MD = 18	6.14	7.63	6.76	0.090	0.384	0.147	6.57 – 6.95
	BL = 18	6.88	9.20	7.95	0.118	0.500	0.250	7.70 – 8.20
Right mandibular molar 1	MD = 19	9.98	9.80	10.80	0.137	0.599	0.359	10.51 – 11.09
	BL = 19	12.10	11.10	10.38	0.079	0.347	0.120	10.22 – 10.55
Right mandibular molar 2	MD = 20	9.71	11.88	10.42	0.114	0.512	0.262	10.18 – 10.66
	BL = 20	8.93	10.27	9.70	0.090	0.400	0.160	9.51 – 9.89
Right mandibular molar 3	MD = 12	9.74	11.57	10.36	0.172	0.595	0.354	9.98 – 10.74
	BL = 12	8.49	10.08	9.22	0.141	0.490	0.240	8.91 – 9.53
Total N	**1014**							

Table A.5 – Descriptive statistics from Eastry (n= 15), pooled sex.

Tooth	N	Minimum Value (mm)	Maximum Value (mm)	Mean	Standard Error	Standard Deviation	Variance	Confidence Interval (mm) (95%)
Right maxillary molar 3	MD = 4	7.73	9.50	8.67	0.388	0.775	0.601	7.43 – 9.90
	BL = 4	10.39	11.73	10.78	0.318	0.637	0.405	9.77 – 11.79
Right maxillary molar 2	MD = 3	8.67	10.35	9.41	0.496	0.859	0.738	7.27 – 11.54
	BL = 3	10.73	11.08	10.94	0.106	0.183	0.034	10.48 – 11.39
Right maxillary molar 1	MD = 5	9.67	10.71	10.23	0.192	0.430	0.185	9.70 – 10.77
	BL = 5	10.01	11.39	10.83	0.244	0.545	0.297	10.15 – 11.50
Right maxillary premolar 2	MD = 3	5.74	7.23	6/36	0.449	0.777	0.604	4.43 – 8.29
	BL = 3	7.88	8.61	8.34	0.233	0.403	0.162	7.34 – 9.34
Right maxillary premolar 1	MD = 3	6.20	6.99	6.67	0.241	0.418	0.174	5.64 – 7.71
	BL = 3	8.20	9.41	8.23	0.350	0.606	0.367	7.32 – 10.33
Right maxillary canine	MD = 5	6.24	7.97	7.21	0.285	0.637	0.405	6.42 – 8.00
	BL = 5	7.85	8.58	8.19	0.150	0.334	0.112	7.77 – 8.60
Right maxillary lateral incisor	MD = 2	6.04	6.59	6.32	0.275	0.389	0.151	--
	BL = 2	6.08	6.34	6.21	0.130	0.184	0.034	--
Right maxillary central incisor	MD = 1	--	--	--	--	--	--	--
	BL = 1	--	--	--	--	--	--	--
Left maxillary central incisor	MD = 3	8.58	9.18	8.93	0.179	0.311	0.097	8.15 – 9.70
	BL = 3	6.99	7.51	7.25	0.150	0.260	0.068	6.60 – 7.89
Left maxillary lateral incisor	MD = 3	5.91	7.78	6.87	0.540	0.936	0.876	4.54 – 9.19
	BL = 3	5.74	6.39	6.07	0.188	0.325	0.106	5.25 – 6.87

Left maxillary canine	MD = 5	7.08	7.82	7.38	0.121	0.270	0.073	7.05 – 7.72
	BL = 5	7.55	8.61	8.06	0.189	0.424	0.179	7.53 – 8.59
Left maxillary premolar 1	MD = 4	6.32	6.63	6.49	0.065	0.129	0.017	6.28 – 6.70
	BL = 4	7.83	9.42	8.67	0.327	0.654	0.428	7.62 – 9.71
Left maxillary premolar 2	MD = 4	5.96	6.80	6.35	0.180	0.359	0.129	5.78 – 6.92
	BL = 4	7.94	9.11	8.43	0.280	0.560	0.313	7.54 – 9.32
Left maxillary molar 1	MD = 4	9.51	10.30	9.94	0.165	0.331	0.109	9.41 – 10.47
	BL = 4	9.68	11.21	10.45	0.338	0.676	0.456	9.37 – 11.52
Left maxillary molar 2	MD = 4	8.56	11.14	9.61	0.551	1.102	1.214	7.85 – 11.36
	BL = 4	9.66	11.74	10.59	0.510	1.021	1.042	8.96 – 12.21
Left maxillary molar 3	MD = 4	8.01	9.64	8.95	0.371	0.742	0.551	7.77 – 10.13
	BL = 4	9.81	10.86	10.28	0.221	0.443	0.196	9.57 – 10.98
Left mandibular molar 3	MD = 3	9.74	10.53	10.17	0.231	0.400	0.160	9.18 – 11.16
	BL = 3	9.43	9.73	9.57	0.088	0.152	0.023	9.19 – 9.94
Left mandibular molar 2	MD = 5	9.51	10.95	9.90	0.269	0.602	0.362	9.15 – 10.65
	BL = 5	9.12	10.20	9.64	0.207	0.462	0.213	9.06 – 10.21
Left mandibular molar 1	MD = 6	10.02	11.49	10.70	0.250	0.612	0.375	10.06 – 11.34
	BL = 6	9.32	10.70	10.16	0.219	0.536	0.287	9.59 – 10.72
Left mandibular premolar 2	MD = 6	6.35	6.97	6.64	0.093	0.228	0.052	6.40 – 6.88
	BL = 6	6.68	8.09	7.61	0.227	0.555	0.308	7.02 – 8.19
Left mandibular premolar 1	MD = 7	6.30	7.34	6.61	0.142	0.376	0.141	6.27 – 6.96
	BL = 7	6.80	8.15	7.49	0.169	0.446	0.199	7.07 – 7.90
Left mandibular canine	MD = 7	6.24	6.77	6.57	0.070	0.186	0.035	6.40 – 6.75
	BL = 7	7.02	8.17	7.56	0.146	0.385	0.148	7.21 – 7.92
	MD = 6	5.47	5.92	5.77	0.070	0.171	0.029	5.59 – 5.95

Left mandibular lateral incisor	BL = 6	5.75	6.82	6.25	0.156	0.382	0.146	5.84 – 6.65
Left mandibular central incisor	MD = 6	4.84	5.46	5.20	0.097	0.238	0.056	4.95 – 5.45
	BL = 6	5.65	6.34	5.96	0.106	0.259	0.067	5.69 – 6.23
Right mandibular central incisor	MD = 3	5.05	5.35	5.19	0.087	0.150	0.023	4.82 – 5.57
	BL = 3	5.68	6.28	6.00	0.175	0.303	0.092	5.25 – 6.76
Right mandibular lateral incisor	MD = 5	5.78	6.19	5.96	0.070	0.156	0.024	5.77 – 6.16
	BL = 5	5.92	6.94	6.27	0.178	0.399	0.159	5.77 – 6.76
Right mandibular canine	MD = 8	6.05	6.93	6.63	0.099	0.278	0.078	6.40 – 6.87
	BL = 8	7.14	8.27	7.57	0.159	0.449	0.202	7.19 – 7.94
Right mandibular premolar 1	MD = 8	6.26	7/45	6.79	0.133	0.377	0.142	6.48 – 7.10
	BL = 8	6.40	8.36	7.61	0.215	0.609	0.371	7.10 – 8.12
Right mandibular premolar 2	MD = 10	6.18	8.09	6.87	0.186	0.589	0.347	6.45 – 7.29
	BL = 10	6.65	8.43	7.76	0.174	0.549	0.302	7.37 – 8.15
Right mandibular molar 1	MD = 7	9.97	11.44	10.71	0.199	0.525	0.276	10.22 – 11.19
	BL = 7	9.74	10.93	10.27	0.143	0.380	0.144	9.92 – 10.62
Right mandibular molar 2	MD = 7	9.36	11.26	10.17	0.247	0.654	0.428	9.56 – 10.77
	BL = 7	9.13	10.70	9.61	0.210	0.556	0.309	9.10 – 10.13
Right mandibular molar 3	MD = 6	8.29	10.25	9.58	0.304	0.744	0.553	8.80 – 10.36
	BL = 6	8.67	9.99	9.33	0.203	0.498	0.248	8.81 – 9.86
Total N	**314**							

8. APPENDIX B

The following is an example of how a tooth's data, the right maxillary first molar from Oakington in this case, would be worked through the statistical analysis in order to be used for identifying potential biological connections between individuals.

Step 1:

Table B.1 - Determine normality of data for a particular tooth using a Shaprio-Wilk test.

Tooth	Measurement	Statistic	df	Significance	Interpretation
Right maxillary first molar	MD	0.989	33	0.976	Normally distributed
	BL	0.985	33	0.921	Normally distributed

The results of this test demonstrate that the data obtained for the right maxillary first molar from the individuals at Oakington are normally distributed. Therefore, this tooth can be included in Step 2 without consideration of alternative testing.

Step 2:

Table B.2 - Determine if cemetery sample influences the size of the tooth significantly using an ANOVA test. Post-hoc Tukey tests used if necessary.

Tooth	Measurement	Test Used	Result	Interpretation
Right maxillary first molar	MD	ANOVA	Df=3, F = 2.066, p = 0.111	Not significant
	BL	ANOVA	Df=3, F = 0.987, p = 0.403	Not significant

The results of this test demonstrate that both the MD and BL dimensions obtained for the right maxillary first molar from the individuals at Oakington are not significantly different than the other three samples. Therefore, this tooth can be included in Step 3 without consideration of alternative testing.

Step 3:

Table B.3 - Determine if biological sex influences the size of the tooth significantly using an ANOVA test.

Tooth	Measurement	Test Used	Result	Interpretation
Right maxillary first molar	MD	ANOVA	Df=1, F = 0.001, p = 0.978	Not significant
	BL	ANOVA	Df=1, F = 3.089, p = 0.088	Not significant

The results of this test demonstrate that the both the MD and BL dimensions obtained for the right maxillary first molar from the individuals at Oakington are not significantly affected by biological sex.

Therefore, this tooth can be included in Step 4 and can be used to compare both males and females in pooled group analyses in subsequent testing.

Step 4:

Table B.4 - Determining if a tooth can be used in hierarchical cluster analysis (HCA). The following criteria need to be met in order to be used in HCA:

Criterion	**Does the right maxillary first molar meet this?**
Normally distributed?	Yes
Both measurements not affected by cemetery sample membership?	Yes
Both measurements affected the same by biological sex (i.e. both metrics significantly affected, or both not significantly affected)?	Yes
Can use this tooth in HCA – however, if wanting to limit further due to number of teeth that fit the above three criteria, can further specify HCA to pole teeth.	
Is this tooth a pole tooth (i.e. first tooth in its class)?	Yes
Where the number of teeth for a particular comparison (i.e. looking at males and females of Oakington) exceeds four, focus on pole teeth over non pole teeth.	

Step 5:

Use the selected teeth for HCA and use dendrograms produced to locate individuals of interest within a cemetery. Use as many teeth as possible that adhere to the above criteria in order to ensure robust comparisons are made. Any connections that showed individuals clustered at a distance of ≤5 were classed as a high level of similarity, distances of 6-15 were classed as moderate levels of similarity and distances of 16-25 were classed as low levels of similarity.