The Use of Teeth for Estimating Biological Similarity in Early Medieval Skeletal Assemblages

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Abstract

An evaluation of familial similarity and identity in archaeology is best examined through multidisciplinary analyses of contextual and biological data. To date, the use of teeth for estimations of biological similarity within skeletal assemblages from the early Medieval period has not been conducted in South-East England. Teeth have been shown to retain morphological and metric features that are linked to genetic inheritance, as such form a particularly useful evidence type from which to obtain biological similarity data from large skeletal assemblages. As teeth are generally found to be better preserved than skeletal remains, their inclusion in such investigations is a worthwhile pursuit.

This project aimed to demonstrate the value of including dental data into discussions regarding social constructs such as identity and kinship patterns within four early Anglo-Saxon cemeteries from Cambridgeshire and Kent: Hatherdene, Oakington, Polhill and Eastry. The recording of dental metrics was done in alignment with anthropological standards. In total, across the four cemeteries, 145 individuals had a total 5988 measurements recorded from their permanent dentition. Through statistical significance testing, it was shown that biological sex and cemetery environments contribute less frequently to differences observed in tooth size compared to genetic inheritance. Furthermore, as a result of subsequent hierarchical cluster analyses, it was shown that biological similarity can be identified successfully within skeletal assemblages using tooth biodata, even in smaller or partial cemetery samples. Validation of this approach was possible with preliminary mtDNA analyses comparing results interpreted from tooth data. In available cases, patterns observed

in tooth data were mirrored in results from mtDNA analyses. This helps to demonstrate that the results from the analyses of dental biodata from the interred individuals within each cemetery could be reliably used as an additional stream of evidence to support and refine theories about social connectivity as expressed through cemetery organisation, familial identity through grave decoration and potential group membership during the early Anglo-Saxon period in South-East England. This methodological approach also highlighted its value by being non-destructive and flexible enough to be used for addressing questions on population, community and local levels. In addition, the method shows promise for use on remains from other archaeological time periods, or even in certain modern forensic contexts.

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1. Introduction

A person's identity, while they are alive, may be based upon a mixture of social constructs and biological variables, including relationships to others (both biological and non), their role or occupation, level of achieved or ascribed status, ethnicity, sex, and age. Making interpretations about a person's living identity is made more difficult in archaeological contexts as only the deceased remain, and those conducting and organising the burial of deceased individuals may have chosen to represent that person's identity according to any, or a combination, of the aforementioned factors or their own personal preferences (Williams 2007; Sayer 2020). Often, in archaeological contexts, only material culture and human bones remain, from which anthropologists and archaeologists must attempt to build interpretations surrounding the identity of the deceased. Due to this, it becomes increasingly difficult for researchers interested in questions surrounding identity or kinship, and the social constructs on which they are based, to be able to convincingly elicit information from the burial record to support such interpretations. While difficult, it is not impossible to establish theoretical discussion relating to the identity of archaeological people and groups. In order to do so successfully, studies must be conducted in such a way to allow for the building of layered concepts supported by a variety of evidentiary sources to help convince others of their ideas (Johnson and Paul 2016). Biological data obtained from the skeleton has been reported in numerous anthropological and archaeological studies with the aim of discussing identity and kinship, and has focused on the presence of nonmetric traits, demographic details, pathology and, more recently, DNA analyses (Adachi *et al.* 2003; Deguilloux *et al.* 2014; Haak *et al.* 2008; Nores *et al.* 2020; Pääbo *et al.* 2004; Vai *et al.* 2020). Teeth have the ability to retain and provide information relating to a person's biological composition that can be obtained

relatively easily by researchers for use in investigations of kinship and identity of past populations. Permanent teeth form early in infancy and childhood and do not remodel or change shape once formed (Hillson 1986; Scott and Turner II 1988). Furthermore, the chemical composition of teeth means they are better suited to surviving longer periods of time and more resilient to taphonomic agents compared to bones which are often affected by factors such as water damage, soil erosion or extreme heat (Galloway *et al.* 1997). Of more relevance to the study of identity and kinship, is that both tooth size and shape have been shown to correlate to patterns of biological inheritance from parent to offspring which can be located when compared to a wider sample (Garn *et al.* 1965; Lee and Goose 1972; Townsend and Brown 1978a; 1978b; Townsend *et al.* 2012). In the context of archaeological studies of kinship and identity, due to better preservation and links to inheritance, teeth can therefore form an integral part of the discussion surrounding a deceased person's identity. This is not to claim that teeth should form the only part of discussions related to identity, rather, the use of teeth can help to discover information regarding the shared biology of individuals interred within the same assemblage, which can then be combined with other forms of evidentiary material to help further interpretations about who each person was or who a particular group of people were in past populations.

It is not a new concept to look for dental data that could be used to link to biological relatedness, and much work has been done on modern populations to help quantify its value, with applications reaching to archaeology. Early work from the 1970s through 1990s focused on the use of teeth in anthropology to highlight evolutionary trends in populations (Alvesalo and Tigerstedt 1974) and as an investigatory tool for studies of skeletal identity and anthropological kinship (Biggerstaff 1975; Townsend and Brown 1978). Biggerstaff (1975) compared the cusp sizes of molars within human twin pairs in order to see if a high degree

similarity could be established. Results demonstrated that molar cusp size alone was not a strong indicator of familial association between pairs, however he acknowledged the issues in studying only cusp size in isolation. Biggerstaff (1975, 137) asserts that other measurements taken from teeth (i.e. overall dimensions) are "composite [in] nature ... [as such] there may be some questions raised relative to the hereditary variability of traits studied in this manner". Individual cusp size contributes to overall tooth size, and therefore it is likely that correlations made between twins were missed by minor size differences when focusing specifically on cusps alone. Measurements of a whole tooth crown would, therefore, yield better correlations to biological similarity. Townsend and Brown (1978a; 1978b) investigated the inheritance of tooth crown size in a polygynous Australian Indigenous population by analysing metric data from the permanent dentition of parents and their offspring. Results indicated relatively high correlations for parent-offspring comparisons (0.64±0.35) and for full and half-sibling comparisons (0.72±0.08 and 0.63±0.30, respectively). In this instance, researchers were able to identify larger 'family units' by associating children, to mothers and fathers with similarly sized permanent tooth crowns. These early studies also suggest the importance of acknowledging that, in addition to genetic factors, environmental factors and randomisation also influence the development of teeth (Townsend *et al.* 2012). However, the authors agree that these external influences, while present, do not detract from the overall ability to study the effects of genetics on tooth development. Other researchers have commented on this environmental impact on dental phenotype and have also observed a link between genetics and dental phenotype. Boraas *et al.* (1988) measured the teeth of human twins who were raised apart in an attempt to quantify the influence of environmental factors on dental development. Their results demonstrated that, although some teeth were more highly correlated between pairs than others, tooth size was statistically similar between

the twins, despite the fact they were raised in different places. Therefore, although environment does appear to affect dental development, the genetic influence on tooth size can still be observed, adding credence to the use of dentition for studies of biological similarity.

Apart from tooth size, nonmetric traits observed on dentition have also been used to comment on potential familial relationships of archaeological populations. Alt and Vach (1995) introduced, at the time, a novel method for recording the presence or absence of dental morphological traits and their 'microsymptoms' (i.e. when a trait is present, but to a lesser degree) in order to estimate biological similarity within a population. Their method recorded traits from a list of 137 morphologic traits known to be hereditary in nature (expanded on a selected list by Turner II *et al.* (1991)). Once traits are recorded, a large data matrix is created and used to establish clusters or small groupings of similarity within the sample. If found, these smaller groups are isolated and further statistical testing will quantify the degree of similarity between individuals present. Interpretations can then be made as to the relationships of these individuals by combining further biological profile information (age, sex, etc...). This method by Alt and Vach (1995) was subsequently tested successfully on an isolated ancient triple burial in the Czech Republic where interred individuals were concluded to represent a family due to the higher than expected incidence of shared traits present on their dentition (Alt *et al.* 1997). While this method supports the concept of teeth being used for anthropological and archaeological research, it is lacking the support of metric analyses. The nonmetric traits described in Turner II (1991), Alt and Vach (1995) and Alt *et al.* (1997) are derived from specific populations which may not be representative for other groups, such as those in the early Medieval period. To this effect, relying solely on the assumption that these traits will be present in every population creates problems for data collection and

analysis if no such traits are present. Therefore, further research of dental morphology of other populations would benefit this area of study.

Validation for the effectiveness of teeth for identification of kinship has been demonstrated by the increase in usage of DNA in cases involving unknown skeletal remains (i.e. Adachi *et al.* 2003; Deguilloux *et al.* 2014). The high preservation rate of teeth can help to protect DNA within the dentin from degradation overtime, making them ideal areas of the skeleton to be sampled for genetic material. There have been various examples of DNA analysis for identification of family members or ancestry in archaeology (i.e. Adachi *et al.* 2003; Deguilloux *et al.* 2014; Haak *et al.* 2008; Pääbo *et al.* 2004). However, despite the protective nature of teeth, there is a risk that ancient samples may result only in mtDNA being recovered which relates to maternal inheritance, rather than a full parental profile (Haak *et al.* 2008). Additionally, the process of extracting DNA from teeth is destructive, time consuming and expensive and may only reveal similarity to the maternal linkages between individuals, which in some societies may not help to further differentiate individuals. Demonstrating the use of teeth in such instances, Adachi *et al.* (2003) utilised a combination of mtDNA analysis with metric and morphologic examination of the dentition of individuals from an ancient double burial in Japan in order to determine the degree of biological similarity present. The authors noted a high correlation between the sizes of teeth from each individual. DNA testing of these individuals was also conducted, and ambiguous results were discovered in regard to the mtDNA sequences of one individual, to which authors attributed the cause of DNA degeneration. After re-testing, Adachi *et al.* (2003) found that mtDNA recovered from the two individuals indicated that they were biologically related, thus the dental analysis supported the mtDNA result. The authors stressed the importance of corroborating evidence from dental analysis to support DNA testing, especially in cases where DNA results are ambiguous

or not possible. While an analysis of dental metrics cannot recreate the robusticity of DNA analyses, validation of results by mirrored findings have shown that it can offer a non-destructive, less time consuming and more cost-effective method of determining presumptive identity in skeletal populations. It is especially advantageous as an approach used to target individuals of interest who could then be selected for DNA analysis to confirm initial presumptions regarding identity and biological connectivity. Furthermore, in cases of advanced degradation of skeletal remains, dental analysis could provide an alternative method of estimating familial relationships in lieu of DNA testing.

Within the body of literature surrounding identity and kinship of archaeological populations, there does appear to be a disconnect regarding the terminology used to describe connections between people. Kinship is a loaded term that many assume relates to shared genetic links among people; under this assumption, a group of kin would consist of individuals who are direct descendants and of shared biology (Morgan 1870). However, in modern and archaeological populations there are numerous examples of relationships between people that would be acknowledged as kin-based yet are not built on the foundation of shared biological traits or inherited genetics (Pilloud and Larsen 2011; Schneider 1984). Moreover, kin groups may change over time based on social events like marriage, death, and the movement of people, resulting in new additions to kin groups or individuals choosing to leave one kin group to join another. Therefore, when discussing kin in archaeology, researchers need to be careful to avoid connotations of the term that are based solely on biological connectiveness between individuals. To combat this, when using biological data such as DNA or dental traits, researchers need to be more prescriptive about what actually is being discussed with that particular type of evidence. When individuals are found to have common traits to others that may be suggesting of a genetic bond, what really has been discovered is

a higher degree of shared biological similarity compared to others within the group. The term biological similarity can be applied to all types of biodata obtained from skeletal remains for use in discussing potential genetic connections between individuals within skeletal assemblages. Thus, biological similarly forms another stream of evidence akin to contextual artefacts, spatial data and historical documentation that can be used in combination with one another to comment on what this means for kinship and identity. Johnson and Paul (2016) have advocated for a more encompassing, holistic approach to the study of identity in past populations, where one form of evidence does not take precedent over another, rather, they are all used as building blocks to construct a stronger interpretation of who people were and who they may have been to one another. An approach such as this, while being standardised, could be adapted and applied to all archaeological populations around the world. In doing so, more refined and supported arguments can be put forward to help discuss broader social concepts such as residence patterns, marriage practices and status divisions that relate to identity in the past.

There have been publications based on historical documentation that have highlighted the likely male-centric nature of later pre-Medieval societies based on examples of law codes (i.e. Lancaster 1958a; 1958b). However, there are also those who comment on how this assumption is too rigid to reflect the more dynamic and fluid social structures across the whole period (i.e. Murray 1983). There have been interpretations made about individuals who have been buried with a wealth of grave goods, in burial structures or in liminal or deviant positions (Buckberry 2007; Gowland 2007; Sayer 2009), but fewer on the identity of individuals who were buried in less unique ways or without furnishing. Discovering the identity of a person within an archaeological assemblage appears to be more fruitful when multiple streams of evidence are consulted to help build this interpretation (Johnson and Paul

2016). However, to date within the early Medieval populations of South-East England, there has been little attempt to include biodata obtained from the dentition of skeletal remains to help develop or refine theories regarding group and personal identity. Demographic data (i.e age and biological sex) from the skeleton overall has factored into discussions, yet the dentition remain a less common source for providing information about identity within this population. This could be due in part to poor preservation at some sites, or the belief that the robusticity of results obtained through studies of gross macroscopic traits are not as fruitful as analyses of DNA for commenting on aspects such as family membership and identity. Whatever the reason, the absence of dental data incorporated into the understanding of broader social structures from the early Medieval period is something that is easily remedied, and able to provide more input into the development and review of social theories from this period.

It is important to offer a final note here on terminology, so far, the term 'early Medieval' has been used to discuss the population under study in this project. From here on, the term will be used synonymously with 'early Anglo-Saxon' to discuss the aspects of the 5th-8th centuries in England. The term 'Anglo-Saxon' herein is not to be misappropriated to discussions of race. It is acknowledged that the term has been misconstrued in parts of the world to support doctrines of white supremacy. racism and sexism, yet these discussions are devoid of archaeological fact. The term Anglo-Saxon has no biological meaning and its use in this project should not be confused for suggesting otherwise. Its use in academia, archaeology and this project is purely chronological (Lucy 2000; Sayer, 2020; Williams 2020). The term serves purpose to describe the period of time after the fall of the Roman empire up until the Normal conquest and evidenced in the burial record through a change in funerary rite and social structure.

1.1 Aims and Objectives

The current project was developed with the following notion in mind: to discover a way to elicit biological information from human remains that could be used to help refine and support theories regarding identity and kinship during the early Anglo-Saxon period in South-East England. In addition, findings from this thesis could be added to the existent literature on use of dental metrics as a form of evidence from which discussions on identity and kinship practices can be developed. A study such as this has not yet been completed on early Anglo-Saxon populations in South-East England, therefore, research on kinship or cultural practices during this time period would benefit greatly by the inclusion of such biological information, if proven successful. As such, the aims of this project were:

1. To establish the utility of teeth for identifying biological similarity within four early Anglo-Saxon skeletal assemblages.
2. To explore the potential for tooth metrics to contribute to discussions on the personal and group identity of individuals within and between the four cemetery sites under investigation.
3. To explore the potential for tooth metrics to be used to help refine discussions on residence patterns and kinship during the early Anglo-Saxon era in South-East England.

In order to achieve these aims, it was essential that the following set of objectives would need to be met:

1. Obtain a large sample of skeletons from four contemporaneous early Anglo-Saxon populations spread across Cambridgeshire and Kent. This would help to determine if

any patterns observed in the dataset were due to local or broader geographic influences.

2. Create and implement a standardised approach to the recording of dental measurements and statistical analyses of raw data to understand the significance of the data obtained. Statistical analyses should focus on demonstrating that variations in tooth size are linked to differences in inheritance compared to geographic location or biological sex as well as the selection of teeth most appropriate for determining biological similarity within an assemblage.
3. Once biological similarity was identified within the raw data, contextualise this by applying it to the cemetery record it was originally obtained from. To do this, spatial, contextual and historical data can be combined to help discuss connections between people.
4. Identity and kinship will then be discussed using inductive and deductive approaches; where interpretations will be led first by spatial and contextual information and compared back to biodata results as well as leading with biodata results to then see what the contextual and spatial data can add.
5. Validate these results by comparing to preliminary analyses that have occurred on these populations investigating mitochondrial DNA and shared haplotypes.

The selection of cemeteries that were geographically and temporally close to one another was important for this project in order to help limit the influence of these variables on tooth size and shape. Irish (2005) has shown that ancestral populations change over time as a result of genetic admixture from migration and that the environment can influence the final size and shape of individual teeth. By limiting the sample selection to cemeteries dated to the early Medieval period and locations kept within the South-East of England, it would allow for

the differences observed in tooth sizes as a result of local level biological differences and family inheritance to be better observed. In addition to contemporaneity and location, the samples selected for in this project were done on the basis of access to collections. The University of Central Lancashire (UCLan) had operated a field-based excavation project for the cemetery of Oakington from 2010 through 2014. It was a collaborative project with Oxford Archaeology East (OAE) and Manchester Metropolitan University (MMU). Over the course of the project, the Oakington cemetery was excavated and all individuals exhumed were examined, cleaned and curated. After receiving permission from the Ministry of Justice, the skeletons recovered were stored within secured facilities at UCLan for further research. Through the partnership with OAE, access was granted to a similarly sized assemblage of human remains recovered in 2017 from Cherry Hinton, Cambridgeshire. These skeletons comprised the Hatherdene collection and are currently stored at OAE offices. The Director of Studies (DoS) of this project was also able to obtain access to parts of the Polhill and Eastry collections from Kent, both dated to similar ranges as Oakington and Hatherdene, though a complete sample was not located for either of those two Kent based cemeteries. The full details and locations of these cemeteries and samples will be outlined in Chapter 4. As this project involved the use of human remains, full ethical approval was granted by the Business, Arts, Humanities and Social Sciences (BAHSS) committee at UCLan (BAHSS-242) before any data collection began. Appendix 8 contains the ethical approval documentation. The project was non-destructive by design and based on samples with Ministry of Justice licenses, so posed no ethical issue for the use of the remains within the remit of this project. A review of Health and Safety and all risk assessments were conducted and adhered to for the data collection phase of the project and all associated activities were deemed to be low risk.

It is hypothesised that, within each cemetery, differences not attributable to sex or location alone will be present within the tooth data. It will then be assumed that these differences are due to inheritance on the local familial level. It will be this remaining variation which will be used as the basis to sort the individuals within and between all four cemeteries selected into groups based on similarity of tooth size. In doing so, highlighting visually those that are more similar to one another and any that are less similar. By sorting the remains based on similarity of tooth data, it will then be possible to know how much similarity is expressed within and between the cemeteries. As tooth form has been shown to be heavily influenced on inherited genetics, it is further hypothesised that some individuals will appear similar to some people while very distinct from others. Hypotheses regarding the application of this method to interpretations of wider social structures will be that it is possible to use biological similarity to comment on populations, communities and individuals in order to support and refine theories related to social mobility, burial organisation and family identity within these assemblages.

After the introductory chapter, Chapter 2 will provide a review of kinship and associated terminology as it pertains to archaeological discoveries and the potential of human skeletal remains to be a part of interpretations in this area. This contextual framework will provide a solid foundation for understanding why terminology used in archaeological and anthropological research surrounding kinship and human remains needs to be modified in order to better reflect what information skeletal evidence is actually providing in such studies. After the discussion on kinship and biological similarity, an overview of dental development and influencing factors on tooth size and shape will be presented in Chapter 3. This chapter will help to provide detailed background related to how it is possible that teeth can be used

as a medium through which to investigate biological connections between individuals. Studies will cover modern and archaeological examples in order to demonstrate the applicability to a wide array of skeletal material. After detailing the background information from which this project is based, details regarding the selected samples and methodological procedure will be included in Chapter 4 to better understand why these cemetery sites were chosen, what data was collected and how it was analysed. This will allow for repetition of method by others in the future. The first results chapter, Chapter 5, will be focused solely on the statistical results obtained from descriptive, multivariate and cluster analyses of the raw data. It is intended this chapter will demonstrate how to take large quantities of data, identify variables that cause differences in tooth form and use this information to dictate which teeth are best suited for additional analyses for the determination of biological similarity. Once biological similarity has been identified in the sample, Chapter 6 will be focused on the application of these results to the cemeteries themselves. Connections between individuals will be presented to demonstrate the contribution tooth data can have to various questions regarding family, identity and kinship in early Anglo-Saxon England. Finally, Chapter 7 will discuss conclusions based on presumptive connections drawn from this project based on the establishment of biological similarity in early Anglo-Saxon populations and will support the utility of teeth and their contribution to more in-depth discussions on social connectivity and identity within this time period. It is not the intention of this project to answer, in depth, all related questions that are generated as a result of observations made herein, rather, one of the main benefits of this project will be demonstrating the vast array of possible areas of study in which data obtained from teeth can contribute to. As many aspects of humanity are intertwining and complex, the more areas that are made available for archaeologists to pull data from to help support interpretations, the more convincing researchers will be in their pursuits. The

development of a method from which reliable biological data can be easily obtained, analysed and applied to skeletal assemblages would benefit archaeologists and anthropologists investigating social identity in past populations, in particular within this context, the early Anglo-Saxon period.

2. Kinship and Identity of Past Populations

Kinship has been said to be one of the original cornerstones of the field of anthropology (Read 2001) and its use in the early parts of the 20th century formed the basis for the establishment of the field as its own science. In modern contexts, the term kinship is often observed in legal or medical settings where individuals may be asked to provide details of 'next-of-kin'. In such instances, this person is almost always a blood relative or someone with a strong social or affine bond (i.e. a spouse). Within the academic field of anthropology, however, there is a much more nuanced approach to its understanding in regard to past and present human populations. Within anthropology and osteoarchaeology, the way in which kinship theory is applied and kinship terminology is understood has developed greatly over the past century. Kinship has been believed to be a guide by which many aspects of social organisation and structuring are based upon. By understanding how people are related to one another, and what interactions these relationships allow for, it is been thought that anthropologists would be able to understand how societies were established and maintained over generations. In modern society, changes to family definitions, adoption practices and artificial procreation have led many researchers to reflect on how to best define kin and how these changes relate to kinship patterns and family units compared to previous generations (Peletz 1995).

While the discussion on the history, use and alterations of kinship theory have been discussed elsewhere (i.e. Johnson and Paul 2016; Lévi-Strauss 1965; Sahlins 2013; Schneider 1984), the focus of this chapter is not to detail this history in full, rather to focus on the impact and application of kinship theory on the analysis of human skeletal remains. As has been alluded to, this is not without some discussion on debates of the study. The use of kinship in anthropology and archaeology has been questioned in the past, and many of the issues

surrounding its use have to do with loose definitions of terminology. In order to best understand the application of kinship theory to the study of archaeological human remains, it is first imperative to understand its terminological uses and misuses throughout its history in the discipline. Afterwards, discussion can focus on what Sahlins (2013) outlines as the distinction between what kinship actually is and how academics can study it, and what kinship is not, but how this information is useful to completing the former task.

2.1 Kinship Theory: What is Kinship? What is Kinship Not?

Throughout its existence in social anthropological literature, kinship had been credited as being the making and unmaking of the discipline (Read 2007). Its presence in early publications of the late 1800s and early 1900s focused on understanding genetic relationships between people in various cultures and appropriating Western terminology to these relationships for sense to be made of complex marriage practices, residence patterns and mating pairs. Morgan (1870) was the first anthropologist to extensively comment on kinship by comparing the familial relationships of various groups throughout the world. According to Morgan (1870, 10), the defining factor for what constituted a family unit, and therefore kin membership, was direct genetic relationships or 'blood ties'. The ways in which parents and offspring centred on an *ego* was noted to vary in different populations, yet the acknowledgement was made that not all uses of the terminology for relatives (mother, brother, father, etc…) were consistent in the groups being studied. One of Morgan's (1870) largest discussion points was to comment on the distinction between descriptive and classificatory kin; the former being representative of the more Westernised ideal of nuclear families and the latter being applied to less developed populations who, according to Morgan,

did not form clear cut family groups. In terms of the terminology itself, descriptive kin were defined as having specific words for specific relationships (i.e. a mother's brother is an uncle) and classificatory terminology found in populations comprised of general terms that could signify a number of relationships (i.e. grandfather and grandson may be denoted by the same term). This distinction formed the basis for early researchers to assume that blood ties were the strongest determinants for group membership and identification, an assumption based on Western ideals regarding family structure (Lévi-Strauss 1965). These theories were quick to be challenged. Kroeber (1909) demonstrated that all societies display elements of both descriptive and classificatory kin, including those groups studied by Morgan. In fact, Kroeber (1909) made the assertion that if Morgan's theory were to be accepted, Western societies would be among the most classificatory in nature as they have fewer words to describe relationships compared to more 'primitive' groups. Furthermore, Kroeber (1909) reached the conclusion that relationship terminology has more to do with psychology rather than sociology, but this is a conclusion that has not been elaborated on by others within the discipline. Malinowski (1930) argued for a more functional approach to understanding kinship by focusing on each society in the present and denouncing the use of classificatory terminology, stating that it does not exist in the sense it was derived for, rather, it is the Westernisation of the use that masks the relationships that these so called terms are describing. This was further imbued by Lévi-Strauss (1965) who made the distinction between two elements of kinship study: the overarching system of people and their relationships, and the model of rules that governed these relationships in the first place. For Lévi-Strauss (1965) it was more important to first understand the rules, which likely had become engrained in societies due to repetition in earlier ancestral groups, before understanding the actual relationships and systems that were created from them.

Due to the early emphasis placed on blood relationships, an interchangeable nature of the terms biological relationships and kinship developed, and many anthropologists continued to structure research questions centred on the understanding of these bonds and how they manifested in various societies. From this foundation, genealogical mapping of relationships and use of kinship terminology became one of the most popular pursuits for anthropologists interested in familial relationships of various cultures. The end goal of establishing links between blood relatives often had to do with interpretations regarding marriage (Lévi-Strauss 1965), inheritance and trade practices, as well as post-marital residence patterns. During the early part of the 20th century, examples of kinship studies ranged from familial terminology in Inuit populations (Guemple 1965), North American Indigenous groups (i.e. Eggan 1937) and various other 'primitive groups'. There appeared limited mention of any types of relationships that could not be defined in biological terms, which is reflective of the overarching framework for research during this time and the importance placed on such genealogical pursuits. However, Lévi-Strauss (1965) was one of the first to publish against this concept by introducing the idea of house societies (Carsten and Hugh-Jones 1995; Lévi-Strauss 1987) wherein kin membership was, in part, based on spatial and residential location within societies as opposed to strictly biological ties. This was argued to be present in cognatic societies where both maternal and paternal kin lived together. Overall, despite a small underlying commentary that not all kinship patterns are based on biological relationships, it was a predominant factor when undertaking studies of this type.

As the century moved on, so did the theoretical framework of kinship research in anthropology. It no longer became acceptable to reduce kinship to basic biological terms and relationships as many aspects of the social structure in various societies were not based on biology alone. This idealistic and simple view was heavily criticised during the 1960s through

1980s, notably by Schneider (1984), for overlooking the dynamic nature of kinship. For him, the concept was more like a continuous system that is ever-changing and adapting rather than a passive process that remains static through time. Also criticised was the concept that these social structures were based on what was perceived to be biological family relationships as blood relations were seen as stronger than other forms of relationships (Schneider 1984). Examples of phenomena that contradict the view that blood ties form the strongest social bonds include adoption practices, wherein children who are not biologically related to parents take on the same terminology and status as those who share genetics (Read 2007) and practical kin, those who form an integral part of a social group yet are not biologically related to any or all members such as close friends (Pilloud and Larsen 2011). Mention of these trends, although not a firm establishment of the idea, was made in earlier work by Lancaster (1958a) who commented that, for later period Anglo-Saxons, it was difficult at times to identify consanguines for any focal kin member as the living members of such a group may not be kin in the most common sociological sense of the word. This can be taken to indicate that not everyone that comprises a kin group was actually a biological relative and that there may have been other forms of kin present within such groups during the later Anglo-Saxon period. Lancaster (1958a) provided a list of example of kin that may fall into these less considered kin groups in later Anglo-Saxon societies: semi kin, half relatives resulting from remarriages, quasi kin, fostering or adoption of children, and ritual kin, those who are ascribed a status otherwise reserved for biological kin (i.e. a godmother or godfather). Schneider (1965) was also one to criticise the use of American or Western terminology to describe the relationships between people observed in other societies; the use of such terminology may have impaired or masked the true social nature of such relationships.

The discordance between biological kinship and the range of behaviours and structures that social kinship can refer to creates a problem for those interested in examining archaeological or modern skeletal populations in order to learn about these concepts. The term biological kinship appears to be an oxymoron; previous research has demonstrated that elements of social kinship surpass direct biological relationships in order to incorporate cultural organisational structures. The difficulty for understanding the fluid concept of kinship in living populations highlights this problem for researchers of past populations. This means that the concepts of biological and social kinship, used to describe aspects of biology, genetic relatedness and culture, are not specific enough to form a basis for current research projects (Schneider 1984), particularly those involving skeletal remains. Despite the notion that social and biological kinship remain entwined, attempts have been made to create distinctions between the two in order to draw attention to specific areas of research. Nolin (2011, 159) explained social kinship as culturally defined according to systems of descent and biological kinship as probabilistic genetic relatedness observed through common descent. As such kinship studies which have focused on ideas of biological kinship have investigated the genetic relatedness between individuals within groups of people by having attention paid to respective sexual mating preferences, marriage partner selection, and the raising of children resultant from these relationships (DeBruine *et al.* 2008). Whereas studies of social kinship have pertained to the much wider notions of rules which govern trade and marriage networks, lineages, and the movement of people between kinship groups. Here, once again, it is difficult to separate the two areas completely as it is the human (biological) aspect which establishes the social.

Sahlins (2013) argued that kinship represents a mutuality of being, wherein people are connected in ways that are intrinsic of and necessary for everyday life in a community. These

relationships could be based on a multitude of factors including social relationships, biology and birth, or a combination of these (Sahlins 2013, 2). Blood relationships, which had been so highly regarded by early anthropologists as the strongest bonds between people, have been demonstrated in many populations and societies to have little to no input into this mutuality of being. Terminology is what demonstrates this point clearly for Sahlins (2013) as he describes multiple societies that use specific relationship terms (i.e. grandmother, daughter, etc.…) in ways that contradict the logic stated by Morgan (1870) and other earlier anthropologists. The point is also made that there are some relationships that are social in structure that afford the same degree of importance as some blood relations, most notably observed in spousal relationships. These bonds are not based on biology, as otherwise would violate marriage taboos of many societies, but are social in creation. It is not until the act of procreation and an offspring generation is established that biology ties these two people together. Franklin and McKinnon (2000) make note of recomposed families, which highlights further instances of blood relations not always being the basis for strong familial relationships. Recomposed families refer to those which are comprised of children and parents from remarriages. Stepchildren, stepsiblings, stepparents and third set grandparents are all members of such groups and all ascribed the same status in communities as their full blood counterparts. As Schneider (1965) made note of, the terminology that Western societies use to describe specific relationships may be more fluid or not at all applicable to every population in the world, therefore trying to make fit relationships in these 'sensible' ways may lead to nonsensical interpretations. There are those that disagree with Sahlins' (2013) distinction between what kinship is and is not by arguing that even social relationships are modelled on those derived biologically (Shapiro 2014). Shapiro (2014) re-presented data from the groups studied by Sahlins in order to make the point that the derivation from use

and acceptance of primary kin and primary kin relationships is baseless. He argued that those who believe the use of primary kin is an assumption created by the West were overlooking ethnographic evidence to suggest that these relationships do exist in ethnography and are used as models for social relationships within groups. Regardless of position in the debate, what is agreed upon is that there is not a straightforward distinction between social kinship and biological kinship, yet there are aspects of each that contribute differently to the wider organisation of a given society.

Recently, there has been a theoretical revitalisation in the appearance of kinship research in osteoarchaeological and anthropological literature (Johnson and Paul 2016). In modern applications, an updated general definition of kinship can refer to a classification system that is able to generate relational worlds that are lived by present or past societies (Franklin and McKinnon 2000, 277). Trends in this area of research appear to be focused on broadening research questions in order to incorporate multi-level or multiscalar approaches to understanding kinship (Johnson and Paul 2016). This shift has been argued for in various forms for the better part of the twenty-first century as a way to study kinship (and other broad social systems) from a bottom-up approach without *a priori* notions as to what constitutes kin membership and implications for group or singular identities. Knudson and Stojanowski (2008) discussed the normative methodologies anthropologists currently use to study biodistance and biological similarity in skeletal assemblages and classed them into two separate approaches: population history, pertaining to ancestor/decedent relationships and evolutionary history and; population structure, where patterns of genetic variations between and within populations are observed to comment on social structure. In the former, comments can be made about how populations change over time and to identify group membership based on lineages, while the latter allows interpretations to be made cross-

sectionally to investigate aspects of social structure that may have been present at a given time in a population's past. While both are useful to assist researchers with understanding aspects of kinship and kinship patterning over time, there are some limitations with stipulating research goals into two broad approaches, neither really addresses the issue as to what is being studied and how it directly or indirectly applies to kinship.

A key aspect, therefore, of this more recent shift towards a multiscalar approach to understanding kinship in past societies should be the stringent consideration of what data can actually be collected from archaeological populations and how it can then form part of the discussion on kinship. Sahlins (2013) approached this from a theoretical vantage yet did not explicitly stipulate the ways in which methodologies should be altered to represent this divide. In fact, many researchers who attempt kinship analyses from skeletal remains continue to use the term kinship to mean a direct biological relationship (i.e. Adachi *et al.* 2003). The problem with this is, as has been demonstrated, kinship is a loaded term; its meaning differs considerably and can relate to a wide variety of both biological and social aspects. There needs to be a clarification of the definition of 'kinship' used for skeletal analysis-based research and further explanation on how this term can being used by researchers in such instances so that results and discussions are not confused with interpretations of wider social aspects. It is for this reason that the term *biological similarity* will be used herein, and encouraged in future publications, in order to denote research into the direct investigation of biological relationships of individuals within and between contemporaneous skeletal populations. Biological similarity relates directly to the information that can be successfully obtained from skeletal remains. Its use is solely for the purpose of understanding biological relationships and, at this starting level, for no mention of wider social implications from this data. This term implies neutrality towards kinship, but that

does not mean that its value in kinship studies is of no worth. Biological similarity can be used in conjunction with other historical, contextual and materialistic evidence as building blocks to construct the wider cultural and biological kinship patterns that may appear within any given population at any given time. It differs from the terms biodistance and biological affinity as the former two often are used for interpretations of broader temporal and spatial connections between populations, rather than smaller scale connections between individuals within contemporaneous and more local communities Table 1 provides an overview of common anthropological terminology currently used to discuss connections between people, both social and biological. To explain it another way, identifying individuals who share biological similarity signifies only that, a likely genetic relationship. In order to move further and define these two as kin, it is imperative to discover further bonds by looking at what other information links them together within the framework of their society.

Table 1 - Anthropological terminology for connections between people.

Term	**Interpretation + Usage in Anthropology**
Biological affinity	Commonly used in anthropological and archaeological to comment on ancestral connections between populations but can also be used to comment on biological and social relationships between people within a community.
Biodistance	A measure of relatedness or divergence among groups separated by time and/or geography based on morphological variation (Pietrusewsky 2014).
Biological similarity	To be used on a smaller scale, within and between contemporaneous and geographically similar populations to comment on suspected biological and social relationships between individuals.

2.2 Biological Similarity and Osteoarchaeology

A review of the literature surrounding kinship and skeletal analyses by Johnson and Paul (2016) surmised that two of the main goals of studies of this kind are to focus on identification of kin members (biologically related kin) and investigations of post-marital residence patterns. Residency patterns have been shown to contribute significantly to the proliferation of inherited genetic traits within a given population (Oota *et al.* 2001) as residence patterns often reflect marriage practices and the development of kinship groups. For example, studies of genetic differences between Y-STRs (representative of male lineages) and mtDNA (representative of female lineages) within patrilocal and matrilocal groups from related geographic regions (Kumar *et al.* 2006; Oota *et al.* 2001; Pérez-Lezaun *et al.* 1999) have shown that genetic differences of biological similarity and diversity can be identified. Kumar *et al.* (2006) found a significant difference in the diversity examined with the mtDNA and Y-STRs in one of the patrilocal tribes studied, where males showed less diversity within the patrilocal groups compared to matrilocal groups. However, the other tribes and castes compared in the study followed the similar pattern, but their results were not statistically significant between the two types of residence patterns. Conversely, Oota at al. (2001) found significant differences in the diversity expressed in mtDNA and Y-STR groups dependent on residence patterns in their Thai sample; mtDNA within matrilocal groups was less diverse compared to patrilocal groups and Y-STRs in patrilocal groups were less diverse than in matrilocal groups. Kumar *et al.* (2006) reflected on their sample, despite the non-significance, and on the fact that patterns present have been replicated in other populations and concluded that the correlation in residence pattern and genetic diversity may not be applicable to populations in India. While novel and informative, there are some considerations to make if this approach

were to be applied to archaeological populations. The time and financial cost of DNA sampling can often be great when undertaking archaeological investigations, especially in larger skeletal assemblages. DNA may not always be recoverable for use in archaeological studies due to taphonomic degradation or possible because its sampling method is destructive. Furthermore, only mitochondrial DNA may be obtained in some instances which relates to maternal inheritance and linkage, which limits complete discussion of residence and marriage patterns within a given society. Additionally, the return on useable DNA from samples may be limited as samples of useable DNA may end up being smaller than the number of individuals sampled for use.

Isotopic analyses of skeletal remains, particularly using strontium, have been used to comment on dietary differences between groups as a way to discuss differences apparent amongst residency patterns (Bentley *et al.* 2002; 2008; Eerkens *et al.* 2014; Ericson 1985). A common approach is to compare the dietary isotopes of individuals pre and post-marriage to see if there is a difference in diet that reflects each location (i.e. Cox and Sealy 1997; Ericson 1985; Sealy *et al.* 1995) which is done by comparing tooth isotope ratio values (reflective of birth location) to bone ratio values (reflective of life closer to death, likely after marriage). Another approach for utilising isotopes is to observe how identity and kin groups have changed over time within populations by identifying the origins of individuals buried together (Gregoricka 2013; Price *et al.* 1994). Isotopic ratios of strontium are determined by geographic locations, which results in a potential limiting factor in regard to the usefulness of this method for groups sharing close proximity or spread across smaller geographic areas as differences in isotope ratios from skeletal tissue may not appear different when error is incorporated. However, Bentley *et al.* (2002) and Eerkens *et al.* (2014) were able to demonstrate the usefulness of strontium isotope variation to identify patrilineal and matrilineal based

societies, respectively. Bentley *et al.* (2002) was able to identify a pattern in strontium isotope ratios where non-local female individuals appeared more frequently in three early Neolithic cemetery sites in Europe, suggesting a local, male based residence pattern. Eerkens *et al.* (2014) sampled skeletal remains from the San Francisco Bay area dated to the Middle Period and found that male strontium ratios were more commonly reflective of non-local values compared to females, indicating a matrilocal-based residence. An issue with isotopic values is the need for larger sample comparisons for robust conclusions to be made. Ericson (1985), although only intended as a pilot study, sampled three individuals from two Californian sites which made it difficult to demonstrate the value of this method on discussing residence patterns. In contrast, Gregoricka (2013) obtained a sample involving 100 individuals which allowed for a more robust understanding of patterns that can be detected on group and population level and allowed for conclusions to be made regarding non-local members adopting local burial practices to be linked to post-marriage adaptations. The success of these methods does, however, create the potential for destructive sampling on wider scales within archaeological populations if this approach is to be employed routinely, which may limit the remains which are available for study.

Non-destructive, macroscopic observations from skeletal remains have also been employed for the identification of residence patterns within past populations (i.e. Konigsberg 1988; Lane and Sublett 1972; Schillaci and Stojanowski 2003; Stojanowski and Schillaci 2006; Spence 1974). Lane and Sublett (1972) were amongst the earliest researchers to publish on the ability for skeletal data to be used alongside cultural information to comment on residence and social mobility. Although they were able to identify patterns in skeletal trait variation between males and females, the authors made the point that any expression of similarity within males and within females is not enough to equate to patrilocal or matrilocal residence patterns

(Lane and Sublett 1972, 187). The justification for this, at the time of publication, was that there was no "quantitative method [to] decide between genetically similar situations" (Lane and Sublett 1972, 187), such as father and son versus mother's brother-sister's son. Despite this, others have helped to validate this approach by attempting to review in detail the theoretical underpinnings, standardising a procedure (Konigsberg 1988) and to showcase its use on other archaeological groups (Schillaci and Stojanowski 2003). Similar results have been found using dental traits (both metric and nonmetric). Prevedorou and Stojanowski (2017) analysed the teeth of individuals from an early Bronze Age cemetery in Greece. Here, tomb burials were common and it was hypothesised that the inhabitants of a tomb were considered families (Prevedorou and Stojanowski 2017). The dental analyses revealed more variation in male tooth phenotype than females, suggestive of a matrilocal based residency pattern (Prevedorou and Stojanowski 2017). Further still, the technological advancements in DNA since the 1980s, have helped to provide robust methodological approaches to differentiating relatives and, as such, provide genetic support for patterns of trait similarity observed on the macro-skeletal level. As further justification for use of this approach, Schillaci and Stojanowski (2003) and Stojanowski and Schillaci (2006) built upon the testable hypotheses presented by Lane and Sublett (1972) to demonstrate how craniofacial dimensions can be used, not just to develop new theories but to refine previous interpretations about social mobility and residence in past populations. In their study, Schillaci and Stojanowski (2003) were able to show the craniofacial features were more variable within the females at Pueblo Bonito, which contradicted the contextual information suggesting a matrilocal residence pattern. However, instead of refuting the concept of matrilocality, the authors suggested that the overarching premise could be true, but the day to day practice of it varied in communities. Thus,

highlighting the benefit of a bioarchaeological approach incorporating biological traits into interpretations alongside contextual or historical documentation (Johnson and Paul 2016).

It is important to note that these types of approaches are dependent on the presence of nonmetric traits evident on the remains of a given sample as these traits are linked to population genetics (Carson 2006; Kaul *et al.* 1979). Stojanowski and Hubbard (2017) investigated the teeth of Kenyan populations to comment on kinship structures evidence from both metric and nonmetric dental traits. They concluded that both performed well in regards to identifying those who likely shared biological connections, but metrics performed slightly better. It was noted that nonmetric traits could also appear randomly dispersed throughout populations and may not be strong enough to indicate a biological connection based on their appearance alone (Stojanowski and Hubbard 2017). Therefore, the rate at which they appear, if at all, may vary considerably between populations making direct comparisons between groups potentially difficult. To combat this, these types of analyses can include the collection of both metric and nonmetric data as well as making qualitative and quantitative comparisons within and between populations in an attempt to obtain some information relating to identity (i.e. Alt and Vach 1995; Howell and Kintigh 1996; Lane and Sublett 1972). It is common for multiple metric and nonmetric traits to appear in populations, and the basis for biological similarity is that those who have more traits in common are determined to be more biologically similar (Berry and Berry 1967; Townsend *et al.* 2012). Examples of such metric and nonmetric traits used successfully to highlight biological similarity between people include: the presence of a persisting metopic suture which appears to be more hereditary in certain populations (Berry and Berry 1967), the presence and location of wormian bones (Berry and Berry 1967), number of lumbar or sacral vertebrae, and dimensions and morphological traits of teeth (Alt and Vach 1995; Howell and Kintigh 1996).

Metric and nonmetric traits of human dentition will be explored in much greater detail in Chapter 3. Additionally, anthropologists can investigate the biological profiles of skeletal remains (age, sex, ancestry, and stature) in order to make initial inferences about the relationships of contemporaneously interred individuals. These initial presumptions of relationships can be corroborated by the analysis of metric and nonmetric traits as well as DNA testing. The development of an alternative non-destructive method for identifying kin groups and residence patterns in past populations based on genetically linked traits that can be readily and easily applied across large skeletal assemblages would be advantageous. In the remit of this project, the analysis and interpretation of biological similarity from human dentition meets these criteria.

Apart from the human remains themselves, there are other ways archaeologists have used burials to discuss relationships within past communities. Multiple burials, especially those with both adult and juvenile skeletal remains, are of great interest to those investigating kinship from skeletal assemblages. Alt and Vach (1998) described three main burial contexts in relation to kin analyses: small graves, structurally spatial graves and unstructured graves. Small graves are defined as being multiple burials within a clearly defined mortuary context and area. Structurally spatial graves are interments that are in a distinct area of the cemeteries and contain individuals that share similar cultural and biological attributes. Unstructured graves, in comparison, are those that display no *a priori* references to spatial structure or cultural and biological aspects within a cemetery context (Alt and Vach 1998; Alt *et al.* 1998). There is often the assumption that those buried together will share either the same family group or are related in some way (i.e. Adachi *et al.* 2003). These hypotheses are often confirmed or refuted via analysis of metric and nonmetric traits from the remains as well as DNA or mtDNA testing, if possible. It is from this point then, that researchers can begin

to build an idea of the type of kinship such societies would practice. An example of the beginnings to this process can be highlighted by a case study by Deguilloux *et al.* (2014) involving sarcophagi burials from a necropolis in Southwest France. Results of metric skeletal analysis and mtDNA testing demonstrated that not all of the individuals interred together were of the same maternal line. Interestingly an infant skeleton discovered interred with two adult female skeletons was one of those that did not share the same mtDNA which would go against assumptions regarding parent and offspring relationships in a purely biological sense. Alt *et al.* (1997) used the occurrence of genetically linked dental morphologic traits to infer the relationship status of an ancient triple burial in the Czech Republic. They stated that the aim of the kinship analysis they were attempting with this sample was "to infer biological relationships from the increased occurrence of … genetically determined traits" (Alt *et al.* 1997, 126). Thus, in this example the authors have taken the term kinship to mean an establishment of direct biological relationships, a focus which excludes a multitude of interactions that can occur at a non-biological level. Results indicated that the individuals within the burial displayed a level of trait similarity that was higher than what would have been expected if the traits were to appear within a population at random. Based on this discovery, and in accordance with biological profile information, the authors concluded that the three individuals belonged to one biological family group. Similarly, Adachi *et al.* (2003) also investigated dental metrics and occurrence of nonmetric dental traits as well as mtDNA testing to discover the degree of relatedness of two juvenile individuals found in a 2000-year-old double burial excavated in Japan. Results indicated similar mtDNA between the two individuals, but also a strong correlation between the metric and nonmetric dental traits (Adachi *et al.* 2003, 357). Based on these results, and the fact that the individuals appeared

to be contemporaneous, it was concluded that these two individuals were biologically related siblings.

At this stage it is important to recognise that what Deguilloux *et al.* (2014), Alt *et al.* (1997) and Adachi *et al.* (2003) discovered was not an element of *kinship*, but rather an estimation of relatedness within their respective studies; they identified biological similarity. Deguilloux *et al.* (2014, 404) used their results to further discussion on the funerary practices of the local population during the observed time period, but they also made the point in their conclusion that the presence of those in the necropolis found with different DNA signatures could be explained by the occurrence of "a kinship [bond] … undetectable by mtDNA". Acknowledgement of this limitation demonstrates the need to consider that biological similarity alone is not enough to infer information about overarching kinship patterns for human populations. To investigate these differences further, information pertaining to the marriage patterns and social organisation of a given population can be inferred biological similarity data in conjunction with other contextual or historical pieces of evidence. Alt *et al.* (1997) and Adachi *et al.* (2003) do not make such an acknowledgement. Their conclusions state that kinship in their studies was inferred by the fact the individuals examined shared similar morphologic and genetic traits. They have implied that their discovery of strong biological similarity is the same as these individuals being kin in a general sense. In order to make this inference stronger, it would have been advisable for these authors to have supported their application of 'kin' status of these biologically similar individuals with other contextual or historical pieces of evidence to substantiate their claims further.

The location of graves within a cemetery has also been used as an identifier of kin relations alongside evidence suggesting biological similarity. Howell and Kintigh (1996) combined age

and sex related information obtained from skeletal analyses of a sample from the North American Zuni settlement of Hawikku with dental morphology, which the authors argued could be used as a marker of biological relatedness in the population. Spatial analyses of the site revealed that distinct areas had been established and were kept purposefully separate from one another. Within each of these distinct areas, it appeared that members of the population who shared similar dental morphology (i.e. those who were more likely to be biologically related) were kept together and the conclusion drawn that cemetery organisation for the Zuni was based on biological family membership. This type of study has demonstrated the potential uses of skeletal analyses in investigations of archaeological kinship. The assumption made by the authors was that a marker of biological relatedness (tooth morphology), in combination with the strategic separation of cemetery groups and spatial patterning of graves was enough to assign kinship status to those individuals sharing similar dental traits. This example highlights the importance of using more than just biological similarity to infer kinship as Deguilloux *et al.* (2014) alluded to. However, as kinship takes into account much more than biological relatedness, there may appear in skeletal populations some outlying skeletal information within distinct spatial groups that do not align with the 'norm' and as a result some aspects of these kinship patterns could be overlooked or misinterpreted in such instances. Johnson and Paul (2016, 98-99) highlight this discrepancy in their recent publication in order to argue there is a need to develop alternative interpretive models when individuals buried in close proximity are not close genetic relatives. A way to perhaps link skeletal outliers within overarching kinship patterns could be the use of grave goods as a potential indicator of kinship in such instances where certain individuals may be overlooked due to specific local customs. Instances such as this help to reinforce the multiscalar approach to understanding kinship, as if only biological data had been investigated

here, it could have been argued that kin membership had no impact on cemetery organisation, yet by supplementing this conclusion with further information from material culture, it could have been better supported or refuted.

Although more difficult than investigations with living populations, it appears as though the interpretations of kinship patterns from archaeological skeletal populations can be made, yet the importance of a multifactorial approach cannot be ignored in this pursuit. It is important to recall what Franklin and McKinnon (2000, 276) asked readers to keep note of: what kinship signifies and what signifies kinship. The more information that can be accessed in addition to skeletal analyses in order to assist with interpretations of kinship, the stronger the support will be for the patterns discovered. Pilloud and Larsen (2011) can be cited as an example of combining multiple sources of information to comment on the kinship pattern for the archaeological populations of Catalhoyuk. Here spatial distribution of house burials, potential neighbourhood demarcations and skeletal traits were investigated, first separately, and then combined, in order to see if burial patterns at this site were based on family groups that were genetically linked or another structural component. It was discovered that skeletal remains found within house burials did not all display strong biological similarity, indicating that group membership within a house was not solely dependent on genetics (Pilloud and Larsen 2011, 523-524). The argument for the inclusion of practical kin, those who contributed to the running of the house but were not biologically related, were just as important as biological kin echoes earlier discussion by Lévi-Strauss house societies (Lévi-Strauss 1965; 1987) and Lancaster (1958a) on the inclusion of alternate forms of kin into a complete understanding of patterns for a given population. Essential to include in any interpretation of burial treatments or cemetery organisation is awareness that it is the living members of groups and societies who are choosing how to bury the deceased, and the way they choose to do so can be

influenced by social memory of the dead and how they want to preserve said memory (Johnson and Paul 2016; Sayer 2020). As such, many aspects of social influence can contribute to the location, contents and skeletal identity of any given grave which is why current researchers need to move towards developing conceptual models for understanding social relatedness in addition to biological relatedness within the archaeological record. Furthermore, it is important that studies investigating social and biological identity consider the dynamic nature of such aspects; these relationships change over time in response to various stimuli, therefore it is imperative that both are included in interpretation as their importance in burial identity may fluctuate (Knudson and Stojanowski 2008).

2.3 Applications to Early Anglo-Saxon Kinship

When the Roman period came to an end in Britain (AD 410), changes occurred to the political, religious and hierarchical aspects of society. How these changes were reflected in the archaeology and burial record has been of great interest to early Medieval researchers. The Anglo-Saxon culture was prominent in England between AD 410-1066, with cemeteries dated to this period appearing across the country, but mainly focused along the Eastern coast with the densest concentrations of cemeteries appearing more in the South (Lucy 2000, 2). Unlike their Roman predecessors who established cemeteries along roads close to towns, early Anglo-Saxon cemeteries appeared in more rural areas, away from pre-established Roman towns. Furthermore, compared to those dated to the Roman period, early Anglo-Saxon graves displayed a range in burial and funerary expression. Grave goods appeared more frequently in burials, cremation became more widespread and burial structures could also become focal

points within a cemetery (Lucy 2000; Sayer 2020). It is important to note here that the Anglo-Saxon period can be divided into early (approximately AD 410-660), middle (approximately AD 660-899) and late (approximately AD 899-1066) phases, and cemeteries (or parts of cemeteries) dated to these phases differed in interment style and funerary rites. Dating of these phases, and the graves associated with each, has been made through a combination of contextual and scientific analyses; seriation in grave good typologies and radio carbon dating are two such methods (Lucy 2000, 17-25). The appearance of grave goods and burial structures varied and over time and across the whole period, however it is the early period which is most famous for its grave goods. Anglo-Saxon culture was not static, and neither were the ways in which communities buried their dead (Lucy and Reynolds 2002; Sayer and Williams 2009; Sayer 2020). For this reason, research from this period has focused on areas such as kinship (i.e. Sayer 2020), identity (i.e. gender, age, status, etc…) (i.e. Gowland 2007, Lucy 2000), social memory (i.e. Williams 1998) and cemetery organisation (i.e. Sayer 2010) to see how these aspects are expressed across this era. Due to the lack of settlement-based data, evidence to structure these discussions comes predominantly from the study of mortuary contexts (Stoodley 1999, 5). As this project utilises the teeth of individuals from the early Anglo-Saxon phase, see Chapter 4 for cemetery overviews, the focus of this subsection will be an exploration of key research themes from this particular phase of the period.

Early Anglo-Saxon cemeteries are, perhaps, best known for their grave goods, with weapons, brooches and buckles being commonly represented (Lucy 2000). Early studies tended to focus on the objects themselves, and their chronology, before more holistic archaeological approaches to comment on social aspects of communities became more popular. Recently, the themes of gender, ethnicity, mobility, age and other aspects of identity have been

explored in detail (i.e. Lucy 2011; Stoodley 1999). For instance, earlier work on gender in early Anglo-Saxon communities tended to rely on what Lucy (2011, 689-691) referred to as the 'common sense' approach, where there tended to be a focus on associating grave goods with either males or females. If present, weapons in a grave were more often associated with male individuals while items such as brooches and beads were more often linked with female individuals. Criticism of this simplistic view between distinctive male and female objects has led to interesting debates on the topic through the identification of 'exceptions' to this supposed dichotomy of objects (i.e. Harrington 2007; Lucy 1997; Stoodley 1999). It is widely accepted and acknowledged that the concept of gender, how it is expressed in death and the decisions made by living members of a community to represent a person's identity with funerary rites are variable across the early Anglo-Saxon community (Stoodley 1999; Sayer 2020). All of which influence the selection of objects for interment with deceased individuals. Despite this acknowledgement, there is a strong evidence base to suggest that there are links between certain objects and gender in the early Anglo-Saxon period. For example, Härke (1990, 36-37) noted during his review on 'warrior graves', that almost all of the individuals interred with weapons (i.e. spears, blades, shields, etc…) were determined to be male based on skeletal indicators. To quantify these differences observed in typical male and female grave objects, Stoodley (1999) analysed the grave good inclusions of 1636 burials from 46 early Anglo-Saxon cemeteries across England, inclusive of both inhumations and cremations. Multivariate statistical analyses demonstrated that there were strong correlations between females and items such as dress fasteners and jewellery, whereas males showed strong correlations to weapons and general tools (Stoodley 1999, 48). As such, despite the widely acknowledged acceptance that exceptions to these norms exist (Lucy 2011), there is also evidence to suggest that decisions made to include certain objects in a grave were linked to

gender, but the meaning for these inclusions does not necessarily equate solely to biological differences. Sayer (2020, 161) discusses the concept of gender, objects and interpretations with the examples of Graves 144 and 164 at West Heslerton. These two graves contained female individuals buried with spears instead of brooches, which may have been more common. For Sayer (2020, 161), this did not indicate that these females were seen as more 'masculine' as a gendered object may imply, rather it is the social meaning behind the inclusion of a spear which could be more flexible and could also relate to females. In these cases, the spear itself may not have been used to designate sex or gender, but potentially to ascribe a more nuanced social meaning to these females, a multifaceted meaning or one which may have been observed in males more frequently. These selected examples show that biological sex alone is not the only determinant for why an object would appear in an individual's grave. Others have also drawn similar conclusions (i.e. Huggett 1996), therefore while patterns can be associated with gender, it would be too simplistic to conclude that it is the main driver behind the choice of interred objects in all communities. To this point, Stoodley's (1999) findings showed that, while strong correlations to gender could be found in the dataset regarding weapons and jewellery, not every male was buried with a weapon or tool and not every female was buried with jewellery.

Age has also been shown to influence the presence of certain objects in a grave (Lucy 2011, Stoodley 1999). Infants and children tended to be buried with fewer grave objects compared to older adolescents and adults. Furthermore, when objects did appear in the graves of children and infants, there tended to be differences as to the frequency of object types in children compared to adults. While what constitutes someone being a child in Anglo-Saxon society is not necessarily linked to skeletal age estimation (Crawford 1999, 26), the age

classifications of work by Stoodley (1999, 105) demonstrate general patterns found in early Anglo-Saxon burials of those aged under and over 12-15 years old based on skeletal development. Gowland (2007, 59) presented similar findings of age-related changes between seven different Roman and early Anglo-Saxon sites. Similarly, Crawford (1999, 28) analysed a sample of Anglo-Saxon inhumations which showed that individuals under the age of 15 were less likely to be found in furnished burials than those over this age. Crawford (1999, 30) also found that the younger the individual, the more variety existed in regard to what was chosen to include in their burials. For example, in furnished infant burials the most common find was a single object in the burial and the choice of what that object was varied (Crawford 1999, 30), though was likely to be gender neutral (Gowland 2007, 59). Along similar lines, Stoodley (1999, 110-113) showed that adults aged 20-30 years old were those most likely to be found with objects, for both males and females, signifying the importance of this age category to identity during the early Anglo-Saxon period. Therefore, evidence suggests that there are patterns regarding the ages of interred individuals and associated artefacts which may also help to explain the decisions made by communities regarding grave furnishings and the appearance of objects in a grave.

Ethnicity and the movement of people from continental Europe into Britain have further contributed to debates regarding identity and material culture from the early Anglo-Saxon period. Before the advent of newer biological technologies involving DNA and isotopes, there were two main areas of thought surrounding the migration of people from Europe to England around the fall of the Roman empire. The first was based on the idea of invasion or mass migration (Higham 1992), where it was postulated that warring groups of Germanic individuals came over to England and in effect replaced the indigenous population of Britons

and their associated material culture. The second idea discusses the concept of smaller groups of immigrants to England, perhaps first those of more elite levels, where material culture and the integration of Britons and immigrants happened more gradually over the period (Higham 1992). Either way, the shift in burial style and grave furnishing apparent during this period is what archaeologists use to distinguish an Anglo-Saxon from pre-cursor groups. There have been recent attempts to understand the scope of migration using biodata from skeletal remains. Weale et al. (2002) and Härke (2011) explored these ideas by incorporating Y-chromosome DNA evidence into their discussion on ethnogenesis in the early Medieval period. Both studies argued that mass migration could have happened, albeit over a much longer time period than hypothesised by pure invasion theory, based on the prevalence of Y-chromosome DNA that was linked to European or British ancestry. For Härke (2011), it appeared as though immigrants and Britons would have been living alongside one another, and for a time, would not have integrated largely, but as the period moved towards the 7th and 8th centuries, this acculturation process intensified.

However, it is important to keep in mind what Lucy (2000, 174-177) discussed in regard to how those living during the transition between the Roman and Anglo-Saxon periods likely did not think of themselves in terms of being an 'Anglo-Saxon', rather this name has been ascribed to this group of people as a means for separating time periods and cultural transitions. Therefore, attempts to utilise material culture and biological data from this time to identify individuals of a potential ethnicity are based on perceptions of past communities that they themselves would not have been aware of (Gowland 2007, 56; Lucy 2000, 175-177). Caution, therefore, must be used when attempting to use objects or biodata to discuss ethnicity or to infer migration. For example, Scull (2011) provided analysis on grave goods and

Anglo-Saxon burials in relation to identity from three cemeteries located in Ipswich, London and Southampton, chosen based on their proximity to water ways and associated trade with the rest of the United Kingdom and continental Europe. For him, the presence of inhumations furnished with continental stylised objects signified the appearance of a non-local individual in English cemeteries. It was, however, acknowledged that these inhumations could contain local individuals who had traded or travelled for these foreign objects in their life and came to be buried with them in death (Hills 1993; Scull 2011). In these cases, additional evidence such as biological data from the human remains would prove useful to refine interpretations.

Lloyd-Jones (1995; 1999) analysed dental nonmetric traits from several cemeteries across the Roman and Anglo-Saxon periods and found support in the continuity-based immigration rather than a larger scale invasion. Here tooth metrics were shown to gradually demonstrate the appearance or disappearance of different traits while retaining others. Additionally, Lloyd-Jones (1995; 1999) was able to show how these dental traits, even with their overlap in appearance between Roman and Anglo-Saxon groups, could be used to differentiate individuals between time periods in some cases. His results showed how geographically similar places did not show significant differences between Roman and Anglo-Saxon dental traits in all cases which would have been expected in the invasion theory was more likely. However, there are some issues with the reliance on nonmetric traits from human dentition, and additional biological data should also be incorporated where possible (i.e. dental metrics or DNA). Tyrrell (2000) presented an overview of the use of dental nonmetric traits to biodistance studies based on his work on early Medieval populations. His review of the use and issues with nonmetric traits for use in identifying population affinities have lost some of the appeal they once had in the 1990s, likely attributable to the caution over studies which

may confuse studies of ethnicity and biological affiliation (Tyrrell 2000, 303). This idea will be explored in more detail in Chapter 3.3.

Further examples of research incorporating biological data and contextual data more holistically to comment on ethnicity and identity during this transition period are work by Evans *et al.* (2006) and Gowland (2007). Using isotopic analysis of skeletal remains in a Roman cemetery, Evans *et al.* (2006) were able to study strontium and oxygen isotopes from individuals thought to represent local and 'exotic' (continental) burials within Roman cemeteries in England. They found that the differences attributable to grave goods, thought to reflect continental styling, were found in burials containing individuals from a variety of places around Europe as well as in graves of those who were likely second-generation migrants to Britain (Evans *et al.* 2006). This work showed that even though grave goods could relate to the presence of non-local individuals, they do not definitively show where a person originated from.

Hughes et al. (2018) also looked at strontium isotope levels of individuals interred in an early Anglo-Saxon cemetery in Sussex. Their work was able to compare groups of individuals identified as 'local' or 'nonlocal' to see where they had been raised. The locals were treated similarly in death, more likely to be found in wealthier burials than the nonlocals, but these were spread across the cemetery evenly. For Hughes et al. (2018) this meant that there was less support for the full invasion theory as it would have been expected to see more strong evidence of this in earlier phases of the cemetery instead of a general consistency amongst elites throughout the cemetery's use. Therefore, the more likely argument for what was occurring in this cemetery was an integration of local and nonlocal individuals and the possible continuous migration throughout the early Anglo-Saxon period (Hughes et al. 2018,

523). Similarly, Gowland (2007) reviewed skeletal and contextual data from seven cemeteries either side of the Roman and early Anglo-Saxon transition in order to highlight the importance of multiscalar analyses regarding the presence of objects in graves rather than a sole focus on ethnicity. Ideas surrounding ethnic divisions between Roman-British and Anglo-Saxon identity in death had previously been discussed (see Lucy 2000, 174-177 for review) and warranted a more holistic approach to study as hypotheses about differences in burial styles being attributed to a single component of identity were unfounded. In her study, results indicated that adornment objects (i.e. bracelets, brooches and finger rings) are linked more strongly to a combination of age, gender or achieved status rather than ethnicity, or any one factor alone (Gowland 2007, 62-63). To this end, Gowland (2007) advocated for the consideration of social identity of past individuals, which can encompass aspects related to all of these areas as a way to more meaningfully explore objects in archaeological assemblages.

Shifting focus from the objects found in early Anglo-Saxon graves to the individuals interred within each, interesting theories regarding identity and kinship have been generated. Multiple burials, in particular, have been investigated in order to discuss cemetery organisation and potential family membership. In a review of the occurrence and use of multiple burials throughout Anglo-Saxon England, Stoodley (2002) noted that the use of multiple burials had little to do with logistics (i.e. less work to dig one larger grave than two smaller ones), therefore must have been based on other factors, such as planned reuse for family plots or the amount of space available in a cemetery. By reviewing data from 59 Anglo-Saxon cemeteries, Stoodley (2002) found that proportions of multiple burials ranged from 0-21% within the assemblages. Within these burials, there appeared graves with mixed sex and same sex adults making up proportions of approximately 15%, and 17%, respectively. As for

the timing of interments, Stoodley (2002) also found proportions for contemporaneous and consecutive burials to be with 17% and 35%, respectively. In these cases, it was argued that contemporaneous burials indicated a familial relationship was present between those interred together as they would have been interred at the same time (Stoodley 2002). The nature of this relationship was not explored in detail by Stoodley (2002), and whether it was based solely on biological, social or on a combination of these factors remains debatable. The most common assumptions would be pairings of husbands and wives or brothers and sisters for mixed sex adult interments, and parents and children for mixed adult and sub-adult interments, though there are other scenarios that could result in such a pairing. For example, Stoodley (2002) suggested that not all children buried with female adults indicate a mother-child relationship, rather, the presence of grave goods may suggest that adults buried within such interments could be involved in the child's life in other ways (i.e. under their care or instruction) which in many ways is akin to Pilloud and Larsen's (2011) discussion on practical kin. Furthermore, Crawford (2011) looked at these types of interments in a different way by suggesting that children themselves could be interpreted as being grave goods in an interment with adult females. In contrast, the relationship of those interred could also have had nothing to do with kin of any sort, and more about a response to a catastrophic loss of life resultant from an epidemic or a superstition about travel to the afterlife, so it is important to think more broadly about these occurrences. Therefore, the inclusion of biological data here to comment in more depth on potential connections, whether biologically linked or not, would be advantageous.

Although the focus of Stoodley's (2002) paper was on contemporaneous interments, there may be more to learn from consecutive interments in regard to familial identity as it could be

argued that these may involve more planning for reuse, much like modern day family grave plots. An example was presented by Stoodley (2002, 111) of a consecutive multiple burial at Deal has potential to support this suggestion. Grave 105 was found with an adult male and adult female buried together contemporaneously but was subsequently reopened at a later time for the addition of a child. This could be indicative of family members being buried in the same burial space by the wider community in order to signify this connection. However, Stoodley (2002) rejects this interpretation in most consecutive burial cases based on the fact that there appeared no pattern regarding demography of interred individuals, the level of care shown by the digging of the grave, and the amount of time that passed between interments. It was argued here that consecutive interments had no link to the nature of the relationship of those buried within. However, future analysis of biological data from the remains of the individuals buried in these grave types could help to comment on the likelihood of this grave being used as a familial plot or be used to further support this conclusion.

As an example of a multiscalar investigation in Anglo-Saxon identity, Sayer (2009) used the presence of grave goods to make inferences about how kinship patterns changed over the early Anglo-Saxon period through discussions of material culture, historical documentation and skeletal demography. He argued that a change took place in burial customs which was related to the importance of family units and their expression after death (funeral rite) by using two Anglo-Saxon cemeteries, Mill Hill and Finglesham. Earlier phase interments of both cemeteries, dated to 5^{th}-6^{th} centuries AD, appeared to place more importance on the identity of a generational head of a household, and such graves likely would be ornately furnished and appeared in centralised locations within grave plots (Sayer 2009, 158-159, 162-165). The

result of having ornately furnished central graves within these plots was that the identity of the whole household would have been reflected by this single marker. In contrast, later phase interments in these two cemeteries, dated to 6th-7th centuries AD, appeared to focus more on individual identity within a household reflecting social changes over the time period, as more wealthy graves became apparent and spacing of burials seemed to become more important as well as the inclusion of external burial structures (Sayer 2009). In support of this, it had been reported elsewhere how burial structures link to identity. Williams (1998) reviewed spatial and structural data from early Anglo-Saxon cemeteries in England to comment on how burial structures linked to identity. He demonstrated that the creation and re-use of ancient structures influenced burial locations of graves and was not solely linked to the status of the interred individual. Rather, through re-use, symbolic relationships to the structures could be maintained (Williams 1998, 102). Another example pertinent to this study appears at the early Anglo-Saxon cemetery of Oakington, where barrows have been linked to the identification of generational figureheads (Sayer 2020, 121-122). Further still, based on contemporary cemeteries in Scandinavia, Thäte (2009) demonstrated how burial mounds were used to signify ancestral claims to land; by burying descendants near this mound, kinship ties were reinforced in such areas.

It was through apparent changes in the use of burial structures and grave good inclusions throughout the 5th-7th centuries AD that Sayer (2009) framed discussion on changes related to identity. The distinction in burial styling was argued to be a response to a change in vertical stratification of these societies, and therefore allowed for the preservation of kinship identity along with the emergence of an elite family as the focus of mortuary expression (Sayer 2009, 168). It was membership of this family, and not the role within it, which resulted in such

treatment and conferred status within the community (Sayer 2009). Further still, Sayer (2020, 84, 167) discussed how graves were created and decorated based on temporal cultural customs as a way to communicate to audiences, past, present and future. If certain aspects related to identity were deemed more important at a given moment in time, they may feature more heavily in burial rite (Sayer 2020, 167). Figure 1 presents an example of this from Sayer (2020, 253) where different patterns were observed at West Heslerton (Plot A), Lechlade (Plot B) and Finglesham (Plot C). These showcase a central core of furnished burials, a dispersed core and barrow burials, respectively, each highlighting different community focused ways to use space as an expression of identity within a cemetery (Sayer 2020, 252-254).

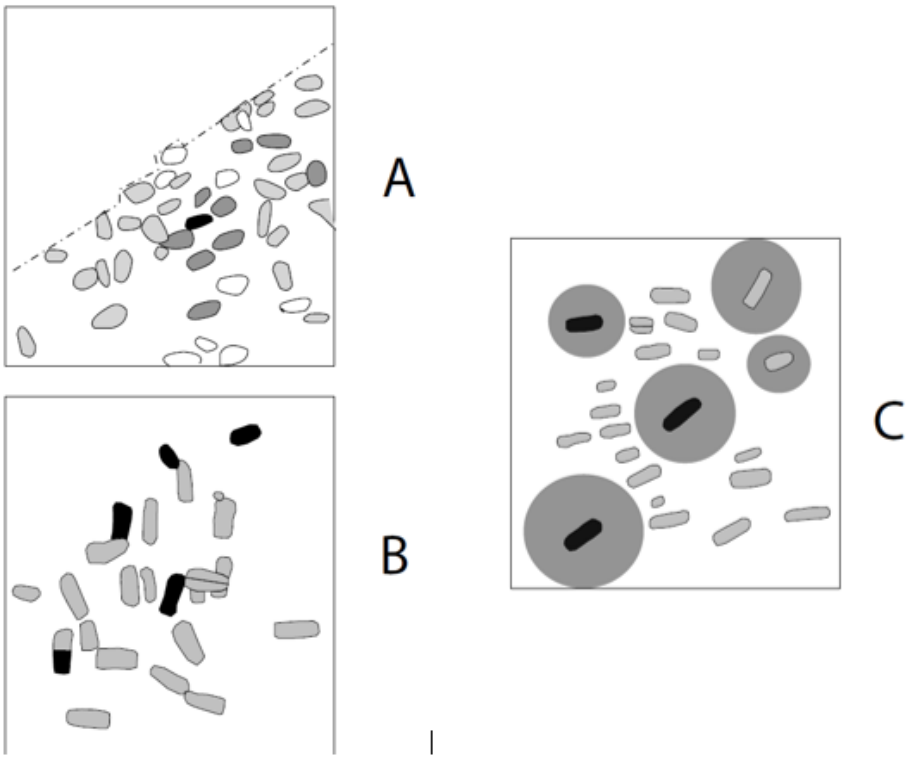

Figure 1 – Three different cemetery patterns from West Heslerton (A), Lechlade (B) and Finglesham (C), which were based on a central core of furnished burials, a dispersed core and barrow burials. The decisions made to bury individuals in such ways were varied and meant to evoke social meaning and memory with the wider living community (after Sayer 2020, 253). The differences in patterns demonstrates how much variation in identity can be expressed in mortuary environments. Darker graves indicate the more highly furnished graves.

In an approach to further understanding cemetery organisation during the early Anglo-Saxon period, Sayer (2010) revisited data from three cemeteries and attempted to understand chronologies of interments by investigating generational usage and shared social time. Cemeteries at Berinsfield, Deal and Apple Down were selected for use in this paper due to their level of preservation, excavation and collection of well-furnished graves for both males and females. Sayer (2010) demonstrated that in these cemeteries, generations of people would have been living and interacting together at any given time; when individuals died their surviving community would be the ones to bury them. As such, variations in burial style, location, or orientation could be attributed to preferences of those in the surviving generations as opposed to the generation membership of the deceased. These themes were further solidified and discussed on a larger scale throughout Sayer (2020). As Sayer (2010) acknowledged, this alternate chronology based on social time is a good approach for understanding the foundation of kinship in early Medieval populations which supports his use of a multidisciplinary approach, including the use of biological data, for investigating kinship during this time period.

To highlight the use of this approach, an example from Sayer (2010) can be employed. A male individual from the Apple Down cemetery was found interred with grave goods indicating a position of importance within the community, yet he was buried in a liminal position in the cemetery away from the wealthier cluster of graves. Sayer (2010) suggested this could be because, while this male was a respected individual of the community, he may not have been part of the same social group identity as those who buried him; a different kin group perhaps. For Sayer (2020) the funerary and burial process changed in response to temporal, political and cultural infrastructures. Those performing the rite on behalf of the deceased, aimed to

communicate messages that would be understood by the community, as it existed in the present, past and for the future. As the decisions regarding burial were made by the living, and the lived experience of individuals in the early Anglo-Saxon period differed between communities, the expression of identity in death would vary across the population too (Sayer 2020). Therefore, recognising that graves represent multiple levels of identity is an interesting concept. Individual identity and group identity could contribute to how an individual is buried, what they are buried with and by whom they are buried (Sayer 2020). In this sense, the combination of furnishings, orientation, grave location and the human remains themselves could be used to further ideas of kin and connectivity between people within early Anglo-Saxon communities.

The above discussion exemplifies how important it is for researchers to be aware of the multiple influences that contribute to the appearance of cemeteries and individual graves. How communities chose to identify certain individuals in death, while showing their connections to the land and to others, has fluctuated over the early Anglo-Saxon period. Studies such as Gowland (2007), Härke (1990), Lucy (2000; 2011), Sayer (2009; 2010; 2020) and Stoodley (1999; 2002), have clearly shown that the attribution of simplistic, single layered explanations regarding the presence of objects in graves, locations of burials or interment structures do not go far enough. Much like the modern day, early Anglo-Saxon communities consisted of complex, dynamic people. Decisions regarding burial would have reflected influences from religious, political, economic and social aspects of these societies over time. As such, a person's gender, biological sex, age, familial connections and status could all contribute to how they were interred, and how these expressions manifested in one community would not necessarily be found in another. For these reasons, researchers

interested in studying broad social aspects of the early Anglo-Saxon period, such as kinship and identity, would benefit from the inclusion of multi-layered data analyses to support their ideas. Conclusions drawn from grave good analyses have been shown to align well with investigations of mortuary space and skeletal data (Sayer 2020). Advancements in areas such as isotopic and DNA analysis have also shown potential to obtain further biological data from skeletal remains to comment on early Anglo-Saxon identity and kinship. Bioarchaeological research, arguably, allows for these various scientific disciplines to work together and develop robust theoretical discussions on these complex topics. Johnson and Paul (2016) and Johnson (2019) recently discussed the importance of these types of study in archaeology. For them, the value of bioarchaeological research is the way in which evidence from multiple fields can be considered together to answer questions related to the lives of past people. Biodata obtained from skeletal analyses can support and refine conclusions made on contextual information, and *vice versa*. As new methods are developed to elicit additional biological data from human remains, such as the method established in the current study using dentition, the way in which they can contribute to discussions on the social aspects of archaeological populations should continue to be encouraged and explored.

2.4 Conclusion

The study of archaeological human remains allows for research in a variety of subtopics within the fields of anthropology and osteoarchaeology. Researchers within osteoarchaeology and burial archaeology tend to fall within two main subcategories when investigating such skeletal remains: those attempting to answer questions pertaining to social constructs for a given

society and, those hoping to use biological indicators to learn more about a population (i.e. health, occupation, violence, etc…). In recent years, the distinction between the two has blurred significantly allowing for more robust interpretations of past populations to be elucidated from data sets. However, its use in the field and related disciplines has not always been globally accepted. Kinship theory, associated mainly with biological and genealogical relationships in its infancy, was questioned through the later part of the 1900s as the rise in feminism and post-structuralism demanded a less constraining definition of kin (Schneider 1965). During its induction into anthropological and archaeological theory, kinship was thought of much differently, resulting in decades of debate on its use and misuse in both disciplines. Regardless of the past criticisms of the theory, the understanding of kinship continues to be a persistent theme in present and, likely, future anthropological and archaeological research. Those criticisms of the past simplistic views on the theory have helped to ensure the disciplines use more pragmatic and methodological approaches in the study of kinship for both modern and archaeological populations. Anthropologists and archaeologists tend to agree that a multifactorial approach to kinship is the strongest way to ensure a full understanding of patterns and systems within specific populations (Johnson and Paul 2016).

Within the remit of the current project, when considering kinship of early Anglo-Saxon populations, terminology must be reassessed and attention should be paid to the distinction between what kinship is, and what kinship is not (Sahlins 2013). In that, the use of the term kinship should only be applied when discussing the patterns of human interaction that have been formalised by the detailed investigation of multiple lines of evidence, including biological similarity, demography, spatial organisation and material culture. This means that the cultural and social organisation of early Medieval societies within a burial archaeological

framework need to be investigated inductively. This is done by first identifying biological similarity between individuals within skeletal populations and then using this information in combination with spatial organisation and contextual material to help rebuild the kinship structure that had been established during this era at particular sites. Comparisons can then be made between sites in order to comment on larger scale interpretations rather than those that appear only locally. Furthermore, understanding the social organisation of a population can help to make sense of any biological data that is recovered from associated cemetery assemblages.

3. Tooth Development and Biological Similarity

The establishment of individual identities and familial relationships are common subjects of study within the fields of archaeology and anthropology. One of the most popular ways to investigate these subjects is to use human remains, as the human skeleton has the potential to reflect numerous traits that correspond to heredity and biological (familial) similarity. These traits can be assessed visually through macroscopic, morphological observations as well as various metric or microscopic histological analyses. The appearance of rare genetic traits present on a few individuals, or those evident in small sub-groups of communities, can also be the starting hypotheses for those interested in locating biological relationships within a given population (Alt and Vach 1995; Vach and Alt 1993). However, in many forensic and archaeological situations, the likelihood of finding complete and well-preserved skeletal remains is low. Therefore, in order to assist with this process, the methodology for assessing biological similarity from human remains needs to focus on robust skeletal elements which have higher survivability rates in order to illicit information relating to identity and familial relationships. Human dentition is a prime example of such a tissue, as their enamel exterior protects and preserves teeth from decomposition and helps to resist various taphonomic processes that damage other skeletal tissues (Adler *et al.* 2011; Galloway *et al.* 1997). Additionally, once a tooth has finished forming, its morphology does not change, rather, it retains its phenotypic expression gained from genetic and environmental influences throughout development. There is a long history demonstrating the use of teeth in order to comment on evolutionary or biological trends, the majority of which has developed through a detailed identification of morphological traits (present on tooth crowns or roots), crown topography, and various metric analyses. Such studies aim to investigate teeth either at an

individual or population focused approach, the former allowing for discussions on interpersonal relationships and genetic inheritance, while the latter provides information as to evolutionary trends and long-term changes (Hughes and Townsend 2013). A critical understanding of the uses and misuses of such types of study is necessary to develop before attempting to use teeth in order to aid in investigations of biological similarity within early Medieval skeletal assemblages. Exploring the genetic pathways through which dental nonmetric and metric traits manifest will frame the discussion on the applications of this information to the fields of dental anthropology and osteoarchaeology.

The overall developmental pattern of human tooth formation is generally well understood and commences as early in humans as six weeks in utero and continues until the mid-to-late teenage years, when the third permanent molar is complete and erupted (Ubelaker 1978; Townsend *et al.* 2012). This regulated pattern has led to the successful use of teeth for assessing the age of human remains in anthropology and osteoarchaeology (i.e. AlQahtani *et al.* 2010; 2014; Moorrees *et al.* 1963; Ubelaker 1978). On a cellular level, the pattern of tooth formation begins with the appearance of a tooth bud, an area of disorganised cells that are waiting to be activated in regard to tooth type. This then progresses to the cap stage where the cells begin to differentiate and form aspects of the enamel and dentine precursors which denote the beginning of hard tissue formation (Hand and Frank 2014). The bell phase is where this differentiation becomes significant and, within later stages of this phase, is where the proliferation of hard tissues (the aforementioned dentine and enamel) occurs in a lamellar format which establishes the foundation for crown development in later stages. Figure 2 provides a visual overview of the tooth formation process. Once the hard tissues have begun to form, the overall tooth itself is able to take shape wherein the crown will form first from the cusps, followed by the roots (Hand and Frank 2014). This process can be divided into three

umbrella categories regarding the molecular processes involved in the patterned phases: initiation, morphogenesis and differentiation.

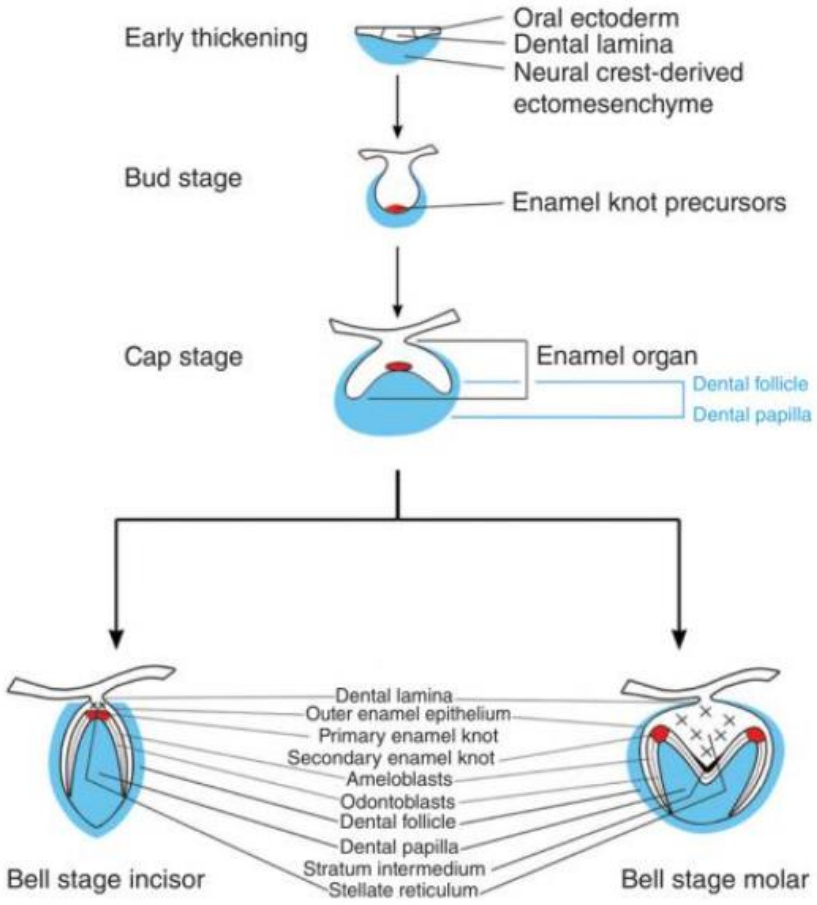

Figure 2 - The cellular process of tooth formation from initiation through bell stage (Hand and Frank 2014, 45).

The molecular and genetic processes that govern tooth formation during early stages of embryo development are becoming better understood, although there are exceptions and gaps in current understanding, such as the timing of defects along the developmental process (Thesleff 2006). It is generally accepted that a variety of genetic interactions are involved in the determination of tooth class (incisor, canine, premolar and molar) and various genes are also thought to be involved in the development of tooth shape and cusp size (Ferguson *et al.* 2000; Vastardis 2000). The formation of teeth occurs under the control of over 300 separate

genes, of various functions, and according to a developmental process that is derived from an interaction between mesenchyme tissue from the neural crest and epithelial cells during foetal development (Thesleff 2006). It is during this process that the variations in tooth form and size are thought to be established (Thesleff 2006). According to Salazar-Cuidad and Jernvall (2002), during the early stages of crown formation, there occurs a predictable sequence of enamel knot and epithelial folding. The shape of a tooth crown is determined by the folding of epithelium and then solidified through the formation of dentin and enamel via odontoblast and ameloblast differentiation. As this process is the sequence which precludes actual crown formation, it is a valid assumption that the genes that determine the expression of metric and nonmetric traits are most influential during this morphogenetic phase. In addition, the fact that these genes are inherent in an individual's DNA means that their activation and control must be at least partly based on genetic material from both parents. It is important to note, as will be discussed in detail, that the presence of these genes alone during this developmental process may not be enough to result in the manifestation of the expression of a particular trait or dimension size as there are additional factors that contribute to their appearance (Hughes and Townsend 2013).

The importance of understanding heritability and what it can be used for in anthropological studies has been noted previously (Vitzthum 2003). The statistic *heritability* does not directly infer the ability of genes to be passed from parent to offspring and appear phenotypically. Rather, it is the proportion of total phenotypic variance that is associated with genetic variance in a specific population (Townsend *et al.* 2012; Vitzthum 2003, 541). It can be used to interpret the variation observed between individuals within the same skeletal assemblage attributable to population genetics (Scott and Turner 1997). However, heritability as a measure of population genetics, is not a static concept (Hughes and Townsend 2013). It can

change to result in varying degrees of influence from the factors that impact dental morphology (i.e. environment and genetics). For example, if the relative percent contribution of genetics' influence on tooth shape increases in a modern population, the overall impact will result in greater phenotypic diversity within the population. This stresses the importance of taking into consideration other factors that affect phenotypic expression (i.e. environment). In order to attempt to quantify the impact genetics has on tooth size and morphology within a specific population, researchers must study the relative levels of influence of genetic, environmental and random contributors that impact upon tooth phenotype (Hughes and Townsend 2013).

It is this pursuit that has fostered the development of dental anthropology as its own discipline, and research within this field has strong ties to orthodontistry, dentistry, archaeology, palaeontology and forensic anthropology. In many studies (i.e. Alt and Vach 1991; Alt *et al.* 1997; Hughes and Townsend 2013; Lane and Sublett 1972, Townsend and Brown 1978a; 1978b; Vach and Alt 1993) within these fields, the aims of research were to comment on biological similarity (though not overtly stated as such), the degree to which individuals or groups of people appear similar in regards to specific traits that are thought to be a result of shared genetics. The more similar traits individuals or groups of people appear to share, the more similar they would be regarding their biological composition. In order to establish the level of influence genetics has on dental phenotype, early dental anthropological studies have tried to investigate the link between parent and offspring in various ways in both living and archaeological populations. In Australia, longitudinal data from Indigenous groups was used as a large sample base from which research was focused on inheritance patterns of both deciduous and permanent dentition (Townsend and Brown 1978a; Townsend and Brown 1978b; Townsend 1980). Correlations were noticed between members of nuclear families

where same sex sibling pairs had the strongest shared level of similarity followed by different sex sibling pairs and, lastly, by parent and offspring pairs. Other studies have looked at siblings of the same and mixed sex (i.e. Garn *et al.* 1965) in order to determine whether X or Y chromosomes demonstrate a stronger affinity for shared biological traits. Alongside these ideas, biological sex in general has been linked to differences in overall tooth size (i.e. Arya *et al.* 1974; İşcan and Kedici 2003) which could further support the ideas surrounding X and Y linked chromosomes and dentition. Additionally, Alt and Vach (1995) have proposed methodology from which to identify suspected members of families within large skeletal assemblages by relying on nonmetric dental traits that have been established to display high heritability within populations. Further still, corroborating studies involving the use of DNA alongside dental traits have demonstrated that there are identifiable correlations between the similarity of DNA and dental traits within groups of people, both living and archaeological (Adachi *et al.* 2003; Hubbard *et al.* 2015). This approach is still developing within the field, therefore, it is currently difficult to be able to demonstrate the true nature of dental traits' corroborative strength with family identifications across various populations (Ricaut *et al.* 2010). This is predominantly because there are other factors that contribute to variations in dental phenotype, making it difficult to understand the influence genetics has solely. While these studies all help to determine, to an extent, that genetic inheritance is involved in the expression of dental traits, some of the strongest evidence to support the theory that a significant portion of trait expression is influenced by genetic inheritance has come from twin studies. Monozygotic (identical) and dizygotic (non-identical) twin pairs are seen to be a gold standard by which the contribution of shared genetics can be quantified and compared to environmental and random factors (Biggerstaff 1975; Boraas *et al.* 1988; Dempsey *et al.* 1995; Hughes *et al.* 2000; Hughes *et al.* 2001; Potter and Nance 1976). The hypothesis behind much

of this research was that if genetics had little influence over tooth size or shape, then monozygotic twins would not show as great concordance between tooth forms compared to other sibling or relative pairs. Common trends throughout these twin studies have demonstrated that identical twins show significantly higher similarities of tooth sizes and appearance of nonmetric traits compared to non-identical pairs (Dempsey *et al.* 1995; Potter and Nance 1976), and stronger concordances when compared to other relative pairs such as parent and offspring or non-twin siblings (Townsend and Brown 1978a). Thus, supporting the notion that shared genetics does appear to be strong indicator of shared similarity in tooth morphology.

3.1 Genetic Basis for Tooth Trait Inheritance and Expression

Early research on the genetic inheritance of tooth crown size and shape aimed to quantify the level of contribution genetics has on these traits compared to other additive sources. The general consensus within the literature is that both metric and nonmetric traits of teeth are under observable genetic influence (Alt and Vach 1995; Biggerstaff 1975; Boraas *et al.* 1988; Dempsey *et al.* 1995; Hughes *et al.* 2000; Townsend 1980; Vach and Alt 1993). It is this premise of genetic inheritance of tooth form that drives much of the research conducted on biological similarity of human populations which can be observed by the appearance of metric and nonmetric traits. The basic hypothesis is that those individuals within a population (archaeological or modern) that display higher than expected levels of similarity in regard to nonmetric or metric traits are more likely to be genetically related (Alt and Vach 1991; Alt and Vach 1995; Alt *et al.* 1997; Vach and Alt 1993). Similarly, this notion can be used to make larger scale comparisons, such as individuals on global scales that share similar traits are more

likely to be from similar founding populations (Hubbard *et al.* 2015). Nonmetric traits refer to the appearance of additional or altered features on the tooth crown or root that do not necessarily occur naturally during normal dental development. Some of the more common traits that have been reported in the literature are: Carabelli's cusps, shovel shaped incisors, and variations in root form or number (Turner II *et al.* 1991). The most common metric traits observed pertain to the main dimensions of the tooth, which are: the buccolingual (tongue side to cheek side length), the mesiodistal (anterior to posterior length), crown height and root length (Hillson *et al.* 2005). Of the four, crown height is the most vulnerable to dental wear and root length can be difficult to assess visually unless aided by radiographs, which makes the mesiodistal and buccolingual dimensions more commonly cited in the literature surrounding archaeological remains.

During the morphogenesis phase of tooth development there are number of genes in varying levels of activation which interact to help guide the developmental process of tooth formation. These genes are said to be pleiotropic (Mossey 1999a; Townsend at al. 2009), as the same gene can impact numerous aspects of dental morphology. The cause of variation in tooth size or shape is said to be a result of any mutation or inhibition of specific genes at this point in developmental process (Salazar-Cuidad and Jernvall 2002; Townsend *et al.* 2012). There have been several competing theories that have been discussed extensively in the surrounding literature as to the processes by which teeth develop: the field theory (Butler 1939; Dahlberg 1945), the clone theory (Osborn 1978), the influence of homeobox code (DNA sequences involved in the regulation of anatomical development) (Sharpe 1995), the cooperative genetic interaction (CGI) theory (Mitsiadis and Smith 2006), and the inhibitory cascade model (Schroer and Wood 2015; Evans *et al.* 2016). The first three, when originally introduced, were seen as competing theories wherein their utility to describe dental

development was thought to be mutually exclusive (Townsend at al. 2009). However, Mitsiadis and Smith (2006) proposed their CGI model of tooth development to encompass the key points of field, clone and homeobox theory as the recent research supports the notion that these theories are actually complementary rather than contradictory, further emphasised by recent developments on inhibitory cascade modelling (i.e. Evans *et al.* 2016).

Butler (1939) was one of the first to note variations in tooth form when investigating the size and shape of non-human mammalian teeth within separate tooth classes. These classes comprised of incisor, canine and cheek teeth (a combination of mammalian premolars and molars) as it pertained to the various animal species he commented on. He noted that there appeared to be 'pole teeth' within each tooth class that appeared to stronger represent the influence of genetic processes during tooth formation as they were less variable in size and shape (Butler 1939; Kieser 1986). It was postulated that the mesial tooth within the incisor class (the one towards the front of the mouth) was the most stable, and the first molar was determined to be the most stable in the cheek tooth classes, with those furthest from it being least stable (Butler 1939; Kieser 1986). Dahlberg (1945) adapted the premise of polarity and applied it directly to human dentition. Differences were made regarding the types of tooth classes as he chose to use four classes in order to reflect the four types of teeth observed in humans: incisor, canine, premolar and molar. Like Butler (1939), Dahlberg (1945) identified a key tooth within each class which was observed to maintain the most consistent morphology across individuals and, therefore, likely to display the strongest expression of genetic information. These key teeth in humans were slightly different compared to their analogues in non-humans; the anterior tooth of each class was thought to be the most stable. However, Kieser (1986) contradicted the polarity effect of these theories by relating morphological differences to developmental stage, rather than location in the jaw. Kieser (1986) observed

that the teeth within each class that appear the most variable are those that tend to be later developing teeth. It was argued that the longer a tooth spent in the morphogenesis phase of development, the more influence various genes would have on their morphology. This theory also supports the idea that genes influence each tooth independently, as the expression of traits is not uniform throughout a set of dentition.

Similar to field theory, clone theory (Osborn 1978) was based on the idea that the development of teeth is variable within the mouth and that there are certain teeth that appear to be more stable within each class. The classes incorporated into clone theory are the same as per Dahlberg's (1945) separations, the difference here was in respect to the timing of developmental stages and the founding cluster of migrated neural crest cells which become ectomesenchyme cells to begin the tooth formation process. The key teeth of each class, as identified by Dahlberg (1945), were thought to develop from a single set of neural crest cells that would begin forming the most anterior tooth of each class before cloning and beginning to form the next tooth within the class, progressing towards the distal part of each jaw. Each subsequent tooth bud within a specific class would, therefore, be formed by the same set of ectomesenchyme initiation cells from the first tooth within the class, yet potentially not be as similar in shape, which is why variation in morphology is presented in each class. The developing tooth buds were not thought to be affected by the influence of a field or gradient as hypothesised by Butler (1939) and Dahlberg (1945). It was believed that the timing of this sequence was more likely to explain the similar patterning of teeth rather than the impact of a field. However, this theory did not explain the process that gave rise to each set of clone cells prior to formation, nor how they result in determining the final shape of each tooth (Mitsiadis and Smith 2006). While this timed developmental process has been replicated in molars of other non-human species, it has not been verified for incisor or

premolar classes (Mitsiadis and Smith 2006). Kieser's (1986) critique of field theory and developmental timings could also be incorporated into this aspect of clone theory as a mechanism to explain the higher levels in variation within distal class teeth.

Currently, homeobox codes are cited as being among the most influential for determining the final size and shape of tooth crowns, as they are main drivers of the initiation phase of tooth formation (Hughes and Townsend 2013; Mossey 1999a; Sharpe 2001). Homeobox codes refer to families of genes that contribute in a variety of ways to embryo development and certain families have been found to relate to dental development (Sharpe 2001). Although there are many, and still much research to be conducted on their effects on dental formation and trait expression, some have been found to play a large role in craniofacial development. Shh and Otx[1] are two examples of such homeobox genes that appear to regulate the early movement of neural mesenchyme cells to become ectomesenchyme cells which will eventually lead to the proliferation of tooth forming cells during the bud stage of dental development (Hughes and Townsend 2013, Sharpe 2001). The first appearance of the impact of homeobox genes relates to the thickening of epithelial bands that will eventually form the mandible and maxillae. A second thickening of these bands and a concurrent invagination of the ectomesenchyme results in the formation of early tooth buds. The *Msx-1*[2] gene is another example that has been shown to link directly to tooth formation (Mossey 1999a). Its link to

[1] Other genes include Fgf, Bmp, Wnt, and Tnf, yet with over 300 individual genes and their interactions to consider, it is difficult for researchers to ascribe specific trait expressions to the influence of a single gene (Hughes and Townsend 2013). Ongoing research in this area will aim to supplement known actions and continue to fill gaps in this area of understanding.

[2] *Msx-1* and *Msx-2* are thought to be instrumental in this initiation process as research on mice has shown that mutations of these genes at this point of the developmental process causes alterations to the patterning of dental development (Sharpe 2001). Furthermore, Mitsiadis and Smith (2006) discuss the impact the *Msx, Dlx, Barx, Lhx,* and *Pitx* genes on the first branchial arch of the embryo; it is this feature that will give rise to the formation of the mandible and maxillae and is therefore likely to be under the influence of these genes and their interactions.

tooth agenesis has been noted during experimental studies on mice. When this gene was inhibited in mice, hypodontia was observed as tooth development was halted after the bud stage. Further research, however, has shown that mutations of the same gene could impact crown morphology at any developmental stage up to completion (Townsend *et al.* 2009). While these gene examples have been linked to dental formation, there are numerous genes whose influence on shape and size of teeth has yet been made explicit. Furthermore, researchers have suggested that, while these genes are involved in tooth formation, their influence on each tooth and tooth class seems to be independent (Townsend *et al.* 2009).

Malocclusion research, the discordance of fit between jaw and tooth, has also provided evidence to suggest multiple independent genetic processes contributing to craniofacial morphology. Many suggest that malocclusion, crowding of teeth or alignment issues due to interactions of tooth and jaw size. result from evolutionary trends in the reduction of jaw and tooth size (i.e. Huang *et al.* 2012). Mossey (1999a) discussed the difference in genetic origin of maxillary and mandibular formation compared to dental development. It was noted that the development of the maxillae and mandible are under the influence of independent genetic processes as these bones are mesodermal structures, compared to teeth being ectodermal features. Sharpe (2001) commented on homeobox genes that are thought to influence the maxillae and mandible in different ways. It appeared that *Msx and Dsx* genes influence both tooth class and development location in mouth, however, mutations in one family appear to influence either tooth class or location, providing support for the notion that each of the jaws has an independent developmental pathway regardless of the presence of the same genes. Townsend *et al.* (2009) also discussed the differential genetic impact through which mandibles and maxillae form, yet they noted that despite current awareness of this phenomenon, it is not known how the neural crest cells are able to respond differently to

what were thought to be fixed signalling pathways. These differences in development would classify as environmental factors and potentially have an impact on dental morphological development as these are the bone structures teeth form within. It is more likely that these various genetic processes have been influenced differently over many generations resulting in the reduction in size of jaws and teeth at varying rates which could cause morphological changes in teeth. Mossey (1999b) also stated that those in homogenous populations tend to have fewer issues with malocclusion which seems to indicate that the addition of new or different genotypes into a population may lead to variations in both tooth and jaw morphology leading to increased appearances of poor fit and altered occlusion.

The aforementioned theories appear to provide many answers for questions relating to the development of teeth (sequence, timing, determination of shape, etc…), yet they do not seem to be able to explain the process completely. While the goal of understanding the complete process of dental formation at a molecular and genetic level will require a lot more research, the merit that each of these theories affords has established the foundation for Mitsiadis and Smith's (2006) theory of cooperative genetic interaction (CGI). The authors have argued that this model encompasses the key elements of each prior theory and would, therefore, prove most beneficial for discussing the process of dental formation in a more comprehensive manner. By incorporating the ideas of field gradients, sequencing patterns and the accepted influence of homeobox codes, the CGI theory can help to make sense of the levels of variation observed on the levels of individual tooth, tooth class and jaw. Recently, more progress has been made regarding the understanding of how tooth size is developed by researching evolutionary changes of tooth size in relation to an inhibitory cascade model (Evans *et al.* 2016; Kavanagh *et al.* 2007; Schroer and Wood 2015). This model has focused on understanding the cellular processes that begin the activation and inhibition sequences of

tooth development. It is based on the assumption that the activation of a further tooth within a class is based on the inhibition of its predecessor, crown size is determined by how much space is left after early teeth form. It has been reported that tooth sizes within a class are proportional which makes it mathematically possible to estimate or predict the size of additional teeth within the class according to the pattern of the cascade effect (i.e. moving distally or mesially within a class) (Evans *et al.* 2016). Again, like CGI, this model appears to utilise key features of earlier theories in order to help explain the variations in tooth phenotype.

Regardless of the theory used to understand the process of dental development, in order to explain the variation in phenotypic expression resulting from the presence, absence or interaction of similar genes, it is important to consider the ways in which genes can impact on tooth morphology. There are: additive effects, traditional concepts of the direct impact of genes or environment; gene interactions at a single locus resulting in dominant or recessive phenotypic expressions; epistasis interactions, when genes interact across loci and; epigenetic, the proportional influence from environmental or random factors on phenotype (Hughes and Townsend 2013). Accepting that tooth formation does not fit a model reflecting complete influence by additive genetic inheritance, researchers needed to focus on the impact of other factors, predominantly the environment and random effects. In order to do so, researchers developed various models in an attempt to isolate the influence of genetic and alternative factors. Hughes and Townsend (2013) and Mossey (1999a) reported the use of ACE or ADE models in order to quantify the contribution of additive genetic (A), common shared environmental factors (C), dominant genetic effects (D) and unique environmental impacts (E) within both living and archaeological populations. The frequency of traits among family members and non-family members can be run through the model in order to see if

comparisons yield information on the proportion of influence from each of these factors. Both metric and nonmetric traits from dentition have been reported to demonstrate strong influences from genetic contributions (Biggerstaff 1975; Boraas *et al.* 1988; Dempsey *et al.* 1995; Hughes *et al.* 2000; Townsend 1980), although it also must be noted that the influence from shared or unique environments is strong. Instead of weakening the argument for use of dental traits for studies on biological similarity within and between populations, these findings rather suggest a more multifactorial approach is needed to fully understand expressions of dental phenotypes before making any interpretations on similarity.

Within the range of dental traits that are possible to observe, divisions can be made into the broad categories of discontinuous or continuous traits (Mossey 1999a). Continuous traits pertain to those that are always present yet follow along a continuum of expression. Apart from the consideration of dentition, alternate anthropometric traits such as stature, body weight, facial height or breadth and cephalic index can all fall within this category. Metric traits (i.e. mesiodistal and buccolingual diameters) and some nonmetric traits (i.e. root and cusp number) can be classed as continuous traits, as they will always be present yet expressed along a continuum (i.e. some will be smaller, others larger). Discontinuous traits, conversely, are those that are either present or absent (although when present can follow a pattern of continuous trait expression) and are said to be a resulting product of the previously discussed gene and environmental interactions (Hughes and Townsend 2013). The Carabelli's cusp is an example that is discontinuous in nature as they are either present or absent, but once present can appear to vary in regard to degree of expression (Guatelli-Steinberg *et al.* 2013). Linking this idea to heritability, those discontinuous traits that appear more frequently within family groups compared to population data are said to have higher heritability than those evenly shared within a population. The correlation of continuous traits can also be used to determine

heritability, wherein sizes of teeth can be compared to elicit information about inheritance patterns, with those exhibiting similarly proportioned teeth compared to the wider population indicating greater biological similarity.

3.2 Metric Traits

As genetics do appear to have a strong influence on tooth morphology, understanding how this information is passed on from parent to offspring is important to consider. Garn *et al.* (1965) were among the first to be able to demonstrate the relationship of permanent tooth size and the X-chromosome in early studies of cranial trait inheritance. They found that sister-sister siblings had the greatest correlation between permanent tooth size, followed by brother-brother sibling pairs and sister-brother siblings had the lowest level of correlation. The results from this study supported the basis for further testing on the Y chromosome's influence as well. Conversely, Bowden and Goose (1969) attempted to recreate results from Garn *et al.* (1965) and found that there were no significantly stronger correlations between mothers and daughters, as would be expected, compared to other pairs (i.e. father and daughter, mother and son or father and son). There are some points of discussion as to why these results may have differed. Bowden and Goose (1969) relied mainly on anterior teeth for their study, and they also separated their sample into 'social classes'. These classes were not defined in the paper, making any differences observed in the results difficult to attribute to a single factor alone as the data could have been manipulated in a way that demonstrated the impact shared environment has on dentition in some cases. While, they did state that maternal environment did not appear to cause significant differences in tooth size between pairs, the conclusion as to the impact of post-natal environments remained unclear.

Townsend and Brown (1978a; 1978b) investigated the role of sex-linked inheritance on tooth size for Australian Indigenous populations. Prior to this work, investigations on tooth size and family relationship focused on twin studies and biologically related family members to demonstrate the positive correlation between these variables (e.g. Biggerstaff 1970; 1975; Garn *et al.* 1965). Results from testing pairs of full and half siblings supported the idea of both X and Y linked inheritance regarding tooth size (Townsend and Brown 1978a; 1978b), reinforcing the idea that tooth size is in part determined in offspring by parental DNA contributions. Similarly, Kabban *et al.* (2001) conducted a study on monozygotic and dizygotic twins to examine the correlation between genetic inheritance and permanent tooth size. Their work compared the concordance of tooth size between twin pairs and non-related pairs of individuals of similar demography (i.e. matched for sex and age). Twin pairs showed stronger similarity on all permanent teeth compared to non-related pairs, therefore genetic influence appeared more substantial than environment or demography in determining tooth size. This finding accepts that there are additional factors that contribute to the expression of tooth size as others have commented (i.e. Küchler *et al.* 2008), yet the importance of the genetic influence cannot be overlooked and can be observed successfully from metric dental traits.

Furthermore, Potter and Nance (1976) investigated the genetic inheritance patterns of tooth size, with a specific focus on investigating whether the buccolingual (BL) and mesiodistal (MD) dimensions were determined by the same genes. They found that BL and MD lengths were determined by different genes, however these genes all influenced the resulting crown size in the same way (either could cause an increase or decrease in each of the individual measurements). Townsend *et al.* (2012) noted that the aforementioned differences in sex linked inheritance contribute overall to the different MD and BL measurements. While both

the X and Y chromosomes are involved with ameloblast initiation and the formation of enamel, only the Y chromosomes have been shown to have a stronger influence on dentine deposition. It is the deposition of dentine that causes changes in the MD length, which has also been hypothesised as to why males generally tend to have larger teeth than females (Biggerstaff 1975; Townsend *et al.* 2012), although in reality these differences may not be significant for all teeth. Kabban *et al.* (2001) also came to the conclusion that there are different genetic influences on each tooth dimension, however they stated that because of this, environmental influences can potentially be stronger on one measurement compared to the other. This idea has been supported by Huang *et al.* (2012) who commented on the fact that the dimensions appear to be influenced differently by environmental and evolutionary factors which they reason has to do with their involvement in mastication. Cusp size has also been researched to identify genetic contributions on metric dental traits (Biggerstaff 1975). As the crown of a tooth is generally comprised of cusps, ridges and grooves, this could be a way for investigators to examine additional aspects of a tooth for genetic influence as minute metric traits on cusps may not be as easily detected by manual measuring techniques. It is likely that, as the cusps form the occlusal level of a tooth crown, similar genetic influences and alterations will impact on cusp morphology as overall crown shape.

3.3 Nonmetric Traits

The gross anatomy and basic development of a tooth are quite straightforward yet, like metric traits, the genetic influences and modes of inheritance for nonmetric traits are not as easily understood. It was first postulated, later corrected, that nonmetric traits were inherited, parent to offspring, via a simple Mendlian inheritance pattern of dominant and recessive

alleles (Garn 1977; Guatelli-Steinberg *et al.* 2013; Hughes *et al.* 2000). This type of inheritance pattern, however, would only result in a simple evaluation of a trait being 'present' or 'absent'. It would not account for the variable nature of trait expression that is observed in the majority of nonmetric traits (Scott and Turner 1997). In order to account for this, researchers hypothesised that incomplete inheritance patterns or threshold patterns, a quasi-continuous expression, are a more likely cause of varying degrees of expression (Alvesalo and Tigerstedt 1974; Howell and Kintigh 1996; Küchler *et al.* 2008; Ricaut *et al.* 2010; Scott and Turner 1997). This theory has been supported by examples of individuals within families and twin pairs who have shared genes yet not everyone in the family or twin pair express a certain trait. Therefore, the presence of genes may not be enough to manifest into phenotypes displaying the trait, which means other factors contribute to surpassing this threshold for expression. As previously discussed, even though these traits are classed as discontinuous, once present they follow similar expression patterns as other continuous individual traits like stature, wherein individuals within populations all display varying degrees of 'tallness'. It is important to reiterate that the expression of such traits is not inherited in a basic sense, rather a multifactorial process, as the appearance of traits are also influenced by environment and the sex of the individual (Küchler *et al.* 2008). Currently, the genes, or mutations of these genes, that cause variations in tooth morphology or size differences are still being investigated as those involved in the appearance of one particular trait, may not be the same as those involved in the occurrence of other nonmetric traits. This is further support for the belief that many of these genes display pleiotropic abilities (Hughes and Townsend 2013; Townsend *et al.* 2009). For this reason, it is difficult to assess the actual level of genetic representation of each trait within a skeletal assemblage as some individuals may have the genetic code required for the presence of a given trait, yet not enough to reach a threshold

value that results in the manifestation of such a trait. This paradox requires researchers to understand the limitations of relying on nonmetric traits alone, as frequency levels can be skewed negatively if low levels of presence are observed.

Dental agenesis (hypodontia), its links to genetic inheritance and evolution, as well as its varying expression have been studied extensively (i.e. Vastardis 2000; Thesleff 2006; Küchler *et al.* 2008; Lavelle and Moore 1973). Theories for the occurrence of such a trait include those that are based on evolutionary changes to the teeth and mouth area such as the shortening lengths of mandibles and maxillae in primate ancestors to remove vestigial structures that become redundant through evolution (Lavelle and Moore 1973; Graber 1978). As human species have developed, jaw length has decreased resulting in fewer and smaller teeth than previous hominid ancestors. This evolutionary approach looks at longer term retention of inherited traits rather than a generational approach (Lavelle and Moore 1973). Molecular theories about hypodontia receive more attention in the literature. Numerous studies on mice have led to the conclusion that the genes involved in dental formation can be influenced by various factors. If this influence results in changes to the timing or sequencing of tooth bud formation during embryo development the tooth may not complete formation or remain as a rudimentary structure (Townsend *et al.* 2009). This seems to corroborate Mitsiadis and Smith's (2006) CGI theory where the development of agenesis in an individual and the fragility of sites where tooth development occurs is influenced by genes and underlying developmental patterns. The common feature of all these theories pertaining to hypodontia is the inherited nature of tooth agenesis, whether via evolution or through the mutation of genes involved in jaw formation or tooth development. The same types of theories can then be applied to other nonmetric traits, or variants of agenesis, including the presence of Carabelli's cusps (Guatelli-Steinberg *et al.* 2013), peg shaped incisors, defined as a shorter

mesiodistal crown length compared to cervical length (Vastardis 2000; Küchler *et al.* 2008), and occurrence of polygenesis, the development of additional teeth (Lavelle and Moore 1973).

With numerous nonmetric traits being reported in the literature, and their aetiologies not completely understood, it becomes a difficult task for a researcher to decide which nonmetric traits to focus on for investigations of biological similarity within a population. The Arizona State University (ASU) recording system has been a positive influence on the standardisation of nonmetric trait recording in dental anthropology (Turner II *et al.* 1991). While it is not inclusive of every potential morphological trait, it focuses on specific traits that are relatively easy to observe and score, those that express little sexual dimorphism, have higher survivability in archaeological populations, are slow to evolve, and are powerful indicators for characterising populations in estimations of biological affinity (Turner II *et al.* 1991). Additionally, the ASU system is accepted as standard recording procedure in forensic anthropological investigations (Buikstra and Ubelaker 1994) which makes its cross disciplinary potential suitable for comparative studies.

3.4 Critical Discussion on Methodologies

Through such discussion it is clear to see that human dentition can be used in various academic pursuits in order to develop an understanding on genetic inheritance, appearance of traits and quantitative analyses. What has not been so widely discussed in the literature, however, is the multimodal approach to tooth analysis, rather, how researchers tend to focus solely on metric or nonmetric traits as opposed to a combination (exceptions include

Haeussler *et al.* 1989; Lease and Sciulli 2005). To assess the strength of each method for analysing teeth, the sample from which data will be collected must be considered. Factors such as environment, socioeconomic status and population size may all contribute to the appearance of certain dental traits, as such limiting approaches to either metric or nonmetric data alone could be problematic.

There are a few main issues with relying solely on nonmetric dental traits for research of this type, including the decision on how to record traits and the subjectivity of determining degree of expression of traits (Scott and Turner 1997). The first issue relates to how researchers will collate the data they observe; a dichotomous distinction between 'absent' or 'present' is generally used when assessing the frequency of traits within populations (i.e. Carson 2006; Howell and Kintigh 1996; Irish 1997). This type of data can then be used to make comparisons of frequencies between populations as is often utilised in studies of ancestry in anthropology (e.g. Hanihara and Ishida 2005; Lee and Goose 1972). However, due to many nonmetric traits displaying a range of expression it is not always straightforward to identify them as being present. Hughes and Townsend (2013) discussed how it is often the researcher's own decision regarding the classification of nonmetric traits and how continuous, binary, interval, and ordinal data can all be used to classify traits. However, the information each is able to elicit may vary. In regard to the subjective nature of recording traits, the issue of which traits to record is raised. In comparison to metric analysis of crown size, nonmetric traits are thought to be less amenable to evolutionary changes and frequencies of such traits may diminish with each new generation (Scott and Turner 1997). Conversely, as there have been discussions amongst practitioners regarding the best way to record the presence of nonmetric dental traits, attempts to standardise and update the recording process of a nonmetric traits (Turner II *et al.* 1991) were devised as ways for researchers to first be able to recognise the most

commonly occurring traits, or at least for those with distinct enough expressions, and to reduce interobserver error in their scoring. As the current standard adheres to scaled descriptions from the Arizona State University (ASU) scoring system, focus is placed on degrees of expression rather than a simple distinction between absent and present. Some (i.e. Scott and Turner 1997) suggest that using scoring systems such as this is the better approach as it reduces the amount of subjectivity between researchers by allowing variations on what is actually representative of the 'present' trait. However, a stronger argument may be made based on the type of study that is being conducted from this data. The ASU scoring system may help to differentiate between levels of expression of nonmetric traits, however most studies interested in frequencies of traits within groups will need to dichotomise the data to maximise potential results. Irish (2005) has suggested using standardised 'cut-off' points for these ranked traits in order dichotomise data for statistical testing. This may also help with reducing discrepancies between researchers for the scoring of traits in cases where expression is slight.

Currently, there is no published research on the degree of expression correlating more strongly to members of the same biological family (i.e. those who display greater expression of a trait are not thought of as more similar than those with lesser expression, as the trait counts as present in both cases). There have been some (i.e. Stojanowski and Hubbard 2017) who have commented on the appearance of nonmetric traits being less sensitive a measure for interpretations of biological relationships in kinship studies compared to metric data. The quasi-continuous theory of expression (Brook *et al.* 2014; Scott and Turner 1997) suggests that parents with the gene for trait expression may pass this along to their offspring, yet due to the combination of other conflating factors, its expression is considered variable.

Metric data recorded from crown diameters are relatively more straightforward to assess compared with nonmetric traits as they are more objectively defined. Metric traits appear on a continuous spectrum, and the well-established landmarks used for measuring help to reduce the interobserver and intraobserver error associated with comparisons among researchers. Crown size, being a continuous trait, can better reflect genetic diversity within each generation which allows for stronger connections between biologically related individuals to be observed in skeletal assemblages. Using a statistical model that allowed for sex-specific family resemblance of traits, Potter *et al.* (1983) determined that a shared familial environment contributes significantly to the determination of tooth crown size among siblings. Arguments can be made to the contribution of other factors on crown size besides common environments (i.e. sex), although this can be overcome by comparing the distributions of crown size separately for males and females of the same group to simplify statistical analysis of traits. Further to the point, however, not all teeth are shown to be sexually dimorphic between groups within a given population (as will be demonstrated in Chapters 5 and 6).

Additional environmental differences that may cause variations in tooth size can be observed at a population level. Smaller, isolated populations tend to be more homogenous in regard to genetics (Howell and Kintigh 1996; Scott and Turner 1997) which means that there may be less variation in expressed traits within the assemblage for two main reasons. The first relates to an absence of certain genes that cause the appearance of nonmetric traits in the founding population, it will be unlikely that they will appear in any great quantity in the population without the introduction of new genetic material (i.e. through marriage with members of different populations or migration). The second continues from the first, wherein the nature of homogenous samples will appear similar within the entire group, and difficulty will arise

when trying to notice any strong similarities or differences within such a group that would indicate various degrees of biological similarity. Bowden and Goose (1969) also touched on this issue when they acknowledged that the variation they observed in their modern sample demonstrated that random mating practices were utilised by the population causing a random influx of various genetic material. Populations that are more isolated, may not have the same degree of random gene mixing that occurs naturally in modern, urban populations. Alt and Vach (1995) suggested a possible solution to determine whether the observed appearance rates of specific traits is confounded by a small population is to use a comparative skeletal assemblage to ascertain whether the levels are within a normal expected range or not. While more resistant to these such of changes, buccolingual and mesiodistal measurements are not immune from sample issues. Bader and Lehmann (1965) highlighted a potential issue involving metric data from small sample sizes. They speculated that lower levels of genetic diversity in small populations resulted in a higher chance of gene mutation which would make these metric traits more variable. However, their research was conducted on lab mice, which do not have the same mating taboos as human populations, mice have a much higher likelihood of mating with closer biological relatives than humans would, which could indicate why this phenomenon was observed in their research.

Within nuclear family units whose members share similar genotypes, there is also the possibility that the phenotypic representation of these shared genes will be dissimilar. Brook *et al.* (2014) acknowledged that the complex pathway and high number of genes involved in the morphogenesis of teeth allows greater potential of gene mutation. According to their research, a mutation at a single gene that contributes to the development of tooth morphology can cause a variation in the appearance of a specific trait. This means that the degree to which genes can impact on tooth morphology is also in part governed by random

factors, those naturally intrinsic to a specific person. This also would have a direct effect on the ability to accurately measure heritability of certain traits within a population (Hughes and Townsend 2013). If the variety of expression in phenotype was masking the true genotypic representation of a specific trait, researchers would not be aware of this and, if not considered in their research, may inflate or understate the true frequency of a specific trait in a given population leading to misinterpretations. Additionally, the gold standard use of twin studies also raises issues observed within nuclear family groups. Due to the nature of heritability, both environmental and genetic influences can each able to contribute relatively more to the expression of a certain phenotype (Hughes and Townsend 2013). The implication of this is that, twins in shared environments (both maternal and post-natal) can lead to a masking of the true influences on trait expression as it would be difficult to discern whether the trait researchers are observing is more related to the shared DNA or rather the shared environment.

The quasi-continuous theory of expression also relates to the fact that multiple variables regarding tooth morphology need to be considered in order to be able to make all-encompassing interpretations about dental phenotypes. Essentially, researchers need to be aware of the interaction of tooth size in regard to the expression of nonmetric traits, otherwise there is the potential problem of making incorrect interpretations of biological similarity from either metric or nonmetric traits without considering the influence they have on one another. Brook *et al.* (2014) demonstrated the congruent nature of their expression during investigation. Individuals in their study with overall smaller teeth compared to the wider population also appeared to have an increased presence of more nonmetric traits associated with reduced or absent teeth (i.e. hypodontia, peg shaped incisors, etc…) (Brook *et al.* 2014, 137). In comparison, those who had significantly larger teeth compared to the

wider population appeared to have increased appearance of nonmetric traits associated with 'extra' tooth development (i.e. supernumerary teeth, extra cusps, Carabelli's trait, etc…) (Brook *et al.* 2014, 138). As these observations can also be noted to work both ways, it provides further justification for researchers to study both of these variables when using dentition to assess genetic influences.

Sex of the individual also needs to be considered here, while others have commented on the dimorphic nature of teeth relating to overall size, Townsend *et al.* (2009) suggested that sex differences in size can contribute to differences in nonmetric traits as well. Females with smaller than average teeth are said to be more likely to display nonmetric traits related to reductions in form or number of teeth. Conversely, males with larger than average teeth are more likely to display traits associated with additional or extra features (i.e. supernumerary teeth or more cusps). Moreno Uribe and Miller (2015) concluded similarly in their discussions on dental malocclusion, which in part was caused by size of dentition, that the complex nature of trait inheritance lends itself to a multivariate phenotypical approach during an investigation. These ideally would combine both quantitative (metric) and dichotomous (nonmetric) phenotypes in order to gain more meaningful results (Moreno Uribe and Miller 2015, 97). The issues highlighted in this section form the foundation for the argument made by Brook *et al.* (2014), who claimed that the distinction between metric and nonmetric traits needs to become more fluid. They proposed utilising the newly emerging concept of *phenomics,* the comprehensive study of a full range of phenotypes expressed on any given individual, subsequently endorsed by Moreno Uribe and Miller (2015). It would be possible to apply this concept and create a new field of *dental phenomics* which would consider all the aforementioned variables in order to explain why variations in human dentition appear between and within populations (Brook *et al.* 2014; Moreno Uribe and Miller 2015). In fact,

Kimura *et al.* (2009) also alluded to the fluid nature of metric and nonmetric by the discovery that the number of *EDAR* 1540C alleles, a receptor gene, is positively correlated to the presence of shovel shaped incisors and larger incisor tooth dimensions. The models used for quantifying genetic and environmental influences described by Hughes and Townsend (2013) also suggested that adopting a phenomics approach would help to better interpret the influences observed from multiple factors. This concept is quite adaptable to the field of osteoarchaeology, if the data is available, as they already rely on multidisciplinary approaches when investigating various social constructs from archaeological populations.

3.5 Applications and Considerations for Practice

The use of DNA and mitochondrial DNA (mtDNA) provide the more robust methods of establishing identity and biological similarity of individuals within archaeological skeletal assemblages. There have been numerous examples where DNA has been able to be extracted from teeth, and other skeletal elements, and used to successfully confirm cases of suspected family relationships or individual identities in archaeological and anthropological contexts (i.e. Adachi *et al.* 2003; Deguilloux *et al.* 2014; Hubbard *et al.* 2015). While DNA analyses have the potential to determine individual identity or establish biological relationships beyond reasonable doubt, there are limitations with such approaches in archaeology. Obtaining samples of DNA or mtDNA from ancient remains is not always possible due to the degradation of genetic material over time and often made more difficult by certain taphonomic processes (i.e. weathering, burning and soil acidity) which may inhibit the ability to collect useable DNA from which to base comparisons. There are also further complications that arise when trying to identify individuals or family units from a larger skeletal population; the task of beginning

to look for individuals that are related in a population of hundreds of unmarked individuals can be daunting. DNA analyses are expensive to conduct so it is less likely that samples will be taken from every member of an archaeological skeletal assemblage for comparative purposes. Furthermore, it is more likely to recover mtDNA compared to nuclear DNA in archaeological populations due to the difference in volume and location of preservation (i.e. within the nucleus vs mitochondria of a cell) and research has shown that mtDNA is not as useful on its own for establishing biological similarity on local or individual scales (Hubbard *et al.* 2015). Mitochondrial DNA is only able to provide information as it pertains to the maternal lineage of genetic inheritance which means that full interpretations on familial connection may not be wholly understood (Hubbard *et al.* 2015). A final issue with DNA sampling is that it is a destructive methodology. In the case of dentition, core samples from teeth must be obtained which damages the crown and would negatively impact on any further data collection of that particular tooth. This is especially problematic if widespread sampling was needed, or in cases where museum collections were involved. For these reasons it seems logical to pursue additional avenues from which biological similarity can be observed and commented on in relation to both paternal and maternal genetic lineages for individuals within archaeological skeletal assemblages.

Reviewing the literature on human dentition and biological similarity, it appears as though dental traits (both metric and nonmetric) can be used successfully for discussions on wider social concepts within archaeological skeletal assemblages, as long as the limits of this type of investigation are noted. The usefulness of dental morphology in anthropological and archaeological applications is dependent on what data researchers decide to use and at what level they are making comparisons between human subjects. Hubbard *et al.* (2015) reported that there are six distinct geographic levels that can be considered as research frameworks:

individual, family, local (within one population), regional (comparisons between populations in close proximity), continental (comparisons between populations across a larger geographic area), and global. These levels must be considered first before deciding what data needs to be recorded from dentition, and how it will be used in studies of biological similarity. Nonmetric dental traits, when dichotomised into either 'present' or 'absent' in order to report frequencies, appear to be better suited for larger scale comparative questions. Nonmetric dental traits are not as sensitive a measure of difference between people and so are better able to pick up on noticeable differences between groups that are separated by larger degrees rather than small discrepancies that are better suited to more sensitive methods of testing like DNA analyses (Hubbard *et al.* 2015). However, context needs to be considered in this regard as larger populations are likely to reflect greater genetic diversity and subsequent admixture effects on smaller scales, of which dental traits may not pick up on, compared to smaller, more isolated populations. When individuals from outside these more isolated populations enter the skeletal record due to migration, marriage or other kinship processes, it could be possible to detect those who are more similar from those who appear different. This enables information from a regional or continental geographic level to be observed more clearly on a family or local geographic level.

When deciding to pursue lines of inquiry into the lives of archaeological populations via their dentition, it needs to be recognised that skeletal assemblages are never a complete likening to a living society and some interpretations of kinship based on cemetery organisation may be vulnerable to misinterpretations. For example, if metric and nonmetric traits are used to determine biological similarity in a population and through analysis it appears that individuals with shared levels of similarity have been buried in close proximity together, it is not enough to conclude with complete certainty that the society buried family members together. The

reason for a grave location could indirectly result in family members being buried in closer proximity but was actually dependent on a factor not observed in the skeletal record (i.e. burial according to social class, occupation or circumstances surrounding death) (Alt and Vach 1991). Considering this, these types of analyses involving human dentition would benefit from a multidisciplinary approach to understanding burial decisions by including aspects of contextual and social theories regarding burial practices and kinship of each population. This was highlighted by Howell and Kintigh (1996) who observed that the kinship practices under investigation need to be considered before interpreting biological data from the skeletal assemblages. Marriage and residence patterns may contribute to the decisions regarding the location of individual burials within a cemetery. If cemeteries are organised according to 'nuclear' families, there may appear biological evidence to suggest the presence of individuals who are not biologically similar as husbands and wives may be from different populations, reflecting less biological similarity. Pilloud and Larsen (2011) have approached the subject of membership within kin groups by investigating the representation of practical and biological kin in skeletal assemblages. Earlier discussions on kinship have clearly demonstrated that not all societies have the same definition of a kin group (e.g. Ensor 2011; Freeman 1973; Schneider 1965), therefore contextual information pertaining to the type of residence and marriage practices utilised by each society will help to make sense of the biological data that is collected from skeletal assemblages. If such information is not known, then interpretations should focus on varying explanations for observations of biological data supported with discussions on kinship theory.

Kinship on a larger, cultural scale has been successfully investigated by researchers who focused on identifying separate kinship groups in American archaeological skeletal assemblages (Howell and Kintigh 1996; Lane and Sublett 1972). These investigations

hypothesised that if physical separations appeared in cemetery organisation and the assumption was that these were based on kin group identity, that there would be similarities in the demography of each cemetery (age, sex distribution) and that the individuals within each separate group would appear more biologically similar via dental morphology. The cemeteries used in these investigations differ in regard to their macro spatial organisation compared to early Medieval cemeteries. The spatial patterning of the former appears more spread out and distinct compared to the latter. Implications of this create an *a priori* starting point for investigations into the representation of distinct kin groups within a contemporaneous assemblage. Howell and Kintigh (1996) also appear to mislead readers with the aim of their study as they stated that individual burials within each distinct cemetery could give information about kin group membership, yet they only compare between cemetery clusters, not within each. In contrast, cemetery organisation in the early Medieval period appears, at the macro-spatial level, to be more unified.

Further studies have focused on larger geographic levels to investigate differences in populations over time in order to support or refute theories of ethnic origins. Haeussler *et al.* (1989) compared a regional level approach for identifying the differences between the dentitions of the San and Central Sotho groups in South Africa. They used metric BL and MD dimensions related to basinasal length, another continuous trait, and found that the two populations were distinguishable. Certain measurements on specific teeth were identified as being more discriminatory than others and could therefore be used for classification. Irish (2005) utilised a dental anthropological approach to understanding the origin of ancient Nubian ethnicity. The ASU recording system for nonmetric traits was used to identify the frequency of several hypothesised founding populations for comparison to a Nubian sample. Quantitative analysis revealed a population theory for the area suggesting that Nubian ethnic

populations arose in the area after an influx of genes from additional populations through history. While all encompassing, it would be interesting to note, considering what is currently discussed regarding dental phenomics, whether results such as these would be further refined if both metric and nonmetric dental traits were both considered, as was not observed in these studies. For example, in Irish's (2005) study there appeared some large differences in the frequency of traits between populations sampled that are considered to be more commonly found in individuals with above averaged size teeth for their population (i.e. Carabelli's cusp, additional cusps and additional root numbers). If metric data were to be included in these comparisons, perhaps it would be possible to identify if these nonmetric traits were correlated to metrics and potentially allow for the inclusions of individuals with larger or smaller than average teeth who may align with those types of nonmetric traits. If so, this combination of traits could be refined in order to shed more light on how population variation is presented in human dentition.

3.6 Conclusion

Due to the taphonomic resilience and early fixed morphology of human dentition, teeth have great potential for eliciting information about biological similarity of individuals within and between archaeological populations. The understanding of dental development at the cellular level is becoming better understood and the influence of specific genes has been shown to relate to variations in patterning and phenotypic expression of individual teeth and tooth classes within human dentition (Evans *et al.* 2016; Sharpe 2001). While genetics do contribute to overall tooth morphology, modelling of this influence has revealed that other factors, such as foetal and postnatal environments, also impact the final morphology of

human dentition (Hughes and Townsend 2013). It is imperative that researchers in dental anthropology understand the interaction of genetic and environmental factors in order to fully understand the processes that lead to the manifestation of metric and nonmetric dental traits. As both types of traits have been shown to correlate with genetic similarity, a more holistic approach to understanding biological similarity can be evoked by a combination of them and environmental factors. Dental phenomics, a newly emerging subfield of dental anthropology, stresses this importance and makes definitive links back to the previously accepted concepts of quasi-continuous expression and threshold values observed in dental morphology (Brook *et al.* 2014; Scott and Turner 1997). For researchers interested in quantifying the similarity of dental morphology within archaeological populations the dental phenomics approach becomes all the more important as archaeological populations have many differences compared to modern populations regarding genetic diversity and environmental conditions. For example, the way in which smaller populations could contribute to a masking effect of certain traits or a general appearance of dental homogeneity within a group could make establishing biological similarity within skeletal assemblages more difficult when investigating only metric or nonmetric traits (Hughes and Townsend 2013). Early Medieval populations, such as the Anglo-Saxons, are often smaller and more isolated than modern populations and would encompass family units which may or may not be further divided in the skeletal record according to burial customs. In order to be able to study the dentition of these skeletal populations effectively, assessing both metric and nonmetric traits would be beneficial, though metric traits could arguably encompass differences in tooth form (Brook *et al.* 2014). By collecting data from these aspects and relating the biological data to contextual and historical data from the time period it may be possible to infer information relating to kinship practices and organisation of family units as reflected in mortuary

practices. Finally, it is vital that researchers have clearly defined questions in place prior to commencing a study on human dentition within archaeological populations as different geographic scales may require additional sets of data, and not all may provide robust answers if used without consideration to alternative variables (Hubbard *et al.* 2015). Within the remit of the current project, identifying kinship patterns in early Medieval archaeology would provide information as to whether any changes in social dynamics reflected in the historical record and contextual chronologies can be observed in the burial record. By examining populations that are contemporaneous and geographically close, similarities in dentition between the compared skeletal assemblages could be used as an indicator of social constructs and organisation during the early Anglo-Saxon period.

4. Cemeteries and Methodological Overview

When establishing the methodological approach for this project, cemetery choice, approach to data collection and process of data analysis all were done with the overarching aim of the project in mind: testing the utility of teeth to comment on biological similarity within archaeological assemblages. As such, this project was not designed to fully explore the in-depth relationship between topics like specific grave goods and identity or changes in burial orientations over time, rather, it was meant to demonstrate whether or not biodata could be easily obtainable from a large number of skeletons, and investigated in such a way that meaningful patterns may be identified which could then add to such discussions. In doing so, fulfilling the suggested approaches of Johnson and Paul (2016) and Johnson (2019) who argue for a more holistic, multifactorial approach for the building of bioarchaeological interpretations of past populations. In this case, in order to comment on overarching social constructs like identify and kinship, evidence streams would need to draw from biological data in addition to what has been published on contextual artefacts, spatial and structural patterning of cemeteries and recorded from later period historical documents.

4.1 Cemetery Sites and Condition of Human Remains

The four sites chosen for investigation were made accessible through projects involving The University of Central Lancashire, Manchester Metropolitan University, Oxford Archaeology East and through loans from council archives. The location of each cemetery in relation to one another in South-East England is presented in Figure 3. Two cemeteries, Hatherdene and Oakington, are from Cambridgeshire, Figure 4, and two cemeteries, Polhill and Eastry, are

from Kent, Figure 5. All individuals exhumed from each excavation had previously been given a corresponding context number (i.e. 999). Within this project, to simplify which skeleton came from which cemetery, each context number was assigned a letter corresponding to the name of the cemetery: H for Hatherdene, O for Oakington, P for Polhill and E for Eastry. Therefore individual 999 from Hatherdene became H999 in this project and could be linked easily to grave catalogues and skeletal reports.

Figure 3 - Overall UK location of the four cemeteries under investigation: Hatherdene (1), Oakington (2), Polhill (3), and Eastry (4) (Google Maps 2020).

Figure 4 - Distance between Hatherdene (blue pin) and Oakington (red pin) cemeteries within Cambridgeshire (approx. 10km) (Google Maps 2020).

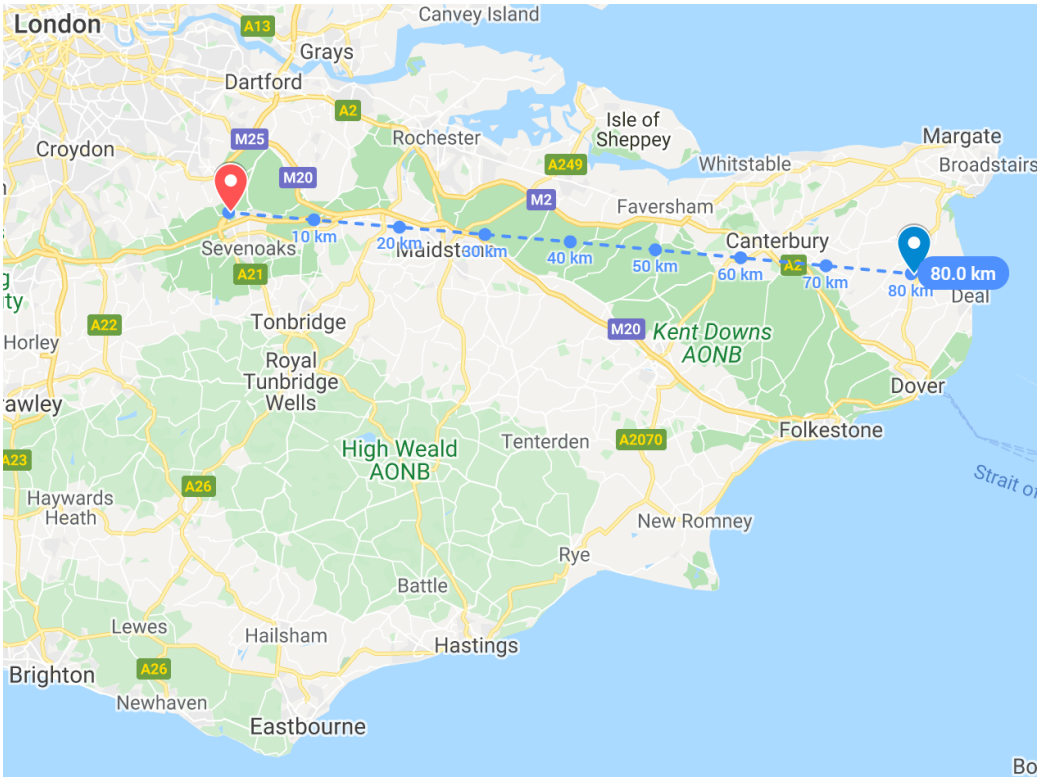

Figure 5 - Distance between Polhill (red pin) and Eastry (blue pin) cemeteries (approx. 80km) within the county of Kent (Google Maps 2020).

4.1.1 Hatherdene

The skeletal assemblage referred to as Hatherdene was recovered from Cherry Hinton, Cambridgeshire and was excavated by Oxford Archaeology East. Initial investigations took place in 2007, and a large-scale excavation and recovery occurred during July through October 2016. The cemetery appears to have been re-used throughout multiple periods, with evidence recovered and dated showing ranges from: prehistory; late Iron Age through Roman; early, middle and late Anglo-Saxon; Medieval and; post Medieval (Ladd *et al.* 2018). By far, the majority of contextual and skeletal evidence was dated to belong to the early Anglo-Saxon period, with dates ranging from the 5th through 6th centuries AD. All individuals used within this project were dated to the early Anglo-Saxon period (5th-6th centuries AD). During the 2016 excavation, the North-West, North-East, and South-West borders of the cemetery were confidently identified. The soil in this area, being comprised of a large proportion of clay, led to good preservation of skeletal and contextual material on site. In total, 126 individuals were recovered from the early Anglo-Saxon portion of the site in single interments, predominantly. Demographic information was estimated from the skeletal remains using standard methods for biological sex and age estimation from Buikstra and Ubelaker (1994). Due to limited time with the remains, the estimations provided by Oxford Archaeology were not verified independently, and these reports remain unpublished currently. There were, however, the interesting inclusion of 'stacked' burials (Ladd *et al.* 2018), where the same grave location was used for multiple interments of individuals, one on top of the other as opposed to a side by side interment. This was a feature not observed to be present in any of the other three cemeteries under investigation within this project, nor was it said to be a common find across contemporaneous Anglo-Saxon sites across England

during this time period (Ladd *et al.* 2018), making it an interesting case study to explore within the remit of this study. As such, the potential to search for patterns within the biological data obtained from the individuals interred in this manner, combined with contextual information, may help to provide theories regarding their use at Hatherdene. Most individuals uncovered were aligned in the graves facing a South-West to North-East position, though there were a small group that deviated from this. Again, the majority of individuals were supinely positioned within their graves, although some were positioned on their side (both left and right) and prone. There was a reported mix of grave furnishings recovered from Hatherdene. Grave goods associated with gender (i.e. shields more common in male graves and brooches found in female graves) and status featured among the collection. Status of grave goods indicated there was a range of structural social diversity within the group associated with this cemetery. Some evidence of settlement was located near to the cemetery and dated to the middle Anglo-Saxon period which has helped to demonstrate the continued use throughout the era. The site of Hatherdene cemetery is located approximately 10km South-East of another assemblage used within this project, Oakington (Figure 5). Oakington and Hatherdene are comparable sample sizes, and have been dated to similar time periods, as such the pair will form the majority of the dataset for this project and be useful to reinforce any patterns observed within and between them, strengthening interpretations about kinship and identity during the early Anglo-Saxon era. Figure 6 presents an overview of Hatherdene cemetery after excavation.

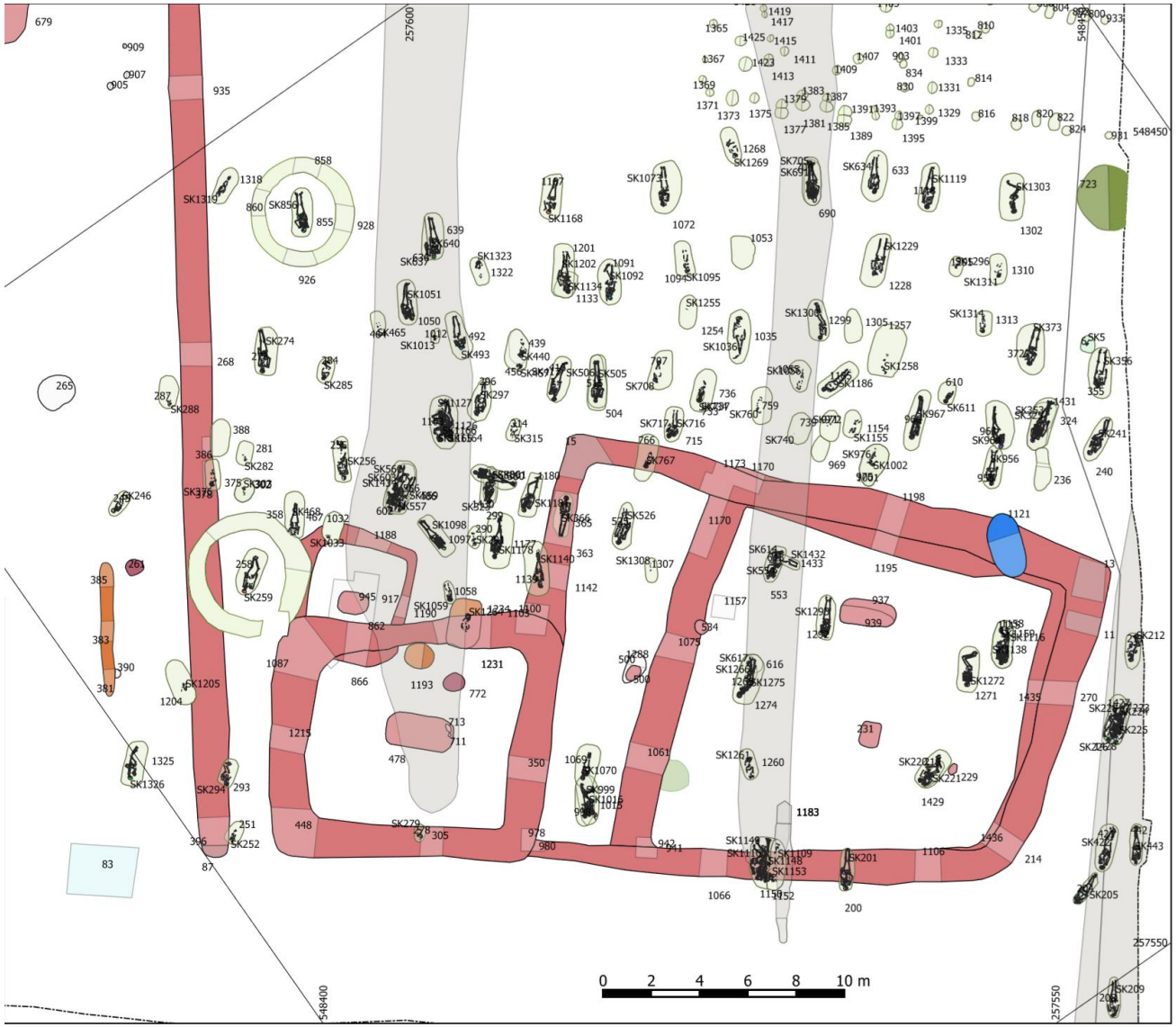

Figure 6 - Overview plan of Hatherdene cemetery excavation by Oxford Archaeology East (Oxford Archaeology East 2018).

4.1.2 Oakington

The cemetery at Oakington is located in a small town in the county of Cambridgeshire. The graves have been dated to the late 5th and 6th centuries AD (Mortimer *et al.* 2017). Sayer (2020, 120-122) provided more specific dating to the following individuals: O1376, O2154 and O2165 were dated to later 5th to early 6th century; O1450, O1747 and O1740 were dated to the mid sixth century and; O1798 and O1799 were dated to the later sixth century. The area surrounding the cemetery is relatively flat with layered soil consisting of sandy and clay levels and there is a stream near to the site. The earliest discovery of human remains at Oakington was in 1926, with a larger discovery and excavation in 1994. Additional excavations took place in 2006, and then as part of a research and teaching excavation run by The University of Central Lancashire, Manchester Metropolitan University and Oxford Archaeology East between 2010-2014. Overall, there was a total of 128 individuals excavated, representing: males and females, adults, sub adults and infants, individuals buried with an assortment of grave goods, multiple and single burials, and individuals in a variety of burial positions. There does appear to be two separate parts of the cemetery (Figure 7) with a smaller satellite interment being located South-East of the larger concentration of burials. The excavations in 2014 helped to identify the likely borders of the cemetery site, though it is possible that the cemetery did extend further under a new housing development to the North-West, due to the discovery of some commingled and disarticulated remains along a residential road adjacent to the cemetery. The site appears to have a higher concentration of infant and female burials compared to other contemporaneous Anglo-Saxon sites (Sayer 2014), which may suggest the associated settlement was favoured for childbirth; perhaps pregnant women were returning to their homesteads to give birth with their biological relatives. There is

evidence at the site of continued use through the dated time period, as ditches and later graves were often found to truncate graves and cut across the cemetery. This caused some disturbance of human remains where upper or lower portions of bodies were found to be missing in some individuals, but overall the preservation of skeletal material was good. There were some unique and ornately decorated graves present, including a woman buried with a cow, the only find of this kind during this time period in Europe (Mortimer *et al.* 2017). Most multiple graves uncovered at Oakington contained two individuals, but there was a grave in which three individuals were interred. The individuals interred in multiple burials comprised of both males and females, as well as adults and sub adults. Infants did not feature in multiple graves, unless they were of neonate age, where there was an instance of a female skeleton recovered with neonate remains found around her pelvic area indicating that she may have died during childbirth (Sayer and Dickinson 2013). Multiple interments have been used previously to discuss potential familial relationships (i.e. Stoodley 2002), so it may be possible that the individuals within the multiple graves at Oakington represent kinship connections. The main osteological report was compiled by Swales (2016) who used cranial and pelvic methods for sex estimation from Buikstra and Ubelaker (1994), and the following methods for degenerative and developmental age estimation, respectively: Todd (1921) and Brooks and Suchey (1990) and; Moorees et al. (1963), Scheuer and Black (2000). One individual, O1870 had been determined to be male by Swales (2016) using morphological methods, but unpublished DNA results have since determined this individual to have been female, therefore this correction was applied for this project, all other estimations by Swales (2016) were used.

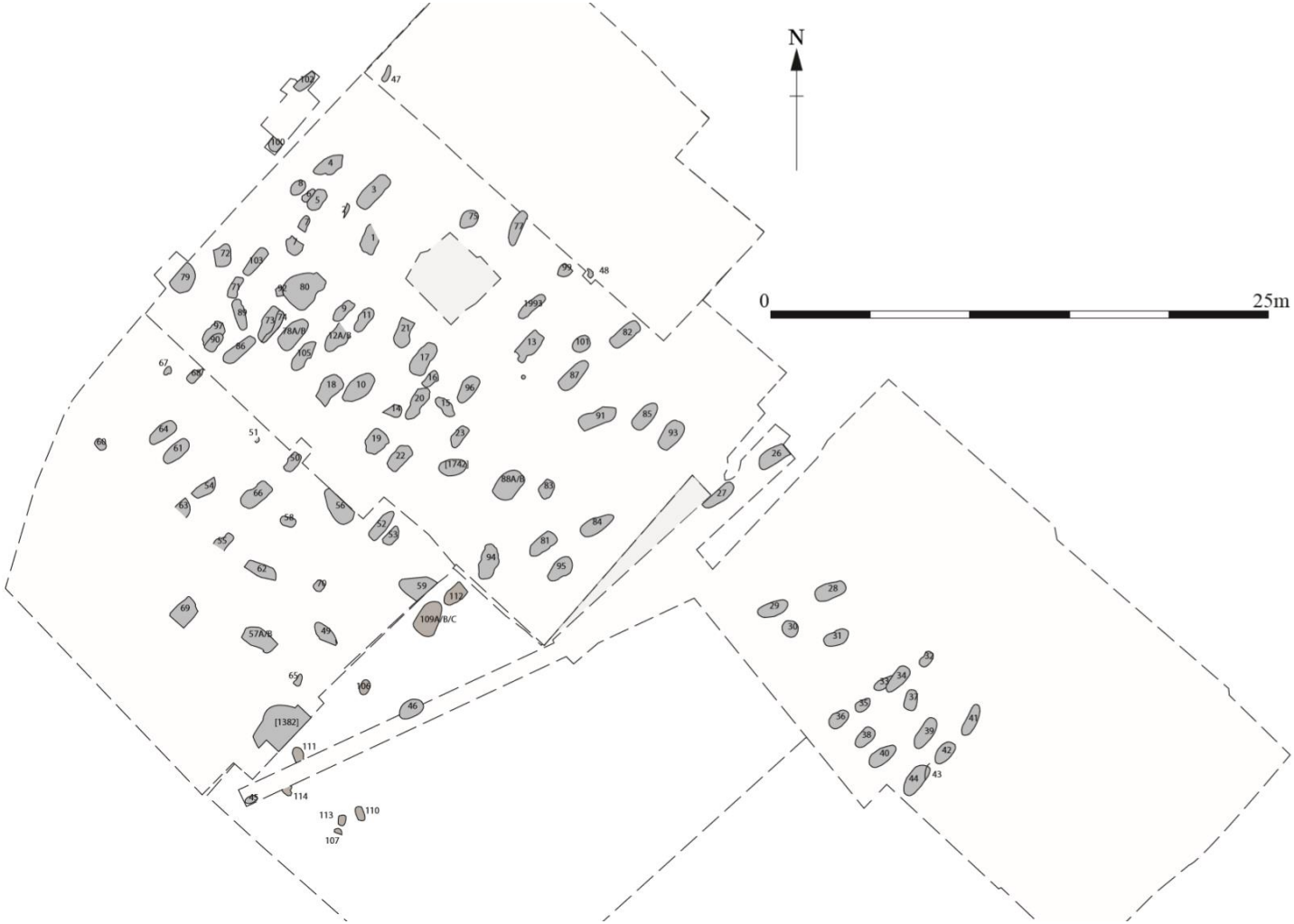

Figure 7 - Overview plan of Oakington cemetery excavation (Duncan Sayer 2017).

4.1.3 Polhill

Located in the county of Kent, a skeletal assemblage from Polhill, near Sevenoaks (Figure 8), was excavated during a series of small and large-scale projects spanning from 1839-1984 as roadworks and alterations to transport links expanded in the area. The cemetery has been dated using grave goods to show use between 650-750 CE (Philip 2002), no more specific dates were discussed for the 1984 sample used for this project. Philip (2002) stated that the graves excavated in 1984 had similar grave goods and burial styles to the rest of the excavation which was in line with the suggested dates of mid seventh-eighth centuries. Due to its location, situated on Upper Chalk and in view of the Darent Valley, it was suggested that the cemetery served a settlement site of similar size nearby, likely Otford, and was in use for generations. Though, it was also possible that the cemetery served smaller, scattered settlement sites as opposed to a single site (Philip 1967). The retention in site use over this time period may be attributable to the landscape being conducive to farming and settlement (Tyler 1992). During the period of excavation, a total of 182 individuals were exhumed from the site. It was only possible to obtain a small subset of this assemblage for use in this project, n=51, corresponding to the latest excavation and recovery effort on site between March and April 1984. The graves uncovered during the 1984 excavation were observed to be within apparent borders of the entire cemetery. The area that the cemetery was found could allow for a much wider dispersal of graves, yet these were kept in a smaller area indicating some planning went into the organisation of the Polhill cemetery (Philip 1967; Philip 2002). In addition to the relatively compact size of the cemetery, graves in this subset appeared less structured than in earlier excavated parts of the cemetery, perhaps indicating the more recently discovered graves were unmarked (Philip 2002). Within this section, there did appear

to be some graves clustered in small groupings (Philip 2002), potentially suggesting that those individuals within these smaller groupings of the assemblage may be representative of family units. An example of such is the presence of three male individuals (Graves 83, 84, and 85) buried in close proximity on the outer edge of the cemetery. Each of these males, in addition to being buried in a similar location, was found buried with a seax. In regards to demography and burial staging, the individuals interred within this section of the cemetery consisted of: adult and sub adult individuals, males and females, most were in single interments but one double burial was recorded, individuals recovered with a variety of grave goods, and some individuals were noted to be supine. The methods used to obtain biological sex and age information from the skeleton were not disclosed in the reports reviewed for this project, and attempts to verify estimations published in Philip (2002) were not conducted due to the poor condition of remains and limited time constraints. The contextual information obtained from the study of the grave goods led to interpretations about this population not being linked to the higher echelons of Anglo-Saxon society, rather, the inhabitants of these nearby settlements were more likely to be from middle ranking groups (Philip 2002). Fourteen barrow covered graves were identified in total across the entire cemetery which were suggested to indicate changing in burial ritual during Pagan to Christianity periods (Philip 2002), as the practice did not appear to be widespread or continuous throughout the occupation.

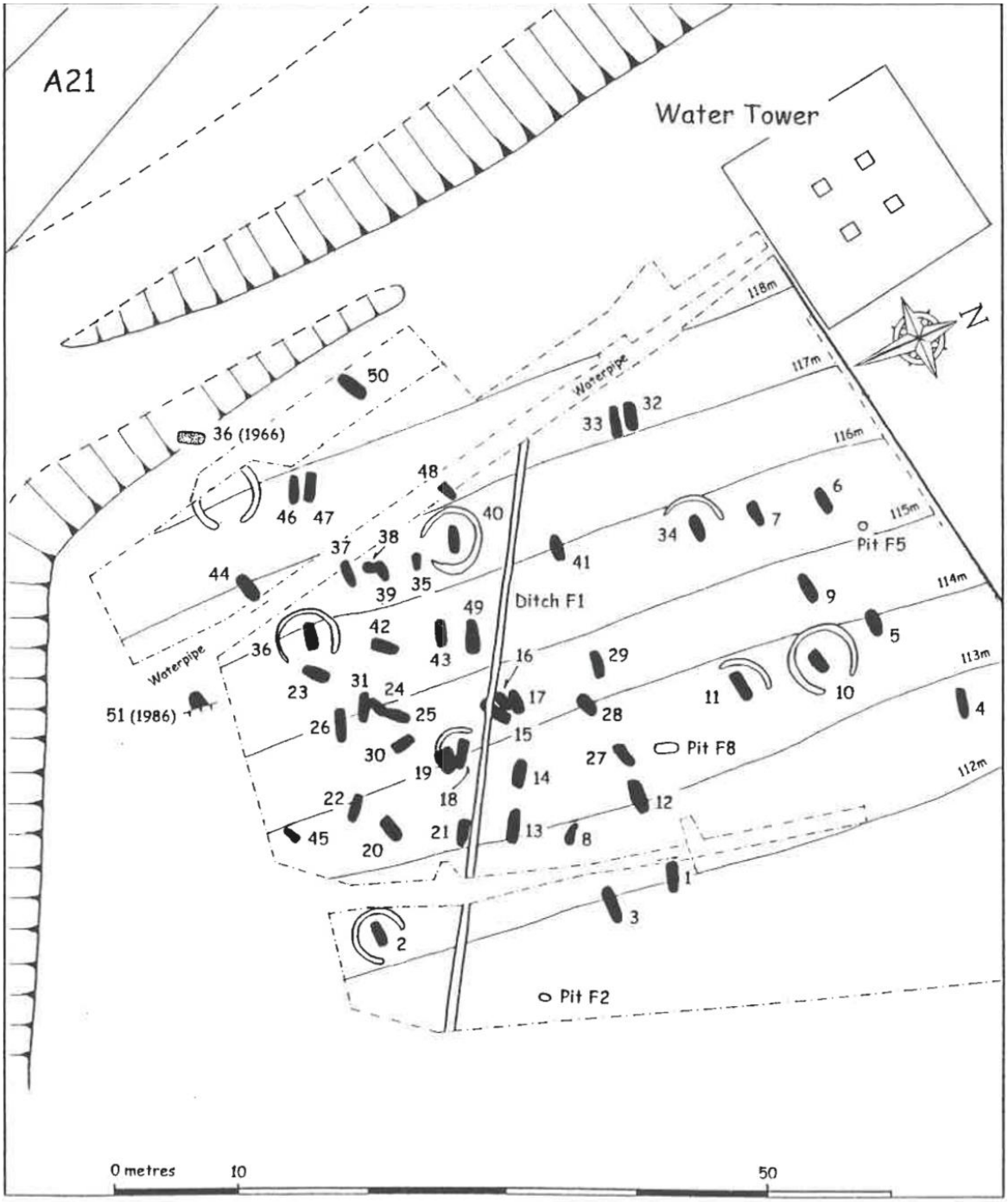

Figure 8 - The excavation plan of the 1984-86 recovery at Polhill, Kent (Philip 2002, 4 (Figure 2)).

4.1.4 Eastry

This cemetery was first formally identified in 1973 using aerial photography near the village of Eastry, in the county of Kent. The cemetery was estimated to contain a minimum of 300 individuals (Welch *et al.* 2008) but has yet to be linked to a settlement site. Excavation first occurred on the site in 1976 after a council proposal to create a water pipeline through the site; 37 graves were excavated and recorded during this period and the Eastern and Western borders of the cemetery were established. The site was further investigated in 1989 prior to the establishment of a bypass through the area, which helped to uncover additional graves bringing the total up to 78 and identified the likely Northern and Southern limits of the cemetery (Welch *et al.* 2008). The cemetery has been dated to the 7th century AD and has revealed two possible phases of use in the beginning and later halves of this century (Welch *et al.* 2008). The phasing applied to some burials was based on certain grave goods, but could not be refined for all graves used for this project. The graves contained a variety of material culture leading to the interpretations of prosperity of the settlement, but not representative of the elite class during this period (Welch *et al.* 2008). The soil conditions were not conducive to good skeletal preservation which prevented osteoarchaeologists at the time from being able to complete biological profile analyses on all recovered individuals, however, the majority were able to be assessed. Anthropological estimations using metric and nonmetric methods for sex estimation (i.e. Ubelaker 1989), and mainly reliant on dental attrition for age due to the poor levels of preservation (i.e. Brothwell 1981). Males, females and individuals of all age categories (infant through later adult) were found in this assemblage. Welch *et al.* (2008) stated the proportion of the two sexes and individuals within each age category was similar to what has been reported in other Anglo-Saxon sites in the Kent area. Most graves

were observed to contain individuals oriented East-West, though one was observed to be West-East. Multiple burials did not feature in this assemblage, however, there were individuals buried within barrows or ring ditches and others located close to or within the same ring. Figure 9 presents an overview of Eastry cemetery.

Unfortunately for this project, it was only possible to obtain a partial sample of individuals from the Eastry cemetery. The individuals obtained were a small subset from the 1989 excavation only. This has resulted in lesser data being obtained from Eastry which, as will be shown in the next section, has affected the ability to generate robust results from this sample alone. Instead, the data from Eastry within this project best serves to help support the interpretations made from the assemblages with larger sample sizes and to assess the potential for utilising this method for the study of partial assemblages.

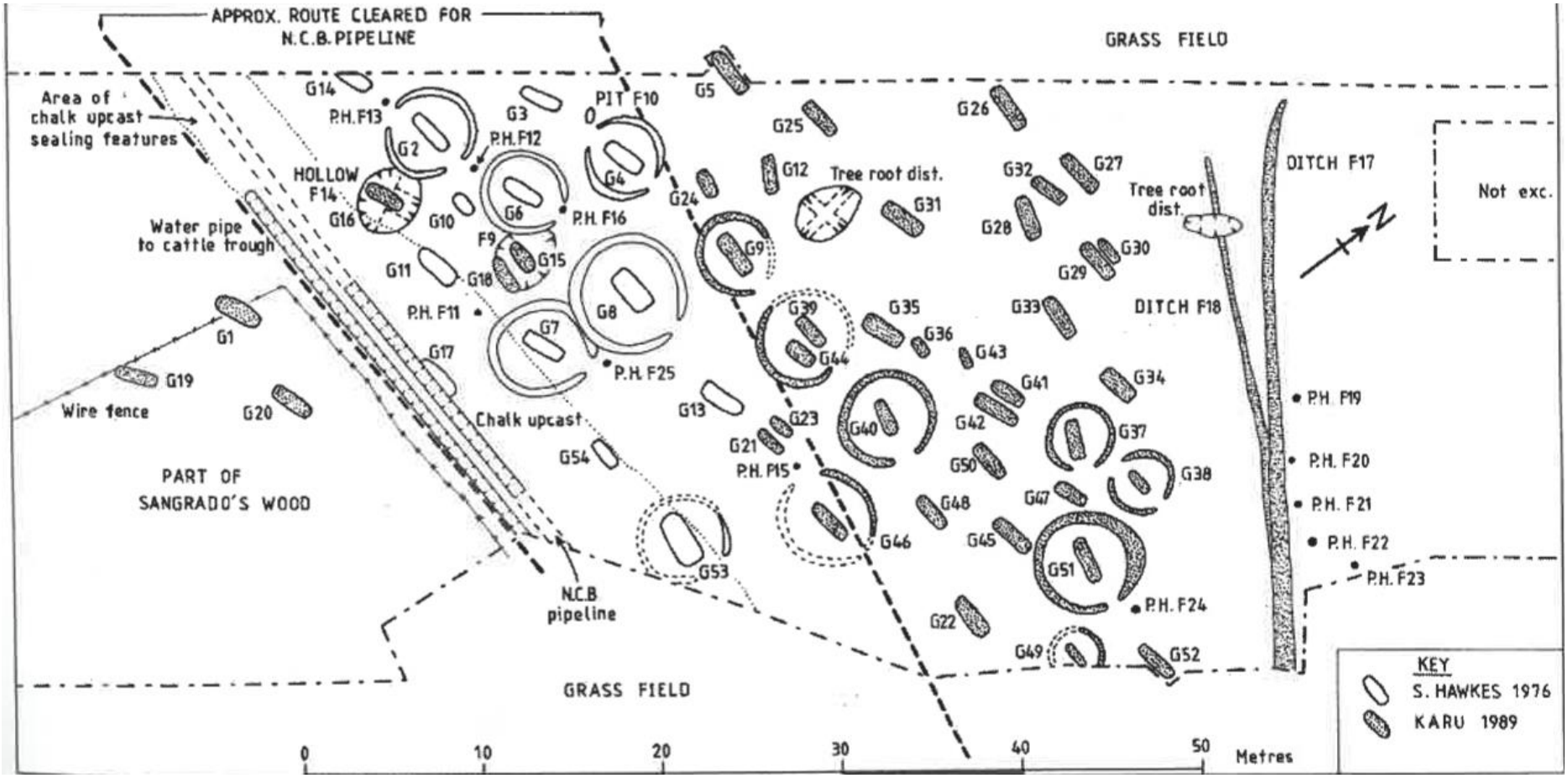

Figure 9 - The excavation plan of Eastry cemetery (Welch et al. 2008, 9 (Figure 4)).

4.2 Condition and Preservation of Remains

The condition and preservation of the skeletal remains from each of the four cemeteries varied. The individuals at Hatherdene and Oakington were well preserved in regard to completeness of skeletons present and the majority of remains were in good condition. There was evidence of truncation of graves, disturbance and skeletal degradation, but overall the remains present in these two cemeteries were structurally solid. Apart from the presence of some dental pathologies, the teeth of the individuals from Hatherdene and Oakington were also in good condition; many remained in situ within the maxilla and mandible and those out of situ were identifiable based on morphology. The individuals from Polhill displayed moderate to poor levels of preservation and the condition of remains ranged from partially complete to fragmented with some individuals being quite friable. The skeletal remains were quite delicate when being handled which resulted in greater numbers of teeth being found out of the maxilla and mandible. The teeth from Polhill displayed erosion in the form of groove patterns along the external surfaces of the crowns and roots. While affecting the integrity of the tooth's strength, these marks did not affect the ability to record measurements. Teeth that were not in situ were more difficult to identify in the Polhill sample compared to those at Hatherdene and Oakington. If identification was not possible, the teeth were not used, though this was rare for this group. The individuals from Eastry displayed the poorest level of preservation and the remains' conditions were very friable and fragmented. The majority of teeth from the individuals at Eastry were found to be out of situ and identification, at times, was hindered by their poor state. Those that could not be identified were not attempted for data collection. Across all four cemeteries, even where skeletal remains were in poorer condition, the tooth structural integrity was greater than that of the skeletal material, thus

supporting the assertion that teeth survive better than bone in archaeological contexts (Adler *et al.* 2011; Galloway *et al.* 1997). This adds further justification for the continued use of teeth in more bioarchaeological research, especially for those interested in recording biodata from human remains, as teeth are more likely to remain identifiable than skeletal remains when recovered during excavation.

4.2.1 Condition of Teeth and Pathology

Pathological conditions on the teeth were observed in all four cemeteries, with the presence of caries and infectious abscesses being most common. There were also numerous teeth within the sample that had calculus present, and some teeth were completely enrobed to the point of not being able to see any part of the crown. The level of dental wear within all four cemeteries was high, particularly in those in the middle and late adult age categories. Attrition was present on all tooth classes and ranged from mild wear on tooth cusps to complete destruction of dental crowns and exposure of pulp cavity. Not all of these conditions, however, resulted in teeth being unusable in the study. As long as the crown was intact enough to allow for the measurements to be recorded according to Hillson (1986) and Buikstra and Ubelaker's (1994) standards (see Chapter 4.3.1), they were used. After observing the teeth from each of the cemetery samples, it became apparent that the presence of nonmetric traits was more variable and inconsistent than had been hypothesised. Nonmetric traits were present, including both additional features like Carabelli's cusps and reduced features like peg shaped incisors. However, the frequency of the appearance of these traits was low among the entire sample which would have prevented robust interpretations to be made here. As a result of this, focus was placed on the metric data, and subsequent inclusion

of nonmetric traits will be linked, in future, to the concept of dental phenomics. Table 2 provides an overview of the number of teeth measured, the number of measurements affected by damage or disease and the number of teeth lost post mortem and antemortem for each cemetery.

Table 2 - Summary table of number of teeth in each cemetery that were used for the recording of mesiodistal and buccolingual measurements.

Cemetery	Teeth Present for Data Collection	Number of MD Measurements not taken*	Number of BL Measurements not taken*	Teeth Absent Post-Mortem (PM)	Teeth Absent Ante-Mortem (AM)**
Hatherdene	1517	123	127	452	39
Oakington	1292	77	48	305	67
Polhill	534	20	26	283	12
Eastry	213	5	8	319	12
Totals	**3556**	**225**	**209**	**1359**	**130**

*Of the teeth present, the number of MD/BL measurements that could not be taken due to wear/damage/disease/calculus. Dental disease (i.e. caries and calculus) was present on many teeth, but only noted in the dataset if it affected the ability to record a measurement.

**The number of teeth observed to be missing ante-mortem. If the bone was too damaged or missing to determine if AM/PM tooth loss, the missing tooth was classed as absent PM.

4.3 Data Collection

In terms of sample composition, this project focused on permanent dentition only. Research has investigated the correlations between deciduous and permanent tooth size (i.e. Hughes et al. 2000; Townsend 1980), however, accurate sex estimation from the skeletal remains of subadults is difficult (i.e. Olivares and Aguilera 2016). As several of the research questions for this project would need to be able to differentiate male and female data, it was for this reason subadult remains of unknown biological sex would be omitted. Therefore, individuals aged 15 years +/- 36 months who had identifiable permanent dentition present as well as an

associated biological sex (estimated via standard anthropological methodology (i.e. Klales et al. 2012; Phenice 1969)) were included in this study.

As this project would be cross checking statistical results against the locations of graves within cemeteries, it was important to ensure that the individuals used were recovered and recorded well to ensure provenience was known. This presented some challenges to overcome from Polhill, Eastry and Oakington. There was a small subset of remains from Oakington that had first been excavated in the 1990s and reburied within a vault structure to allow for the development of the land. Decomposition of the cardboard boxes within the vault led to the commingling of the remains within this context. These remains were excavated and exhumed well, and detailed provenience and corresponding context sheets were available to help re-associate remains as much as possible. Therefore, those individuals from the reburial vault that were re-associated and could be matched reliably to original excavation records were used in this project, and those that could not be reliably matched to such records were omitted. Issues arose with the samples at Polhill and Eastry were archival records did not always match up with skeletal remains associated with a grave or context number. In these cases, those individuals were not included in this study. After these eliminations, a total of 145 adult individuals were selected for use: 56 individuals from Hatherdene, 48 individuals from Oakington, 26 individuals from Polhill and 15 individuals from Eastry. From this sample, a database of 5988 measurements was generated for statistical analyses, as well as a small range of nonmetric traits. A complete overview of sample sizes, proportions of males and females and number of associated measurements is presented in Chapter 5, Table 2.

4.3.1 Metric Data

Metric data was recorded in the form of mesiodistal and buccolingual diameters from each tooth present in the sample. Figure 10 presents an overview of the location these measurements can be recorded from on the tooth crown.

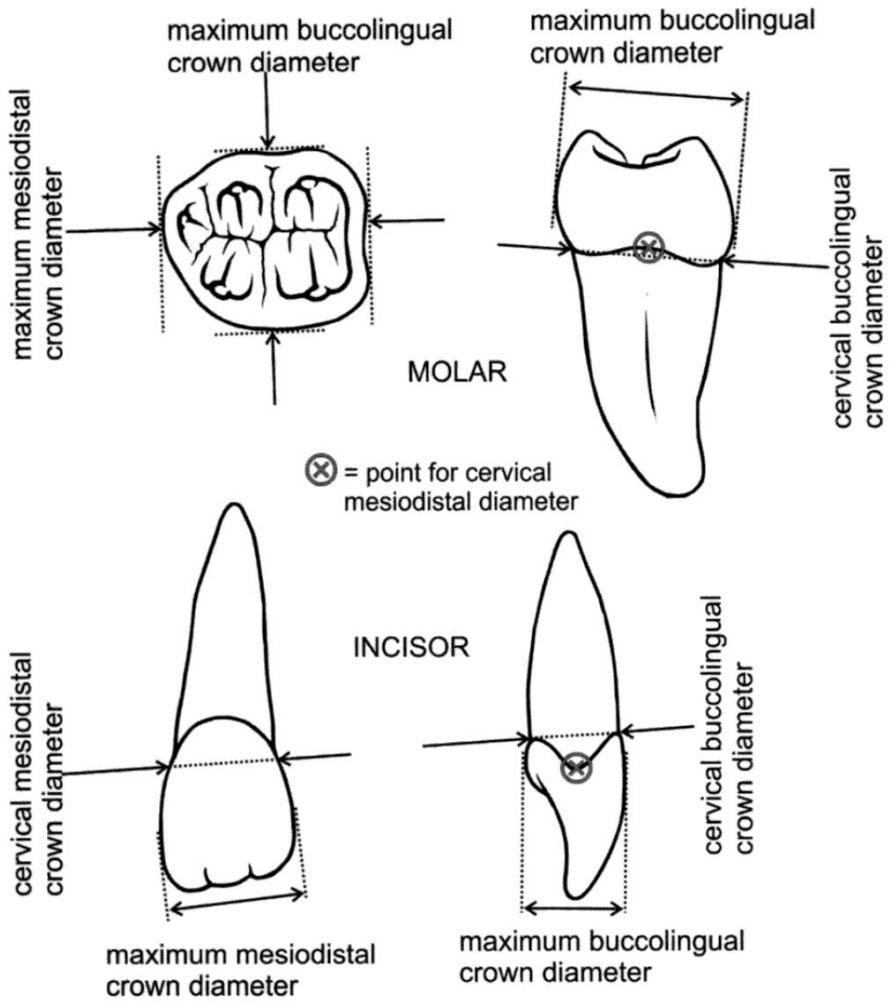

Figure 10 - Diagram of measurement points for mesiodistal and buccolingual tooth dimensions (Hillson 1986, 261).

Within the field of dental anthropology, it is generally accepted that these measurements provide the most genetically influenced data in regards to individual 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; Turner and Brown 1978a; 1978b) while being relatively simple to take. Mesiodistal diameters refer to either a measurement being taken between two interproximal contact points which are parallel to the occlusal surface of the tooth or as the maximum width of the tooth crown in the mesiodistal plane (Hillson 1986; Buikstra and Ubelaker 1994; Mayhall 1992), with the preferred option being the latter, as there is greater potential to retrieve data from teeth which are more worn (as is observed in many archaeological populations, including those within this study). Buccolingual diameters are defined as the widest measurement taken across a plane perpendicular to that of the mesiodistal (Hillson 1986; Buikstra and Ubelaker 1994). Thus, mesiodistal measurements were taken first during this sequence, followed by buccolingual. Crown height has also been used in similar research, however, this measurement is more vulnerable to the effects of dental attrition (Buikstra and Ubelaker 1994) and as a large proportion of the individuals within these four assemblages displayed dental wear, the decision was made to rely on the aforementioned mesiodistal and buccolingual measurements and forgo crown height.

It was important to ensure that measurements were taken consistently throughout the course of data collection, therefore the same researcher recorded all the measurements from all teeth. Gordon and Bradtmiller (1992) tested the level of inter-observer error on a series of anthropometric measurements. Their discussion noted that each researcher develops their own measuring style over time which adds support to the idea of one person conducting a series of data. To account for intra-observer error in this project's dataset, all measurements were taken three times and the average was used as the final measurement. In the event that the three measurements were more than 0.5mm different, three more measurements were

taken and an average used. If tooth antimeres appeared to differ dramatically in their dimensions, these teeth would have their measurements taken again (three times each) in order to ensure consistency and repeatability in measurements.

While acknowledged as being likely, inter-observer error was not assessed in this study. Time restraints and the lack of available experienced researchers to re-measure teeth were the main reasons why this decision was made. Research has shown that experience level can influence repeatability of results, increasing inter-observer error (Langley et al. 2018). However, standardised points from which to take the measurements from (i.e. Hillson 2005) are designed to help minimise error between different observers as all measurements are taken with the same kit, from the same places (Adams and Byrd 2002; Buikstra and Ubelaker 1994).

4.3.2 Nonmetric Data

Nonmetric trait data was recorded according to the Arizona State University (ASU) system for identifying and classifying morphological differences in tooth appearance. While this system is not inclusive of every potential morphological trait that exists (Alt and Vach 1995 cite over 700 traits can be observed), it does focus on specific traits that are relatively easy for researchers to observe and score, those that express little sexual dimorphism, have higher survivability in archaeological populations, are slow to evolve, and are powerful indicators for characterising populations in estimations of biological affinity (Turner II *et al.* 1991). Additionally, the ASU system is accepted as standard recording procedure in forensic anthropological investigations (Buikstra and Ubelaker 1994) which makes its use, along with

mesiodistal and buccolingual diameters, a suitable choice for comparative studies. While this method was employed and utilised, the appearance of such traits was relatively low in this study and would not have led to as meaningful statistical results compared to the metric data. The future use of this data will be discussed in Chapter 7.3, where an approach to using this data to corroborate ideas presented in Chapter 3 regarding dental phenomics and potential work with geometric morphometric analyses will be discussed.

4.3.3 Tooth Nomenclature

A combination of nomenclature was used to identify individual teeth throughout this project. The Universal Numbering system (American Dental Association 2010) was used to distinguish each individual tooth during the recording of data. This system uses the numbers 1-32 to identify every permanent tooth individually across the maxilla and mandible. In addition, for results and interpretations, short-form word versions of each tooth were used as it may be easier for those not familiar with the Universal Numbering system to identify teeth. These shorter versions denote if a tooth was from the right (R) or left (L) side of the mouth and whether the tooth was maxillary (Mx) or mandibular (M). In addition, they show if the tooth was a central incisor or lateral incisor (CI or LI), canine (C), premolar (P) or molar (M). In the case of premolars and molars, numbers were used to signify which one was being referred to. Table 3 provides an overview of the Universal Number assigned to each tooth, the full name of each tooth and its corresponding shortened version used within this project.

Table 3 – Overview of nomenclature used to refer to individual teeth within this project. A combination of Universal Numbering system and short-form versions of the full tooth name were used throughout.

Universal Tooth Number	Full Tooth Name	Short-Form Name
1	Right maxillary third molar	RMxM3
2	Right maxillary second molar	RMxM2
3	Right maxillary first molar	RMxM1
4	Right maxillary second premolar	RMxP2
5	Right maxillary first premolar	RMxP1
6	Right maxillary canine	RMxC
7	Right maxillary lateral incisor	RMxLI
8	Right maxillary central incisor	RMxCI
9	Left maxillary central incisor	LMxCI
10	Left maxillary lateral incisor	LMxLI
11	Left maxillary canine	LMxC
12	Left maxillary first premolar	LMxP1
13	Left maxillary second premolar	LMxP2
14	Left maxillary first molar	LMxM1
15	Left maxillary second molar	LMxM2
16	Left maxillary third molar	LMxM3
17	Left mandibular third molar	LMM3
18	Left mandibular second molar	LMM2
19	Left mandibular first molar	LMM1
20	Left mandibular second premolar	LMP2
21	Left mandibular first premolar	LMP1
22	Left mandibular canine	LMC
23	Left mandibular lateral incisor	LMLI
24	Left mandibular central incisor	LMCI
25	Right mandibular central incisor	RMCI
26	Right mandibular lateral incisor	RMLI
27	Right mandibular canine	RMC
28	Right mandibular first premolar	RMP1
29	Right mandibular second premolar	RMP2
30	Right mandibular first molar	RMM1
31	Right mandibular second molar	RMM2
32	Right mandibular third molar	RMM3

4.4 Statistical Analysis

All statistical analyses were conducted using SPSS (IBM Corp 2016) and R (R Core Team 2017) statistical software packages. The exploratory approach to data analysis for this project focused on the data set as a whole first, by broadly investigating any trends or patterns observed. Analysis then proceeded to investigate the influence of biological sex and cemetery location as variables that may influence tooth metrics before finally using the information gained from the former statistical tests to investigate patterns regarding similarity of individuals. The key findings of all analyses are presented in Chapter 5, and the overall raw results are provided in Appendices 1-6.

4.4.1 Descriptive Statistics

It was first important to explore the dataset on a basic level to assess the quality and spread of data within each cemetery site as well as between the cemetery sites. Descriptive statistics were generated for each tooth to showcase the: minimum and maximum measurements, the standard deviation and error, the 95% confidence interval range, and variance. Patterns and general trends within these measures were explored and reported in Chapter 5. Testing was also done with the data to assess whether or not the values were normally distributed; normal distribution is advantageous, but not preventative from additional statistical testing (Buthmann 2018). However, it is important to know if a particular data set is normally distributed or not before employing multivariate analyses to ensure the data is being treated appropriately. Finally, bivariate plots were produced to observe the level of covariation between the mesiodistal and buccolingual tooth dimensions.

4.4.2 Outliers

Outliers were detected using box and whisker plots to help identify which individual measurements fell outside of the inter-quartile range for each tooth and dimension. In general data sets, it is recommended that outliers are removed before continuing with further analyses (Motulsky and Christopolous 2004), however, in biological data sets, this advice is not the same. As differentiation between biological specimens can cause outlying data points to appear, it is important to retain them for future analyses (Motulsky and Christopolous 2004). As this project is using tooth biodata in order to look for patterns of similarity or dissimilarity between individuals, it was pertinent to leave outliers in, but helpful to identify who these measurements were attributable to. SPSS allowed for the tagging of data points according to known context number which made it possible to easily identify which individual possessed an outlying tooth dimension within the sample. These were recorded and discussed further in Chapters 5 and 6.

4.4.3 Variation due to the Influences of Cemetery Location and Biological Sex

After running analyses for descriptive statistics and normality, the exploratory approach continued by choosing two variables to focus on to assess their influence on tooth size: cemetery location and biological sex. The testing process for both of these was similar, with analysis of variance (ANOVA) testing completed for tooth data that were normally distributed, and Kruskal-Wallis tests completed for those that were not normally distributed, both with a level of significance set at <0.05. These tests are designed to determine if the variance between the means of groups are significantly different or not (Spiegel and Stephens 2017).

In the case of biological sex this was used to determine if being a male or female would contribute to the differences in variance observed in descriptive statistics. For cemetery location this, similarly, tested the hypothesis that belonging to a particular cemetery group would attribute to the differences in variance observed within the tooth data. If significant differences were observed in the results of cemetery site membership, post-hoc tests were performed using Tukey tests to find where these differences were attributable to across the four sites. Post-hoc tests were not needed in the case of biological sex differences as there were only two groups being compared.

Although not a new topic, there has been a recent resurgence in the wider scientific community regarding the use of p-values and the often-inflated level of important placed on their interpretation. Benjamin et al. (2018) provide an overview of the history of this issue, first commented on by Fisher in the early part of the 20th century, regarding the 0.05 threshold for significance. However, there are issues with reproducibility, large sample sizes and choice of statistical tests that can affect the final p-value (Benjamin et al. 2018; Lin et al. 2013). As this project has a large dataset to compute, it is likely that these issues will apply to results obtained here. However, this section of analyses where p-values are being calculated are not being used to support interpretations of identity or for use in excluding any data based on the outcome of a significance test. In these instances, the p-value is only being used to help better group tooth data to prevent other variables from confounding the discovery of biological similarity in tooth data. Whether or not a tooth measurement is found to differ between biological sexes, only will determine to which group the data is best compared.

In the event future research wants to focus on biological sex related differences or differences attributable to environments, it would be advisable for researches to consider using

alternative measures of significance to better understand what a p-value is representing. Effect sizes, confidence intervals and intuitive Bayesian approaches are such solutions put forward to use alongside, or instead of p-values to better understand how variables are being affected in scientific research (Benjamin et al. 2018; Price et al. 2020).

4.4.4 Hierarchical Cluster Analysis

Hierarchical cluster analysis (HCA) was used to enable the detection of patterns in the grouping of individuals within and between cemeteries based on the cluster patterns generated across multiple teeth. There are other exploratory methods by which to identify similarity between individuals in a data set, such as principal component analysis (PCA) or multidimensional scaling (MDS). Often times, PCA is used to identify the variables that are the strongest determinants of similarity between individuals in a dataset and is recommended for use when there are three or more response variables being assessed (Granato et al. 2018; Oliveira et al. 2015). However, as this project only utilises two variables (MD and BL dimensions), and the inclusion of both was important as they are under different genetic influences (see Chapter 3.2), it was decided to use HCA in favour of PCA. MDS is again similar to both PCA and MDS and allows for the visual depiction of similarity in individuals in a dataset. Both PCA and MDS focus on the similarity in variables separately and depict how that contributes to similarity between individuals within a dataset. However, HCA focuses on clustering the individuals into groups based on combinations of variables, which works well for this project's dataset. Furthermore, the output of MDS does not display clear clusters and the visualisations can be difficult to interpret with larger sample sizes.

While HCA is not seen as a statistically 'perfect' approach to identifying true clusters (Abu-Jamous *et al.* 2015; Baker and Hubert 1975; Milligan and Cooper 1986), there are many benefits to its inclusion in a project such as this. HCA does not rely on the use of a pre-determined set number of clusters, rather, it is an agglomerative process that allows data to naturally group until all groups have been joined within the data set (Fraley and Raftery 1998; Grubesic and Murray 2001). The agglomerative approach begins with each individual being a part of their own cluster and are then linked along the way by specific criterion (a linkage method) (Fraley and Raftery 1998). Along similar lines, in contrast to 'flat' clustering methods like K-means, the hierarchical aspect of HCA allows for distances between groups of data points to be identified via a dendrogram; it is possible to identify some clusters that are more closely related than others (Abu-Jamous *et al.* 2015). Furthermore, the ability to select a particular linkage method to guide the clustering process provides flexibility to better match the statistical process with the questions being asked of the data. This project used the Ward's linkage method (Ward 1963) for HCA, an approach where distances between clusters is based on the increase of their sum of squares when merged. Ward's method is also cited to minimise the total within-cluster variance (Abu-Jamous *et al.* 2015, 161) and appropriate for use with Euclidean distances. As the process of HCA in SPSS first determines a dissimilarity matrix based on Euclidean distances, and efficiency in the creation of small clusters was welcomed, Ward's method was determined to be the best fit for this project. In addition, Ward's method for cluster analysis uses standardised score values rather than actual scores for each variable included in the analysis which helps to avoid inflation of similarity between individuals. As the clusters derived from HCA are difficult to quantify in terms of actually how true they are (HCA will create clusters in the data no matter what data is entered) a way to support the patterns observed is necessary. One way to help validate these patterns is through repeated testing

across new data sets (Tee *et al.* 2013); as this project utilised multiple teeth for HCA, it was possible to observe if similar clustering between individuals appeared to be consistent across multiple teeth as opposed to just one. It is important to note that this project utilised HCA as a precursor to explore potential levels of similarity between individual's via dental metrics, not as definite measures of relatedness. Squared Euclidean distances of 5 or less were used to indicate a high level of similarity, distances of 6-15 were indicative of moderate levels of similarity, and distances 16-25 were indicative of low levels of similarity. Key findings from HCA are presented in the Chapters 5 and 6 and all dendrograms produced to aid interpretations are presented in Appendix 7 (Figures 1 – 54).

4.5 Application of Results

Chapter 5 is focused on the statistical results from analyses of metric data obtained from the teeth within the four assemblages. While demonstrating the value of teeth for the identification of biological similarity within skeletal assemblages, this alone does not fully demonstrate the value of teeth for interpretations about kinship and identity. Results from the hierarchical cluster analyses will demonstrate that there are individuals within and between each cemetery whose mesiodistal and buccolingual measurements are either more similar or less similar to others, these dendrograms are not enough evidence to help validate or refute theories of social constructs during this time period. In order to better add to such discussions, Chapter 6 presents a three-part approach to the application and interpretation

of statistical results. First, comparisons across all four sites will be made to comment on patterns observed on a population level. Links will be drawn back to literature surrounding topics of mobility and residence patterns during the early Anglo-Saxon era in order to see if the biodata can add another level of support for what is currently hypothesised. The second and third parts of this approach to applying the data will be on community and individual levels. Community level interpretations will focus on burial structures, outlier individuals and grave goods. Individual level explorations within each cemetery will be look at factors like how certain people were buried or who they were buried with. Each comparison will add another perspective into social constructs like individual and group identity and burial organisation during the early Anglo-Saxon period in South-East England.

4.6 Conclusion

The overall aim of this project was to establish the utility of teeth for estimating biological similarity within skeletal assemblages. In order to help replicate this process, care was taken into the decision regarding the samples selected to ensure contemporaneity between sites existed which would allow for more robust results. Furthermore, the type of data obtained from the skeletal remains was chosen carefully in order to be repeatable and standardisable across current and future studies. Alongside this, it was important that the approach to statistical analysis worked through the raw data logically to find the areas that would be of most use for addressing questions of biological similarity within the sample. The results from

these approaches are presented over the next two chapters to help demonstrate and discuss interpretations that can be made based on the amalgamation of various data streams.

5. Results

5.1 Overview

The aim of this project was to determine the usefulness of teeth as an indicator of biological similarity among individuals within a skeletal assemblage. To best assess whether the data collected could be used in such a way, univariate and multivariate approaches needed to be undertaken statistically to understand and quantify patterns observed within this dataset. An exploratory approach to statistical analysis was chosen for this project as the amount of data collected was extensive. Furthermore, it was unlikely that data from every tooth would be necessary to factor into final discussions on the utility of dental metrics to understanding biological similarity in archaeological populations. A variety of methods have been employed within the literature for the investigation of dentition and identity (i.e Alt and Vach 1995; Haeussler *et al.* 1989; Howell and Kintigh 1996; Irish 1997; Irish 2005; Tinoco *et al.* 2016; Townsend and Brown 1978b), which demonstrates that there is not yet a standard statistical approach for this type of research, rather, analysis is much more dependent on the questions being asked of the data and the type of data recorded. In this case, where there was not an *a priori* assumption on which teeth would be most useful for investigating biological similarity, it was important to start by broadly reviewing the data in general and then progressively get more focused. This progression of statistical testing began by generating the descriptive statistical data from the mesiodistal (MD) and buccolingual (BL) dimensions of each tooth for the whole sample and subdividing those into separate biological sex and cemetery groups. From these values it was then possible to look at the causes of variation in size between and within all groups to help determine what is accounting for differences in tooth size overall. In

doing so, it was made possible to determine which teeth were most helpful for continuing statistical analysis into biological similarity.

Overall, n=145 individuals were observed and had dental data recorded, from which a total of 5988 measurements were taken in accordance with the methodological procedures described in the Chapter 4. Table 4 presents the overall sample sizes, corresponding number of measurements as well as the datasets for individual cemetery samples and a breakdown of male and female data. Hatherdene and Oakington provided the larger contributions to the sample compared to Polhill and Eastry. Eastry had the smallest sample of the four cemeteries investigated which has led to some interpretive issues surrounding the results of statistical analyses. As such, results obtained from Polhill, and especially Eastry, are to be treated cautiously as to whether they support trends and patterns observed at Hatherdene and Oakington. However, the inclusion of Polhill and Eastry has helped to add to the descriptive data regarding dental metrics for early Anglo-Saxon populations, and therefore their inclusion was important for the full statistical analysis.

Table 4 - Overview of the sample size for the combined cemetery sample (pooled sex and separated by sex) and for each individual cemetery site (pooled sex and separated by sex).

Comparative Group	Sample Size (n)	Number of Corresponding Measurements
Combined cemetery, pooled sex	145	5988
Combined cemetery, males	65	2656
Combined cemetery, females	80	3332
Hatherdene, pooled sex	56	2500
Hatherdene, males	28	1360
Hatherdene, females	28	1140
Oakington, pooled sex	48	2150
Oakington, males	21	872
Oakington, females	27	1288
Polhill, pooled sex	26	1014
Polhill, males	10	314
Polhill, females	16	700
Eastry, pooled sex	15	314
Eastry, males	6	110
Eastry, females	9	204

5.2 Descriptive Statistics

Descriptive statistics were looked at for each tooth's mesiodistal (MD) and buccolingual (BL) measurements separately and data were presented for the: minimum measurement, maximum measurement, mean, standard error, standard deviation, variance, and confidence interval (95%). These measures were chosen to best understand the spread and variation within the datasets of each tooth and their associated dimensions. Descriptives were recorded for the entire sample with pooled sex individuals, combined cemetery groups but separated by sex, and then repeated for each individual cemetery as a whole and then separated by sex. Full results from these analyses can be seen in Appendix 1 (Tables 1 – 15), but key findings are discussed below.

From the combined cemetery group, the descriptives revealed a level of consistency within the data regarding spread of data points for both the MD and BL measurement of each tooth. The value for standard error (SE), standard deviation (SD) and variance (VAR) were all relatively low across all tooth classes and for each dimension. Table 5 provides the ranges of SE, SD and VAR for the combined cemetery group as well as each individual cemetery. The low standard error indicates that the MD and BL measurements from the sample population are not likely to be too dissimilar from the actual population. The low values for standard deviation indicate that the data points within each dimension are closer to the mean as there is less spread of data within both MD and BL measurements. Similarly, the low variance reiterates the closeness of data points to the mean but also on the close proximity of individual points to one another. This all demonstrates that, overall, the metric data gathered within these four cemeteries are similar to one another and displays consistency among the levels of observed variation in tooth size.

Table 5 – An overview of Standard Error (SE), Standard Deviation (SD) and Variance (VAR) ranges from the descriptive statistical analysis of the mesiodistal and buccolingual tooth dimensions.

Site	Sex	SE Range	SD Range	VAR Range
Combined cemeteries	Combined sex	0.037-0.107	0.328-0.849	0.108-0.801
	Male	0.051-0.157	0.333-0.867	0.111-0.752
	Female	0.045-0.134	0.310-0.848	0.096-0.719
Hatherdene	Combined sex	0.057-0.182	0.317-0.896	0.101-1.088
	Male	0.065-0.231	0.312-0.915	0.097-0.837
	Female	0.071-0.235	0.248-1.050	0.117-1.103
Oakington	Combined sex	0.054-0.189	0.060-0.854	0.124-0.729
	Male	0.076-0.234	0.262-0.826	0.069-0.682
	Female	0.068-0.312	0.313-1.080	0.090-1.168
Polhill	Combined sex	0.072-0.273	0.236-0.907	0.056-0.823
	Male	0.060-1.530	0.078-2.163	0.006-4.682
	Female	0.070-0.265	0.210-0.795	0.044-0.904
Eastry	Combined sex	0.065-0.551	0.129-1.102	0.017-1.214
	Male	0.000-0.840	0.000-1.188	0.000-1.411
	Female	0.079-0.885	0.105-1.302	0.011-1.694

This trend of low variation is repeated when the combined cemetery group was divided into males and females. Both males and females reflected low levels of variation across all parameters for MD and BL measurements (Table 3) and there appeared to be consistency in size with the potential for corresponding teeth of either or male or female to fall into the 95% CI presented for each measurement. Once again, these values demonstrate that the data recorded from MD and BL measurements are close together, close to the mean of comparative samples and display levels of consistency. Within the combined cemetery group, biological sex does not appear to influence the level of variation observed in these descriptive statistics, but targeted testing in Chapter 5.5.2 will investigate this further. Regarding variation in tooth class or differences between upper and lower dentition, there appeared no patterns that suggest tooth type relates to the amount of variation observed. Each tooth class appears to have variation values that fall across the spectrum of overall calculated standard error, standard deviation and variance. In addition, being part of the maxillary or mandibular dental arcade appeared not to influence the amount of variation observed within

measurement data, as both maxillary and mandibular teeth displayed higher and lower amounts of variation within the reported range of values for the overall sample.

After separating data into individual cemeteries, and then looking at differences between sexes and as pooled sex groups, similar findings were reported as the combined cemetery group. Table 3 provides the SE, SD and VAR ranges for pooled sex, males and females from Hatherdene, Oakington, Polhill and Eastry. Data showed little in the way of sex specific or tooth specific differences in regard to amount of variation expressed in each tooth's measurements, building on findings observed within the combined cemetery group. Again here, being a maxillary or mandibular tooth reflected no consistency with higher or lower amounts of variation and data spread, nor did tooth class. Additionally, like the combined cemetery group, there appeared overlap between measurement values for each tooth when comparing across sex and cemetery and the 95% CI were similar when comparing across the teeth and between sexes. When looking at the breakdown of descriptive statistics from each cemetery separately, there were some apparent issues with sample size. Eastry and Polhill proved to be difficult due to their smaller sample sizes, especially when separated into male and female groups. As such, it was not possible to make comparisons for each tooth within this subset of the sample. It was also difficult to compare levels of SE, SD and VAR of these small samples to larger samples as there is not as much data present to understand patterns and trends. Therefore, levels of SE, SD and VAR displayed more extreme values compared to the groups with larger sample sizes, see Table 3. It was not unexpected to see higher and lower values for these descriptive measures with a smaller sample sizes like Eastry, as it is expected that if there were fewer data points differences would seem further away and similarities would seem closer together.

In comparison to Polhill and Eastry, Hatherdene and Oakington were mainly found to have similar values to the combined cemetery group, for both males and females. Interestingly, for both Hatherdene and Oakington the females displayed higher levels of SD and VAR compared to the combined cemetery group and the females in Polhill and Eastry. The higher values for SD and VAR represent a greater spread of data points not only from the mean, but that the points are further away from one another as well. This could indicate that there are lower levels of similarity within the female dentition at Hatherdene and Oakington compared to males of the same groups, however additional testing in Chapter 5.7 will help to validate this point. Overall, despite differences observed due to sample size issues, the data analysed does display variation in MD and BL measurements, however, this variation is relatively small. Additional statistical analyses were subsequently computed, presented further in this Chapter, in order to better understand where this variation in size is attributable and how it will affect interpretations made from this data.

Using the combined cemetery, pooled sex group, bivariate plots were produced to look at the correlation between MD and BL measurements, too see what extent one accounts for the size of the other. MD values were plotted along the x-axis and BL values were plotted against the y-axis. Sex was separated in order to look at correlation across male and female values to see if any patterns based on sex could start to be revealed. In each case the mean for each sex was also plotted along with the raw data for each measurement. The coefficient of determination (R^2) $R^2 = 1 - \frac{RSS}{TSS}$ was calculated for each tooth for males and females to better interpret the closeness of data points to the line of regression. Appendix 2 (Figures 1 – 32) contains the bivariate outputs for each tooth, separated by sex along with their respective regression equations and R^2 values. The regression lines of the bivariate plots revealed some interesting differences. For some of the lines' slopes, there were differences

between males and females resulting in the crossing of regression lines. The 12 teeth where this crossing was observed were the: right maxillary first molar, right maxillary canine, right maxillary lateral incisor, right maxillary central incisor, left maxillary lateral incisor, left maxillary first premolar, left maxillary first molar, left mandibular second molar, left mandibular first molar, left mandibular central incisor, right mandibular first premolar, and right mandibular second molar. As differences in tooth size between sexes were expected based on discussion in Chapter 3.2, these results demonstrated the need to follow up with additional statistical analyses on the effect of sex on tooth measurement correlation in order to see which teeth are more affected by this than others, see Chapter 5.5.2. The lowest R^2 value was attributed to males' right first maxillary molar ($R^2 = 0.003$) and males' right maxillary canine ($R^2 = 0.003$), whereas the highest R^2 value was attributed to females' right maxillary first premolar ($R^2 = 0.594$). Like the results from the descriptive data, there appeared no real patterns to suggest that tooth class or location in the mouth (i.e. either maxillary or mandibular) would contribute to the level of correlation between variables as all tooth types and locations were represented across the range of correlation values. However, an unpaired t-test (two tailed) revealed significant differences between the level of correlation observed between MD and BL measurements and sex $t(62) = 2.182$, $p = 0.036$. Here, biological sex does appear to contribute to the correlation between the MD and BL measurements, with females having a stronger correlation between measurements than males. This reiterates findings from Townsend *et al.* (2012) who discussed the differences in sex-based inheritance and MD and BL dimensions, refer to Chapter 3. However, as has been shown, knowing either the MD or BL measurement does not allow researchers to reliably predict the size of the other for these groups.

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{s^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$$

5.3 Normality of Data

Shapiro-Wilk tests $W = \frac{\left(\sum_{i=1}^{n} a_i x_{(i)}\right)^2}{\sum_{i=1}^{n}(x_i - \overline{x})^2}$, for normality were conducted on the combined cemetery, pooled sex group, the combined cemetery groups, separated by sex and each individual cemetery for pooled and separated sex. Complete results from these tests can be found in Appendix 3 (Tables 1 - 15) and key findings are discussed below. These statistical tests are used to quantify whether or not continuous data is normally distributed. If this is not found to be the case, the variables are said to be non-normally distributed. In such instances, data can still be used but alternative statistical analyses would have to be computed using non-parametric tests which do not assume normal distribution of data. Within the combined cemetery group, eight of the possible 64 measurements (each person could have 32 MD and 32 BL to compare) were found to be non-normally distributed ($p<0.05$): the MD of the right maxillary canine, the BL of the right maxillary lateral incisor, the BL of the left maxillary central incisor, the BL of the left maxillary lateral incisor, the MD of the left maxillary first molar, the BL of the left maxillary third molar, the MD of the left mandibular second premolar and the BL of the left mandibular second premolar, see Table 6. All other tooth measurements were found to be normally distributed ($p>0.05$).

Table 6 - The measurements that were not found to be normally distributed after Shapiro-Wilk's testing for the whole group, pooled sex. Degrees of freedom indicated by df.

Tooth	Measurement	Statistic	df	p-value
RMxC	MD	0.940	101	< 0.001
RMxLI	BL	0.961	83	0.013
LMxCI	BL	0.965	81	0.026
LMxLI	BL	0.960	86	0.009
LMxM1	MD	0.972	89	0.049
LMxM3	BL	0.945	68	0.005
LMP2	MD	0.830	116	0.000
LMP2	BL	0.955	116	0.005

Separating the sample into individual cemetery sites revealed a similar trend in normality with the majority of data found to be normally distributed and abnormal distribution ($p<0.05$) occurring in five measurements from Hatherdene, four measurements from Oakington, three measurements from Polhill, and three measurements from Eastry, see Table 7. All remaining measurements displayed normal distribution ($p>0.05$) within each cemetery site when sex was not being taken into consideration.

Table 7 - The measurements that were not found to be normally distributed after Shapiro-Wilk testing within each cemetery site, for pooled sex groups. Degrees of freedom indicated by df.

Cemetery	Tooth	Measurement	Statistic	df	p-value
Hatherdene	**LMxCI**	BL	0.895	29	0.007
Hatherdene	**LMxLI**	MD	0.942	39	0.045
Hatherdene	**LMxC**	BL	0.932	41	0.017
Hatherdene	**LMP2**	MD	0.795	47	0.000
Hatherdene	**LMP2**	BL	0.930	47	0.008
Oakington	**RMxC**	MD	0.872	35	0.001
Oakington	**RMxLI**	BL	0.921	33	0.019
Oakington	**LMxM3**	MD	0.865	19	0.012
Oakington	**LMxM3**	BL	0.881	19	0.023
Polhill	**RMxLI**	MD	0.681	12	0.001
Polhill	**RMxLI**	BL	0.779	12	0.006
Polhill	**LMM2**	MD	0.887	19	0.028
Eastry	**RMxM3**	BL	0.723	4	0.021
Eastry	**LMM2**	MD	0.735	5	0.022
Eastry	**RMC**	BL	0.816	8	0.042

When each site was split by sex, again the majority of values were normally distributed, and only a small subset from each cemetery appeared to be non-normally distributed, see Table 8 for all these normality results. Hatherdene males had 10 measurements at $p<0.05$, while the female only group had four measurements at $p<0.05$. Oakington males had five measurements at $p<0.05$, while the female only group had four measurements at $p<0.05$. Polhill males had three measurements at $p<0.05$, while the female only group had five measurements with $p<0.05$. Eastry males had two values at $p<0.05$, while the female only data was all normally distributed. The differences in numbers of abnormally distributed

measurements between the cemeteries can partially be explained by sample sizes. Again, with Polhill and Eastry having fewer measurements to analyse, data was either missing and Shapiro-Wilk testing could not be conducted, or the few data points meant that a spread of data was more difficult to quantify reliably. Another possible explanation for the appearance of non-normally distributed data could be attributable to outliers within the data set. Many outlying points were present within this sample, and as such, it was necessary to explore them in more depth to demonstrate their importance within this study of biological similarity, see Chapter 5.4. In order to accommodate data that was not normally distributed, non-parametric testing was employed to quantify results later on in analysis.

Table 8 - Abnormally distributed data within each cemetery when data was separated by sex. Degrees of Freedom indicated by df.

Cemetery	Sex	Tooth	Measurement	Statistic	df	p-value
Hatherdene	Male	RMxM3	BL	0.878	16	0.036
Hatherdene	Male	RMxLI	BL	0.814	18	0.002
Hatherdene	Male	LMxCI	BL	0.872	18	0.019
Hatherdene	Male	LMxLI	BL	0.901	21	0.037
Hatherdene	Male	LMxC	MD	0.885	23	0.012
Hatherdene	Male	LMxC	BL	0.839	23	0.002
Hatherdene	Male	LMP2	MD	0.884	27	0.010
Hatherdene	Male	LMP2	BL	0.871	27	0.003
Hatherdene	Male	RMLI	MD	0.908	21	0.049
Hatherdene	Male	RMM3	MD	0.879	19	0.020
Hatherdene	Female	LMP2	MD	0.725	20	<0.001
Hatherdene	Female	LMP2	BL	0.899	20	0.039
Hatherdene	Female	LMC	BL	0.915	25	0.040
Hatherdene	Female	RMM1	BL	0.812	17	0.003
Oakington	Male	RMxM3	BL	0.783	9	0.013
Oakington	Male	RMxC	MD	0.784	14	0.003
Oakington	Male	RMxCI	BL	0.841	12	0.028
Oakington	Male	RMM1	MD	0.878	15	0.044
Oakington	Male	RMM2	MD	0.753	13	0.002
Oakington	Female	LMXM3	MD	0.823	13	0.013
Oakington	Female	LMC	BL	0.882	21	0.016
Oakington	Female	RMC	MD	0.900	22	0.030
Oakington	Female	RMC	BL	0.910	22	0.047
Polhill	Male	LMxC	MD	0.741	5	0.025
Polhill	Male	LMC	MD	0.821	8	0.048
Polhill	Male	RMP2	MD	0.757	6	0.023
Polhill	Female	RMxLI	MD	0.610	8	<0.001

Cemetery	Sex	Tooth	Measurement	Statistic	df	p-value
Polhill	Female	RMxCI	MD	0.799	8	0.028
Polhill	Female	LMxM1	BL	0.812	13	0.009
Polhill	Female	LMM2	MD	0.783	13	0.004
Polhill	Female	LMLI	MD	0.786	10	0.010
Eastry	Male	RMP2	MD	0.745	5	0.027
Eastry	Male	RMM2	BL	0.764	3	0.032

5.4 Outliers

The detection of outliers within the dataset was also made possible through the analysis of descriptive statistics. Box and whisker plots were formulated to visually depict the range of measurements for MD and BL dimensions of individuals within the sample. These plots displayed the median, lower and upper quartiles for each tooth's dimensions and those at the minimum and maximum points within two standard deviations from the mean of the sample. Data values that fell outside this range were identified as outliers as they did not fall within the expected range for 95% of the sample for that particular measurement. Outliers were identified for the combined cemetery group, as well as each individual cemetery site and tests were repeated in each instance for pooled sex and separated sex groups. Outliers are commonly removed when identified in statistical analyses as they contribute to abnormal distribution of data resultant in skewing. However, Motulsky and Christopolous (2004) concede that, in biological research, outliers should be left in for further analyses as outliers can be useful for finding differences between species, taxa and individuals. As the focus of this project is to investigate similarity in biological traits, outliers could be representative of those who are least similar in regard to tooth size within the sample, therefore are important to retain with the dataset.

All identified outlying measurements were linked to an individual within the sample and those individuals that appeared most frequently were noted within the overall group and in each

individual cemetery. Appendix 4 (Tables 1 – 15) provides a complete overview of outlier analysis. While many individuals appeared as outliers within the data, the ones that were highlighted as most meaningful for future interpretations were those that appeared across several teeth and within both their respective pooled sex and separated sex groups within each cemetery. These individuals are presented in Table 9 and will be featured in later discussion in Chapter 6.2.2 regarding interpretations about outliers in these skeletal assemblages. Outliers were found across male and female individuals, for both MD and BL measurements of all tooth classes and within all cemeteries. There did not appear to be any pattern to suggest the likely reason as to why an individual measurement was an outlier, though females did appear slightly more frequently than males did. This finding could be explained due to there being more females within the sample compared to males overall. Interestingly while the male outliers tended to be for larger measurements than their comparative groups' means, female outlying measurements appeared as either larger or smaller than comparative groups' means. This trend was evident within individual cemeteries and separate sex groups, but also for the pooled sex groups, meaning that some females had significantly larger teeth to other females and males within the group. This reiterates the idea that there are multiple influences on permanent tooth size.

Table 9 – Most commonly identified individuals with repeated outlier measurements across the whole, pooled sex sample, separated sex and individual cemetery samples for multiple teeth and measurements.

Outlier ID	Number of Outlier Measurements	Cemetery	Sex	Larger or Smaller Than Mean
H1293	13	Hatherdene	Male	Larger
H205	20	Hatherdene	Female	Smaller
H241	38	Hatherdene	Male	Larger
H493	11	Hatherdene	Female	Larger
H560	13	Hatherdene	Male	Larger
H956	13	Hatherdene	Female	Smaller
H999	13	Hatherdene	Female	Larger
O1424	30	Oakington	Male	Larger

Outlier ID	Number of Outlier Measurements	Cemetery	Sex	Larger or Smaller Than Mean
O1616	11	Oakington	Female	Larger and Smaller
O1636	12	Oakington	Female	Larger
O1709	20	Oakington	Female	Larger
O2165	17	Oakington	Female	Smaller
P2	16	Polhill	Female	Smaller
P3	11	Polhill	Female	Smaller
P42	11	Polhill	Female	Larger
P50	20	Polhill	Male	Larger
E5	6	Eastry	Male	Larger and Smaller
E50	7	Eastry	Male	Larger

5.5 Inter-cemetery and Intra-cemetery Variation

5.5.1 Influence of Cemetery Membership on Tooth Size

As differences in tooth size varied within the descriptive statistics for each cemetery and between both biological sexes, quantification of these factors as influencing variables on tooth dimensions was carried out. In order to analyse this in a meaningful way, assumptions had to be made about the meaning of 'cemetery'. For the purposes of this investigation, each cemetery was taken to be representative of a local environment resulting in four different geographic environments for comparative testing. As the cemeteries were separated by space and time (more marked were the differences between the two Cambridgeshire sites compared to the Kent sites), these assumptions can be warranted for these statistical analyses. It is acknowledged that not every interred individual would have been a local inhabitant, but this testing approach was done to observe any overall differences in patterns between the four sites.

Environment has been cited to be an influencing factor on tooth size (Hughes and Townsend 2013; Townsend *et al.* 2012), as such it was important to demonstrate within this overall sample whether or not the differences in cemetery location (environment) were large enough to cause significant differences in the size of teeth between assemblages. First, data was looked at as a combined cemetery, pooled sex group in order to determine whether or not membership to a cemetery population had a statistically significant impact on tooth size. This approach was repeated on the combined cemetery group but separated into males and females to see if differences appeared when sex was accounted for. For the data that were normally distributed, analysis of variance tests (ANOVA) $F = \frac{MST}{MSE}$ were used as they can work well with continuous dependent variables, in this case the MD and BL measurements, as well as categorical independent variables (i.e cemetery site). For data that was not normally distributed the Kruskal-Wallis test $H = (N-1)\frac{\sum_{i=1}^{g} n_i(\bar{r}_{i\cdot} - \bar{r})^2}{\sum_{i=1}^{g}\sum_{j=1}^{n_i}(r_{ij} - \bar{r})^2}$ was utilised as it is designed to work with non-parametric data in a similar way to one-way ANOVA tests. These tests are designed to determine whether there are statistical differences in group means. For any significant differences found, a Tukey test $q_s = \frac{Y_A - Y_B}{SE},$ was used post-hoc to determine where exactly the significant difference was found. The hypothesis being tested for these initial tests was that cemetery site (environment) had an impact on the tooth dimensions of people interred within each. Appendix 5 (Tables 1 – 3) provides the full analysis of these results, and key results are presented here. Within the combined cemetery, pooled sex group of 145 individuals, only two measurements were shown to be significantly different between the four sites: the MD of the right maxillary lateral incisor and the MD of the left mandibular second molar, see Table 8. The remainder of the measurements had p-values greater than 0.05 which means that the hypothesis is rejected, and the null hypothesis accepted; being found in a particular early Anglo-Saxon cemetery had no significant influence

on tooth size. These tests were repeated on males from the combined cemetery sample and females from the combined cemetery sample. Within the male group, only the MD of the left maxillary third molar was found to have significant differences between sites, Table 8, all other p-values were greater than 0.05, again accepting the null hypothesis. The female group appeared to have more values that were significantly different between the sites with six measurements finding statistical significance: the MD of the right maxillary lateral incisor, the MD of the left maxillary central incisor, the MD of the left maxillary first molar, the MD of the left mandibular second molar, the BL of the right mandibular first premolar and the MD of the right mandibular second premolar, see Table 10.

Table 10 - Statistical results from ANOVA testing for the significance of cemetery site on mesiodistal and buccolingual measurements. Significant results presented at the p<0.05 level.

Group Comparison	Statistically Significant Measurement + corresponding tooth	ANOVA Significance Value	Tukey Test Post Hoc Results
Combined cemetery, pooled sex	MD RMxLI	Df=3, F = 2.989, p = 0.036	No significant differences found.
	MD LMM2	Df=3, F = 3.376, p = 0.021	Significant difference found between Oakington and Polhill only.
Combined cemetery, males only	MD LMxM3	Df=3, F = 4.176, p = 0.017	Not possible to compute due to low case numbers in groups.
Combined cemetery, females only	MD RMxLI	Df=3, F = 3.723, p = 0.018	Significant difference found between Hatherdene and Oakington.
	MD LMxCI	Df=3, F = 3.034, p = 0.040	No significant differences found.
	BL LMxM1	Df=3, F = 3.481, p = 0.023	Significant difference found between Polhill and Eastry.
	MD LMM2	Df=3, F = 3.542, p = 0.021	Significant differences found between Hatherdene and Polhill as well as Oakington and Polhill.
	BL RMP1	Df=3, F = 3.528, p = 0.020	Significant differences found between Hatherdene and Eastry as well as Oakington and Eastry.
	MD RMP2	Df=3, F = 3.006, p = 0.038	No significant differences found.

By separating out the male and female data it was revealed that more differences are observed between the cemeteries in terms of the variation within each. Males overall appear to be more similar between cemeteries, whereas there appears more variation in female data. This is not visible when combined into a pooled sex group, because female values become less significantly different, masking this pattern. Outlier values could have contributed to these values being significant, as was shown previously female outliers outnumbered males and displayed a range of size differences, from being much smaller than expected or much larger than expected compared to the rest of the group. This could have caused more variation and significant differences to appear within female only data, especially for cases where females had larger than expected teeth. These individuals could have contributed to greater significance when males, who may have a more similar range of dimension values, were removed from comparison. Another reason for these apparent differences observed between males and females could be that there are greater levels of biological similarity between some males and females within the whole sample which could, when combined, lessen the differences between female individuals who share more similarity with males in the group compared to other females. To explain, if brothers and sisters are compared together, their tooth measurements may be more similar compared to two unrelated females, exaggerating differences when sexes are separated and masking others when combined. This concept supports the idea that tooth size is dictated not only by environment, but by inherited genetics as well (Hughes and Townsend 2013). Compared to female data, the male group appeared more uniform in regard to the influence of cemetery membership on tooth size as there appeared no real differences between the four sites being investigated. This can indicate that, overall, males within the combined sample express greater levels of similarity compared to a pooled sex sample or the separated female group.

It was notable that seven of the nine significant values found within these analyses were MD dimensions. This finding supports the idea that dimensions of teeth are not influenced in the exact same manner in regard to formation and development, rather that each tooth and its dimensions should be looked at individually in order to best assess the usability of an individual tooth in analyses of biological similarity. From these results it is possible to conclude that, in general, cemetery environment or being buried within a certain location did not relate to differences expressed in tooth size for MD or BL dimensions. This indicates that despite differences in dates of occupation and geographic location, these differences were not large enough to have caused significant variation in tooth size between the four sites sampled within this project.

5.5.2 Influence of Biological Sex on Tooth Size

Once cemetery environment was shown not to be a large influencing factor on tooth size between the four assemblages, differences attributable to biological sex were quantified. ANOVA and Kruskal-Wallis tests were used to analyse the significance of MD and BL measurements (dependent variables) between males and females (independent variables) for a combined cemetery sample, and within each individual cemetery.

Results from the combined cemetery group revealed a mixture of measurements that were determined to be significantly different between the sexes. From the 64 measurements looked at (32 teeth in total, therefore a potential 32 MD measurements and 32 BL measurements for each person), 29 measurements had p-values of <0.05, equating to significant differences between males and females. The pattern in these instances were

reflective of males having larger measurements compared to females for these particular dimensions. All other measurements within the group were non-significant ($p>0.05$) and demonstrated no statistical difference between males and female tooth dimensions. Appendix 5 (Tables 4 – 8) provides the full analysis of these results, and key results are presented below. These significantly different measurements appeared across both the maxillary and mandibular dentition, and across all tooth classes. Of the 29 that were determined to be significantly different between the sexes, 22 were BL dimensions as opposed to MD dimensions. This contrasts with what was found previously regarding the results found when testing the influence of cemetery environment on tooth size where MD dimensions were shown to be more commonly significant than BL. The differences in pattern between the two variables further demonstrates the complexity of genetic and environmental interactions that contribute to tooth size. While significant differences were present amongst all tooth classes, only six teeth were found to be significantly different across *both* of their MD and BL dimensions (Table 11). From these results it is evident that canine teeth appear to be the most sexually dimorphic within the combined cemetery sample as three of the four are represented by differences between both sets of dimensions.

Table 11 - Teeth present within the combined cemetery group that were found to have significant differences in tooth size across both the mesiodistal (MD) and buccolingual (BL) dimension.

Tooth	Measurement	Significance Value
Left maxillary canine	MD	Df=1, F = 10.066, p = 0.002
	BL	Df=1, F = 12.273, p = 0.001
Left mandibular second molar	MD	Df=1, F = 7.434, p = 0.008
	BL	Df=1, F = 16.011, p <0.001
Left mandibular canine	MD	Df=1, F = 19.623, p <0.001
	BL	Df=1, F = 57.943, p <0.001
Right mandibular canine	MD	Df=1, F = 24.014, p <0.001
	BL	Df=1, F = 34.547, p <0.001
Right mandibular second molar	MD	Df=1, F = 6.482, p = 0.012
	BL	Df=1, F = 8.612, p = 0.004
Right mandibular third molar	MD	Df=1, F = 4.923, p = 0.029
	BL	Df=1, F = 7.896, p = 0.006

Within each tooth class, there appeared no difference to whether mesial (towards the front of the mouth) or distal teeth (towards the back of the mouth) within the arcade were affected any differently by sex. The first molars present had measurements that were found to be both significant or non-significant, as did the second and third molars. Similarly, both premolars and incisors within the arcade had a mix of measurements found to be significant and non-significant. Overall, from the combined sample it was clear that while there were notable differences between male and female measurements, with the exceptions of the canine teeth and the pattern observed with BL dimensions, it is difficult to comment exactly on how sex affects each tooth individually.

When looking at each cemetery separately, there were issues that meant that any patterns observed would also need to be discussed in a broader way by looking at differences across cemetery site, dimension and tooth class. The first issue to address related to differences in sample sizes. Hatherdene and Oakington were the two largest samples with 56 and 48 individuals, respectively, where in comparison Polhill had 26 and Eastry had 15 individuals. As a result of this, there appeared more variation in the Hatherdene and Oakington assemblages between male and female measurements compared to Polhill and Eastry. For Polhill and Eastry, overall results indicated that there were no real differences between the sexes for both MD and BL dimensions of teeth. Out of the possible 64 different tooth measurements from the permanent dentition, Polhill presented six as being significantly different between males and females: the MD of the left maxillary third molar, the BL of the left mandibular third molar, the MD of the left mandibular first molar, the BL of the left mandibular canine, the MD of the right mandibular central incisor, and the BL of the right mandibular canine, see Table 10. All other measurements within Polhill expressed no significance ($p>0.05$) between the sexes. Similarly, Eastry presented two measurements out of the possible 64 with

significant differences between males and females: the BL of the right mandibular canine and the BL of the right mandibular first premolar, Table 12. Unfortunately, some comparisons of measurements within Eastry were not possible because the comparative group had too few individuals within it. For example, most of the incisors only had one or two individuals of the same sex, therefore no between sex comparisons could be made. All other measurements from Eastry displayed no significant differences in size attributable to sex ($p>0.05$). Of the statistically significant measurements, canines appeared most consistently. This corresponds with the findings from the combined cemetery testing. Within the dental arcades, canine teeth do appear more consistently dimorphic compared to other tooth classes. Unlike the combined cemetery group, no single tooth in either Polhill or Eastry subgroups was identified to be significantly different across both of their MD and BL measurements. Within data from both Polhill and Eastry, there did appear to be differences between how sex affected each tooth dimension with the majority of significant values being BL measurements as opposed to MD measurements. Polhill had three of its six significant values being BL, while both significant values from Eastry were also BL measurements. As this pattern was observed within the combined group sample as well, its reflection in these two sub samples likely indicates that this finding is not restricted to larger samples but can be found in smaller groups as well.

Table 12 - Significant ANOVA and Kruskal-Wallis results for size differences between males and females within Polhill and Eastry cemeteries.

Cemetery Site	Significant Measurement + Corresponding Tooth	Significance Value
Polhill	MD LMxM3	Df=1, F = 11.422, p = 0.008
	BL LMM3	Df=1, F = 5.299, p = 0.044
	MD LMM1	Df=1, F = 7.081, p = 0.016
	BL LMC	Df=1, F = 15.727, p = 0.001
	MD RMCI	Df=1, F = 6.712, p = 0.024
	BL RMC	p = 0.029*
Eastry	BL RMC	Df=1, F = 23.326, p = 0.017
	BL RMP1	Df=1, F = 8.792, p = 0.025

*Kruskal-Wallis test for significance for non-parametric data.

Results from Hatherdene revealed that 26 of the 64 measurements were statistically significant ($p<0.05$) between males and females. All other measurements showed no significant differences between sexes ($p>0.05$). Like the combined cemetery group, these values were distributed across the maxillary and mandibular dentition, as well as having each tooth class represented. Within each tooth class, there appeared no relationship between significant differences and location within the arcade as earlier appearing teeth had just as much of a show of significance compared to later appearing teeth within the class. This finding was consistent with observations made of the combined cemetery group. Of the 26 significant values, 17 were from BL dimensions, again demonstrating the consistent pattern in BL measurements being more affected by differences in sex compared to MD measurements. Similarly, to the combined cemetery sample, there were certain teeth that were found to be significantly affected by sex across both dimensions. Nine teeth from Hatherdene were identified to fit this description, see Table 13. Consistent with findings from the combined sample and from Polhill and Eastry, canine teeth appeared to be the tooth class most commonly observed to differ statistically between the sexes as all four canine teeth were

found to be significantly different between males and females for both dimensions at Hatherdene.

Table 13 - Teeth present within the Hatherdene cemetery subsample that were found to have significant differences in tooth size across both the mesiodistal (MD) and buccolingual (BL) dimension.

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

*Kruskal-Wallis test for significance for non-parametric data.

Oakington, like Hatherdene, displayed more variation in tooth measurements between the sexes compared to Polhill and Eastry. Fourteen of the 64 measurements recorded displayed significant differences between male and female tooth dimensions. Interestingly, compared to Hatherdene, Polhill, Eastry and the combined group, there was less difference between how sex affected each tooth dimension at Oakington. Of the 14 measurements found to be significant within the Oakington subgroup, six were BL dimensions and eight were MD dimensions. Similarities were observed, however, within the Oakington group to the others, in that there were five teeth that had both MD and BL measurements differ significantly between males and females, see Table 12. The canine tooth, yet again, appeared to be the tooth class most affected by sexual dimorphism with three of the four canine teeth being

represented in Table 14. Additionally, the location within the dental arcade and position within tooth class did not appear to relate to the occurrence of statistically significant differences between measurements as mesial and distal teeth each displayed significant and non-significant results.

Table 14 - Teeth present within the Oakington cemetery subsample that were found to have significant differences in tooth size across both the mesiodistal (MD) and buccolingual (BL) dimension.

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

*Kruskal-Wallis test for significance for non-parametric data.

Overall, biological sex does appear to influence the size of teeth within these four early Anglo-Saxon populations, but not in a purely bimodal way. While there are differences observed between the sexes, the majority of tooth measurements between and within these cemetery groups show no statistical difference between male and female data. Along similar lines, the influence of sex is not consistent between or within the groups tested. When the combined cemetery group was compared to the individual cemeteries there were some apparent differences in the representation of teeth showing significant values. Not all tooth measurements that appeared significantly different in the combined cemetery group were found to be so in the separated cemeteries. Likewise, some values that appeared to be significant within individual cemetery sites, showed non-significance when combined into the combined cemetery group.

5.6 Selection of Teeth for Cluster Analysis

The results from the descriptive data analysis along with the ANOVA and Kruskal-Wallis tests to determine the influence of environment and biological sex on tooth size demonstrate that variation is present in the sample and not all is attributable to these aforementioned variables. Based on literature that suggests the main influences on tooth size are random mutations, environment, sex and genetics (i.e. Hughes and Townsend 2013; Townsend *et al.* 2012) (see Chapter 3), it is reasonable to assume that a significant portion of the remaining variation is attributable to inherited metric traits. For additional statistical analyses focused on observing the level of biological similarity between individuals within the sample, it was necessary to compare only the teeth that were consistently affected by sex and environment in the combined and separate cemetery samples. This was to ensure that any evidence of similarity found in subsequent statistical cluster analysis could not be due to the influence of environment or sex alone. Therefore, decisions had to be made regarding the inclusion or exclusion of certain teeth from the next set of analyses and it was decided to exclude the teeth that may obscure patterns related to biological similarity from the sample for use in cluster analysis.

When analysed for differences between cemetery sites, no single tooth from the pooled or separate sex comparisons was found to have significant differences across both the MD and BL dimension. Therefore, the decision was made to eliminate any teeth that were found to have a significantly affected measurement. Additionally, teeth were eliminated from use if they had a mix of significant and non-significant values across their MD and BL dimensions when statistically analysed for biological sex differences. This means that only teeth which had *both* dimensions as significant or *both* dimensions as non-significant were used. For teeth

that were found to be significantly different in size between males and females, it was important that their use in cluster analysis was for sex-specific comparisons only while those that were found not to differ significantly could be used for both pooled sex and separate sex cluster analysis. As a final limiting criterion, as the teeth were tested for normality, any remaining tooth that displayed abnormal distribution in either the MD or BL dimension was eliminated. These exclusions made it possible to ensure that no overarching factors could be attributable to any patterns observed in the hierarchical cluster analyses.

5.6.1 Teeth Selected for Inter-Cemetery Comparisons

The teeth selected based on these criteria differed between the combined cemetery group and individual cemeteries. Because of this, only teeth that met the above criteria and were consistent across all four cemeteries were included for inter-cemetery comparisons. Table 15 presents the teeth selected for inter-cemetery comparisons based on these criteria for inclusion in cluster analysis. The teeth associated with males or females could only be used to for respective sex comparisons across all four cemeteries. Teeth associated with the whole group can be used to compare males, females and a pooled sex group across all four cemeteries.

Table 15 - Selected teeth for subsequent statistical analyses for inter-cemetery investigations of biological similarity between Hatherdene, Oakington, Polhill and Eastry cemeteries.

Comparative groups	Selected Teeth
Female comparisons only	Right maxillary canine, left maxillary lateral incisor, right mandibular third molar
Male comparisons only	Left mandibular lateral incisor
Whole group comparisons	Left maxillary first premolar, left mandibular first premolar, left mandibular central incisor

5.6.2 Teeth Selected for Intra-Cemetery Comparisons

The same criteria were then applied when looking at teeth within each cemetery for future intra-cemetery analysis. However, when separated into individual cemeteries it was found that a lot more teeth fit these criteria compared to the combined cemetery group. In order to help with standardisation and future replication of this process, it was decided to limit the number of teeth for use in subsequent statistical testing for biological similarity. Additional limiting criteria for the teeth selected for intra-cemetery, where the list of potentially useful teeth exceeded four for either female, male or pooled sex comparisons, they were only included if they were the first formed in each class, as these have been thought to be the most stable in terms of development (Dahlberg 1945; Osborn 1978), see Chapter 3.1. Previous literature has suggested that such teeth tend to be the most stable regarding development (Mitsiadis and Smith 2006, 178) and within this project, they also tended to have the highest sample representations. Table 16 presents the selected teeth for each cemetery site, and for separated sex samples within each.

Table 16 - Selected teeth for subsequent statistical analyses for intra-cemetery investigations of biological similarity within Hatherdene, Oakington, Polhill and Eastry cemeteries.

Comparative groups	Selected Teeth
Hatherdene male comparisons only	Left mandibular canine, right mandibular first molar
Hatherdene female comparisons only	Left maxillary lateral incisor, left maxillary canine, right mandibular lateral incisor, right mandibular third molar
Hatherdene whole group comparisons	Right maxillary canine, right maxillary central incisor, left maxillary first premolar, left mandibular first molar, left mandibular first premolar, left mandibular central incisor, right mandibular central incisor, right mandibular canine
Oakington male comparisons only	Left mandibular canine, right mandibular canine
Oakington female comparisons only	Right maxillary third molar, right maxillary canine, right maxillary central incisor, right mandibular first molar
Oakington whole group comparisons	Right maxillary first molar, right maxillary first premolar, left maxillary first premolar, left mandibular first molar, left mandibular first premolar, left mandibular central incisor
Polhill male comparisons only	Left mandibular lateral incisor

Comparative groups	Selected Teeth
Polhill female comparisons only	Left maxillary canine, left maxillary second molar
Polhill whole group comparisons	Right maxillary first molar, right maxillary first premolar, right maxillary canine, left maxillary first premolar, left mandibular first premolar, left mandibular central incisor, right mandibular first molar
Eastry male comparisons only	Right maxillary first molar
Eastry female comparisons only	Right maxillary first premolar, right maxillary canine, left maxillary canine, left maxillary first premolar, left mandibular first premolar, left mandibular canine, left mandibular central incisor, right mandibular first molar
Eastry whole group comparisons	Left mandibular first molar, right mandibular third molar

A complete overview of how tooth metric data is progressed through the above statistical process is provided in Appendix 6.

5.7 Cluster Analysis and Identification of Biological Similarity

The results discussed above have helped to understand some of the underlying causes of variation in tooth size within these four skeletal assemblages. It has been shown that not all the variation expressed was attributed to cemetery site, outliers or sexual dimorphism. Based on these results, and theoretical research that suggests environment, sex and genetics contribute most significantly to overall tooth morphology (Hughes and Townsend 2013; Townsend *et al.* 2012), it was assumed that the remaining variation yet to be accounted for within this sample is likely attributable to inherited biological traits. As has been previously discussed in Chapter 3, biological similarity relates to the appearance of traits within a skeleton that can be used to help quantify the level of likeness between individuals within skeletal assemblages. In order to statistically separate those that are more similar from those that are less so, hierarchical cluster analysis was employed to sort through the MD and BL data from all cemeteries.

Hierarchical cluster analysis (HCA) was used to sort individuals based on their proximity (level of similarity) of their MD and BL dimensions. This type of clustering method allowed for natural clusters to be formed without pre-selecting a set number of clusters for the data to be divided into. It was not the aim of this work to identify the exact number of clusters presented by each tooth, rather, it was more important to determine overall patterns that could be observed when looking between and within groups as a whole population, separate communities and at individual levels. Therefore, it was important to allow the data to naturally organise itself via the selected linkage method, rather than to ascribe an *a priori* number of clusters for the sample to divide into. Regarding linkage methods, it was decided to employ Ward's linkage (Ward 1963) to help sort the data into clusters via hierarchical cluster analysis. Ward's linkage works well for quantitative data and focuses on separating points based on the error sum of squares and total sum of squares for the data points present (Abu-Jamous *et al.* 2015). This approach helps to maximise the differences between clusters that are formed by having those that are grouped closest together represent a high degree of similarity compared to those that had branched from a node (separate branch) at a further Euclidean distance. Ward's method is also seen as favourable in data sets as it helps to reduce the variance between clusters (Ward 1963). As discovered in the descriptive statistics section, there were fluctuations in variance within and between sexes and across all teeth, so it was postulated that Ward's method would be a suitable way to incorporate these observations. Appendix 7 (Figures 1 – 54) displays the hierarchical cluster dendrograms from all teeth listed in Tables 13 and 14. Once all dendrograms had been produced, they were looked at for pooled sex and separate sex differences observed for the combined group and separate cemetery sites. Dendrograms were looked at to compare: number of clusters present at a squared Euclidean distance of 1, 3 and 5 (the smaller the distance, the more similar the tooth

measurements), the Euclidean distance of the second node (branch) separation, the percentage of the sub group that was separated after the first node division, and size of largest cluster as a proportion of sub group. These features of the dendrograms were considered to try and standardise an approach to comparing results from different teeth within and between skeletal assemblages. These measures were also considered as they could be used to infer connections at a population level as well as at community and individual levels. Within this project, the term connection is used primarily in response to biological similarity and the suggestion of a biological link between individuals. Results that indicate higher amounts of similarity in tooth data are interpreted as showing a biological connection between such individuals.

Within the sample, comparisons of pooled sex groups were made first. The combined cemetery group and each individual cemetery were looked at to investigate the patterns of similarity expressed within each subgroup. Tables 17 – 19 and Figures 11 – 14 present the general observations from these groups.

Table 17 - Number of clusters observed within the combined and separate cemetery groups with pooled sex. Distances recorded at squared Euclidean distances of 1, 3 and 5. Average number of clusters calculated based on data from all teeth used for each comparison.

Group	No. Clusters at 1 Squared Euclidean Distance	No. Clusters at 3 Squared Euclidean Distance	No. Clusters at 5 Squared Euclidean Distance
Combined cemetery	8.67	6.33	3.33
Hatherdene	7.13	5.38	3.88
Oakington	7.67	5.67	3.83
Polhill	6.71	5.00	3.71
Eastry	4.00	3.50	2.50

The number of clusters was linked in part to sample size, with Eastry and Polhill having fewer clusters than Hatherdene and Oakington. There appeared three main clusters within each group which further subdivided into smaller clusters with decreasing squared Euclidean

distances, and this pattern was consistent across all groups compared, Table 17 and Figure 11.

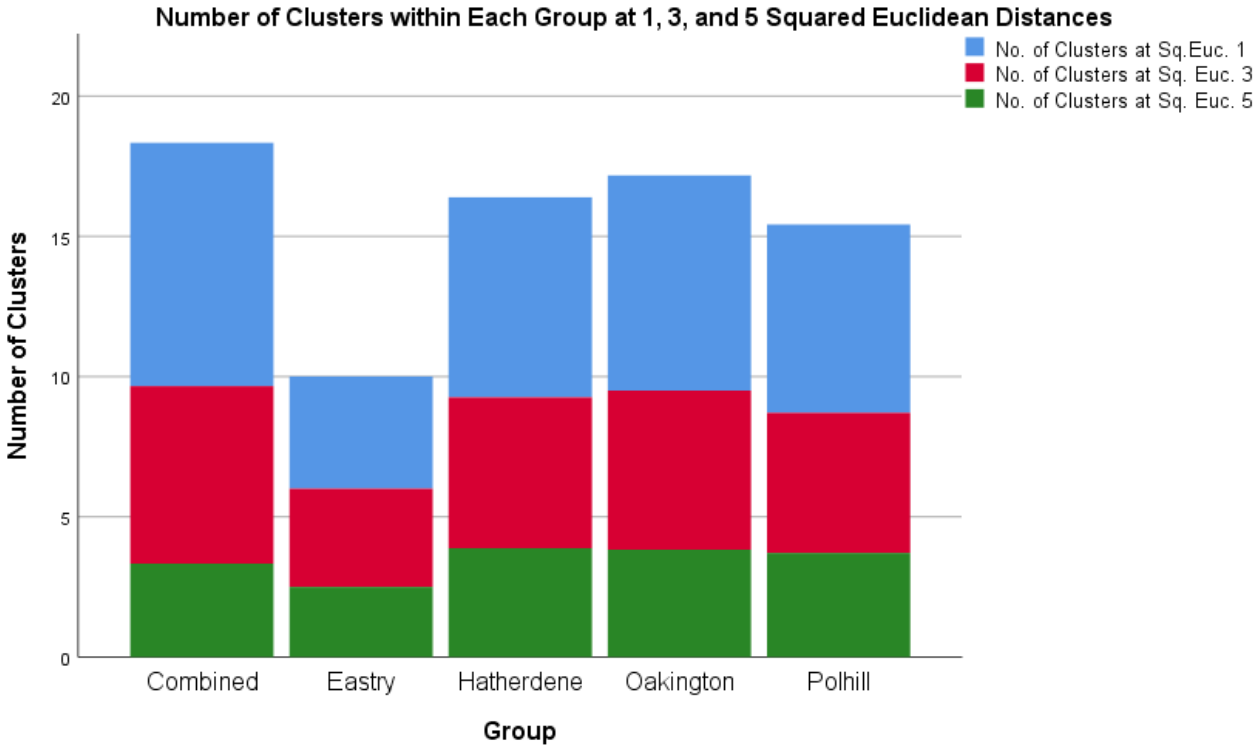

Figure 11 - The number of clusters identified within each cemetery group at 1, 3, and 5 squared Euclidean distances. The number of clusters increased as the Euclidean distance decreased which indicates that the separation of individuals based on tooth size was effective at locating those that were most similar to one another.

The majority of the population also split off at the first node division which is indicative of higher levels of similarity among the group, Table 18 and Figures 12-13. This trend was reflected in the distance of second node split, 25 represented the maximum split difference in this analysis and was consistent for all groups being joined at the first node. Therefore, the distance of second node split was more telling for the level of similarity within the group. The closer this split appeared to the maximum distance of 25, the more variation present within the subset. Average distance values for this second split ranged from 8.50 – 13.14 further supporting the concept of spread of variation of tooth size within these groups, Table 18 and Figures 12-13.

Table 18 - Maximum distance for split of second node for the combined cemetery and separate cemetery groups with pooled sex. Distance is recorded as squared Euclidean distances; averages represented in the table. Average percentage of population that separated after first node split also presented.

Group	% of Group Split after Node 1	Distance of Node 2 Split
Combined cemetery	54.83	11.00
Hatherdene	62.41	10.00
Oakington	61.50	9.17
Polhill	69.33	13.14
Eastry	66.65	8.50

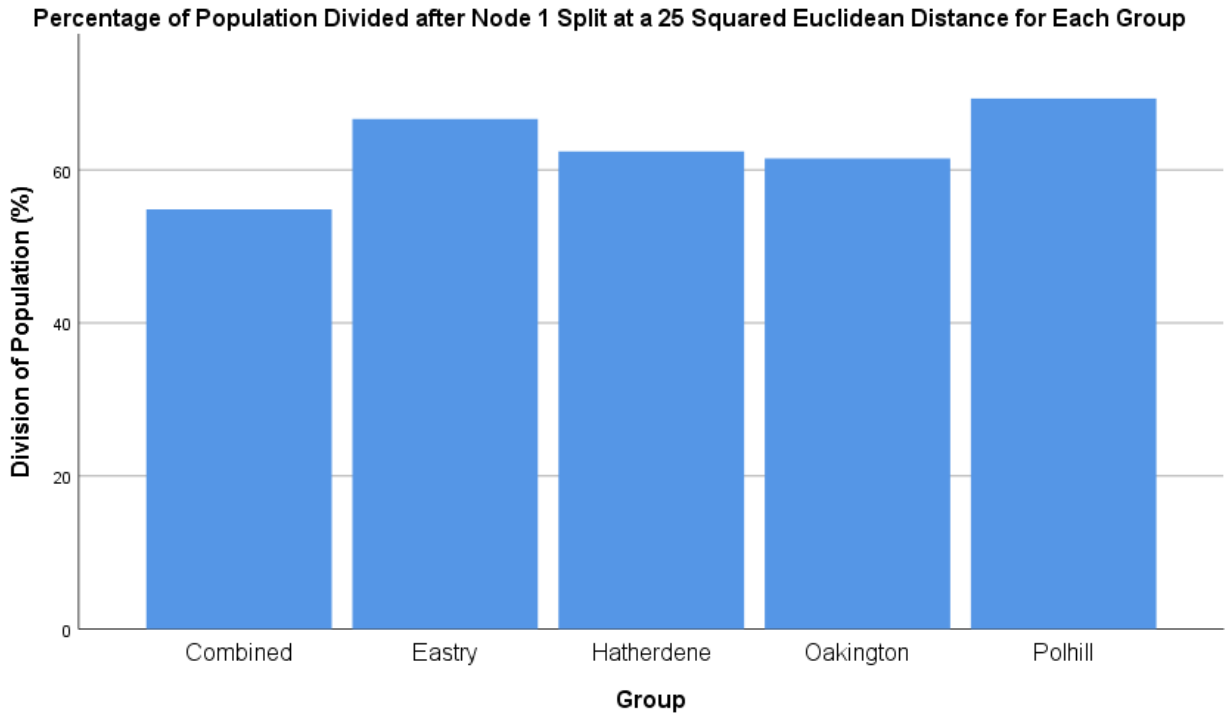

Figure 12 - Percentage of population divided after node 1 split at a squared Euclidean distance of 25. These results indicate that while some diversity appears, there are high levels of similarity within each group under investigation in regard to their tooth data.

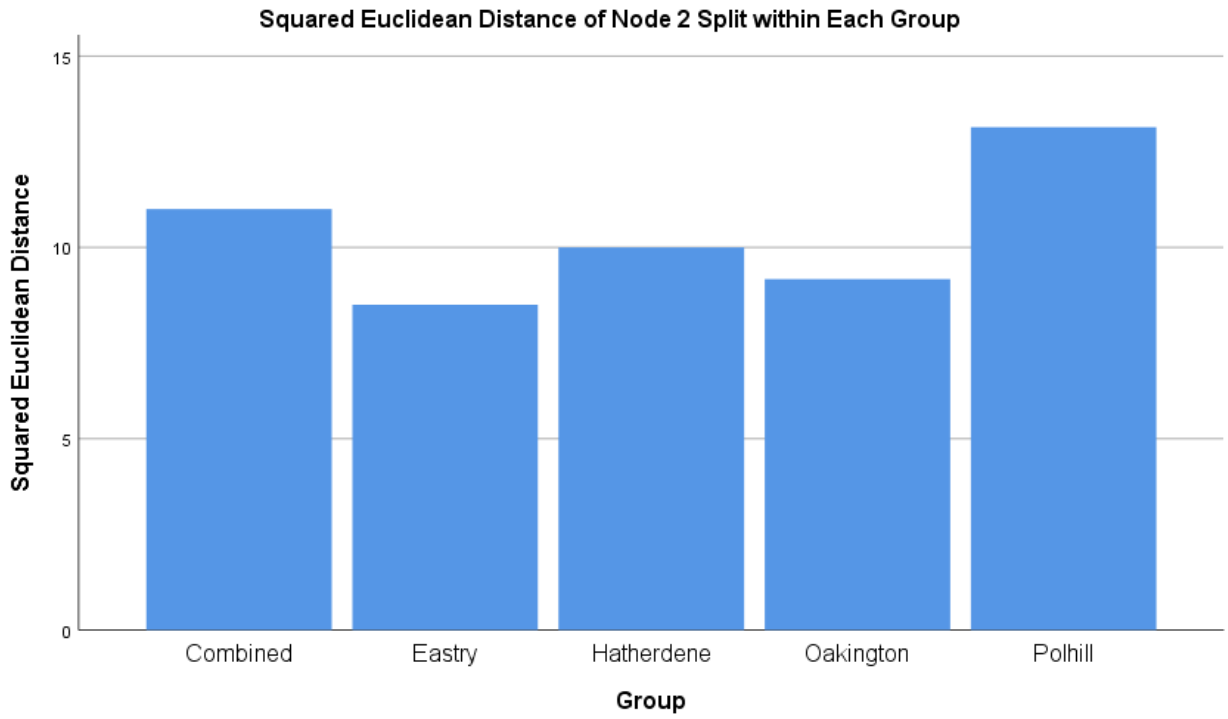

Figure 13 - The squared Euclidean distance corresponding to the split of the second node for each comparative group. The smaller the distance value here, the more similar the individuals within the group are to one another.

Table 19 and Figure 14 also demonstrates the trends discussed above regarding tooth size similarity within each cemetery compared to a combined group. In these comparisons the average size of a largest cluster, proportionally, was similar for all four cemeteries and the combined cemetery group. These results suggest that approximately a third of each population shows higher levels of similarity, therefore supporting the idea of a core lineage based on biology.

Table 19 - Average size of largest cluster (at a Euclidean distance of 1) within the combined cemetery and separate cemetery groups. Presented alongside this is the average percentage that reflects the proportion this cluster size represents within each comparison. These results display that approximately 1/3 of the individuals in each group display the highest level of similarity found.

Group	Average Size of Largest Cluster	Proportion of Group (%)
Combined cemetery	21.33	22.67
Hatherdene	9.88	26.13
Oakington	7.67	22.00
Polhill	5.29	32.57
Eastry	2.00	33.00

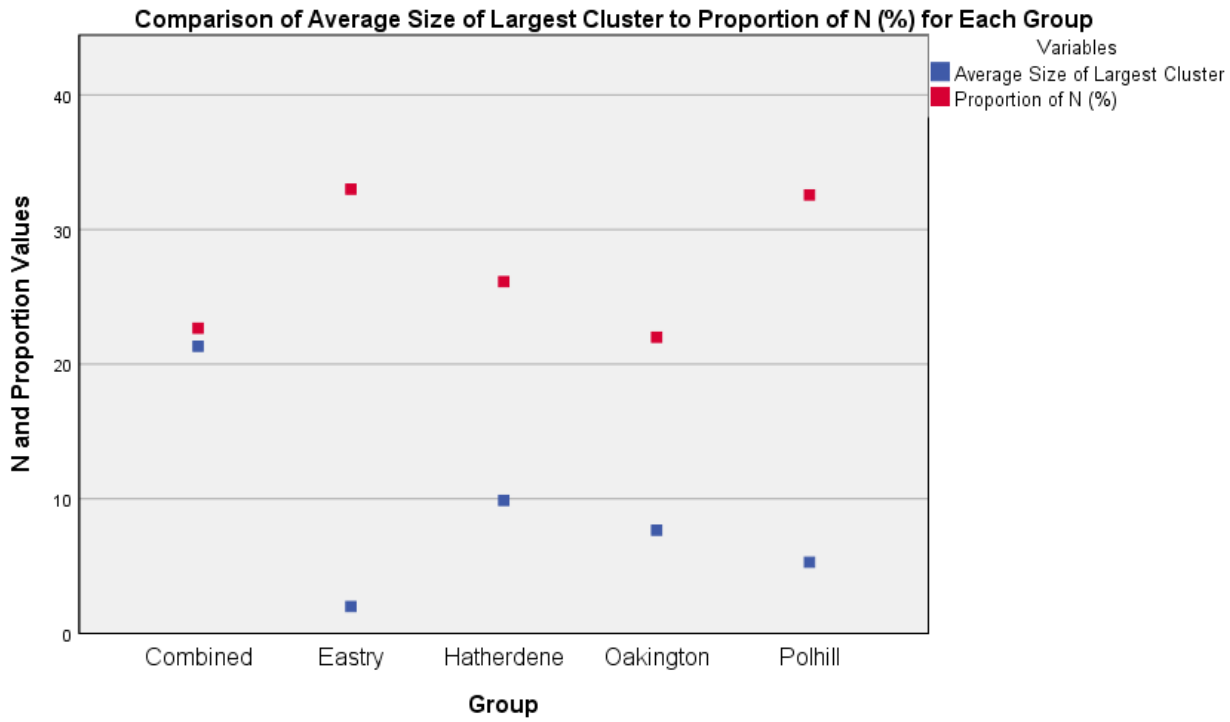

Figure 14 - Comparison of average size of largest cluster as a proportion of n for each comparative group. It is important to consider both proportion and cluster size together to prevent over or underrepresenting similarity within a group.

There did not appear to be one cemetery that had significantly more variation in terms of the distances clusters were separated out compared to others. Similarly, the overall sizes of clusters when looked at as a percentage proportion of each comparative sample were similar across all four sites. There did not appear to be a cemetery that had a lot of higher levels of similarity within it compared to others. This means that each cemetery demonstrated the same patterns when being sorted through HCA. It was possible to identify individuals who shared higher levels of similarity from those that did not.

After the pooled sex groups were looked at, the same measures were looked at separately for males and females within the combined cemetery group and for each individual cemetery site. Tables 20 – 22 and Figures 15 – 21 present the observations for these comparisons.

Table 20 - Number of clusters observed within the males and females of the combined and separate cemetery groups. Distances recorded at squared Euclidean distances of 1, 3 and 5. Average number of clusters calculated based on data from all teeth used for each comparison. Differences were apparent in number of clusters formed between the sexes with females having more clusters overall compared to males.

Group	No. Clusters at 1 Squared Euclidean Distance	No. Clusters at 3 Squared Euclidean Distance	No. Clusters at 5 Squared Euclidean Distance
Combined cemetery males	9.00	7.00	5.00
Combined cemetery females	8.00	6.00	4.00
Hatherdene males	8.50	6.50	4.50
Hatherdene females	5.75	5.25	3.50
Oakington males	5.00	4.00	3.00
Oakington females	6.75	5.25	3.75
Polhill males	5.00	4.00	3.00
Polhill females	6.50	5.00	3.50
Eastry males	2.00	2.00	2.00
Eastry females	3.25	3.13	2.63

Based on the data in Table 20 and Figures 15-17, it appears as though within each cemetery male data appears to share higher levels of similarity compared to female data.

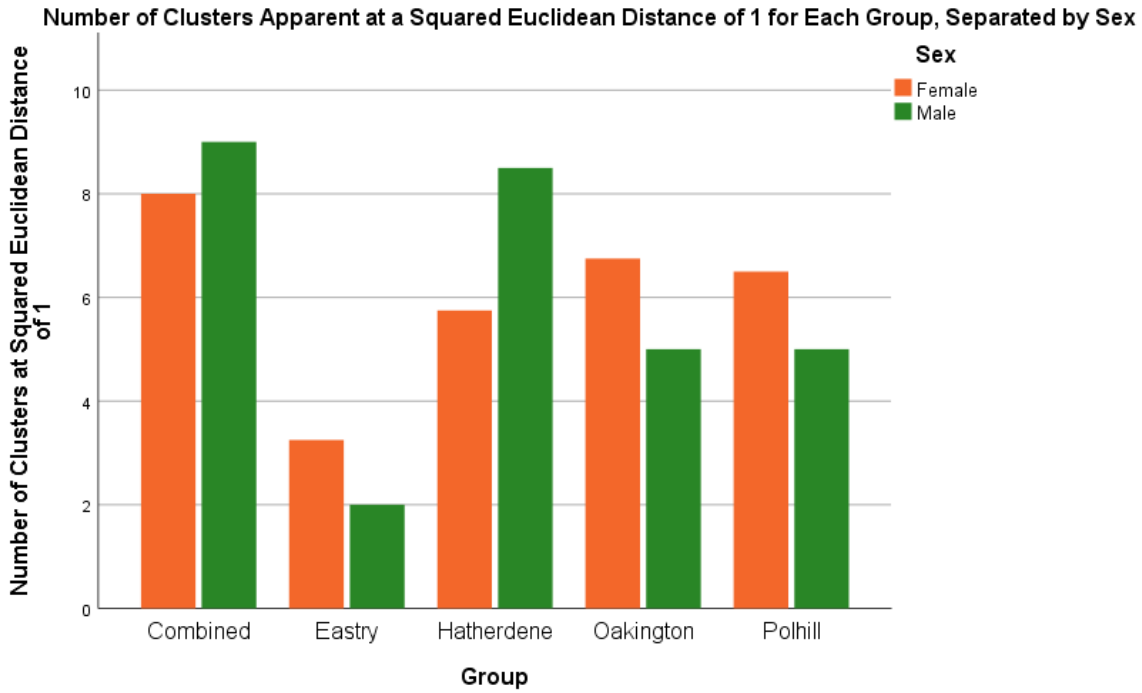

Figure 15 - The average identified number of clusters within each comparative group across all analysed teeth at a squared Euclidean distance of 1, separated by sex. Within each individual cemetery females appeared to have more clusters overall, however when combined into a complete sample, males had more clusters.

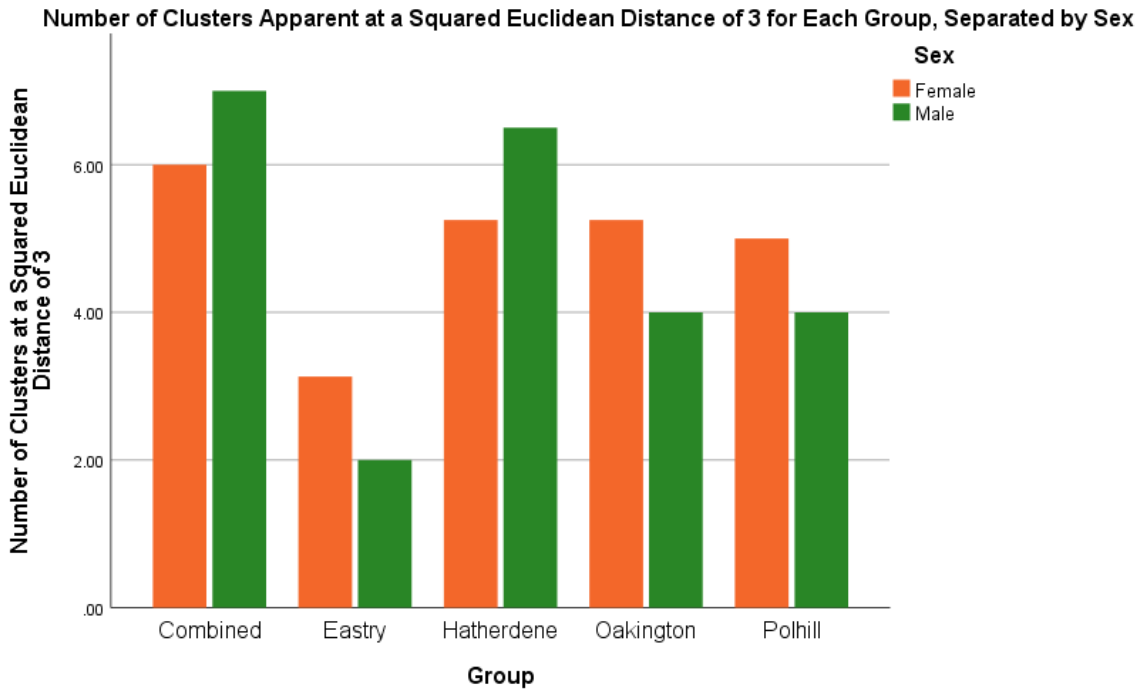

Figure 16 - The average identified number of clusters within each comparative group across all analysed teeth at a squared Euclidean distance of 3, separated by sex. Within each individual cemetery females appeared to have more clusters overall, however when combined into a complete sample, males had more clusters.

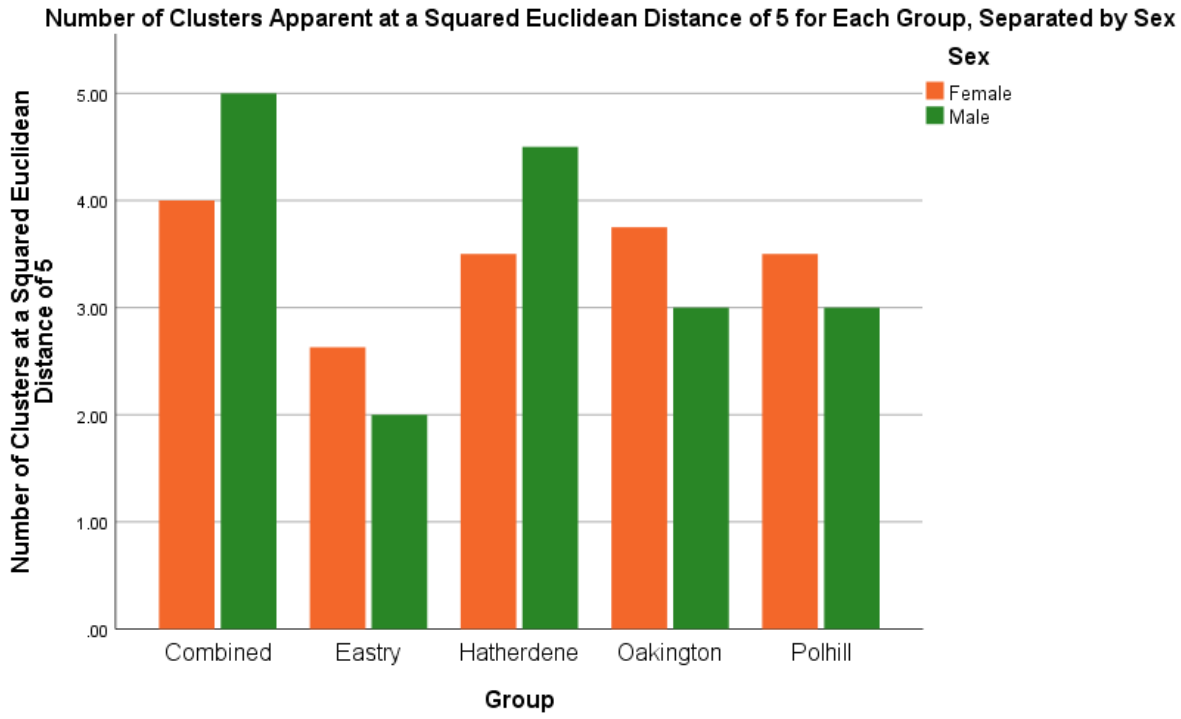

Figure 17 - The average identified number of clusters within each comparative group across all analysed teeth at a squared Euclidean distance of 5, separated by sex. Within each individual cemetery females appeared to have more clusters overall, however when combined into a complete sample, males had more clusters.

While there are exceptions, overall males tended to cluster into fewer, larger groups compared to females within each cemetery. However, this trend was reversed when all cemeteries were combined into a single group, Table 20 and Figures 15-17.

When looking at the percentage of the population that split after node 1 and the distance of the second node split, again males appeared to show greater levels of similarity in their data compared to females within each cemetery. Table 21 and Figures 18-19 display these results.

Table 21 - Maximum distance for split of second node for the combined cemetery and separate cemetery groups for males and females. Distance is recorded as squared Euclidean distances; averages represented in the table. Average percentage of population that separated after first node split also presented. Overall, males appeared to have higher percentages split (greater similarity) compared to females.

Group	% of Group Split after Node 1	Distance of Node 2 Split
Combined cemetery males	46.70	11.00
Combined cemetery females	62.00	8.33
Hatherdene males	79.60	15.00
Hatherdene females	57.50	9.50
Oakington males	78.90	8.00
Oakington females	68.30	12.25
Polhill males	85.70	14.00
Polhill females	58.70	11.00
Eastry males	66.70	4.00
Eastry females	70.40	8.38

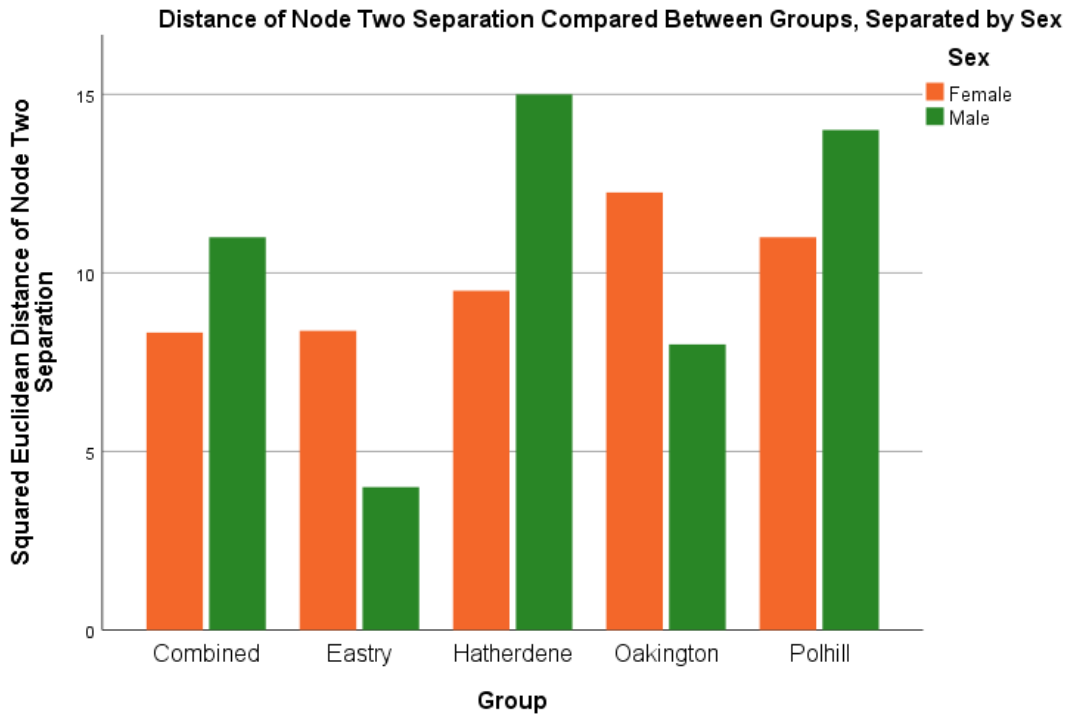

Figure 18 - The squared Euclidean distance of second node separation within each comparative group, separated by sex. A clear difference between males and females was not observed for this measure alone.

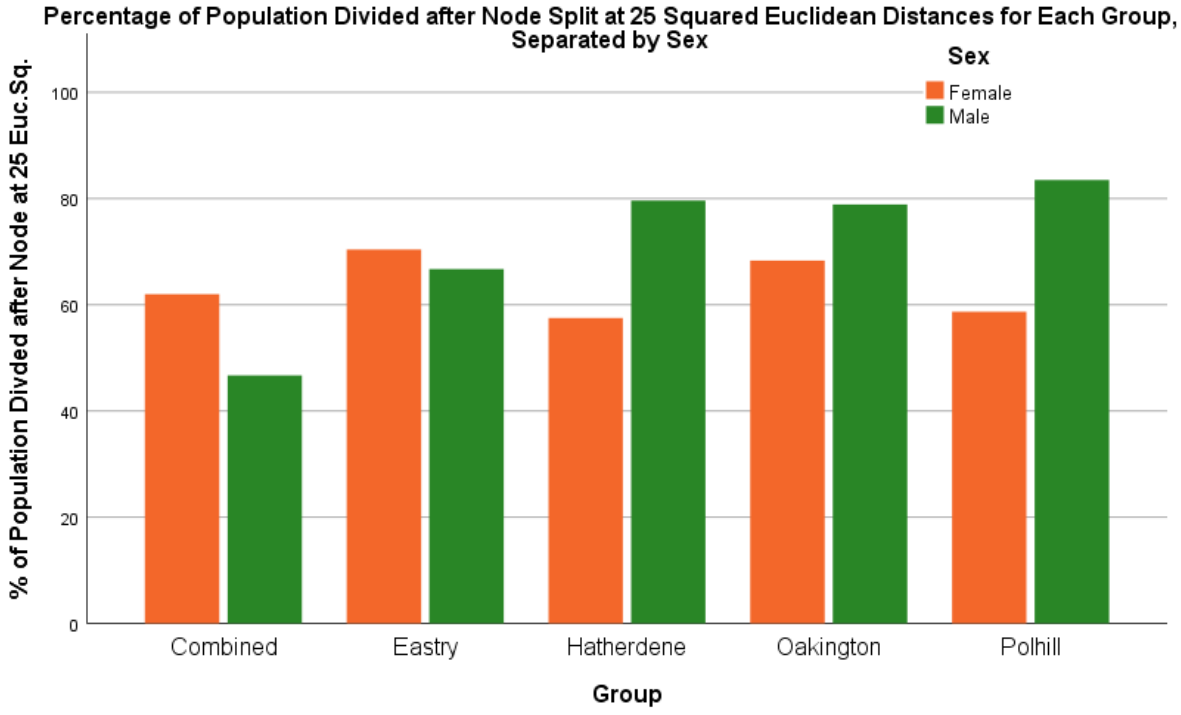

Figure 19 - The percentage of population that divided after the first node split at a squared Euclidean distance of 25 within each comparative group, separated by sex. Within each cemetery, overall, males showed higher percentages for the first split which represents higher levels of similarity overall.

When comparing the average sizes of largest clusters and the proportion of the population this comprised of in the group, again within each cemetery males tended to have larger and fewer clusters compared to females. Whereas in the combined cemetery group, females had larger and fewer clusters compared to males, Table 22 and Figures 20-21.

Table 22 - Average size of largest cluster within the combined cemetery and separate cemetery groups for males and females. Presented alongside this is the average percentage that reflects the proportion this cluster size represents within each comparison. Within individual cemeteries males tend to display larger clusters overall than females.

Group	Average Size of Largest Cluster	Proportion of Group (%)
Combined cemetery males	8.00	18.00
Combined cemetery females	11.33	24.00
Hatherdene males	4.50	20.50
Hatherdene females	4.25	26.50
Oakington males	6.50	43.50
Oakington females	4.75	27.00
Polhill males	2.00	29.00
Polhill females	3.00	25.00
Eastry males	2.00	67.00
Eastry females	2.00	49.30

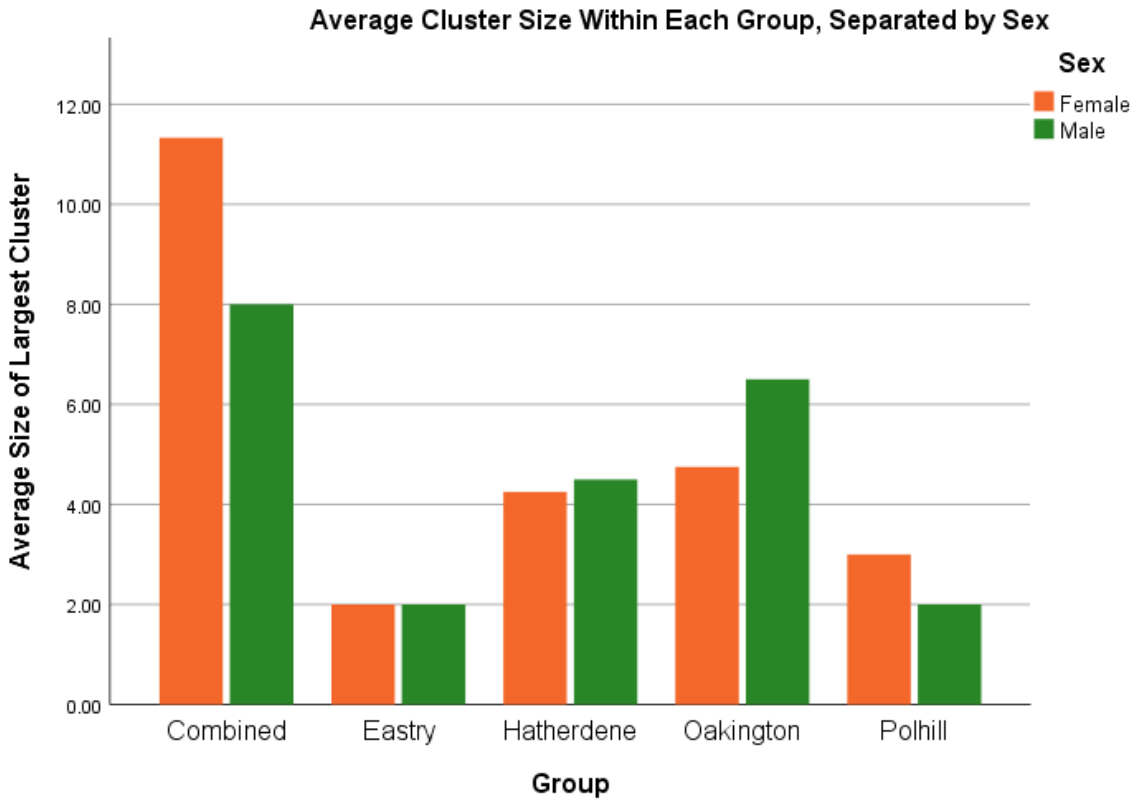

Figure 20 - Average cluster size within each comparative group, across all analysed teeth and separated by sex. Within each cemetery, overall males had larger cluster sizes than females.

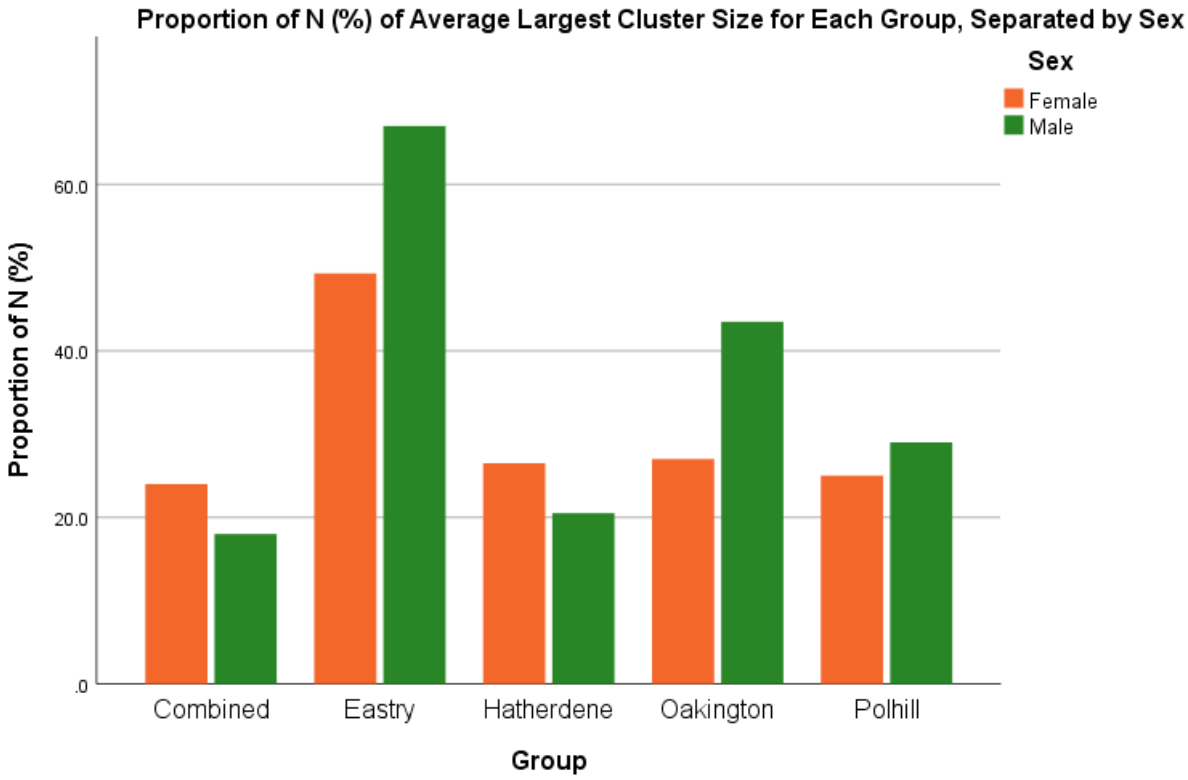

Figure 21 - The largest cluster size, on average, within each comparative group and across all analysed teeth as a proportion of n. Within each individual cemetery males had larger clusters compared to females.

Based on the results presented in Tables 20 – 22 and Figures 15 - 21, the patterning of clusters between males and females within each of the five comparative groups, overall, appears similar. With the exception of Hatherdene, females within the other three cemeteries had higher numbers of clusters compared to males. When this result is combined with the percentage of group that separated after the first node, this pattern is better observed. Smaller numbers of females were being separated out after the first node split. For comparative sake, a higher percentage split would indicate more similarity overall within the sample as only a small group would be shown to be most different to the rest. Female percentages for this split ranged from 57.5% - 70.4%, whereas male percentages ranged from 66.7% - 85.7% demonstrating the trend in more similarity overall within the male groups of these four cemetery sites. With the exception of Oakington males, the size of clusters within each group appear to be similar relative to sample size. This meant that similarity in tooth size was spread evenly within each group. Eastry had the smallest sample sizes for males and females, therefore their values appear elevated proportionally. Overall, from these parameters, the general trend observed within Hatherdene, Oakington, Polhill and Eastry was that female tooth dimensions were observed to have more diversity within each cemetery compared to their male counterparts. This result also furthers those made in the descriptive statistical analyses which revealed females appeared to have more variance in the spread of their data compared to males within the cemetery groups.

Interestingly, the reverse trend was observed when looking at the males and females in the combined cemetery group. In this case, males were seen to have more clusters overall compared to females, and the percentage split after node one was smaller in males than in females. This indicates that there was more diversity overall in males when individuals from Hatherdene, Oakington, Polhill and Eastry were combined. This difference is important to

highlight, as looking at a combined group provides more information regarding *population level* patterns, while investigating cemeteries individually provides interpretations about *community level* patterns. The reasons why this discrepancy appears within the sample will be discussed in Chapter 6.2. However, in general, the patterns observed from the hierarchical cluster dendrograms for combined group, individual sites and for male and female sub samples have shown that there are multiple levels of influence contributing to the overall size of teeth. Patterns reveal that teeth from males and females look different when combined as a whole group compared to when they are viewed as separate cemetery sites. This means that any interpretations from these results need to be cognisant of the fact that population level patterns may be masking community level patterns in biological similarity.

Once population level comparisons (between sites) for both pooled and separated sexes had been made, the same dendrograms were used to comment on targeted relationships at the community and individual levels (within each site) in more detail. Individuals were targeted for further investigation based on those that were found in multiple graves, burial structures, in close proximity or those with consistency in artefacts present in burial. Results obtained from these approaches are discussed in detail in Chapter 6.2 to highlight the applications and value of information derived from statistical cluster analysis to understanding social organisation within archaeological skeletal assemblages.

5.8 Conclusion

Results from the descriptive statistics revealed variation in tooth size throughout the four cemetery populations appeared to be consistent in terms of them showing relatively low levels of variation overall, but interesting patterns within this variation. After additional analyses, there were some patterns observed regarding females from Hatherdene and Oakington displaying more variation than females at Polhill and Eastry and compared to males from the same cemeteries. Some of the variation in the dataset was likely attributable to the number of outliers present within the combined cemetery group as well as the individual cemeteries. The explorative approach to statistical analysis allowed for simple questions to be asked of the data to determine which factors were likely to contribute to the variation in tooth size observed. While being a member of a particular cemetery site was overwhelmingly observed not to influence tooth size significantly, the same could not be argued for the influence of biological sex. With the exception of canine teeth, which were found most commonly to reflect significant sex related differences in tooth size, the way in which the influence of biological sex was expressed in all other teeth was complex. All tooth classes appeared susceptible to the influence of sex, however not consistently across all four cemetery sites. Similarly, each tooth dimension appeared to be differently affected by sex with BL dimensions being more likely to show dimorphism than MD, though this pattern was not observed as strongly in the Oakington sample. Furthermore, by testing for differences separately with the MD and BL dimensions of the teeth, it was possible to uncover patterns responsive to overarching factors of cemetery and sex that demonstrated there are multiple layers that contribute to tooth size, and intrinsic and extrinsic factors contribute to variations in size in different ways. From these explorative approaches to data analysis, it was

determined that it was possible to observe variation in size that was not accounted for by cemetery environment or sex alone, therefore, the remaining influences are attributable to biological similarity based on the inherited traits shared amongst closely related individuals.

The results from the hierarchical cluster analysis have revealed the ability to locate individuals that share greater amounts of similarity within and between cemetery groups. It was possible to observe the influences that sex can contribute at a population level compared to a local level and the issues that may arise with masking trends within a dataset. When looking at teeth within pooled sex groups, again differences were noticed. The spread of variation became a lot more homogenous within the individual cemetery sites and combined cemetery group. When looking at teeth that were not sexually dimorphic, the sample appeared more similar overall. It was not until sex was taken into consideration and males and females were separated that differences in patterns within each cemetery compared to the combined group sample became evident. When sexually dimorphic teeth were included to look at males and females separately, patterns were detected within the sample. Females within the individual cemetery sites appeared to be more diverse in their tooth sizes overall compared to males within the same samples. This was reflected in the percentage of population that was separated at the greatest distance (node one), overall number of clusters and percentage of cluster size relative to sample size. In contrast, on the population level, males appeared to be more dissimilar than females when looking at all cemetery sites combined.

From these results, it is clear to see that there are several influencing factors on tooth size. Cemetery site, biological sex, and level of comparison (whether broadly referring to a population or a group on a community level) need to be addressed and understood in order to help develop meaningful interpretations from this type of biodata. Biological similarity can

be clearly identified within skeletal assemblages, but not in a consistent way. An exploratory approach to data analysis to work through these confounding variables has proved to be a useful way to better understanding tooth data which in turn will help to build up stronger interpretation about social constructs within early Anglo-Saxon England. The next chapter will focus on developing these interpretations based on these results, particularly the cluster analysis, where kinship patterns and biological connections between individuals at the population and local level will be explored in more detail.

6. Applications of Tooth Data and Biological Similarity

This chapter will attempt to demonstrate how results obtained from the analysis in Chapter 5 from the individuals of Hatherdene, Oakington, Polhill, and Eastry can be incorporated into the current theories regarding early Anglo-Saxon kinship and identity. Discussion will begin at the population level to demonstrate how patterns evident in the teeth across all four cemetery sites can link to existent research on early Anglo-Saxon residence and mobility patterns. Once established, each cemetery's tooth data will be looked at separately to comment on community level connections between the individuals interred within the sites. This section will focus on spatial patterning of graves, burial structures and grave goods interred with certain individuals in the community. Finally, the focus of this chapter will shift to the individual grave level through discussion on multiple interments and case study burials. By arranging the discussion in such a way, the aim of this chapter is to highlight the utility of teeth for adding to multi-scalar conversations on early Anglo-Saxon kinship that could be explored in more depth in future. For discussion on validation of method, preliminary mtDNA results from a different project have been used to corroborate findings from dental analyses. The notion of kinship being direct manifestations of blood relationships between individuals is, by far, a simplistic view on a complex topic within the study of archaeological populations (see Schneider 1984). Furthermore, linking a person's or group's identity to shared biological traits alone is also misleading and preventative of in-depth discussion on what actually contributes to the 'selfhood' of an archaeological individual. Rather, as has been argued for here, a holistic approach to the understanding of identity and kinship between and within archaeological populations needs to start from a foundation involving multiple streams of evidence. These can then work together in order to best understand and interpret kinship

patterns from the past. Tooth biodata is one such stream of evidence that can be useful in conjunction with cemetery spatial data, biological profile data, contextual artefacts and historical information in order to help build a more robust image of how people were identified, at least in death, during the early Medieval period. Furthermore, even with the addition of biological similarity from tooth size, caution must be applied to interpretation of what suggested connections may be. Most of the phasing information from the four cemeteries dated graves within ranges spanning a century or more. Therefore, without knowing the exact timing of interment it will be difficult to identify exactly what the underlying connection may be. The exception to this would be in multiple interments of concurrent burial where timing is clearer.

6.1 Population Level Interpretations

In order to investigate residence and mobility patterns present within early Anglo-Saxon England using tooth biodata, patterns resultant from the clustering of males and females across the four skeletal populations and within each individual population (Hatherdene, Oakington, Polhill and Eastry) needed to be reviewed. The first set of results discussed are based on the groups with both males and females being compared in a pooled sex group. It was important to consider pooled and separate sex comparisons as there will be siblings and offspring of both sexes that are present within each lineage and family unit, contributing to the levels of similarity expressed. As previous research has shown, tooth measurements in offspring correlate with tooth dimensions of parents (i.e. Townsend and Brown 1978a; 1978b) therefore, discussions on patrilocal/patrilineal (or matrilocal/matrilineal) societies need to encompass pooled sex and sex specific patterns. Additionally, statistical testing revealed that

not all teeth present in the human dentition were sexually dimorphic within these four cemeteries (see Chapter 5.5.2 and Tables 11-14), allowing male and female comparisons to focus more on genetic similarity in tooth size rather than sex-related size differences.

Working with the hypothesis that, if each cemetery represented a separate lineage or kinship group within the population, the tooth data should reflect this by the hierarchical cluster analysis (HCA) outputs appearing to show more similarity within each cemetery, but less so when they are combined into one group. From the clusters generated by HCA, Tables 17-18 and Figures 11-12 show that there were an average 8.67 clusters of individuals at squared Euclidean distances of 1 in the combined cemetery group compared to averages of 4-7.67 clusters when data was separated by cemetery site. Furthermore, around half (54.83%) of the population of the combined cemetery group divided after the first node, compared to approximately two thirds (61.5 – 69.33%) for each site when cemeteries were looked at individually. In a more homogenous group, it would be expected that higher percentages of individuals would still group together (separate) after the first node split at a squared Euclidean distance of 25. Therefore, each of these four individual cemeteries were showing higher levels of similarity compared to when they were combined into one group. The greater number of clusters in the combined cemetery group also supports this idea; in a more diverse group, you would expect more clusters to appear. When looking at the proportion of each sample the largest cluster comprised at a squared Euclidean distance of 1, the largest clusters at Hatherdene, Polhill and Eastry made up around 30% of the corresponding site sample (26.13 – 33%, see Table 19 and Figure 14). In comparison, the largest cluster from the combined cemetery group represented 22.67% of the whole sample. This indicates again, higher levels of similarity among the individuals within each cemetery compared to the combined cemetery group. Interestingly Oakington appeared to be an exception to this as the

largest cluster within this site made up 22% of the overall population, the lowest of the five comparisons. However, the tooth data from Oakington does follow the rest of the patterns observed regarding the number of clusters and node-split percentages as the other three sites under investigation. Based on these findings, each individual cemetery was found to have a higher amount of similarity expressed amongst its members than when observed in the combined cemetery group. This supports the notion that each cemetery includes at least one dominant lineage as, when treated as its own entity, each cemetery displayed more similarity within the group than when combined with the others at a population level.

As discussed in Chapter 2, females and males may reflect differences in population residence and mobility patterns, so it was important to review the above trends for both males and females within each cemetery and compare them across the population. By separating data in this way, it was possible to identify patterns between the sexes that may be based on residence patterns. Overall, when looking at each cemetery individually, the results indicated that there appeared to be greater levels of biological similarity within the males of each site compared to the females. This was represented by the lower percentages of females (57.5-70.4%) being separated out after the first node split at Hatherdene, Oakington and Polhill compared to males (66.7-85.7%) (see Table 21 and Figure 19). At this population level, it is presumed that the more similar individuals are within a group the higher the percentage after first division should appear. In conjunction with this, females buried at Oakington, Polhill and Eastry were observed to have higher numbers of clusters compared to males (see Table 20 and Figures 15-17). Along similar lines, the proportion of the group that the largest cluster comprised of was smaller for females than males at Oakington, Polhill and Eastry (see Table 22 and Figures 20-21). Across the population females tended to be arranged into greater numbers of smaller sized clusters compared to males. These results are indicative of higher

amounts of diversity among the female members of the population compared to males in relation to tooth size. An interesting exception to this was observed with the Hatherdene data where females were observed to cluster into fewer groups compared to males (5.75 and 8.5, respectively, see Table 20) and the overall proportion of the largest cluster size was larger in females than males (26.5% and 20.5%, respectively, see Table 20). While there do appear these differences between males and females, it would be incorrect to assume that there would be significant differences between *all* males and females in each cemetery due to sibling relationships as well as those between parent and offspring. It is possible that within each cemetery site there would be males and females that appear more similar to one another than to other same sex individuals. This may help to explain the differences observed with the data from Hatherdene. Therefore, conclusions drawn related to sex specific differences in regard to population should be based on repeated patterns present across multiple variables under investigation. In this case the data is suggesting that, across the population, there is more similarity in male tooth sizes compared to female tooth sizes. These findings were also echoed in the ANOVA results for significance testing on the impact of site and biological sex on tooth size; when looked at separately, males appeared to have less variation in their measurements compared to females (see Chapter 5.5.2). In addition, Chapter 5.5.1 showed that more female teeth appeared to be significantly affected by cemetery site membership than males with six teeth being found to differ between the sites compared to one for males. Combined, these results suggest that some female individuals were quite different to the rest of the population, perhaps indicating they are coming from different communities altogether apart from these four cemeteries. This means that females could have been more mobile across the population compared to males.

For these results to make sense when discussing residence patterns for this early Anglo-Saxon population, however, one further comparison needed to be made. Instead of looking at males and females between the four cemeteries separately, it was also important to compare the sexes within a combined cemetery group. When the combined cemetery population compared males and females separately, an interesting pattern was observed. In contrast to what was found with males showing higher levels of similarity in their tooth sizes, when all four sites were combined, it was females who showed higher levels of similarity in their tooth sizes. In this case, it was the male data that had more clusters, fewer individuals being separated out after the first node split and the size of the largest cluster represented a smaller proportion of the group compared to the female only results (see Tables 20 – 22 and Figures 15-21). However, if patrilocality and patrilineality were employed within this early Anglo-Saxon population, later phases of the period were thought to be based on historical documentation (i.e. Lancaster 1958a; 1958b), this result should be expected. If each cemetery represents a separate kin network based on connected lineages, when combined these differences should become more striking. Females marrying in from elsewhere may still appear different, but as what separates kin groups from one another in patrilocal groups is determined along the male line, it would be expected for these differences among males to become more pronounced when combined at the population level (Kumar *et al.* 2006; Oota *et al.* 2001; Pérez-Lezaun *et al.* 1999). It could also be considered that the pool of eligible females available for marriage comes from a smaller group of families than the males which would heighten the diversity of male data when combined a population level (Sayer, *personal communication).*

The working idea for patrilocal residence and patrilineal groups has been identified in these four early Anglo-Saxon cemeteries which are representative (due to geographic spread and

occupation dates) a subset of the wider contemporary population. As such, this biological evidence helps to solidify theories regarding male-centric residency during this time period in England. It appears that there are identifiable lineages between the four cemetery sites, and that greater affinity between individuals is linked more to similarity between males. Brothers, fathers and sons would have formed the same consanguine group. In addition, this would suggest that, due to the greater variation in female dentition compared to males, females were the ones entering these communities from elsewhere, bringing with them dental metrics reflective of other lineages which caused increased variation within these four cemetery sites. As previous research has supported the notion of the mobility of females during this era (Montgomery *et al.* 2005; Sayer 2014; Sayer and Dickinson 2013), the differences observed in tooth morphology and size may be reflecting differences found in local and non-local groups of people. The data presented here through dental metrics supports these population level findings and further highlights the complexity of looking at biological data to infer kinship patterns in archaeological populations. While the bimodal representation between similar and dissimilar may be easier to locate, how these distinctions came to be is more difficult to understand completely. Further still, results at a population level may differ at a community and individual level, which is why all need to be considered in equal measure.

6.2 Community Level Interpretations

While there is documentary evidence to suggest that patrilocal residence and patrilineal descent were apparent in later Anglo-Saxon England, there have been alternative perspectives that suggest, in practice, on a community level these patterns were not so rigid

(Lancaster 1958b; Murray 1983). Additionally, identity and kin relations on a community level may be expressed very differently to residence patterns on a population level (Sayer 2020). As such, eliciting additional information from skeletal remains to build up ideas of kinship at a community level is a worthwhile pursuit. Biological profile data (age and sex of individuals in particular) has been used previously to help explain ideas of biological relationships between individuals in archaeological populations (i.e. Alt *et al.* 1997; Howell and Kintigh 1996, see Chapter 2). By doing so, identifiable features about a specific individual combined with presumptive biological relationships to others (via hierarchical cluster analysis of tooth metric data) can be compared alongside spatial patterning regarding the location of individual interments within a cemetery site or the appearance of certain grave goods in order to comment on identity in death on a community level. For instance, deductively, assumptions have been made about grave structures and the geographical locations of graves in a cemetery and how they may relate to kinship (Stoodley 2002).

The four cemeteries under investigation in this project displayed commonalities with other early Anglo-Saxon cemeteries within this region and time period in regard to presence of grave goods and apparent placement of graves around centralised areas (i.e. Sayer 2020, 121-122). As these decisions are attributed to cultural and social narratives at time of interment (Sayer 2020), these features reflect messages on the local or community level. In order to explore these community level differences in detail, this subsection will frame discussion around the location and connections of those interred in structured ring ditch burials, the location of outlier individuals within the cemetery, and the presence of connections represented by grave good inclusions.

6.2.1 Ring Ditch Burials within the Cemeteries

Further explorations of community level influences on burial were done through the investigation of individuals interred within grave structures. Ring ditch burials were found at Hatherdene, Polhill and Eastry cemeteries, while no such structures were found at Oakington. It was decided to investigate each individual buried within a ring ditch in order to locate those in the cemetery that displayed the closest degree of biological similarity to them through dental metrics, as well as comparing the individuals within ring ditches to one another. Patterns discovered were able to inform on the community level regarding connections between notable individuals and those within the rest of the group. For the purposes of this analysis, to be consistent between across the four cemeteries, individuals within ring ditches had all connections noted between one another, but when compared to the rest of the group, connections were only recorded if other individuals were connected to those in ring ditches at a squared Euclidean distance of 1, signifying the closest connection possible across the teeth under comparison.

There were two individuals found within ring ditches at Hatherdene cemetery: H856, a male aged 26-44 years at time of death, buried with a knife, mixed beads, a shield boss with grip, and a spearhead and; H259, a male aged 26-44 years at time of death, buried with a belt plate, a buckle, and a knife. Table 23 presents an overview of common teeth and corresponding distances between H259 and H856.

Table 23 - Squared Euclidean distances between individuals within ring ditches for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance Between Individuals
Right maxillary canine	Hatherdene only, pooled sex	2
Right maxillary central incisor	Hatherdene only, pooled sex	25
Left maxillary first premolar	Hatherdene only, pooled sex	4
Left mandibular first molar	Hatherdene only, pooled sex	6
Left mandibular first premolar	Hatherdene only, pooled sex	4
Right mandibular canine	Hatherdene only, pooled sex	25

As can be seen in Table 23, the two individuals who were buried in the ring ditches appear to share moderate to high levels of similarity in regard to their tooth dimensions because four of the six teeth available for comparisons showed higher levels of similarity between one another. This, combined with the presence of similar grave goods and burial style, suggests a level of social importance as well as a biological connection shared between these two males. Elsewhere researchers have suggested social levels of importance due to the appearance of grave structures like mounds or ditches (Williams 2011), therefore, due to these two graves being the only ones encircled with rings within the assemblage at Hatherdene it could be argued that these two males were from the most central patrilineal family group at the site. Due to the closeness in tooth data observed, combined with their demographic data, it is likely these two males were genetically related. If burials were contemporaneous, this relationship could potentially indicate brothers or first cousins.

Within the community, H259 was found to be most similar to: H526 (found with a spear, buckle and knife); H1164 (buried with a buckle, spear and knife) and; H1275 (found with a knife, spear and buckle). All of these individuals were middle aged adult males between the ages of 26-44 years old at time of death and buried with the same array of grave goods. For H856, the four most similar individuals in the cemetery were: H201, an adult male of unknown

age and no associated finds; H557, a male aged over 46 years old at time of death, buried with a knife; H1181, a male aged 26-44 years old at time of death, buried with a shield, buckle, knife and spear and; H1092, a female aged 26-44 years at time of death, buried with a knife and small long brooch. The majority of close biological connections to these two males in ring ditches were also males. It is also interesting as there appears no cross over between the three males who are closest to H259 and those that are closest to H856. This could add more support for the idea that the males may have been cousins as opposed to brothers, as it would be expected that the two would appear similarly as close to the same individuals if they had the same set of parents and close relatives. The location of the individuals in the ring ditches and their associated close connections are displayed in Figure 22 and Table 24 provides a brief summary of all individuals at Hatherdene associated with the ring ditch burials.

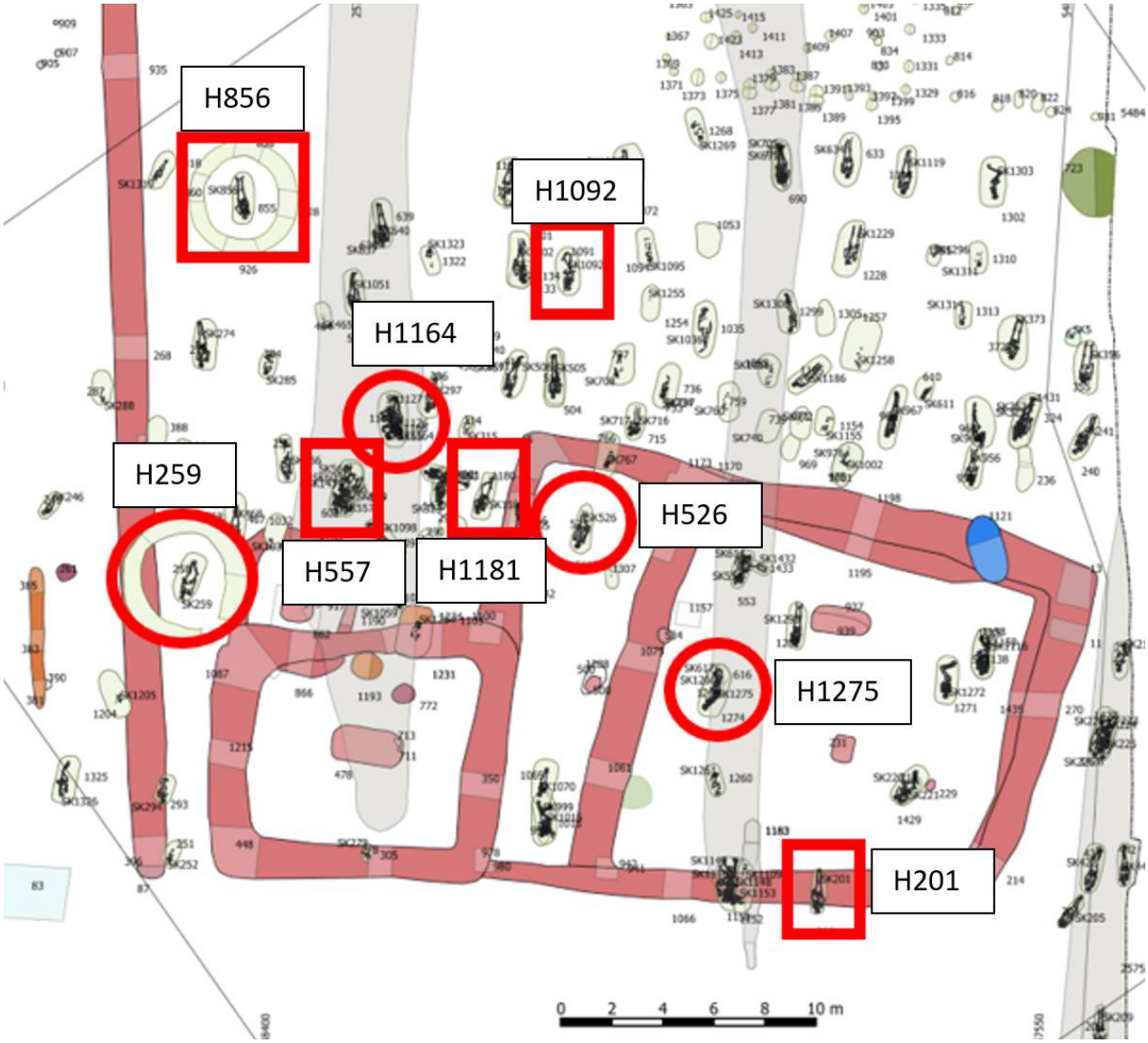

Figure 22 - The spatial distribution of individuals with the highest level of biological similarity to each individual buried within the ring ditches. Circles indicate H259 and connections, and rectangles indicates H856 and connections (after Oxford Archaeology East, personal communication 2018).

Table 24 – Brief summary of findings related to the ring ditch interments at Hatherdene cemetery.

Cemetery	Individual	Demography	Grave Goods	Notes
Hatherdene	H856 (buried in ring ditch)	Male, 26-44yrs	Knife, beads, shield boss, spearhead	High degree of similarity to: H259, H201, H557, H1181 and H1092
	H259 (buried in ring ditch)	Male, 26-44yrs	Belt, buckle, knife	High degree of similarity to: H856, H526, H1164 and H1275
	H201	Male, age unknown	N/A	High degree of similarity to H856.
	H557	Male, >45yrs	Knife	High degree of similarity to H856.

Cemetery	Individual	Demography	Grave Goods	Notes
	H1181	Male, 26-44yrs	Spear, buckle, knife, shield	High degree of similarity to H856.
	H1092	Female, 26-44yrs	Knife, small long brooch	High degree of similarity to H856.
	H526	Male, 26-44yrs	Spear, buckle, knife	High degree of similarity to H259.
	H1164	Male, 26-44yrs	Spear, buckle, knife	High degree of similarity to H259.
	H1275	Male, 26-44yrs	Spear, buckle, knife	High degree of similarity to H259.

Within Eastry, there were nine individuals interred within ring ditches. Table 25 provides an overview of individuals interred within ring ditches along with their demographic details and associated artefacts, if applicable. There were an additional six individuals at Eastry buried in ring structures, however, these individuals were curated in the 1976 excavation, and therefore unable to be located for this project.

Table 25 - An overview of individuals interred within ring and partial ring ditches within the Eastry cemetery. Where two individuals are listed in the same row, they were interred within the same structure.

Individual	Sex	Age (years at time of death)	Grave Goods
E9	Female	35-45	Knife
E39 E44	Sub adult Female	9-13 25-30	Fitting/mount, beads, knife, purse mount N/A
E40	Female	18-21	Knife, spearhead
E51	Male	35-37	Buckle, knife, spearhead
E37	Male	25-35	Seax
E38	Sub adult	N/A	Knife, pin
E46	Female	32-36	Girdle hanger, knife, beads
E49	Sub adult	N/A	Pot, nail, knife, spearhead

There was one ring structure that had two individuals interred within it, E39 and E44. However, E39 was a sub adult, so no comparisons were available to be made within this project. Additionally, the teeth of E44 were not in good enough condition for measurements

to be recorded so this adult female could not be compared to any of the others within the ring ditches either. E37 had very few teeth available for comparison, and unfortunately none of the teeth selected for hierarchical cluster analysis, see Chapter 5.6, corresponded to the teeth this individual had present. As such, no further comparisons were made to E37. Comparisons of the remaining four adults were made to the rest of the group from Eastry to locate individuals who appeared to be the most similar based on tooth size. Due to overall poor levels of preservation, there was limited comparative data within the entire sample set. Few individuals were observed to have strong affinity for another as there simply were not enough teeth to compare between them. However, some connections could still be made, although with less certainty compared to the other two cemeteries.

In the wider cemetery, E9 was found to be most closely affiliated with: E45, a young adult female aged 16-24 years at time of death, recovered with a cowrie shell, workbox, chatelaine fitting, knife, buckle, latchlifter, ring, beads and a pendant and; E12, an adult female aged 20-30 years at time of death and recovered with an iron strip and a buckle. E40 was found to be most similar to: E46, E45 and; E20, an adult female aged 30-36 years at time of death, recovered with a cowrie shell, oyster shells, beads, rings, and a pin. E51 was only found to have one close connection, E28 a young adult male aged 18-24 years at time of death, recovered with a knife. Finally, E46 was found to be most similar to E40 and E12. The majority of these graves were given the same general phasing date of 7th century (Welch et al. 2008). Figure 23 provides an overview of the location of these ring ditch individuals and their affiliations within the cemetery at Eastry. Table 26 provides a brief summary of all individuals associated with the ring ditch interments at Eastry.

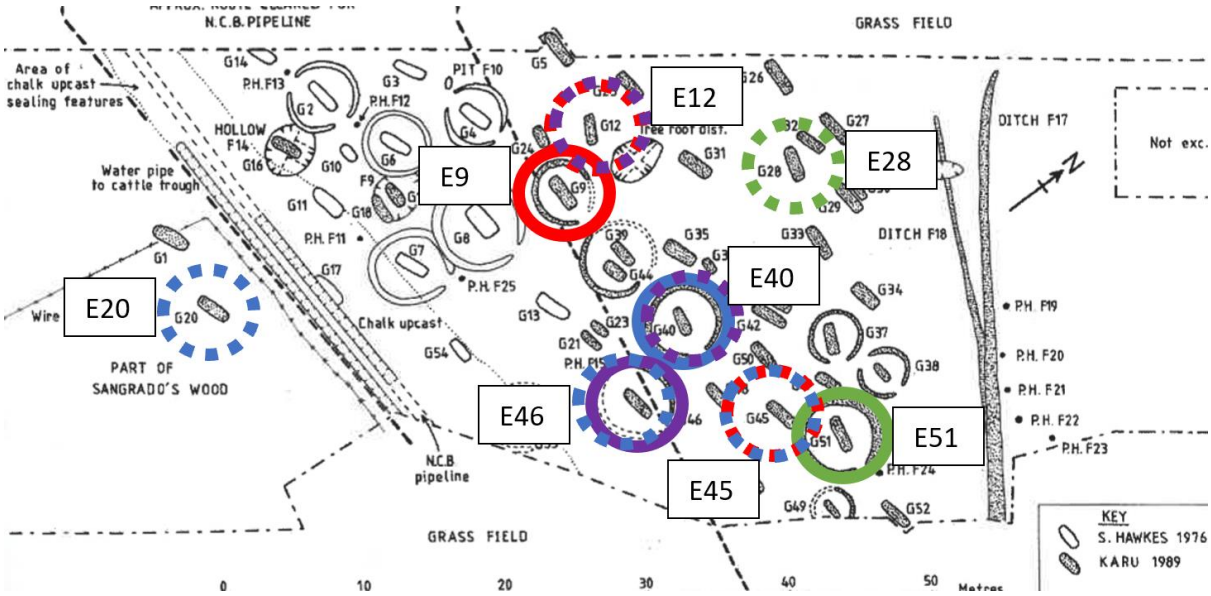

Figure 23 - A visual representation of the individuals interred within ring structure (for whom teeth were available for comparison) and their affiliated connections. Red indicates E9 and connections; blue indicates E40 and connections; green indicates E51 and connections and; purple indicates E46 and connections. Dashed circles of same colour indicate closest connections to ring ditches (after Welch et al. 2008, 9).

Table 26 – Brief summary of findings related to the ring ditch interments at Eastry cemetery.

Cemetery	Individual	Demography	Grave Goods	Notes
Eastry	E9 (buried in ring ditch)	Female, 35-45yrs	Knife	High degree of similarity to E45 and E12.
	E40 (buried in ring ditch)	Female, 18-21yrs	Knife, spear	High degree of similarity to E46, E45 and E20.
	E46 (buried in ring ditch)	Female, 32-36yrs	Knife, girdle, beads	High degree of similarity to E40 and E12.
	E51 (buried in ring ditch)	Male, 35-37yrs	Spear, buckle, knife	High degree of similarity to E28.
	E12	Female, 20-30yrs	Iron strip and buckle	High degree of similarity to E9 and E46.
	E20	Female, 30-36yrs	Shells, beads, and pin	High degree of similarity to E40.
	E28	Male, 18-24yrs	Knife	High degree of similarity to E51.
	E45	Female, 16-24yrs	Knife, buckle, beads, pendant	High degree of similarity to E9 and E40.

There does appear some overlap between ring ditch individuals and their corresponding close connections with E12, E45, E46 and E40 appearing to cross over the most. All these individuals are female and three of the four of these women were classed as young adults ranging from teenage years to early 20s at time of death. Out of all the above connections, E9 and E45 appeared to be linked the strongest as they had the most teeth available to support this connection. Based on the demography of these two females it is possible that they represent, sisters, cousins or a mother-daughter relationship, depending on timing of interments within the 7th century. With consideration paid to the presence of grave goods for E45 and the structure surrounding E9, it could also be hypothesised that they were part of a larger, centrally important familial network within the community.

At Polhill, nine individuals were interred ring ditches, Table 27 provides an overview of these individuals along with their demographic details and associated grave goods, if recovered.

Table 27 - An overview of individuals interred within ring and partial ring ditches within the Polhill cemetery.

Skeleton	Sex	Age (years at time of death)	Grave Goods
P40	Male	32-50	Buckle
P36	Male	30-36	Buckle
P34	Female	>50	Buckle
P19A	Female	22-28	Beads
P19B	Infant	N/A	None
P18	Female	20-24	None
P11	Male	44-52	None
P10	Female	42-50	None
P2	Female	18-25	Beads

P34 unfortunately had no teeth available for comparison, so no connections could be derived for this particular female. Additionally, P11 only had data present for a single tooth which rendered the results less robust compared to the remainder of the individuals which had multiple teeth available for comparison. P40 displayed no strong affinity for a particular individual, there were others within ring ditches that appeared similar on a single tooth (P36

and P18), but due to the lack of repetition across multiple teeth, connections were not deemed to be as strong as they could have been. P36 appeared to be most similar to P14, a young adult female who was aged to be 18-22 years old at time of death and buried with a pin and a buckle. P19 displayed closest affinity to: P14, previously mentioned and P37, an adult female aged 30-34 years at time of death who was buried with a buckle. P18 did not really show strong affinity to any particular individuals but was closest in regard to tooth data to: P36 and P19, also in ring ditches, as well as P14 and P37, both previously mentioned. P10 appeared most similar to P14 as well. Finally, P2, like P18, did not demonstrate strong affinity to a specific individual, but shared closest similarity with: P42, a young adult female aged 18-22 years old at time of death who was recovered with beads and P46, an adult female aged 25-28 years old at time of death who was recovered with shears. Figures 24 and 25 provide an overview of the noted connections and their locations within the section of excavated cemetery. Table 28 provides a brief summary of the individuals interred in ring ditches and their closest connections within Polhill cemetery.

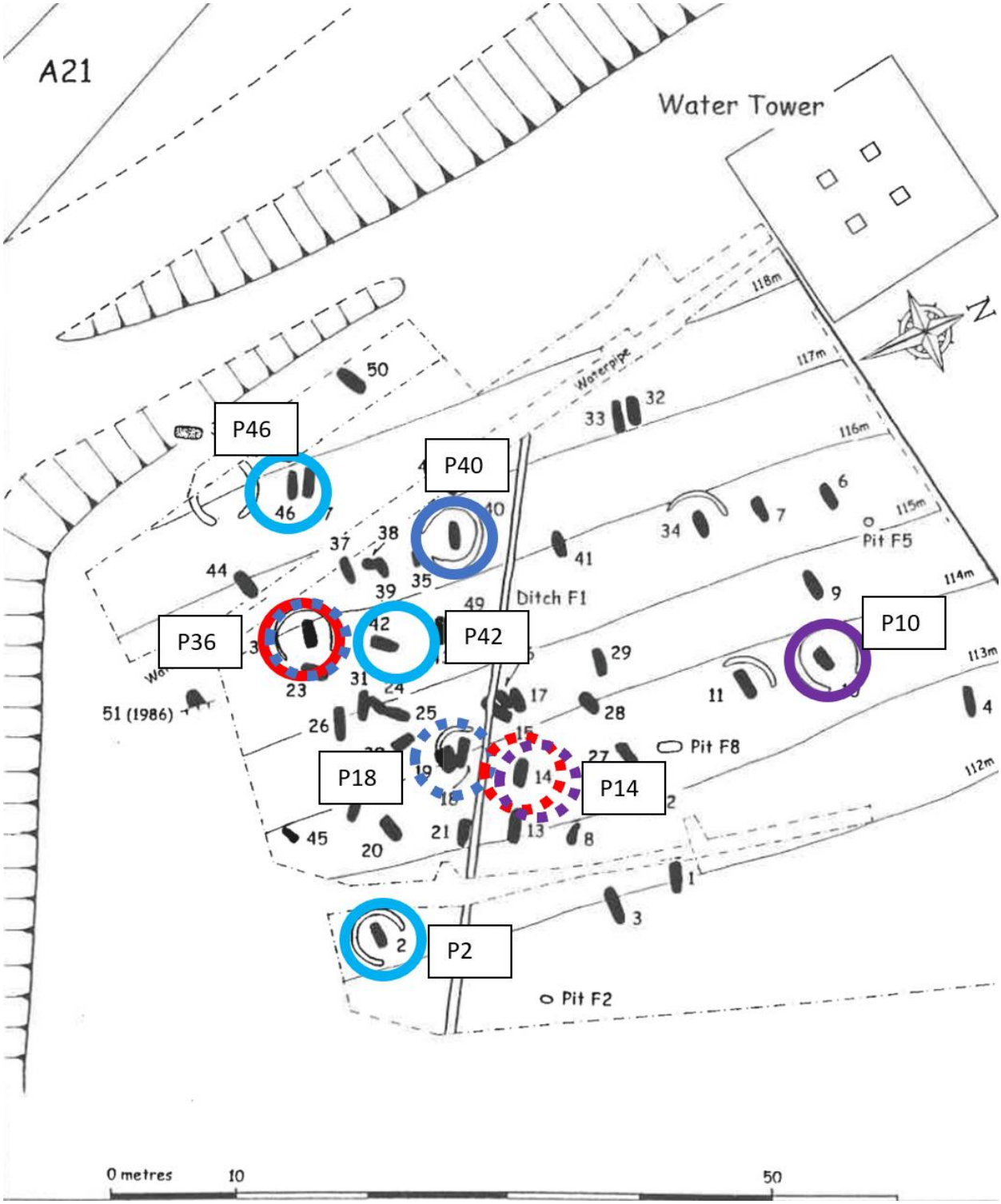

Figure 24 - An overview image of the ring ditch individuals from Polhill and their identified connections relative to close biological similarity. Dark blue relates to P40; red relates to P36; purple relates to P10 and; light blue relates to P2. Dashed lines indicate identified connections (after Philip 2002, 4).

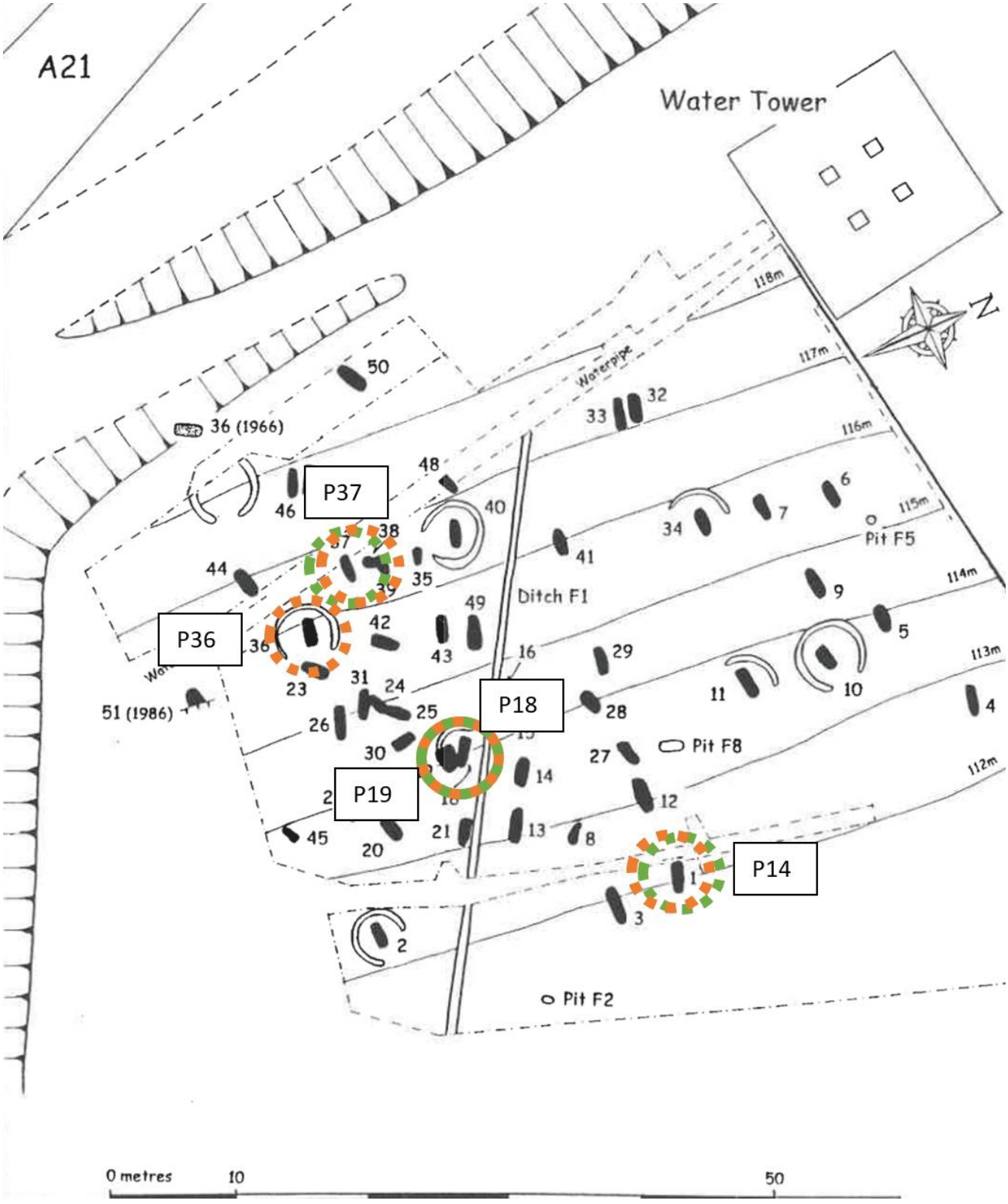

Figure 25 - An overview image of the double ring ditch interment from Polhill and their identified connections relative to close biological similarity. Green indicates P19 and orange indicates P18. Dashed lines indicate identified connections (after Philip 2002, 4).

Table 28 - Brief summary of findings related to the ring ditch interments at Polhill cemetery.

Cemetery	Individual	Demography	Grave Goods	Notes
Polhill	P2 (buried in ring ditch)	Female, 18-25yrs	Beads	Most similar to P42 and P46.
	P10 (buried in ring ditch)	Female, 42-50yrs	N/A	High degree of similarity to P14.
	P18 (buried in ring ditch with P19)	Female, 20-24yrs	N/A	Most similar to P36, P19, P14 and P37.
	P19 (buried in ring ditch with P18)	Female, 22-28yrs	Buckle	High degree of similarity to P14 and P37.
	P36 (buried in ring ditch)	Male, 30-35yrs	Buckle	High degree of similarity to P14.
	P40 (buried in ring ditch)	Male, 32-50yrs	Buckle	Most similar to P36 and P18.
	P14	Female, 18-22yrs	Buckle and pin	High degree of similarity to P10, P19 and P36. Similar to P18.
	P37	Female, 30-34yrs	Buckle	High degree of similarity to P19. Similar to P18.
	P42	Female, 18-22yrs	Beads	Similar to P2
	P46	Female, 25-28yrs	Shears	Similar to P2

The spatial distribution of the ring ditch individuals and the individuals most similar to them was quite interesting. Although some of the ring ditches were located away from the centre of the cemetery, the connections amongst this group were often overlapping, especially in the case of P14. In addition, the overlapping connections appeared to be clustered in the dense, central area of the cemetery. This pattern is quite strong, especially with the overlap between individuals interred in ring ditches and between individuals such as P37 and P14 who appeared to be very similar in regard to tooth measurements amongst the ring ditch group. This observation could mean that there may have been more consideration to close relations at Polhill in regard to choosing where to bury family members. Although, it must be

acknowledged that this section of the cemetery is only represented by the 1984 excavation, the entire cemetery has yet to be explored via dental metrics and may provide different interpretations if the remainder of individuals were included.

There also did appear some consistency among grave goods recovered amongst the ring ditch individuals at Polhill and those that were determined to be most similar in tooth sizes. Buckles were the most common grave artefact to have been recovered with the group discussed above, which included male and female individuals. Furthermore, of the nine individuals interred in burial structures, five of them were females and the connections made to closest individuals within the cemetery were also mainly to females. Similar to the females' connections at Eastry, at Polhill the connections discussed above also tended to be between females in the young adult age category.

When reviewed across these three cemeteries, interesting patterns have been revealed regarding the connections between ring ditch interments and the wider community. At Hatherdene, it was shown that the only two individuals within burial structures were males of a similar age. Their connection to one another was relatively strong in terms of tooth biodata. In addition, their strongest biological connections to the rest of the group were to six other males and one female. In a patrilineal society, it would be expected to see higher levels of similarity between the males of the group compared to females as they are the ones remaining and residing in their home area. The appearance of an adult female does not deviate from this pattern of patrilineality as it was common in the later period for daughters to reside with the family until marriage (Lancaster 1958a; 1958b) or return to their homestead to give birth (Sayer 2014).

However, at both Polhill and Eastry, the majority of connections found to those interred within ring ditches were amongst females. This may be attributable to different customs in the Kent locations compared to Cambridgeshire or could link to patrilineality through a closer look at demography. In both sites, many of the female individuals highlighted as sharing similarity amongst the ring ditch burials were classed as young adults based on their demographic data. It is possible, that if females were yet to marry at time of death, they would still reside at their paternal homestead and then may contribute to the homogeneity of females present therein. Therefore, it could be possible that these females represent members of a central paternal lineage which is why they have been treated differently in death with their interment in ring ditches compared to other females. At Polhill, there was the added layer of shared grave goods between ring ditch individuals and their close connections. The consistency regarding the inclusion of buckles between the ring ditch individuals and others is a further visual signifier to the community of the connections between certain individuals. While this was not found to be as clear with those in Hatherdene and Eastry, this finding highlights the range of community level narratives possible to express between different cemetery sites.

6.2.2 Outlier Individuals within the Cemeteries

During the statistical investigation of the raw data, outliers were identified within all four cemeteries within this project, see Chapter 5.4. In this context of biological similarity, these outlier individuals were interpreted to represent those that were least similar to the rest of the group. In that, the individuals identified as being an outlier were shown to have tooth

dimensions that were significantly larger or smaller than the expected range of variation within each cemetery, see Table 7. These differences in size were interpreted to mean that it was unlikely the individuals listed in Table 7 shared close biological connections to anyone in the rest of the cemetery group. As such, it was decided to locate the graves containing these individuals in order to comment on spatial patterning related to those that unlikely to have a biological connection to the rest of the group.

There were two individuals within Eastry cemetery who were identified as statistical outliers during analysis: E5, an adult male aged 36-38 years old at time of death, recovered with a buckle and knife and; E50, an adult male aged 22-28 years old at time of death, recovered with a pot. Figure 26 presents the location of these two outlying individuals within the cemetery at Eastry.

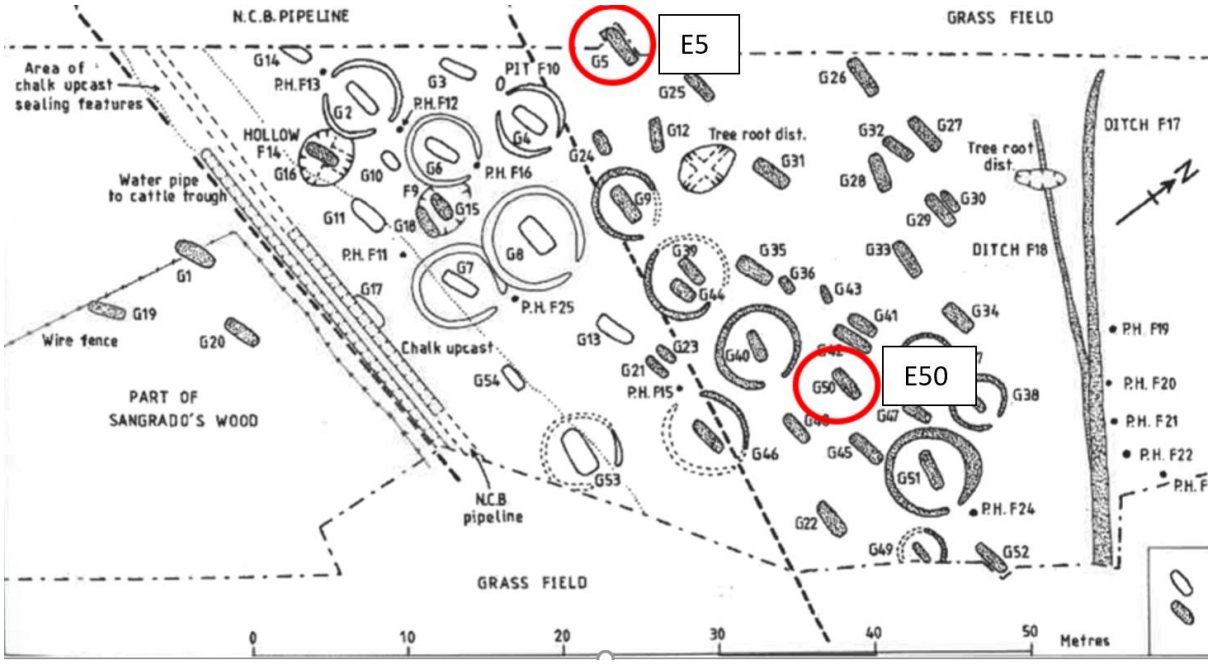

Figure 26 - Red circles indicate the interment location of the individuals identified as outliers based on their tooth metrics within Eastry cemetery (after Welch et al. 2008, 9).

The location of these two males are varied with E5 appearing on an edge of the Western border of the cemetery while E50 has been interred within a densely populated area.

Contrasting again are the inclusions of grave goods in both burials. While E5 was recovered with a wide assortment of grave goods, E50 had very few. These contradictions between the two do not reveal a set pattern in terms of the treatment of outliers, while the position of E5 could be argued as being liminal, the inclusion of an array of grave goods implies a connection to the society. The opposite pattern was observed with E50 where he was buried in a central area of the cemetery, yet sparsely furnished. These two burials were also phased slightly differently (Welch et al. 2008), though there was some overlap, so their treatment could also be a product of their time of interment.

Within the Polhill cemetery there were four identified outlier individuals: P2, a young adult female aged 18-25 years at time of death recovered with beads; P3, an adult female aged 25-30 years at time of death, recovered with beads; P42, a young adult female aged 18-22 years at time of death, recovered with beads and; P50, an adult male aged 38-45 at time of death, recovered with a pot. Figure 27 presents the interment location of these outliers within the Polhill cemetery.

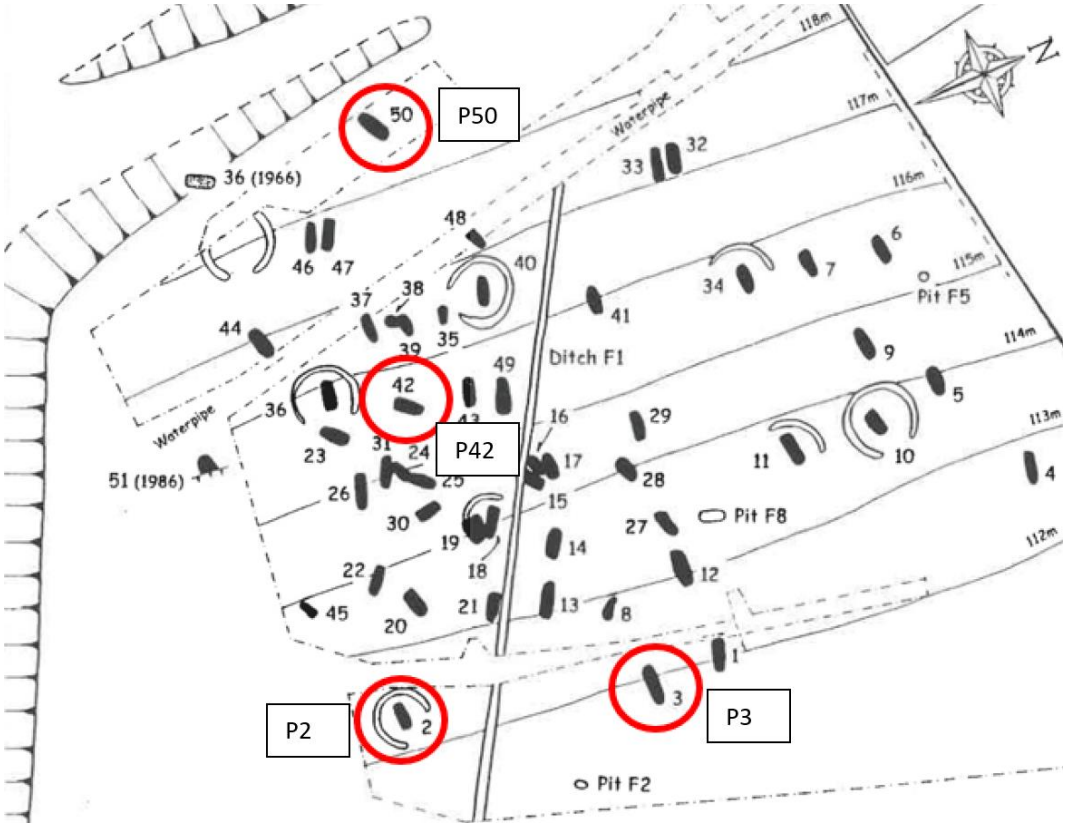

Figure 27 - Red circles indicate the interment location of the individuals identified as outliers based on their tooth metrics within Polhill cemetery (after Philip 2002, 4).

Three of the four outliers have been interred further away from the densest part of the cemetery, towards the Eastern and Western limits. Furthermore, P42 and P50 show a different orientation to the majority of East-West aligned graves, despite P42 being located in the denser area of the cemetery. Therefore, there does seem to be a pattern overall for the placement of these individuals, towards the external borders of the cemetery. For P2 this appears to be a dichotomy as this female has been buried within a ring ditch suggesting a strong social connection to the group, yet along the edge of the cemetery which may be in contrast to perceived status based on burial structure. Philip (2002, 3) does suggest that this edge of the cemetery was in the contour of a large hill which could indicate importance for those buried along it. Therefore, it could be argued that this choice in location for P2 was due

to needing room to construct the ditch surrounding the grave to show importance, rather than a decision based on biological connections.

There were five outliers identified within the Oakington cemetery: Grave 62, O1424 a young adult male aged 18-23 years at time of death and not buried with associated artefacts; Grave 21, O1616 a male aged 25-35 years at time of death and buried with a knife; Grave 10, O1636 a female aged 45-49 years at time of death and buried with cruciform, small long and disc brooches as well as a knife; Grave 71, O1709 an adolescent female at time of death and buried with a disc brooch and; Grave 109, O2165 a young adult female aged 18-25 years at time of death and not associated with grave goods, though was interred in a triple burial. The location of the graves containing these outlier individuals within the Oakington cemetery is displayed in Figure 28.

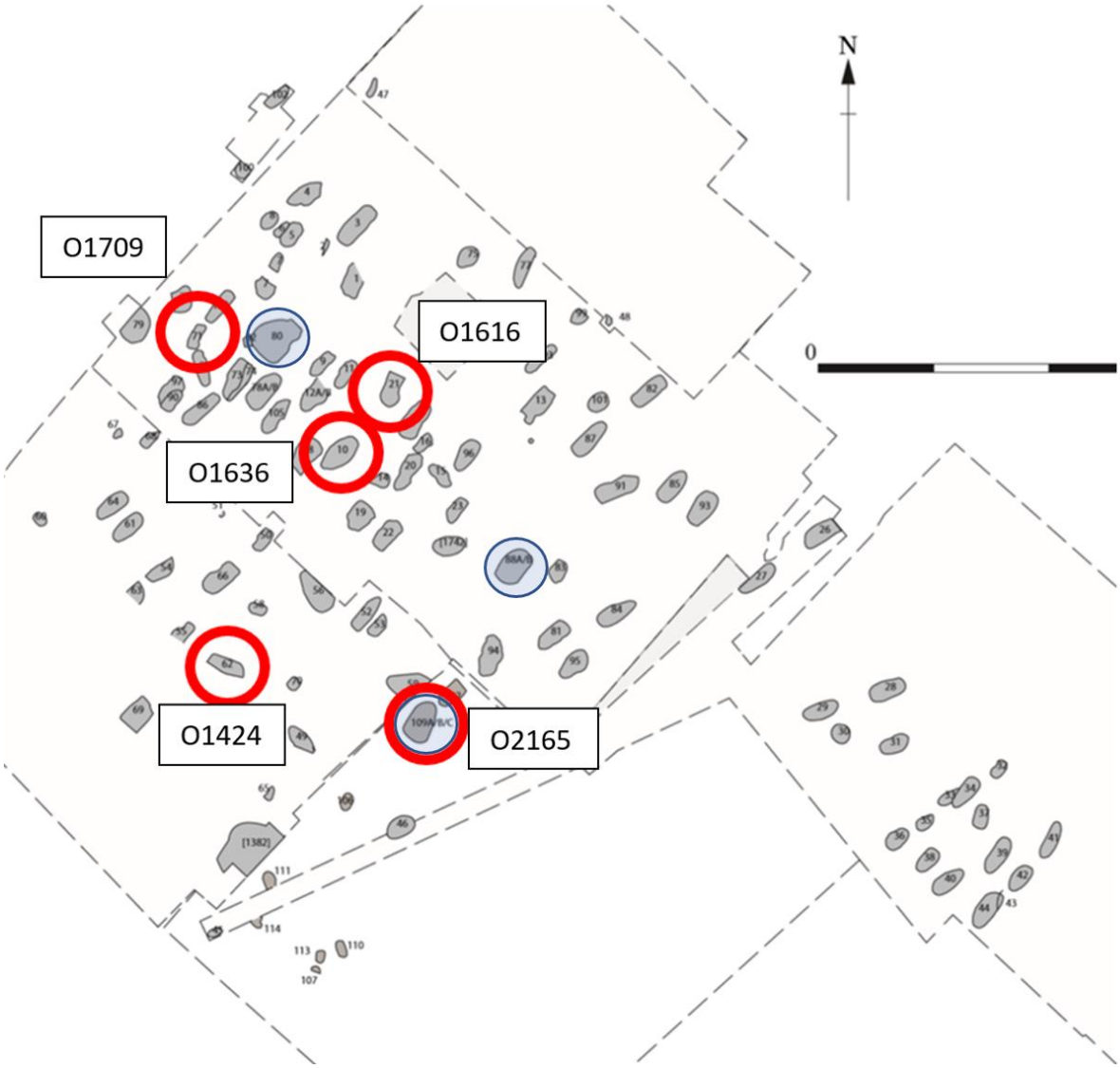

Figure 28 - Red circles indicate the interment location of the individuals identified as outliers based on their tooth metrics within Oakington cemetery. Blue highlighted graves indicate generational figure heads for the Oakington cemetery (see Sayer 2020, 122 for full discussion) (after Sayer, personal communication 2017).

The location of the five outliers within Oakington, initially, does not reveal any particular pattern regarding their placement. Graves 62 and 109 appear in less dense areas of the cemetery but the other three individuals appear within the most densely populated area of the cemetery. However, knowing the chronology of the cemetery and how the cemetery was populated over time has helped to better identify patterns in the position of outlier individuals. Sayer (2020, 122) indicated which graves were marked with barrows at Oakington

(three examples highlighted in blue in Figure 28); barrows were used to highlight generational figureheads which were used as beacons for the community who would continue to bury their dead around these notable graves during each phase of occupation. Figure 28 showcases these barrow burials, and when looked at in combination with the location of outlier individuals based on tooth data, it appears that the locations of some of these graves were further away from these central generational figures.

Within the Hatherdene cemetery, seven individuals were found to be outliers: H205 a female aged over 45 years at time of death, not associated with any grave goods; H999, a male aged 26-44 years at time of death, buried with a knife; H956, a young adult female aged 13-18 years at time of death, not associated with any grave goods; H493, a young adult female aged 19-23 years at time of death, buried with a small long, brooch, annular brooch and knife; H1293 an male aged 26-44 years at time of death, not associated with any grave goods; H241, a young adult male aged 19-25 years at time of death, buried with a shield, spear and knife, and; H560, a male aged 26-44 years at time of death with no associated finds. These individuals were located on the Hatherdene cemetery plan and are presented in Figure 29.

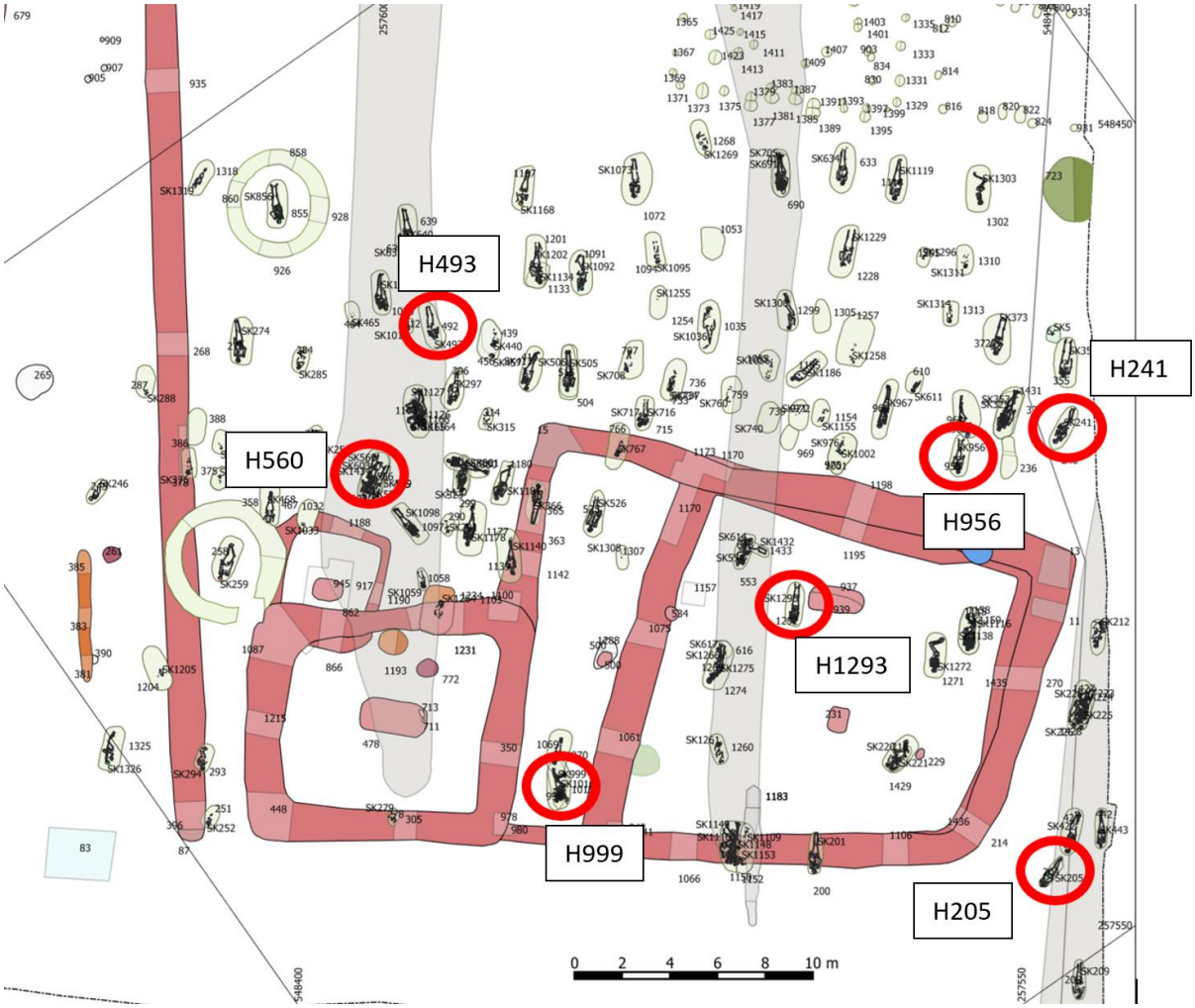

Figure 29 - Red circles indicate the interment location of the individuals identified as outliers based on their tooth metrics within Hatherdene cemetery (after Oxford Archaeology East, personal communication 2018).

The outliers identified within Hatherdene were found in denser areas of the cemetery as well as the less dense borders. However, the majority of the outlier burials, five of the seven, do appear to be located more towards the less populated South-East corner of the cemetery where the density of graves seems lesser than towards the North-West area of the cemetery. These graves were mostly single interments, but the stacked burials containing H560 and H999 contradict this pattern.

Across all four cemeteries there appeared no consistent trend regarding the decisions made by the community surrounding the burial of male and female individuals who were likely not biologically related to the rest of the group. In that, there appeared no real difference in the location, furnishing, or occupancy of the graves that these individuals were interred within compared to the rest of the community. Within Hatherdene and Oakington, outlier individuals were found in multiple graves in the case of H999 and H560, both in stacked burials of at least three individuals and O2165 found interred with a child and another adult female. The remainder of the identified outlier individuals were in single interments. In regard to grave goods, artefacts were found in some of the outlier graves that were also found in non-outlier graves, for instance: H493 with brooches, H241 with a shield, O1636 and O1709 with brooches, and E5 with a buckle. Alternatively, several of the outlier individuals were not found to be associated with any artefacts. The locations of the graves themselves at Hatherdene, Oakington, Polhill and Eastry showed that these individuals appeared in dense areas of the cemeteries, as well as on the periphery or towards cemetery limits. Furthermore, as was found at Polhill, outlier individuals also appeared interred within burial structures with P2 having a ring ditch surrounding her grave.

This demonstrates that, while these individuals had little shared biological similarity compared to the rest of the group, they were being interred amongst the general population. There was no standardised treatment in place for those genetically more divergent than others. This helps to support the notion that burial locations at Hatherdene, Oakington, Polhill and Eastry were not based solely on closeness in biology between individuals. The implications of this on a community level indicate that decisions regarding identity in death were not linked solely to biological connections between members. Rather, just because an

individual was biologically different, this did not negate them from being fully incorporated into a community, at least based on how they were represented in death.

6.2.3 Grave Goods within the Cemeteries

Grave goods, as briefly expressed above, can also be used as means to connect deceased individuals within a community. Due to this, it was decided to investigate the connections between those interred with certain grave goods. Those interred with spears, seaxes, knives and shields were taken to represent weapon burials and individuals interred with each were looked at for similarity within each cemetery site. Furthermore, brooches were investigated and subdivided into cruciform, small long, saucer or disc and annular or penannular types. Finally, buckles were investigated due to the connections raised in the previous subsection at Polhill.

Hatherdene, Oakington, Polhill and Eastry were all looked at separately and connections between individuals found with these goods were categorised according to the squared Euclidean distances of these links. 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. Once all connections had been made across all available teeth, percentage proportions of high, moderate and low levels of similarity connections were calculated for each grave good type to see if those who were buried with the same objects were likely to biologically linked. The following results do not present a uniform pattern regarding biological relationships and consistency among grave good inclusions across the four communities. Some goods that

showed to be linked well with biological relationships in one cemetery did not follow this trend in another. As such, interpretations drawn from the results below help to support the notion that burial designs reflect the ever-changing social narrative reflective of each individual community (Sayer 2020). This is also reflective in work looking at lifecycles or life courses and the appearance of artefacts in graves (i.e. Gowland 2006). In these cases individuals dress and object associations can change throughout life which mean that the items interred with people in death could vary depending on age and accomplishments. The comparison between grave goods and dental metrics is interesting as the size of permanent teeth remain consistent through life but the choice of burial objects does not. By adding biological data into discussion of lifecycles, results are expected to further support the idea of variation within and between communities.

6.2.4 Weapon Burials

Spear burials were investigated first across the four cemeteries. From the available sample at Polhill cemetery only one male individual (P27) had a spear, so no further interpretations were made for spear burials at this site. From the available sample at Eastry, there were two individuals buried with spears, one male (E51) and one female (E40), but due to limitations of the sample regarding tooth preservation, these two could only be compared once using only the left mandibular first molar (though they were from the same phase). This single connection was at a squared Euclidean distance of 25 indicating low level of similarity between the two. At Oakington, three male individuals (O1441, O1618 and O869) were buried with spears. From the six teeth available to compare across these males, 12 connections were made: 50% of the connections show a high level of similarity, 33.3% of the connections show

a moderate level of similarity, and 16.7% of connections show a low level of similarity. From the Hatherdene cemetery, nine males (H1275, H241, H506, H526, H640, H856, H1036, H1164 and H1181) were buried with spears. From the 10 teeth available for comparison across these nine individuals, 186 connections were made: 42.5% of the connections show high levels of similarity, 16.9% of the connections show moderate levels of similarity, and 40.9% of the connections show low levels of similarity. The Oakington example strongly supports the notion that the three individuals interred with spears shared a biological connection. The results from Hatherdene are less strong, however, they do show that nearly 60% of the connections made between the individuals buried with spears show either moderate or high levels of similarity to one another.

For those buried with knives, no individuals at Polhill were interred with them, therefore no further connections could be made within this site. At Eastry, three males (E5, E28 and E51) and five females (E9, E34, E40, E45 and E46; most from the 7th century) were recovered with knives. Ten teeth could be compared for these eight individuals, which resulted in 40 connections between them: 25% of the connections show high levels of similarity, 17.5% of the connections show moderate levels of similarity, and 57.5% of connections show low levels of similarity. At Oakington nine males (O1622, O1618, O1616, O731, O1308, O1862, O1909, O2160 and O2222) and nine females (O1636, O1615, O887, O1747, O1779, O1785, O1793, O1843 and O2154) were buried with knives. Twelve teeth could be compared for these 18 individuals, which resulted in 430 connections between them: 34.2% of the connections show high levels of similarity, 26.5% of the connections show moderate levels of similarity, and 39.3% of the connections show low levels of similarity. There were 30 individuals buried with knives at Hatherdene, 18 males (H228, H241, H259, H274, H353, H373, H422, H526, H557,

H640, H705, H856, H964, H999, H1036, H1164, H1181 and H1275) and 12 females (H1326, H205, H209, H220, H225, H325, H493, H554, H634, H1092, H1202 and H1272). From the 13 teeth available for comparison, 1763 connections were made: 34.6% of the connections show high levels of similarity, 20% of the connections show moderate levels of similarity, and 45.4% of the connections show low levels of similarity. Overall, due to the lower percentages of high-level similarity connections, the presence of a knife in burial does not appear to be linked to biological closeness between individuals.

No individuals from the samples of Polhill or Eastry were buried with shields so no further interpretations could be made. Three males at Oakington (O1618, O1631 and O1799) were found buried with shields. Seven teeth could be compared across these three males, which resulted in 15 connections between them: 26.7% of the connections show high levels of similarity, 20% of the connections show moderate levels of similarity, and 53.3% of the connections show low levels of similarity. Five male individuals from Hatherdene (H241, H640, H856, H1165 and H1181) were buried with shields. Nine teeth could be compared between these five individuals, which resulted in 42 connections between them: 26.2% of the connections show high levels of similarity, 16.7% of the connections show moderate levels of similarity, and 57.1% of the connections show low levels of similarity. These results together indicate that shields were not used to denote biological connections between individuals.

Shields and spears were then combined together to see if there were connections between those buried with each type of grave good, this could only be done for Hatherdene and Oakington. As all the individuals buried with spears also had shields at Hatherdene, the corresponding percentages of high, moderate and low-level connections would be the same as for spears alone. At Oakington five males were identified as having either a shield or spear

(O1618, O1631, O1799, O1441 and O869). Eight teeth could be compared across these five individuals, which resulted in 42 connections between them: 35.7% of the connections show high levels of similarity, 21.4% of the connections show moderate levels of similarity, and 42.9% of the connections show low levels of similarity. These results are similar to those for just shields, where the presence of both of these grave goods does not seem to support a biological connection between these males.

Overall, from these weapon types, only the presence of spears alone showed a possible link with biological connections between the individuals who were buried with them. The other types of weapon goods (knives, and shields) did not reveal to equate to strong biological connections between those interred with them. At a community level, this reflects the decisions made related to weapon burials and identity. Not all males who were chosen to be interred with such weapons were biologically related, therefore the messages communicated via their inclusion is not solely based on biology. At Oakington, however, it was possible that the biological connection between the males with spears was being highlighted by the decision to include this type of artefact in these three graves.

6.2.5 Brooch Burials

No individuals within the available samples from Eastry and Polhill cemeteries were found buried with brooches. Therefore, this section focuses solely on those interred within Hatherdene and Oakington. From Hatherdene, three females were buried with cruciform brooches (H220, H225 and H1202). Twelve teeth could be compared across these three females, resulting in 22 connections between them: 50% of the connections show high levels

of similarity, 31.8% of the connections show moderate levels of similarity, and 18.2% of the connections show low levels of similarity. Seven females at Oakington were found buried with cruciform brooches (O1612, O1636, O1615, O820, O1793, O1823 and O2430). Ten teeth could be compared across these seven individuals, resulting in 95 connections between them: 36.8% of the connections show high levels of similarity, 12.6% of the connections show moderate levels of similarity, and 50.5% of the connections show low levels of similarity. It appears from these results that the females at Hatherdene who were buried with cruciform brooches most likely shared close biological relationships, while those at Oakington did not.

Small long brooches were found in abundance at both Hatherdene and Oakington. At Hatherdene, 12 females were found to be buried with this type of brooch (H220, H225, H325, H356, H493, H554, H634, H1092, H1202, H1229, H1272 and H1326). Twelve teeth were available for comparison across these 12 females, resulting in 333 connections between them: 34.8% of the connections show high levels of similarity, 18.6% of the connections show moderate levels of similarity, and 46.5% of the connections show low levels of similarity. At Oakington there were also 12 females who were buried with small long brooches (O1376, O1395, O1450, O 1626, O1636, O1747, O1779, O1807, O1823, O1843, O1882 and O2430). Ten teeth could be compared across these 12 females, resulting in 412 connections between them: 32% of the connections showed high levels of similarity, 20.4% of the connections show moderate levels of similarity, and 47.6% of the connections show low levels of similarity. From both cemeteries, it appears as though the small long brooches are not linked to biological connections between females.

Only one female (H325) was found with a saucer or disc brooch at Hatherdene and therefore no further connections could be made using this brooch type at this cemetery. There were

eight females at Oakington who were buried with saucer and disc brooches (O1411, O1636, O820, O1709, O1740, O1782, O1615 and O2154). Ten teeth were compared across these eight individuals, resulting in 171 connections between them: 28.7% of the connections show high levels of similarity, 19.9% of the connections show moderate levels of similarity, and 51.5% of the connections show low levels of similarity. There is no strong evidence presented here to suggest saucer or disc brooches were used to signify biological relationships between these females at Oakington.

No individuals at Oakington were found with annular or penannular brooches. Hatherdene cemetery had three female individuals buried with penannular or annular brooches (H443, H493 and H1300). Nine teeth were available for comparison across these three females, resulting in 19 connections between them: 10.5% of the connections show high levels of similarity, 15.8% of the connections show moderate levels of similarity, and 73.7% of the connections show low levels of similarity. These results demonstrate that biological relationships were not used to determine which female was buried with an annular or penannular brooch at Hatherdene cemetery.

Comparisons of biological similarity in tooth size between those interred with brooches has revealed some interesting findings. The first is that differences appeared between Hatherdene and Oakington in terms of how brooches may have been chosen for burial inclusion. The cruciform brooches at Hatherdene strongly suggest a biological relationship between those interred with them, whereas this was not found to be the case at Oakington. As was observed with the weapon burials, those buried with brooches could show higher levels of similarity to some, but not all of those with the same type of brooch. Therefore, there are other reasons decided at a community level for the use of brooches in burial decoration

in addition to those based on biological relatedness. Stoodley (1999), Gowland and Penny-Mason (2017) and Gowland (2006) have looked at the difference in grave goods in females (and males) and have noted that the presence of brooches may be linked better to the achievement of life milestones (i.e. marriage, child birth or menopause), or the lifecycle rather than aspects like gender or age alone. It is acknowledged by these authors that these milestones can vary between places, which may be part of the reason why brooch variation existed between Oakington and Hatherdene. It may have been that brooches in general were linked to social milestones, but certain brooches were used by Hatherdene to demonstrate additional biological narratives in death.

6.2.6 Buckle Burials

Eastry had four individuals buried with buckles, two males (E5 and E51) and two females (E12 and E45). Only two teeth were available for comparison across these four individuals, resulting in two connections between them. One of these connections showed a moderate level of similarity and one showed a low level of similarity. Within the Oakington cemetery, six males (O1441, O1613, O1618, O1799, O794 and O1909) and one female (O1843) were buried with buckles. For these seven individuals, seven teeth were available for comparison which resulted in 39 connections between them: 33.3% of the connections show high levels of similarity, 15.4% of the connections show moderate levels of similarity, and 51.3% of the connections show low levels of similarity. At Hatherdene cemetery 10 males (H1275, H259, H274, H373, H506, H526, H640, H1036, H1164 and H1181) and three females (H443, H325 and H1272) were buried with buckles. Thirteen teeth were compared across all individuals resulting in 433 connections being made: 41.7% of the connections show high levels of

similarity, 15.9% of the connections show moderate levels of similarity, and 42.4% of the connections show low levels of similarity. At Polhill, three males (P27, P36 and P40) and three females (P14, P34, and P37) were buried with buckles. Eight teeth were compared across these six individuals which resulted in 30 connections between them: 40% of the connections show high levels of similarity, 40% of the connections show moderate levels of similarity, and 20% of the connections show low levels of similarity.

The patterns expressed between Oakington and Polhill are contrasting. At Oakington there did not appear to be a biological link regarding the inclusion of buckles in the graves of these identified individuals, whereas, arguably, at Polhill there was. The majority of connections (80%) of those interred with buckles at Polhill were divided among the moderate and high levels of similarity categories. This is strong evidence to suggest that those interred with buckles in this cemetery shared close biological relationships. The results from Hatherdene were less clear, there appeared a split between high- and low-level connections regarding the presence of buckles.

6.3 Individual Level Interpretations

Once community level interpretations had been explored, the focus of analysis shifted to the individual grave level. This section will explore connections discovered between case study graves that were selected due to being unique or particularly wealthy graves found in Hatherdene and Oakington, as well as investigating connections between those interred in the same grave space. Of the samples available from Polhill and Eastry there were not any specific individuals that stood out for being treated in a particularly unique or elaborate way

compared to examples at Hatherdene and Oakington. As such, the decision was made not to investigate any individual further at this time for Polhill and Eastry, unless in a multiple burial, see Chapter 6.5. However, in future, if researchers were interested in a particular question or specific grave, it is possible to go back to this data (Appendix 7) and select any individual needed for further comparisons from any of these four sites.

Arguably, one of the most intriguing burials at Oakington was that of O1740 (Grave 80). This burial contained the remains of a young adult female between the ages of 20-25 years old at time of death. In addition to being buried with an abundance of grave goods including beads, disc brooches, rings and an assortment of iron objects, she was also interred with an articulated cow (Mortimer *et al.* 2017), Figure 30 displays this grave during excavation. This was the first of its kind discovered in Europe, and as such is a unique interment for the early Anglo-Saxon period. As such, it was decided to focus on O1740 and use the HCA dendrograms to help identify the individuals who were most similar based on their tooth metrics to this female. Two individuals were identified in the cemetery to share high levels of similarity across multiple teeth at a squared Euclidean distance of 1. These individuals were: O1411 (Grave 61), an adult female aged 30-40 years at time of death and O1747 (Grave 78), an adult female aged 30-40 years at time of death, who had been interred in a multiple grave with a sub adult. O1747 and O1740 also shared a similar phasing range with both being more specifically dated to the mid-sixth century. Figure 31 presents the location of O1740 and her closest connections in the Oakington cemetery.

Figure 30 – Burial 80, containing O1740 and an articulated cow (Mortimer et al. 2017, 312).

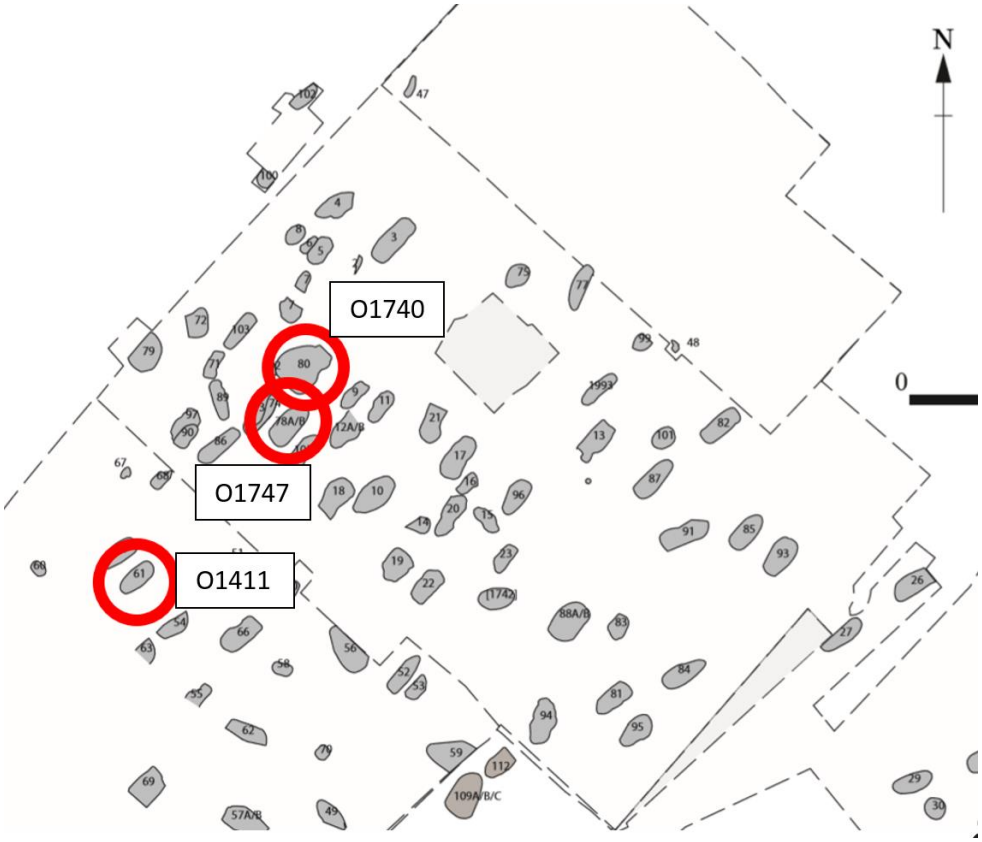

Figure 31 - The location of Grave 80 containing O1740 and the two closest individuals to this female based on tooth data: O1411 in Grave 61 and O1747 in Grave 78 (after Sayer 2017).

The proximity of O1740 and O1747 is noticeably close within the cemetery, however O1411 has been buried towards the South-West edge of the cemetery despite there being space closer to the others. This, in addition to the examples outlined above, reiterates that burial location was not fully dictated by shared biology. The grave goods interred with O1747 included: a wrist clasp, a small long brooch, a knife and an assortment of beads. The goods recovered with O1411 included: two saucer brooches, two wrist clasps, a ring, a knife and an assortment of beads. There are parallels to draw between these three women. They were all buried with similar grave goods, though brooch type differed, and were all adults. The female buried with the cow was noticeably younger than the two other females, yet was buried, arguably, in a more elaborate way. These commonalities in ornately decorated females, combined with the similarity of their tooth measurements and interment dates does suggest a close social and biological connection between them. It is hard to identify what these connections could be without narrower age estimations, but likely attributable to them being sisters, cousins or even a possible mother and daughter relationship present, though these interpretations are dependent on exact timing of interments.

Another unique burial at Oakington was Grave 57 (O1376), an adult female aged 22-35 years at time of death, found with foetal remains in the pelvic area, interpreted to signify she was pregnant at time of death (Mortimer *et al.* 2017; Sayer and Dickinson 2013). Figure 32 displays this burial during excavation. She was buried with an assortment of beads and small long brooches. Using the HCA output, three individuals were identified as sharing high levels of similarity with O1376: O1308 (Grave 49), an adult male aged 40-44 years at time of death, buried with a knife; O2165 (Grave 109B), a young adult female aged 18-25 years at time of death and no associated grave goods, but was interred in a burial with another adult female

and a child and; O1321 (Grave 52), an adult male aged around 45 years at time of death with no associated finds. Figure 33 presents the location of O1376 and the three individuals who share the highest amounts of similarity with her in their tooth data in the Oakington cemetery. It is interesting that her closest connections are mainly to males within the Oakington cemetery. This could link back to discussions on females returning to their paternal homestead to give birth (Sayer 2014).

Figure 32 - Grave 57, containing O1376, a female skeleton recovered with foetal remains in her pelvis area (after Sayer et al. 2013, 24).

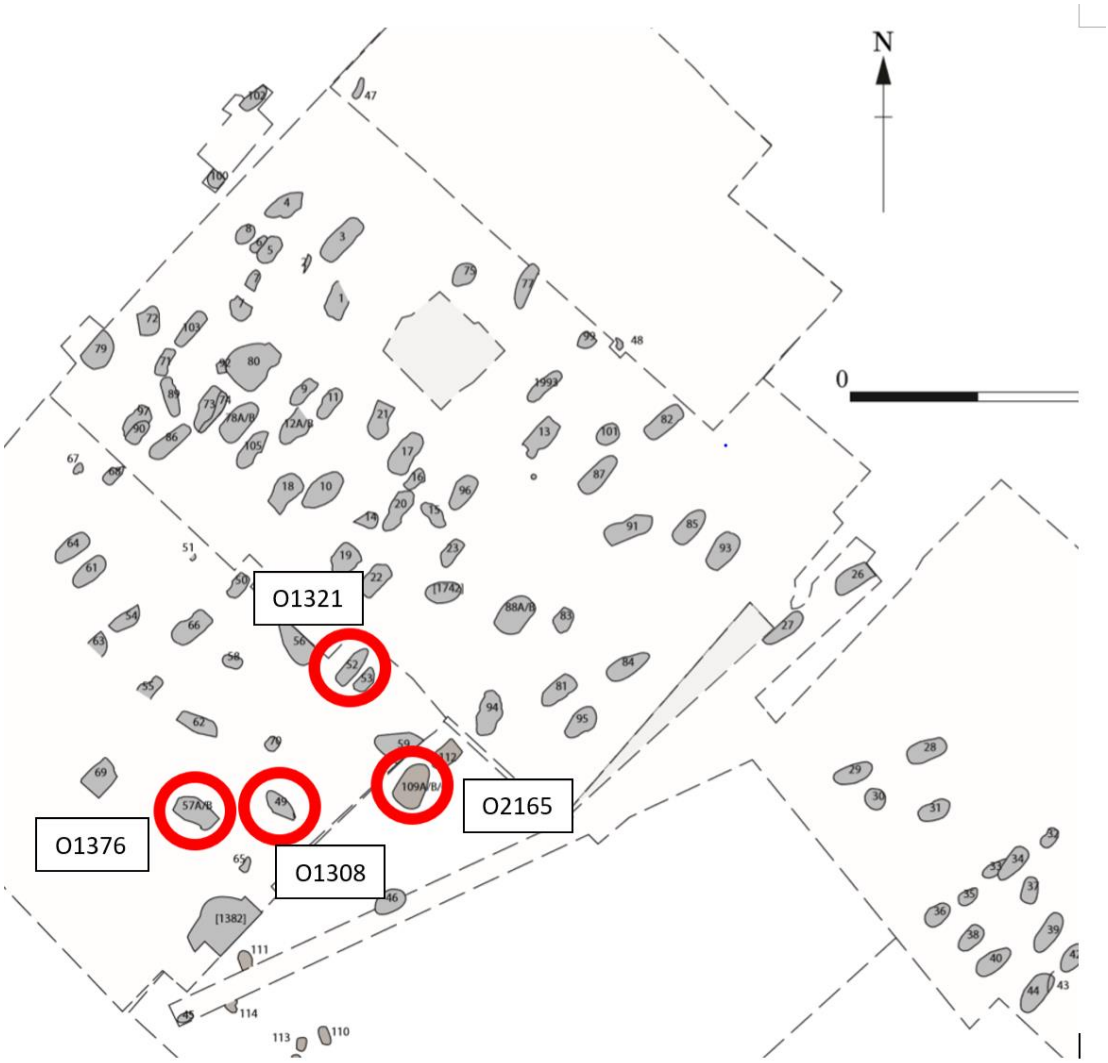

Figure 33 - The location of O1376 (Grave 57) and the individuals identified as sharing the highest amount of biological similarity: O1308 (Grave 49), O2165 (Grave 109B) and O1321 (Grave 52) (after Sayer 2017).

The grave good inclusions show no real pattern among O1376 and those who were most likely to be biologically related, but the spatial distribution of the graves is interesting. All four of these graves are located more towards the South-West corner of the Oakington cemetery, in relatively close proximity, particularly close was O1308. Based on skeletal demography and timing of interments, the two male individuals are old enough to be a father or uncle to O1376 but could also be representative of brothers. The similarity to O2165 was surprising as this individual had previously been identified as an outlier in the dataset, see Chapter 6.3.1. Therefore, while O2165 is different from the majority of individuals within the data set, she

did appear to share a connection with O1376. O2165 was younger than O1376, but depending on timing of burials, the connection between these two females could represent sisters, cousins or mother and daughter. While these two individuals have both been more specifically dated to the late 5th through early 6th century, caution still needs to be applied to the interpretation not what their exact biological connection could have been.

In terms of wealth, at Oakington, apart from O1376 who was a highly decorated female, three additional decorated male burials were: Grave 64 containing O1441, an adult male aged 36-45 years at time of death, buried with a spearhead, knife, sheath, belt buckle and pottery; Grave 88 (a double burial) containing O1799, a male aged 18-25 years at time of death and recovered with a shield boss, a belt buckle and fastener and; Grave 100 containing O1909, an adult male aged 30-35 years at time of death, buried with knife, tweezers, and buckle. Grave 100 was chosen as there were many objects associated with the male, yet the types of artefacts were not typical of other decorated males in the wider community. Once these graves were located, the hierarchical cluster dendrograms were consulted to identify individuals who appeared to have high levels of biological similarity to each of the decorated males.

O1441 had three individuals that exhibited higher levels of biological similarity: O1793 (Grave 86), a female aged 25-28 years at time of death; O1779 (Grave 82), a young adult female aged 20-25 years old at time of death and; O1798 (Grave 88) an adult male aged 25-35 years at time of death. O1799 connected to six individuals displaying higher levels of biological similarity: O1866 (Grave 94), an adult male aged 36-45 years at time of death; O1441 (Grave 64), one of the highly decorated males aged 36-45 years at time of death; O2154 (Grave 109A), an adult female aged 25-30 years at time of death O1870 (Grave 95), an adult female

aged 25-36 years at time of time of death; O1747 (Grave 78), an adult female aged 30-40 years at time of death and; O1618 (Grave 13), an adult male of unknown age due to poor preservation. It is important to note, however, that these connections to O1799 were not that strong as they were based on fewer numbers of comparative teeth. Some interesting chronological information was presented here, however, as O1799 has been more specifically dated to the later 6th century, O1747 was dated to the mid 6th century and O2154 was dated to the late 5th through early 6th century. This demonstrates the possibility that teeth may pick up on shared genetics across multiple generations, though again caution is noted as there were not that many teeth available to support these connections.

It was determined that O1909 had two individuals displaying higher levels of similarity: O1450 (Grave 66), an adult female aged 35-40 years at time of death and O731 (Grave 29), an adult male. The location of these three individuals and their associated connections based on biological similarity are indicated on Figure 34. The spatial distribution for each of these males and their associated connections appears to be quite dispersed throughout the cemetery, only slight clustering of graves appears for O1799.

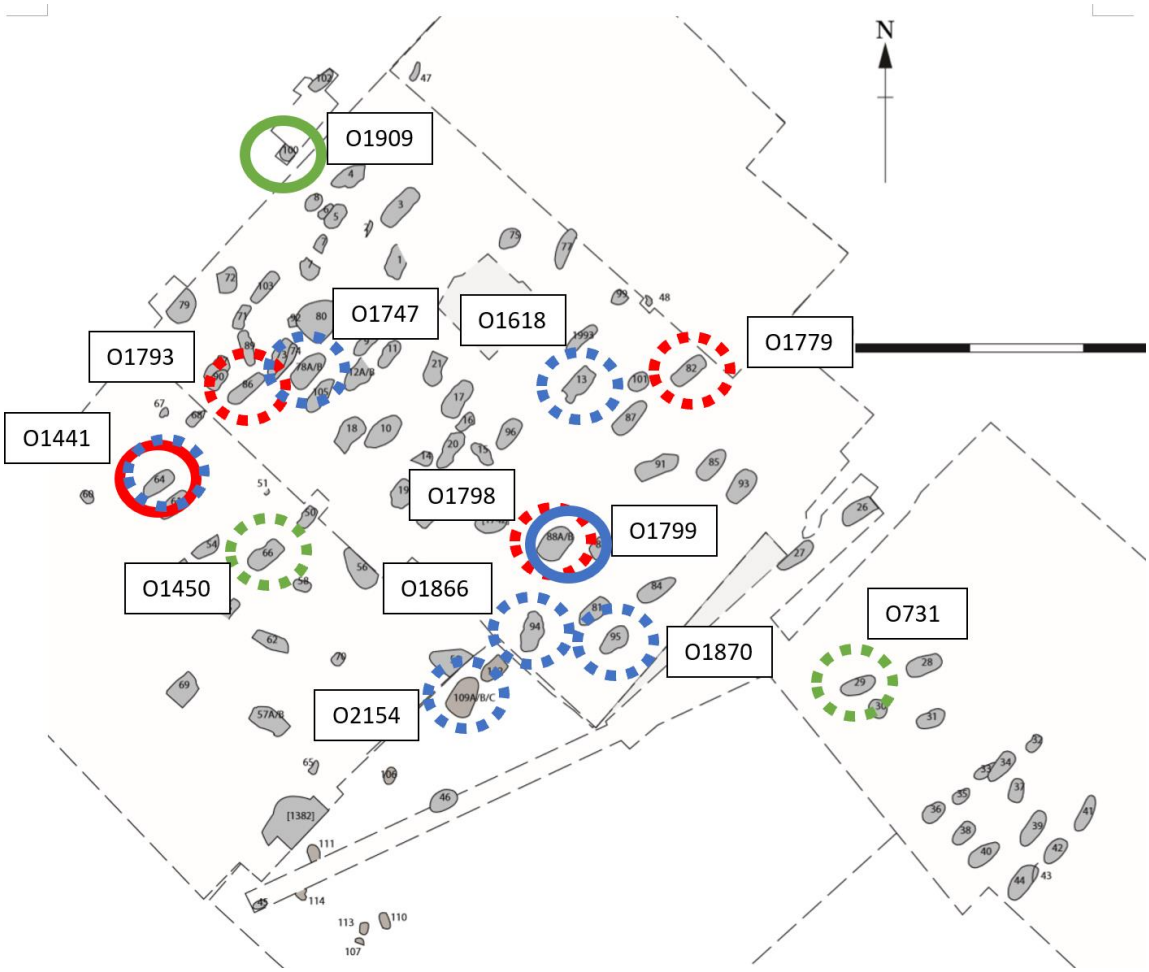

Figure 34 - The location of three decorated male individuals at Oakington and their associated connections. Grave 64 (O1441) represented by red circles; Grave 88 (O1799) represented by blue circles and; Grave 100 (O1909) represented by green circles (after Sayer 2017).

At Hatherdene H1275 was the individual who was associated with the most high-value artefacts. He was an adult male, aged 26-44 years at time of death and buried with a spear, knife and buckle. The strongest connection to another individual was to H259, one of the ring ditch burials discussed in Chapter 6.3.2. In addition to this connection, H1275 was found to be most close to eight other individuals: H526, a male aged 26-44 years at time of death buried with a spear, knife and buckle; H274, a male aged 26-44 years at time of death, buried with a knife and buckle; H999, a male aged 26-44 years at time of death buried with a knife; H1164 a male aged 26-44 years at time of death buried with a spear, buckle and knife; H506 a male aged around 18 years at time of death buried with a spear and buckle; H1092 a female

aged 26-44 years at time of death buried with a small long brooch and knife and; H228 a young adult male aged 19-25 years at time of death, buried with copper remnants and beads. Figure 35 presents the location of H1275 and his most similar connections in the wider cemetery.

Figure 35 - The location of wealthy burial H1275 and the individuals that share the highest amount of similarity in regard to tooth dimensions (after Oxford Archaeology East 2018).

The spatial distribution of these individuals appears spread throughout the cemetery rather than being clustered around H1275, and both single and multiple interments are represented. This result reiterates previous findings regarding burial location wherein the location of graves at Hatherdene do not appear to be based solely on biological relationships. The skeletal

demography shows that the majority of connections to H1275 were also adult males aged between 26-44 years old at time of death. This finding is noteworthy as it shows that the closest biological connections to a wealthy male are other wealthy males. This pattern was also observed when ring ditches were investigated in Chapter 6.3.2, further demonstrating the biological closeness of males at Hatherdene.

Looking at the differences in wealthy graves at Oakington and Hatherdene revealed a contrast between the two sites. The wealthiest male burials at Oakington had connections to a relatively equal mix of male and female individuals; six males and five females were identified during this process. Whereas, at Hatherdene, the connections found to the wealthy male case study were all to males apart from one. There were more ornately furnished female burials at Oakington compared to Hatherdene which, in combination with the above pattern, reflects differences between the two cemeteries in regard to the burial customs practised within each site. Table 29 provides a brief summary of all of the grave case studies discussed above and their associated connections in the wider cemeteries of Hatherdene and Oakington.

Table 29 – Brief summary of grave case studies and their associated connections to their corresponding wider community.

Cemetery	Individual	Demography	Grave Goods	Notes
Oakington	O1740 (cow burial)	Female, 20-25yrs	Disc brooches, rings, beads	High degree of similarity to O1411 and O1747.
	O1411	Female, 30-40yrs	Saucer brooches, ring, knife, beads	High degree of similarity to O1740.
	O1747	Female, 30-40yrs	Small long brooch, knife, beads	High degree of similarity to O1740.
Oakington	O1376 (pregnant female)	Female, 22-35yrs	Small long brooches, beads	High degree of similarity to O1308, O2165 and O1321.
	O1308	Male, 40-44yrs	Knife	High degree of similarity to O1376.

Cemetery	Individual	Demography	Grave Goods	Notes
	O2165	Female, 18-25yrs	N/A	High degree of similarity to O1376.
	O1321	Male, >45yrs	N/A	High degree of similarity to O1376.
Oakington	O1441 (wealthy male)	Male, 36-45yrs	Spear, knife, buckle	High degree of similarity to O1793, O1779 and O1798.
	O1793	Female, 25-28yrs	Knife, cruciform brooch	High degree of similarity to O1441.
	O1779	Female, 20-25yrs	Knife, small long brooch	High degree of similarity to O1441.
	O1798	Male, 25-35yrs	N/A	High degree of similarity to O1441.
Oakington	O1799 (wealthy male)	Male, 18-25yrs	Shield, buckle	Most similar to O1866, O1441, O2154, O1870, O1747 and O1618.
	O1866	Male, 36-45yrs	N/A	Similar to O1799.
	O2154	Female, 25-30yrs	Beads, purse, metal objects	Similar to O1799.
	O1870	Female, 25-36yrs	N/A	Similar to O1799.
	O1747	Female, 30-40yrs	Small long brooch, knife, beads	Similar to O1799.
	O1618	Male, unknown	Spear, buckle, knife	Similar to O1799.
Oakington	O1909 (wealthy male)	Male, 30-35yrs	Knife, tweezers, buckle	High degree of similarity to O1450 and O731.
	O1450	Female, 35-40yrs	Small long brooch	High degree of similarity to O1909.
	O731	Male, adult	Knife	High degree of similarity to O1909.
Hatherdene	H1275 (wealthy male)	Male, 26-44yrs	Spear, knife, buckle	High degree of similarity to H259, H526, H274, H999, H1164, H506, H1092 and H228.
	H259 (buried in a ring ditch)	Male, 26-44yrs	Belt, buckle, knife	High degree of similarity to H1275.
	H526	Male, 26-44yrs	Spear, knife, buckle	High degree of similarity to H1275.
	H274	Male, 26-44yrs	Knife, buckle	High degree of similarity to H1275.
	H999	Male, 26-44yrs	Knife	High degree of similarity to H1275.
	H1164	Male, 26-44yrs	Spear, knife, buckle	High degree of similarity to H1275.
	H506	Male, ~18yrs	Spear, buckle	High degree of similarity to H1275.

Cemetery	Individual	Demography	Grave Goods	Notes
	H1092	Female, 26-44yrs	Knife, small long brooch	High degree of similarity to H1275.
	H228	Male, 19-25yrs	Beads	High degree of similarity to H1275.

6.4 Multiple Burials

Within early Anglo-Saxon research, Stoodley (2002) noted the presence of individuals in shared burial space has been used to infer stronger kin and family connections between individuals in this period. Within the four sites investigated in this project, there were several multiple burials present. Multiple burials refer to the presence of more than one individual within the same grave. Hatherdene, interestingly, had a subset of stacked burials where, instead of being laid side by side, individuals were stacked on top of one another (Ladd *et al.* 2018). The multiple burials within each cemetery were looked at separately and the HCA dendrograms were used to establish the level of similarity observed between the individuals buried together. In these cases, the timing of interment is assumed to have been contemporaneous and therefore the suggested biological connections may be more likely. The following sections provide intricate details of each grave and the interpretations developed based on dental analyses, but a brief summary of all multiple graves discussed below is provided in Table 30.

Table 30 – A brief summary of all multiple graves investigated from Hatherdene, Oakington and Polhill and associated interpretations based on dental analyses.

Cemetery	Grave Number	Number of Teeth Compared	Interpretation based on Similarity of Tooth Dimensions
Hatherdene	Grave 223	8	H228 and H225 share moderate to low levels of similarity.
	Grave 299	4	H361 and H300 share moderate to low levels of similarity.
	Grave 324	7	H353 and H325 share a high level of similarity.
	Grave 486	11	H557 and H560 share low levels of similarity, H557 and H603 share moderate levels of similarity and H560 and H603 share high levels of similarity.
	Grave 636	3	H637 and H640 share a low level of similarity.
	Grave 1150	10	H1148 and H1149 share high to moderate levels of similarity.
	Grave 1163	8	H1127 and H1164 share a low level of similarity, H1127 and H1165 shared high to moderate levels of similarity and H1164 and H1165 share a low level of similarity.
Oakington	Grave 88	6	O1798 and O1799 share a moderate level of similarity.
	Grave 109	12	O2154 and O2165 share a low level of similarity.
Polhill	P19/P18	9	P18 and P19 share high to moderate levels of similarity.

6.4.1 Polhill and Eastry

Within the sample obtained from Eastry cemetery for this project, no multiple burials were present. From the sample obtained from Polhill cemetery, only one double interment was noted. This was Grave 19 and contained a young adult female, P19, who was between the ages of 22-28 years at time of death and an infant skeleton. As there was only one adult present within this interment, there were no possible comparisons to make to other adults within the same grave. However, Grave 19 was located within a ring ditch and, though not in the same grave cut, another individual, P18, was interred within the same ring structure. P18 was another young adult female, aged 20-24 years at time of death. Therefore, the decision was made to compare these two adult female individuals as their proximity within the same

burial ring ditch, for some (i.e Stoodley 2002; Thäte 2009) may infer a type of kinship relation is present. Table 31 provides an overview of the teeth available for comparison between P18 and P19.

Table 31 - Squared Euclidean distances between individuals P18 and P19 within Graves 18 and 19, respectively, for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison Group	Squared Euclidean Distance Between Individuals
Left maxillary first premolar	Combined cemetery, pooled sex	11
Right maxillary canine	Combined cemetery, females only	3
Left maxillary lateral incisor	Combined cemetery, females only	9
Right maxillary first molar	Polhill only, pooled sex	7
Right maxillary first premolar	Polhill only, pooled sex	1
Right maxillary canine	Polhill only, pooled sex	6
Left maxillary first premolar	Polhill only, pooled sex	1
Right mandibular first molar	Polhill only, pooled sex	8
Left maxillary canine	Polhill only, females only	25

The results from Table 29 display a moderate level of biological similarity between P18 and P19. The females showed a strong affinity of a squared Euclidean distance of 3 or less across three of the nine teeth used in comparison. However, the maximum distance of 25 was also noted across one comparative tooth. This suggests there is a high to moderate biological connection between the two females which could be akin to sisters or cousins, further supported, in part, by their similar age categorisations. Both individuals were relatively under-decorated with P18 having been recovered with no finds and P19 only having beads present on recovery. As there were no real similarities in grave goods present, it was difficult to ascertain how this information could help relate to a potential biological connection, though the shared lack of goods could indicate equitable status between them.

6.4.2 Oakington

There were four multiple burials found within the Oakington cemetery. The details of these graves and the individuals within them are presented in Table 32. While all individuals were listed, only the adult individuals were investigated in this project.

Table 32 - Overview of multiple graves excavated at Oakington cemetery. Details of interred individuals and corresponding grave numbers are included.

Skeletal ID Number of Interred	**Notes**
O1376 and 1375	O1376 is an adult female, 1375 is a sub adult. Grave 57
O1747 and 1748	O1747 is an adult female, 1748 is a sub adult. Grave 78
O1798 and O1799	O1798 and O1799 are both adult males. O1799 is younger than O1798. Grave 88
O2154, O2165 and 2168	O2154 and O2165 are both adult females, though O2154 is older than O2165. 2168 is a sub adult. Grave 109

*Skeletal ID numbers without 'O' indicate individuals were not included in data collection due to age.

In regard to general patterns of multiple graves, there does not appear to be a distinction in sex or location. Both males and females appear in multiple interments (though females appeared more frequently) and the location of the graves varies from being centralised within the densest area of burials (i.e. Grave 78) as well as peripheral locations (Grave 57) of the cemetery. Both Graves 88 and 109 appear to be located away from the main central cluster of the cemetery, though not completely isolated from the rest of the group. As only adults were investigated in this project, there were two multiple graves for consideration and further analysis, Graves 88 and 109, as Graves 57 and 78 each contained a single adult with a sub adult or infant. Figure 36 highlights the location of Graves 88 and 109 on the Oakington cemetery plan.

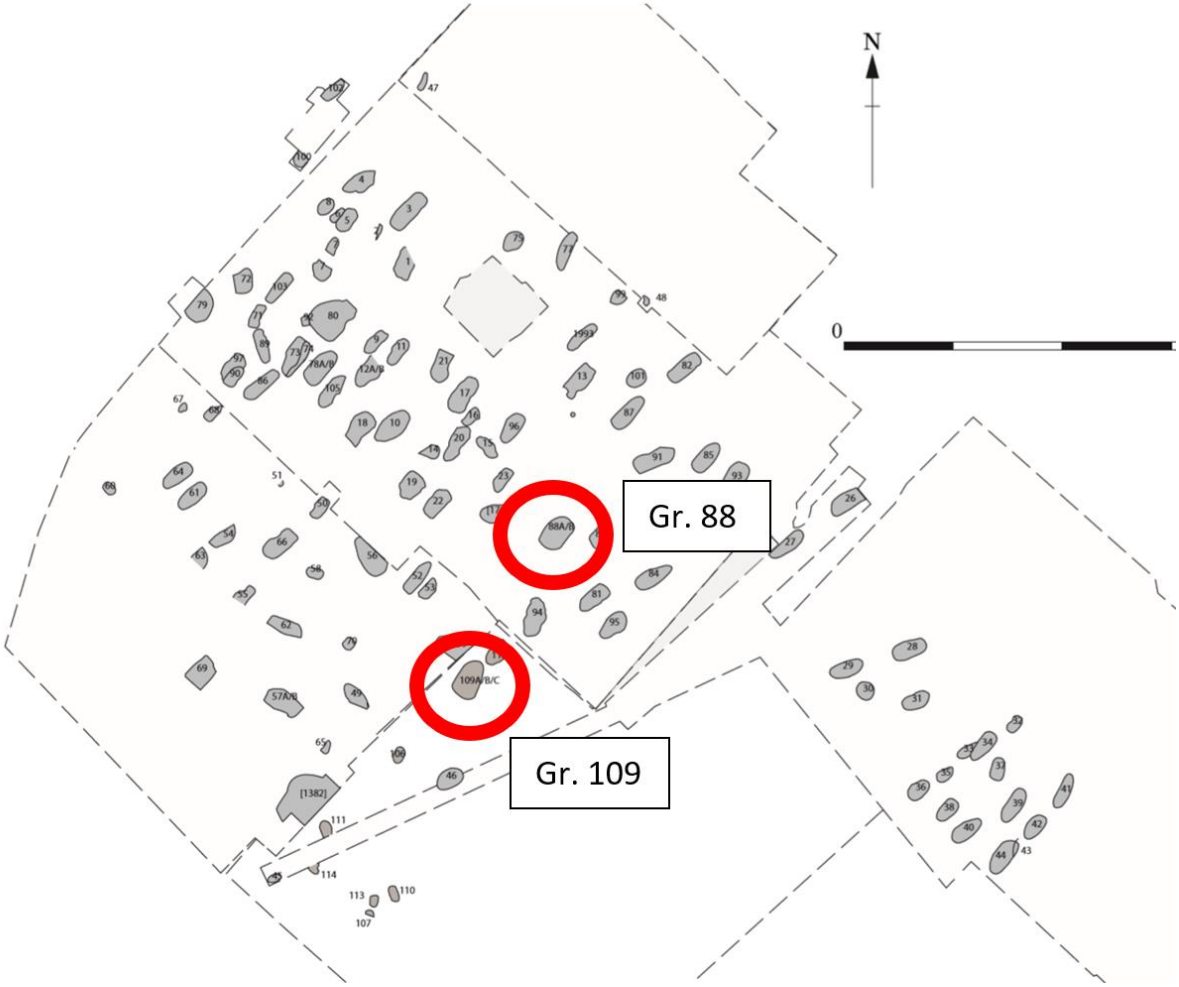

Figure 36 - Overview of Oakington cemetery, the multiple burials investigated for biological similarity were Graves 88 and 109. Locations of these graves are highlighted in red (after Sayer 2017).

By comparing the individuals within each grave to their corresponding dendrograms from the hierarchal cluster analyses, it was possible to make observations on the level of biological similarity of each person's tooth measurements. Appendix 7 (Figures 1 – 54) presents all the dendrograms from the HCA, however, the key pieces of information pertaining to distances between the multiple burial individuals at Oakington are summarised in Tables 33 and 34.

Table 33 - Squared Euclidean distances between O1798 and O1799 within Grave 88 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison Group	Squared Euclidean Distance Between Individuals
Left mandibular first premolar	Combined cemetery, pooled sex	1
Left mandibular central incisor	Combined cemetery, pooled sex	25
Left mandibular first molar	Oakington only, pooled sex	2
Left mandibular first premolar	Oakington only, pooled sex	25
Left mandibular central incisor	Oakington only, pooled sex	6
Left mandibular canine	Oakington only, males only	25

Table 34 - Squared Euclidean distances between individuals O2165 and O2154 within Grave 109 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison Group	Squared Euclidean Distance Between Individuals
Left maxillary first premolar	Combined cemetery, pooled sex	25
Left mandibular first premolar	Combined cemetery, pooled sex	25
Right maxillary canine	Combined cemetery, females only	25
Right mandibular third molar	Combined cemetery, females only	8
Right maxillary first molar	Oakington only, pooled sex	25
Right maxillary first premolar	Oakington only, pooled sex	25
Left maxillary first premolar	Oakington only, pooled sex	25
Left mandibular first molar	Oakington only, pooled sex	10
Left mandibular first premolar	Oakington only, pooled sex	25
Right maxillary canine	Oakington only, females only	10
Right maxillary central incisor	Oakington only, females only	14
Right mandibular first molar	Oakington only, females only	25

From these observations, interpretations can be made about the relative level of biological similarity between the individuals interred within Grave 88 and Grave 109. Grave 109 contained three individuals, two female adults and one sub adult. In terms of inferring kin-based relationships between these two adults, evidence from spatial, contextual and biological aspects must all be considered together. Spatially, being interred together suggests a closeness of some sort between the two (Alt *et al.* 1997; Stoodley 2002), and the position of the adult individuals within the grave, Figure 37, shows they were somewhat overlapping or intertwined, which could also possibly be interpreted to signify a close relationship.

Figure 37 - Grave 109; a triple burial consisting of two adults and one subadult. The two adult females, O2154 and O2165, appear to have been interred overlapping one another, possibly suggesting a close relationship between the two (Duncan Sayer photograph).

The interpretation of closeness could be interpreted to suggest a biological relationship. In terms of skeletal age, O2154 was between 25-30 years old at the time of death while O2165 was between 18-25. This would likely allude to a biological relationship more akin to sisters or cousins rather than a mother-daughter relationship. However, this is only one evidentiary stream to base such interpretations on. The grave goods associated with these two individuals differed dramatically; O2154 was buried with beads, a purse and a variety of metal objects, whereas O2165 did not appear to have any associated artefacts. Interestingly, the sub adult skeleton had artefacts associated with it that were similar to what was present with O2154.

As O2165 did not have any artefacts buried alongside her, it was not possible to comment on what this could infer regarding a potential biological relationship.

When the biodata from the dental analyses were included, a contradiction to the presumptive relationship suggestions was observed. From a biological similarity perspective, it was shown that, based on dentition, the two adult females are quite dissimilar to one another. Of the 12 teeth observed for comparing the level of similarity between these two females, the minimum distance separating them was a squared Euclidean distance of 8, while the most common distance (67% of dental comparisons) was reported to be 25, the maximum distance possible within these analyses. This demonstrates that their tooth sizes are very different to one another. Perhaps not surprising given that O2165 had previously been identified as an outlier individual based on tooth size. If these two females were supposedly sisters, which may have been inferred based on skeletal age, biological sex and interment positioning, it would be expected that their teeth be more similar in size. Townsend and Brown (1978a) have shown that same sex sibling pairs, especially female-female siblings, have had the highest level of correlation between tooth sizes when compared within certain populations. This is not the case to be observed here. What can be inferred strongly in the case of Grave 109 is that the females interred within it were not biologically related but, rather, may have shared a social connection that may have ascribed them a similar status which resulted in them being buried together. Within a patrilineal community, suggestions of plausible relationships could be something like sisters-in-law.

Grave 88 was more complex to interpret compared to Grave 109. Grave 88 contained two adult male individuals, O1798 and O1799. O1798 was aged skeletally to be between 25-30 years old at time of death, whereas O1799 was aged at 18-25 years old at time of death. Like

Grave 109, the position of the individuals within the burial does suggest a closeness between these two, so much so that initial skeletal assessment from an early version field report (Sayer *et al.* 2013) had suggested a male and female were interred together here, a finding later adjusted by a subsequent skeletal report which showed these were two males (Swales 2016). Figure 38 shows the position of the individuals within the grave; the right arm of O1799 appears to be placed over the left arm of O1798 and Sayer *et al.* (2013, 48) noted "[t]heir heads are touching and they are both leaning into each other".

Figure 38 - Grave 88 containing two male individuals, O1798 and O1799. The position of the remains could be suggestive of a close personal relationship between these two individuals (after Sayer et al. 2013, 48).

Using the provided age data, a likely suggestion of brothers or close cousins may be suggested in this case. However, again, like findings from Grave 109, additional streams of evidence must be consulted to provide a more complete and holistic view of what could be interpreted from this interment. The presence of grave goods varied between O1798 and O1799. O1798 was not interred with any objects at all, while O1799 was buried with an iron shield boss and belt fittings. Shield bosses have been used elsewhere to discuss links to role, occupation or status in Anglo-Saxon England (i.e. Dickinson and Härke 1992). The lack of comparative goods between the two males prevents further discussion on group membership but could infer a difference in status or, perhaps, a shared status.

The biodata observed from comparing dendrogram outputs of various teeth have revealed some discrepancies between these two individuals. Overall, six teeth were comparable between O1798 and O1799, but were less clear in regard to biological similarity. Half of the teeth under investigation showed a high degree of biological similarity, with squared Euclidean distances of 1, 2, and 6, equating to higher levels of similarity between these males. In contrast, the other three teeth showed low amounts of similarity between the two males by presenting the maximum possible distance of 25 for each. These conflicting results are less convincing than what was observed in Grave 109 as there is equal evidence to suggest both high levels of similarity and low levels similarity between these two males. If the assumption were to be based on high levels of similarity, the ages of these two males could be used in addition to support a notion of a close biological relationship like brothers, as same sex sibling pairs again have been shown to have highest correlations between tooth measurements (Townsend and Brown 1978a). However, as not all tooth measurements are showing this high degree of similarity, an alternative hypothesis could be that these are more distantly related individuals on the paternal line. If patrilineal descent and residence was common here at

Oakington, it is possible for paternal male cousins to be buried in the same cemetery which may be why these teeth are showing a moderate level of correlation to one another here. If these results were interpreted based on the low level of similarity, however, the close positioning and shared burial of these two males in the grave may indicate a type of practical kinship based on social relationships rather than biological connections.

6.4.3 Hatherdene

There were 19 multiple burials excavated at Hatherdene, more than were found at Oakington, Polhill and Eastry. Additionally, the layout of some of these multiple interments was quite different to what was observed in the other cemeteries; instead of being interred side by side, individuals in several of the graves were 'stacked' on top of each other. Dickinson (2004, 34) discovered similar stacked burials at the Anglo-Saxon cemetery at Quarrington, Lincolnshire, and commented on the rarity of such finds, regardless of whether the stack had been established contemporaneously or with successive interments over time. The construction of such grave types may be linked to social aspects like family, identity or kin relations. As has been suggested elsewhere (i.e Adachi *et al.* 2003; Alt *et al.* 1997), the interment of multiple individuals within the same grave could be used as evidence to discuss family units and kin groups in past populations. Table 35 presents an overview of the individuals who were interred in multiple burials within the Hatherdene cemetery. Once again, while all are listed, as only adults were focused on for this project not all of these graves will be used in further discussion. Figure 39 presents the location of the multiple interments containing more than one adult individual.

Table 35 - Overview of multiple graves excavated at Hatherdene cemetery. Details of interred individuals and corresponding grave numbers are included.

Skeletal ID Number of Interred	Notes
H220 and 221	H220 is an adult female and 221 is a subadult. Grave 219
H228, H225, 226 and 224	H228 is an adult male, H225 is an adult female, and 226 and 224 are sub adults. Grave 223
H361, 323 and H300	H361 is an adult male, 323 is an adult female with no teeth, and H300 is an adult female. Grave 299
H353 and H325	H353 is an adult male and H325 is an adult female. Grave 324
457 and 440	Both 457 and 440 are subadults. Grave 439
505 and H506	505 is a subadult and H506 is an adult male. Grave 504
614, 1432 and H554	614 and 1432 are subadults and H554 is an adult female. Grave 553
H603, H560, 1434, 559 and H557	H603 is an adult female, H560 is an adult male, 1434 and 559 are subadults, and H557 is an adult male. Grave 486
H1275, 1266, 617	H1275 is an adult male, 1266 and 617 are subadults. Grave 616
H637 and H640	H637 is an adult female and H640 is an adult male. Grave 636
H705 and 691	H705 is an adult male and 691 is a subadult. Grave 690
716 and 717	Both 716 and 717 are subadults. Grave 715
737 and 734	Both 737 and 734 are subadults. Grave 733
1002 and 976	Both 1002 and 976 are subadults. Grave 975
1016 and H999	1016 is a subadult and H999 is an adult male. Grave 998
1110, H1148, H1149 and 1109	1110 is a subadult, 1109 was an adult without recoverable dentition and both H1148 and H1149 are adult males. Grave 1150
1159, 1116 and 1136	All of 1159, 1116 and 1136 are subadults. Grave 1158
H1164, H1165 and H1127	H1164 and H1165 are adult males and H1127 is an adult female. Grave 1163
H1202 and 1134	H1202 is an adult female and 1134 is a subadult. Grave 1133

*Skeletal ID numbers without 'H' indicate individuals that were not included in data collection due to age or no present dentition.

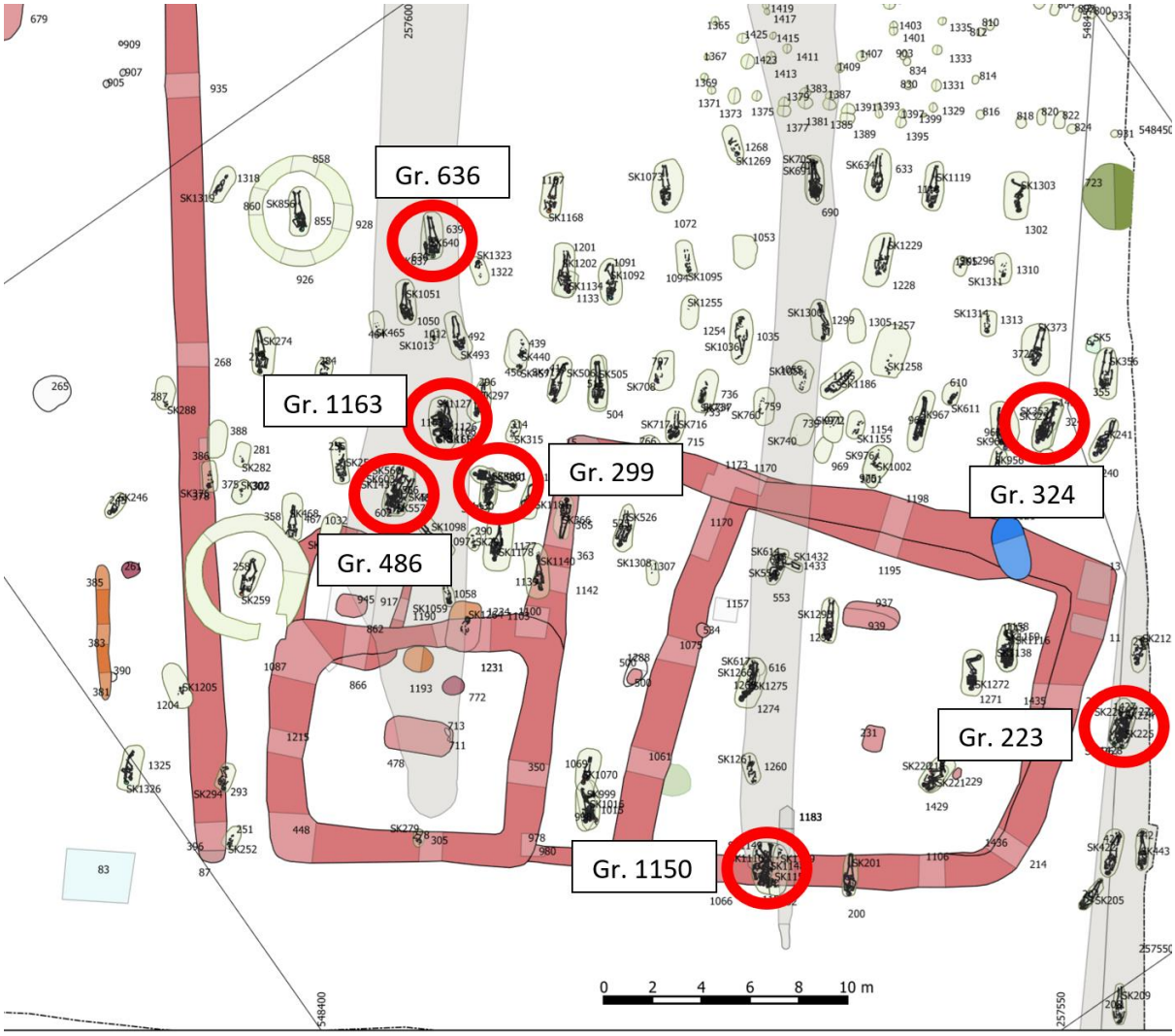

Figure 39 - Multiple burials within the Hatherdene cemetery. Red circles indicate graves where more than one adult was present, while blue circles indicate only one adult was present, or no adult remains were found within the grave (after Oxford Archaeology East, personal 2018).

The multiple interments were not situated in spatially distinct locations in the cemetery to single interments, as both types of graves were found across the entire site. As Table 35 displays, it was possible for both adult males and females to be interred in multiple graves and to either be interred with another adult or with a subadult. Therefore, the membership of a multiple grave is not attributable to differences in biological sex or age within the Hatherdene cemetery. Of the 19 multiple interments excavated at Hatherdene, only seven were investigated in greater detail as they contained more than one adult from which to base comparisons of tooth metrics. The comparison of dental analyses outlined below are for Graves: 223, 299, 324, 486, 636, 1150 and 1163.

Grave 223 contained two adult individuals: H225, an adult female aged 26-44 years at time of death and H228 a young adult male aged 19-25 years at time of death. Upon reviewing the spatial information from the position of each in the stack, H228 was the first interred in this stacked burial, with H225 being above him, followed by the subadults with 226 on the same level as H225 and 224 as the most superficial interment. Grave goods were also considered, H225 was interred with an iron object and brooches, but preservation was too poor to make any reliable identification of good type. H228 had present a number of belt and copper remnants and beads. Few comparisons could be made between the artefacts present here and the individuals to comment on whether they show kin or group membership. In order to refine these suggestions, the hierarchical cluster output from the dental analyses were reviewed, Table 36.

Table 36 - Squared Euclidean distances between H225 and H228 within Grave 223 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance Between Individuals
Left maxillary first premolar	Combined cemetery, pooled sex	25
Left mandibular first premolar	Combined cemetery, pooled sex	25
Left mandibular central incisor	Combined cemetery, pooled sex	4
Left maxillary first premolar	Hatherdene only, pooled sex	11
Left mandibular first molar	Hatherdene only, pooled sex	25
Left mandibular first premolar	Hatherdene only, pooled sex	25
Left mandibular central incisor	Hatherdene only, pooled sex	13
Right mandibular canine	Hatherdene only, pooled sex	7

The majority of teeth available for comparison revealed low levels of similarity present between H225 and H228, rather than high levels of biological similarity. Biologically related brothers and sisters would be expected to share higher levels of similarity (Townsend and Brown 1978a), therefore it is more likely these two individuals are not siblings or any other type of biological relation. Friendship between males and females has been commented on in the literature (Lancaster 1958a; 1958b) which demonstrates the potential for practical kin relationships to have been formed during this time period. Marriage between a male and female would also show as differences in tooth size between individuals. The fact these two individuals appeared to be less similar when compared within the combined cemetery group, helps to support the notion that they are less likely to be biologically related. Biological similarity between two genetically related individuals would be expected to increase in comparative groups where individuals come from a variety of lineages. However, where individuals are not genetically related, these differences in tooth size may become even more divergent when compared to a broader mix of individuals.

Grave 299 contained an adult male (H361), adult female (H300) and another adult female (323) who was not recovered with any dentition skeleton. It was a stacked burial with the

adult male being interred first, followed by 323 and then H300 being the most superficially interred. All three individuals were aged to the mature adult category. Table 37 provides an overview of the teeth available for comparison and the distances observed between H361 and H300 for each corresponding tooth.

Table 37 - Squared Euclidean distances between individuals H361 and H300 within Grave 299 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance Between Individuals
Left mandibular first premolar	Combined cemetery, pooled sex	25
Left mandibular first premolar	Hatherdene only, pooled sex	4
Right mandibular canine	Hatherdene only, pooled sex	7
Left mandibular first premolar	Hatherdene only, pooled sex	25

Unfortunately, there were only four teeth available for comparison between H361 and H300 which will affect the reliability of interpretations made from these results. There does appear to be a moderate to low level of biological similarity between H361 and H300. The similar ages of these individuals, both being over 45 years at time of death, can be discussed in relation with the moderate levels of similarity to suggest a sibling relationship between these two individuals. Opposite sex sibling pairs have been shown to have moderate levels of correlation between tooth metrics (Townsend and Brown 1978a), partially due to the additional influence of biological sex on tooth size, which would help to explain why not every tooth within this comparison is showing the degree of closeness as one another. However, these presumptions are only supported by two teeth. No grave goods were recovered alongside H361 or H300, though 323 was found with a single amber bead. As there were no grave goods recovered within this grave, interpretations on identity and relationships were not possible with this evidence type. The large distances between two of the four teeth, however, are noteworthy. Equally, these could be taken to interpret no close biological

relationship between these individuals; cousins may fit as an interpretation or another form of ascribed or practical kin. Overall, the fact that these individuals were buried stacked on top of one another in the same grave, with partial display of biological similarity helps to demonstrate the potential that the male individual and one of the female individuals would have shared some connection, whether a more distant biological relationship or an ascribed kin status.

Grave 324 was another stacked grave, containing an adult male (H353) on the bottom and an adult female (H325) interred above. H325 was aged between 26-44 years at time of death and H353 was over 45 years old at the time of death. Table 38 provides an overview of the teeth available for comparison between these two individuals and their corresponding distances apart.

Table 38 - Squared Euclidean distances between individuals H325 and H353 within Grave 324 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance Between Individuals
Left maxillary first premolar	Combined cemetery, pooled sex	2
Left mandibular first premolar	Combined cemetery, pooled sex	4
Right maxillary canine	Hatherdene only, pooled sex	1
Left maxillary first premolar	Hatherdene only, pooled sex	1
Left mandibular first premolar	Hatherdene only, pooled sex	3
Right mandibular central incisor	Hatherdene only, pooled sex	11
Right mandibular canine	Hatherdene only, pooled sex	25

In comparison to Grave 299, Grave 324 provides much more clear evidence of high levels of biological similarity within the tooth data. As the age categories are so broad for adult age estimation, it is difficult to differentiate on biological data alone what this could mean in regard to relationships. The two most likely interpretations are to assume a father-daughter or brother-sister relationship. However, Townsend and Brown (1978a) suggests that stronger

correlations in tooth measurements are observed between sibling pairs as opposed to parent-offspring pairs due to the greater likelihood of shared dental traits in siblings than between parents and siblings. As the teeth here demonstrate high levels of similarity overall, this could be used as evidence to argue for a brother-sister pairing as opposed to a father-daughter relationship. H353 was buried with a ceramic vessel, an iron knife and a rod whereas H325 was decorated with an applied saucer brooch, a belt ring, buckle, knife and an assortment of beads. The fact that both individuals were interred with grave goods could indicate a more equitable status between them, or membership of a wealthier family unit within the population (Sayer 2009). This further acknowledges that there is likely a close kinship bond here, likely based on biological relations. Applying this finding to social constructs would suggest that family level patterns were expressed during burial, though this will be discussed in more detail in Chapter 7.

Grave 486 was a large stacked burial containing five individuals in total: H603 is an adult female (aged 26-44 years at time of death), H560 and H557 are adult males (aged 19-26 and over 45 years at death, respectively), 1434 is a foetus and 559 is a subadult. H603 was interred on the bottom level of the stack, with H560, 1434 and 559 on the level above, followed by H557 on the most superficial level. Table 39 presents an overview of dental comparison between the three adult individuals interred in Grave 486.

Table 39 - Squared Euclidean distances between individuals H603, H560 and H557 within Grave 486 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance between individuals
Left maxillary first premolar	Combined cemetery, pooled sex	603-557 = 3
Left mandibular first premolar	Combined cemetery, pooled sex	603-557 = 9 603-560 = 1 560-557 = 9
Left mandibular central incisor	Combined cemetery, pooled sex	557-560 = 13
Left mandibular lateral incisor	Combined cemetery, males only	557-560 = 12
Right maxillary canine	Hatherdene only, pooled sex	603-557 = 9
Right maxillary central incisor	Hatherdene only, pooled sex	603-557 = 25
Left maxillary first premolar	Hatherdene only, pooled sex	603-557 = 1
Left mandibular first molar	Hatherdene only, pooled sex	603-560 = 2
Left mandibular first premolar	Hatherdene only, pooled sex	603-557 = 11 603-560 = 1 557-560 = 11
Left mandibular central incisor	Hatherdene only, pooled sex	557-560 = 6
Left mandibular canine	Hatherdene only, males only	557-560 = 25

In order to best explain the results from Table 39, each pairing was looked at in turn to discuss the results found. H603 and H557 shared six teeth for comparison with corresponding distances between each other as follows: 3, 9, 9, 25, 1, and 11. Based on those values, a moderate degree of biological similarity was apparent between the female and mature male. H603 and H560 shared only three teeth for comparison, with corresponding distance values as: 1, 2 and 1. Based on these values alone, it appears as though there are higher levels of similarity between the female and the young adult male. H557 and H560 shared six teeth in common for comparison, with corresponding values as: 9, 13, 12, 11, 6 and 25. Out of the three pairs, the two males appear to have the least amount of similarity between their tooth dimensions. Figure 40 depicts these levels of similarity visually, the darker the line, the greater degree of biological similarity the individuals share between them.

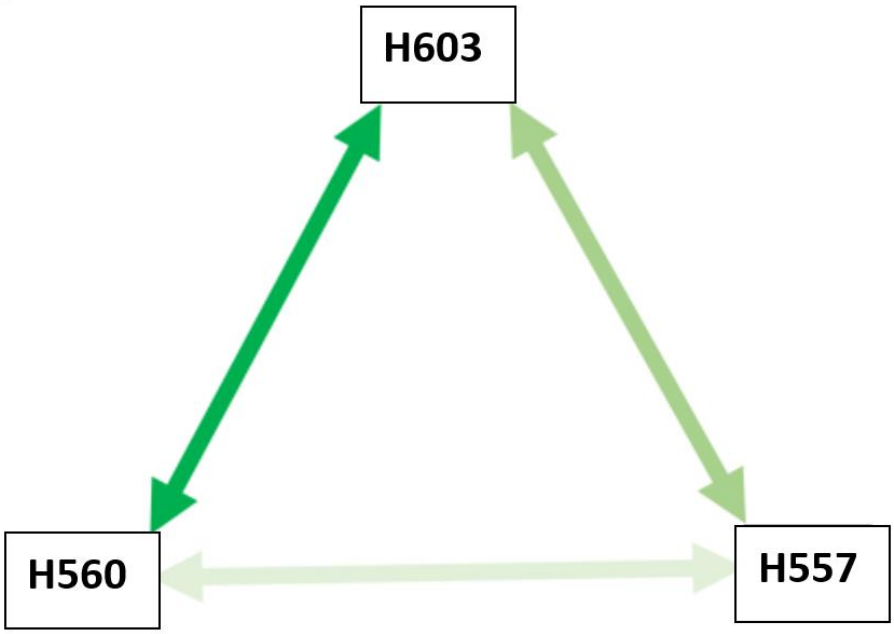

Figure 40 - A visual depiction of the varying levels of similarity between H560, H557 and H603 in Grave 486. The darker the line connecting the individuals, the greater the level of similarity between them.

Grave goods were present among two of the three adults under investigation here: H603 was found with an assortment of beads, H557 had a knife an array of mixed beads, and H560 was not recovered with any artefacts. Elsewhere, arguments have been put forward regarding identity and shared grave goods (i.e. Huggett 1996; Lucy 2000; Sayer 2009), the commonality of beads between H603 and H557 may demonstrate a further kin connection between the female and the older male, though this is not very convincing as a standalone point. Taking all these evidence streams into account when considering potential interpretations about relationships between these three individuals has helped to develop more robust ideas about who they may have been to one another. Due to the shared burial, commonalities in grave goods and evidence of high levels of similarity between some pairs' biodata, the following was hypothesised. Due to the closeness of H603 and H560, a mother-son or sister-brother relationship is possible; mother-son could be possible here if the male was on the younger end of his associated age category and the female was towards the upper limits of the age

category assigned to her. H603 and H557 could have been husband and wife, who would be expected to show lower levels of similarity between them but the commonality in interment location and grave good may help to demonstrate a social connection akin to marriage here. H557, however, is most dissimilar in his biodata compared to H560, which perhaps indicates that H560 (if assuming the son of 603) is not his biological kin, but perhaps adopted. Or, the same information could be applied to support the fact that H560 is H603's brother as opposed to son, which would signify a greater difference to H557 as they would be from different paternal lineages.

Grave 636 contains two adult individuals: H637 is a female aged 26-44 years at time of death and H640 is an adult male aged 26-44 years at time of death. They were stacked one on top of the other with the female skeleton having been interred first. Table 40 provides an overview of the teeth available for comparison between the two individuals and their corresponding distance values.

Table 40 - Squared Euclidean distances between H637 and H640 within Grave 636 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance Between Individuals
Left mandibular first premolar	Combined cemetery, pooled sex	25
Right maxillary canine	Hatherdene only, pooled sex	25
Left mandibular first premolar	Hatherdene only, pooled sex	25

Grave 636 is another case where unfortunately, limited interpretations could be made based on tooth biodata as only three teeth were found in common for H637 and H640 within the dataset. In regard to grave goods, the female individual was not recovered with associated artefacts, but the male individual was heavily decorated. H640 was recovered with five arrow heads, several board fittings and studs, a buckle, a knife, a ring, a shield boss and grip and a

spearhead. Being highly decorated has been shown to relate to status and occupation in the Anglo-Saxon period which could indicate this male was part of the main paternal identity group or had an important role in society (Sayer 2009). Based on the shared grave area, and lack of similarity between tooth measurements between H637 and H640 it could by hypothesised that the female and male were a husband and wife. However, it is odd that if the husband is so ornately decorated that his wife would be buried without some sort of grave offering as elite women were often to be found with grave goods as well during this time period (Lucy 2000). While not impossible to suggest, this discrepancy in grave objects may lead to different relationships being investigated for this particular pairing. Ross (1985, 14), for example, describes the practice of concubinage within Anglo-Saxon societies and discusses how, while it was socially recognised and practised, there were no laws or customs to formally recognise it. However, it must be reiterated that these ideas are coming from spatial, contextual and a limited amount of biodata from these two individuals. These evidence streams have helped to form starting points for discussion on potential relationships, but each idea should be explored in greater depth.

Grave 1150 was a stacked burial that contained four individuals in total; the bottom level contained 1110 (a subadult), H1148 and H1149 (both of whom were adult males aged 26-44 at time of death. The most superficial level contained 1109, an adult but preservation was too poor to provide an age range or sex estimation and no teeth were recovered with this skeleton. Table 41 provides an overview of the teeth available for comparison between the two adult males.

Table 41 - Squared Euclidean distances between individuals H1148 and H1149 within Grave 1150 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance Between Individuals
Left maxillary first premolar	Combined cemetery, pooled sex	11
Left mandibular first premolar	Combined cemetery, pooled sex	1
Left mandibular lateral incisor	Combined cemetery, males only	7
Right maxillary canine	Hatherdene only, pooled sex	25
Right maxillary central incisor	Hatherdene only, pooled sex	1
Left maxillary first premolar	Hatherdene only, pooled sex	25
Left mandibular first premolar	Hatherdene only, pooled sex	4
Right mandibular canine	Hatherdene only, pooled sex	2
Left mandibular canine	Hatherdene only, males only	25
Right mandibular first molar	Hatherdene only, males only	1

The two adult males in Grave 1150 were both aged similarly when they died, they were buried in the same plot and, overall, show a relatively high degree of biological similarity when comparing their tooth dimensions. Of the 10 teeth available for comparison, seven of them were reflective of higher levels of similarity. This leads to the interpretation of a biological connection between these two males, likely akin to a brother-brother pair or a pair of first cousins. No grave objects were recovered with either of the two males within this grave, so it was impossible to make an interpretation based on their inclusion, though the fact they both lacked goods may suggest equitable status. As the overarching assumption that these populations were based on patrilineal residence, the assumption about the relationship between these two individuals was that they were brothers or cousins.

Grave 1163 was the final multiple burial to be investigated from Hatherdene. It was a stacked burial containing three individuals: H1164 was an adult male aged 26-44 at time of death, H1165 was an adult male aged 19-25 at time of death, and H1127 was an adult female aged over 46 at time of death. The female individual was interred overtop the two male individuals, which were interred on the same level as one another. Like Grave 486, comparisons between

the three individuals were broken down, and Table 42 provides an overview of the teeth available for comparison and their corresponding distances.

Table 42 - Squared Euclidean distances between individuals H1164, H1165 and H1127 within Grave 1163 for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance Between Individuals
Left maxillary first premolar	Combined cemetery, pooled sex	1164-1165 = 25
Left mandibular first premolar	Combined cemetery, pooled sex	1127-1165 = 4
Left mandibular lateral incisor	Combined cemetery, males only	1164-1165 = 25
Right maxillary central incisor	Hatherdene only, pooled sex	1164-1165 = 25
Left maxillary first premolar	Hatherdene only, pooled sex	1164-1165 = 11
Left mandibular first molar	Hatherdene only, pooled sex	1127-1164 = 25 1127-1165 = 6 1164-1165 = 25
Left mandibular first premolar	Hatherdene only, pooled sex	1127-1165 = 3
Right mandibular canine	Hatherdene only, pooled sex	1127-1164 = 25 1127-1165 = 7 1164-1165 = 25

In order to best explain the results from Table 42, each pairing was looked at in turn to discuss the results found. H1127 and H1164 shared only two teeth in common for comparison, both with corresponding distances of 25 between each other. Based on limited assumptions that could be made solely from those two distances, it is unlikely that H1127 and H1164 shared a biological connection. H1127 and H1165 had four teeth in common for comparison, with corresponding distance values as: 4, 6, 3 and 7. Based on these values, it appears as though there are higher levels of similarity between the female and the young adult male. H1164 and H1165 shared six teeth in common for comparison, with one corresponding distance value at 11 and the remaining five at 25. Out of the three pairs, the two males, and the female and middle-aged male appear to have the least amount of similarity between their tooth dimensions, whereas the female and young adult male appear to share the most similarity.

Figure 41 depicts these levels of similarity visually; the darker the line, the greater degree of biological similarity the individuals share between them.

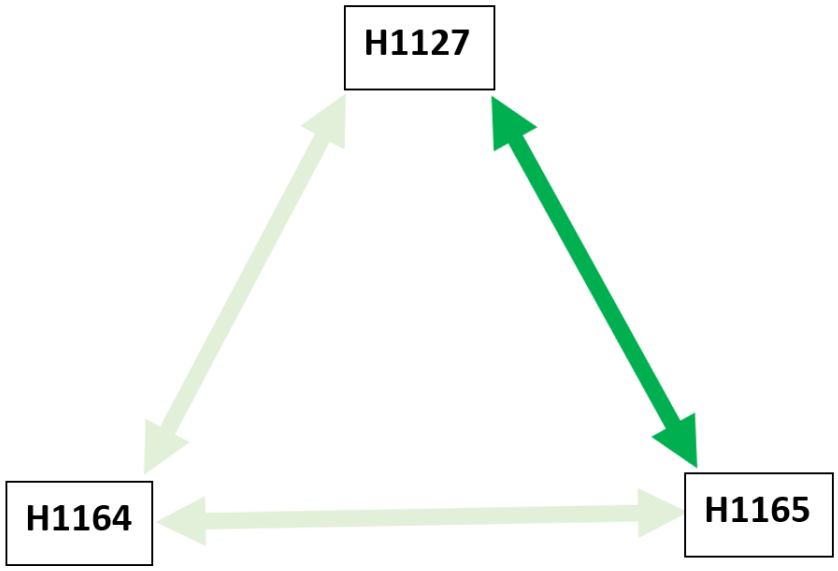

Figure 41 - A visual depiction of the varying levels of similarity between H1165, H1164 and H1127 in Grave 1163. The darker the line connecting the individuals, the greater the level of similarity between them.

H1127 was recovered with an assortment of beads, while the male individuals had more objects recovered with them. H1164 was found with a buckle, a ferrule, a knife, a spearhead and mixed beads. H1165, the young-adult male, was recovered with mixed beads and a shield boss and grip.

The interment of the two males side by side on the same level of this stacked burial, in combination with the presence of similar grave goods may suggest a strong relationship or connection between them. However, this relationship does not appear to be based on shared biology as their dental measurements show a lack of similarity between one another. Blood relations such as brother-brother or father-son pairing here would have the expectation of more shared biological similarity, which was not observed. This is not to suggest, however, these roles could have ascribed via an adoptive or practical focus. Adoption of children was evident in later Anglo-Saxon England (Lancaster 1958a; 1958b) where males would adopt the

children of new wives. If this was the case within Grave 1163, it could help to explain why the female is more similar to the young male (mother-son), and not the older male (wife-husband). In contrast, it could be that the two males shared a connection beyond kin, more relative to occupation or status as signified by their grave goods, however the interment of a biologically similar female to the younger male in the same plot may put more strength behind an argument based on family interment and adoptive kin.

6.5 DNA Validation of Methodological Approach

The general premise from which this methodological approach is based is that the biological similarity observed amongst individuals from Hatherdene, Oakington, Polhill and Eastry can be used in two separate ways. Firstly, to lead hypothesis testing based on those the biodata results highlight as being similar and, secondly, to use the spatial and contextual data to lead back to the biodata for corroboration and comparisons regarding relationships, kinship and identity. However, it was important that the method used herein be validated, if possible, in order for the results to carry significance. As part of a separate project, DNA samples were obtained from a random selection of individuals from early Anglo-Saxon cemeteries, including Hatherdene, Oakington and Eastry, in order to undergo genetic testing that would help to lead to country of origin, confirmation of biological sex and comments on kinship (Schiffels and Gretzinger, *nd.*). Mitochondrial DNA could be amplified in these cases, which relates to maternal inheritance as opposed to nuclear DNA which reflects both maternal and paternal inheritance. This preliminary work was useful in the remit of the current project as some of the individuals tested were the same ones whose tooth measurements were recorded and analysed here. Though there was overlap between individuals sampled for DNA and the ones

used within this project, the DNA project and the current project did not always use the same individuals, therefore not all results could be corroborated with DNA analyses. Despite this, two very strong examples from Oakington and one from Eastry have helped to demonstrate the validity of this methodological approach for basing inferences about biological relationships between individuals in archaeological assemblages. Grave 88 and Graves 56 and 78 from Oakington each demonstrated the potential to look at multiple and single interments together to elicit and compare biodata to help comment on potential social connections based on biological similarity. Similarly, dental based observations made between E45 and E46 at Eastry have also supported connections discovered via mtDNA analysis. Consistency found among mtDNA results and tooth metric data has shown that this method does appear to pick up on biological connections between individuals and, as such, it can be shown that teeth do provide a strong evidence base from which to discuss and hypothesise about connections between archaeological people.

From Oakington, Grave 88 contained two males, O1798 and O1799 whose dentition provided a mix of high and low similarity across the six teeth compared. Chapter 6.5.2 presented the full results from the dental comparison between these two males, but it was concluded that there was evidence to suggest some sort of biological connection, although likely a more distant one. In support of this, the preliminary mtDNA analysis (Schiffels and Gretzinger, *nd.*) also revealed that these two individuals are not closely related maternally based on the identification of two different mitochondrial haplogroups: U5b2b1a1 for O1798 and X2b4a for O1799. Therefore, while not maternally connected, it could be possible these two males share a closer connection on their paternal side, which the mtDNA results are not able to pick up on but is reflected in their dentition as they presented a combination of high and low levels of similarity. The fact that half of their tooth measurements are strongly similar to one

another may still demonstrate some degree of blood relation, likely paternally linked as was suggested in Chapter 6.5.2. Figure 42 highlights the mtDNA linkage for O1798 and O1799.

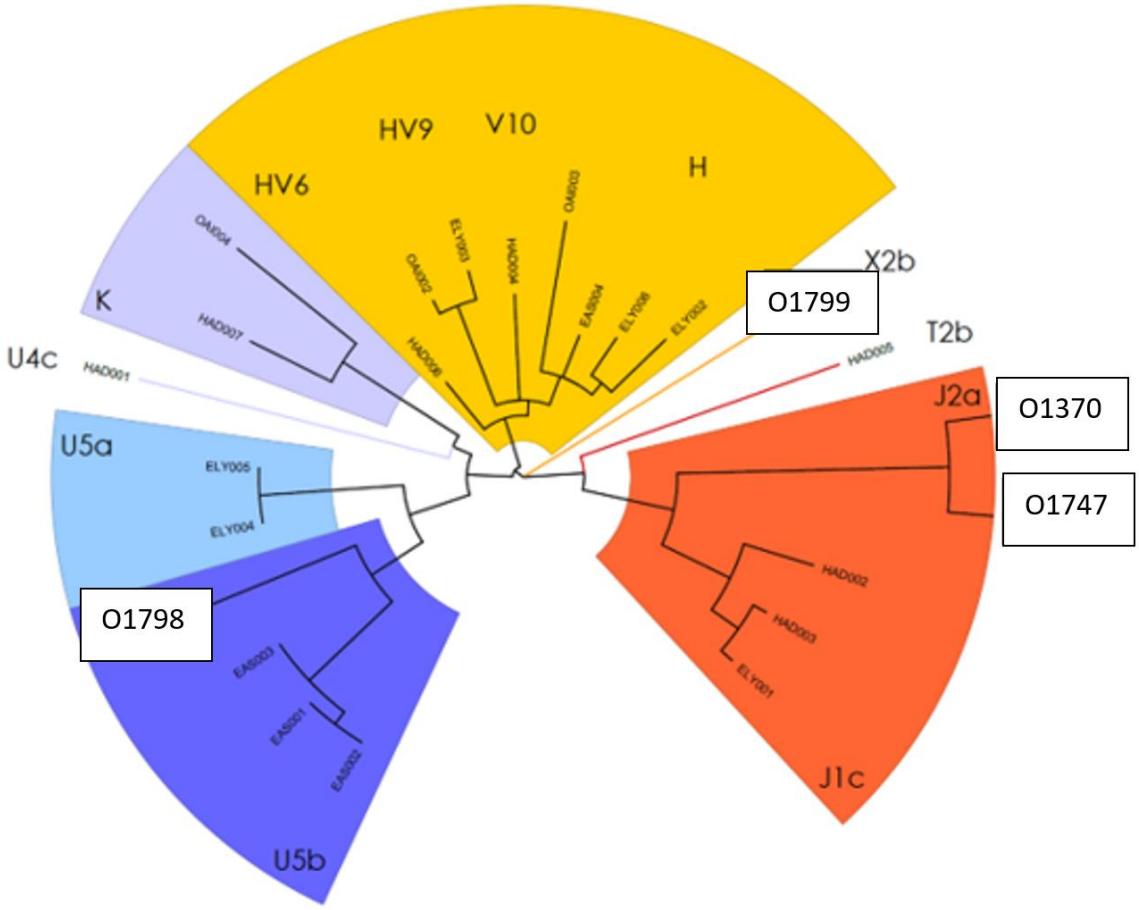

Figure 42 - Genetic kinship output from Schiffels and Gretzinger (nd.), demonstrating the genetic diversity along the maternal line for the individuals in Grave 88: O1798 and O1799 and the relative similarity between O1370 and O1747 (after Schiffels and Gretzinger nd.).

Additional genetic data had been processed from Oakington remains, connecting two individuals as blood relatives, O1370 and O1747, which had not yet been investigated together in the current project. O1370 was an adult male between the ages of 30-35 years at time of death and O1747 was an adult female between the ages of 30-40 years old at time of death. O1747 was buried in a double interment with a sub adult, and O1370 was buried in single grave. The location of the graves to one another in the cemetery is displayed in Figure

43. The graves are both located closer towards the densest area of the cemetery, though not in very close proximity to one another.

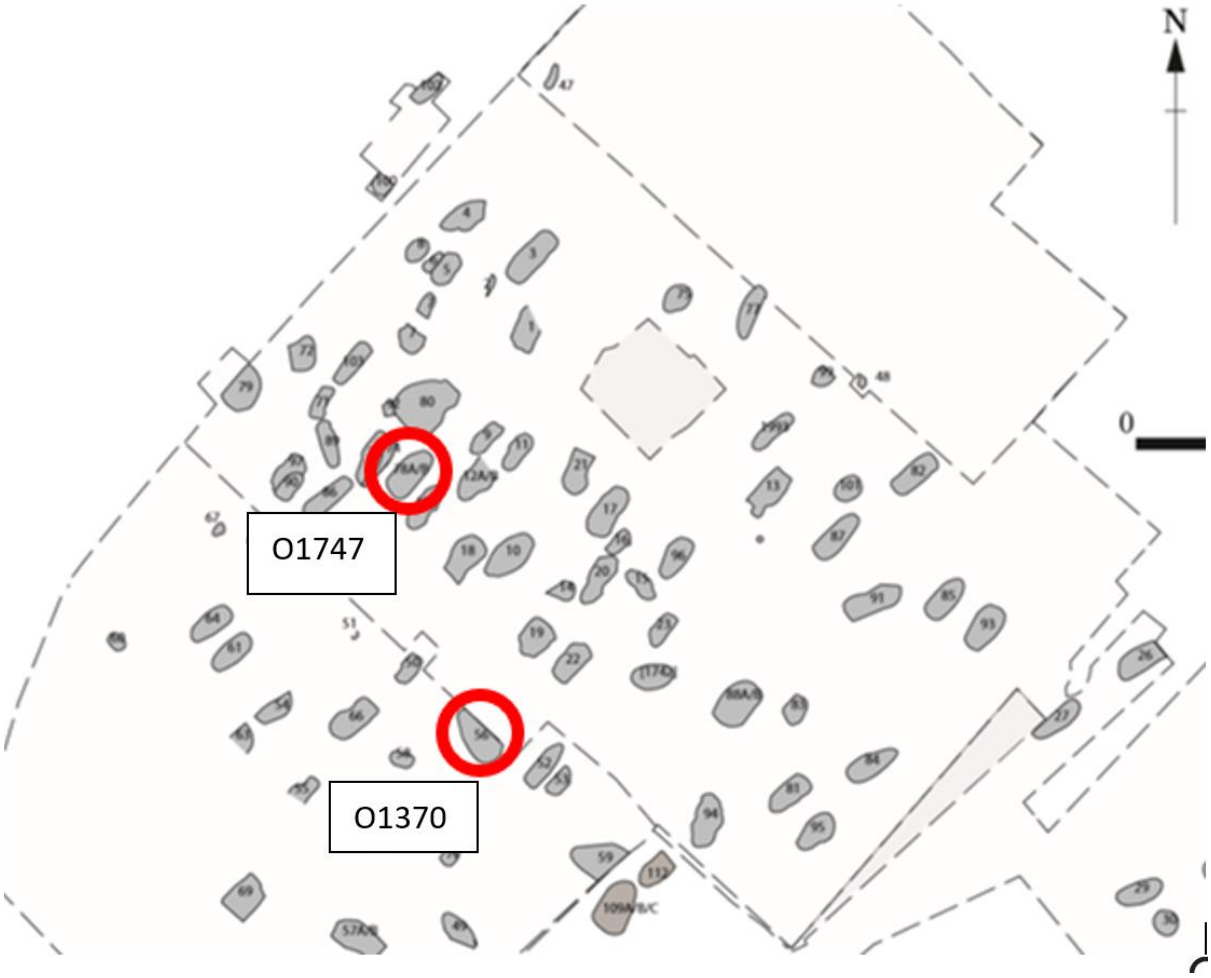

Figure 43 - Location of Graves 56 and 78 at Oakington cemetery, containing O1370 and O1747, respectively. Graves indicated by red circles (after Sayer 2017).

Figure 42 also depicts the genetic interpretation regarding kinship between these two individuals. As can be seen, they appear to share a close maternal connection based on their mitochondrial haplogroups: O1370 had J2a1a1a2 and O1747 had J2a1a1c (Schiffels and Gretzinger, *nd.*). This finding, in combination with their demographic details would suggest a biological relationship akin to brother-sister or close maternal cousins. As both of these individuals had yet to be compared together in this project, the HCA dendrograms were

consulted to verify this with dental data. The dendrograms were used to locate the levels of similarity across as many teeth as possible between these two individuals. Table 43 provides an overview of the teeth available for comparison between O1370 and O1747 and their associated distances.

Table 43 - Squared Euclidean distances between individuals O1370 and O1747 within Oakington cemetery for each tooth involved in hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance between individuals
Left maxillary first premolar	Combined cemetery, pooled sex	2
Left mandibular first premolar	Combined cemetery, pooled sex	2
Left mandibular first molar	Oakington only, pooled sex	25
Left mandibular first premolar	Oakington only, pooled sex	25
Left maxillary first premolar	Oakington only, pooled sex	1
Right maxillary first premolar	Oakington only, pooled sex	2
Right maxillary first molar	Oakington only, pooled sex	3

As can be seen in Table 43, O1370 and O1747 share a high level of biological similarity as the majority of teeth (five of seven) available for comparison show connections at squared Euclidean distances of 1-3. This is strong evidence to suggest a genetic link between the two individuals, which was corroborated with the mtDNA analysis by Schiffels and Gretzinger (*nd.*). As the mtDNA results suggest a close maternal bond this suggests, in combination with the similarity in tooth sizes, these individuals may have been brother and sister.

Preliminary mtDNA results have also revealed some valuable insights into the identity of individuals at Eastry, particularly E34 (adult female aged 25-45 years old at time of death, recovered with a ring, nail, three knives, beads, shears and a girdle-hanger), E45 and E46 previously discussed in Section 6.3. The results from the mtDNA analyses by Schiffels and Gretzinger (*nd.*) have indicated that E34 and E45 are likely first-degree relatives akin to sisters as they carry the same mitochondrial haplogroup, U5b1c2b. Unfortunately, poor preservation

of the remains meant that there was only one tooth in common (right maxillary first premolar) between E45 and E34 for comparison which showed a maximum distance of 25 between them. A single tooth is not enough from which to base strong interpretations of similarity. As has been shown in numerous examples in Chapter 6, the overall pattern of multiple teeth is much more reliable than results from a single tooth. Schiffels and Gretzinger (*nd.*) also suggested, however, that E46 was a third-degree relative of E34 and E45, and so it was possible to discover more about the connection between E45 and E46, which in turn helped relate back to E34. Figure 44 presents the preliminary mtDNA results for these three individuals from Eastry and Table 44 presents an overview of the similarity amongst the teeth of E45 and E46 which were used to compare results between mtDNA and dental metrics.

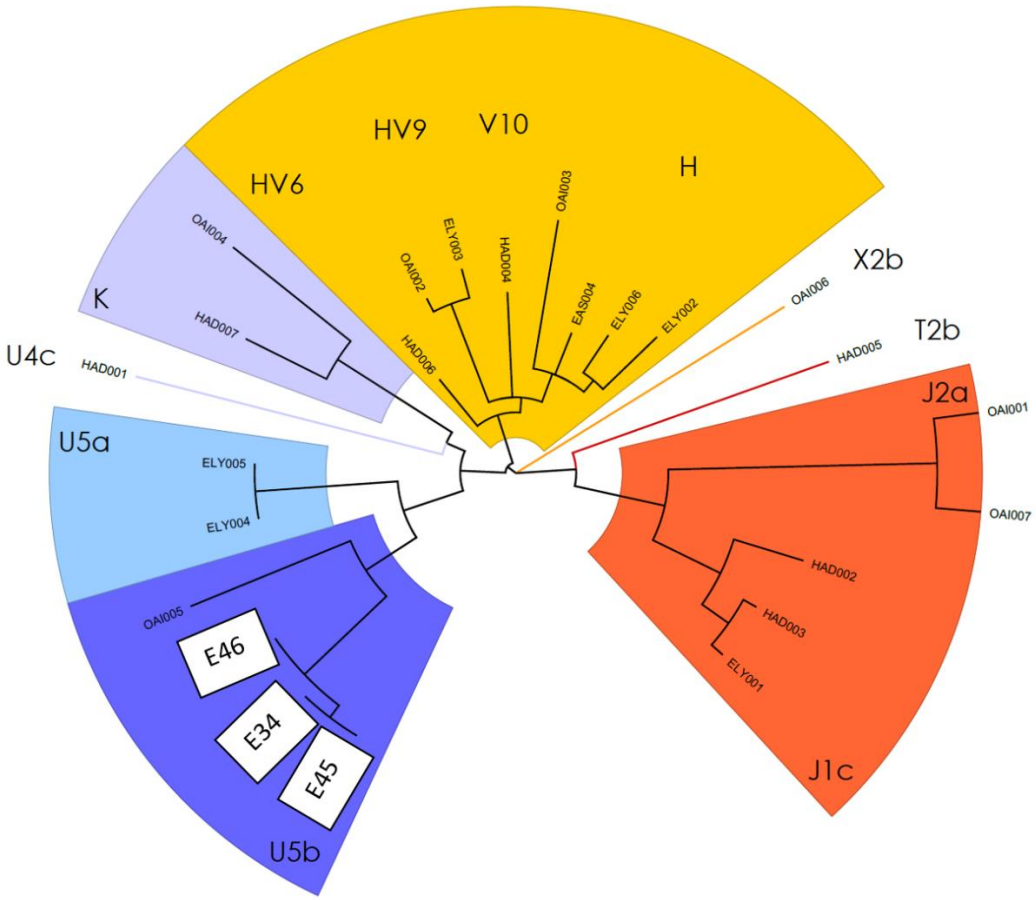

Figure 44 - A visual representation of the mtDNA results for E34, E45 and E46 from Eastry cemetery (after Schiffels and Gretzinger nd.).

Table 44 - Squared Euclidean distances between individuals E45 and E46 within Eastry cemetery for each tooth available for hierarchical cluster analysis.

Tooth	Comparison group	Squared Euclidean Distance between individuals
Left mandibular first premolar	Combined cemetery, pooled sex	9
Right maxillary canine	Combined cemetery, females only	4
Right maxillary canine	Eastry only, females only	12
Left mandibular first premolar	Eastry only, females only	14
Left mandibular canine	Eastry only, females only	12

The biological similarity observed between the teeth of E45 and E46 supports the results discovered from the mtDNA analysis as the teeth show a likely biological connection between these two females. The moderate levels of distance measures from the teeth suggest a more distant biological relationship than direct first relatives, exactly what was suggested from the mtDNA analysis. Considering the demographic details from these two females, it is likely they represent cousins, or third-degree relatives as Schiffels and Gretzinger (*nd.*) suggested. This could then more loosely be applied to E34, as it was suggested E34 and E45 were sisters, this result would also indicate that E34 and E46 were cousins as well. Figure 45 displays the burial location of these three individuals within the 1989 excavated area at Eastry.

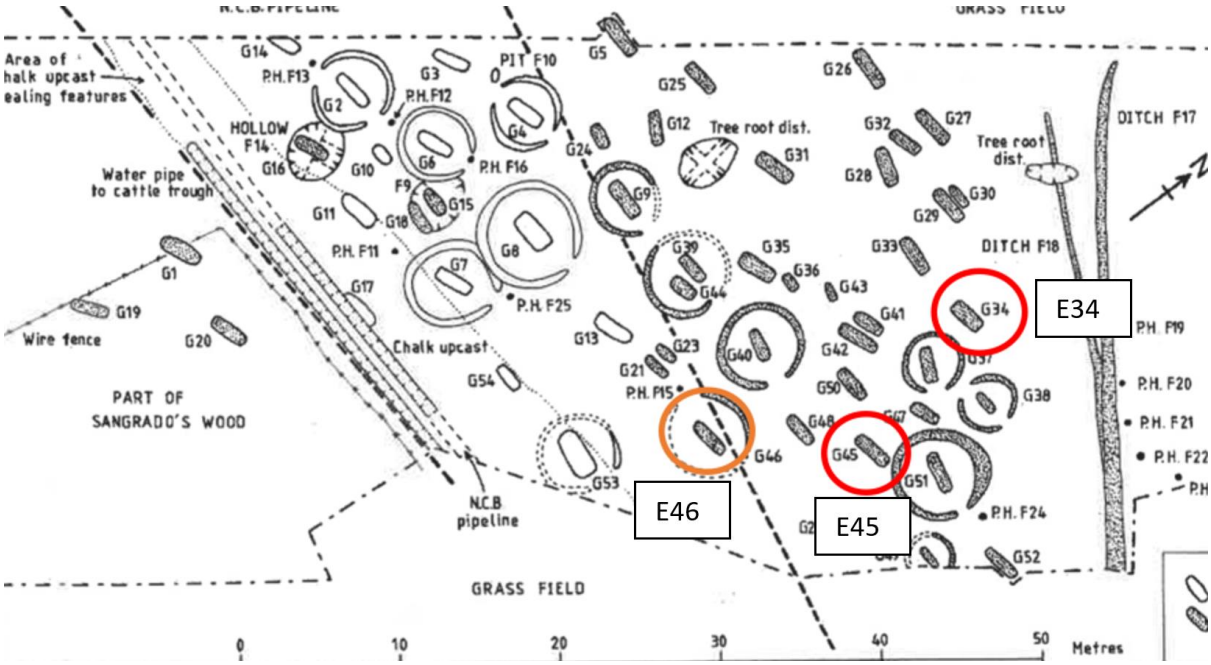

Figure 45 - The locations of individuals E34, E45 and E46 within the cemetery at Eastry. The red circles indicate a first-degree biological relationship and the orange circle indicates a third-degree biological relationship as per the preliminary mtDNA analyses (after Welch et al. 2008, 9).

E46 was also cited as being quite different in terms of genetic ancestry and was noted as having strong ties to extant Icelandic or Norwegian groups with genetic background indicating about 67% Anglo-Saxon ancestry with about 33% West-African ancestry (Schiffels and Gretzinger, *nd.)*. While this mix was noted on the mtDNA results, it was not reflected in the teeth as clearly as E46 was not identified as a statistical outlier, rather, showed closer affinity to multiple individuals within the sample, see Chapter 6.3. This, once again, helps highlight the various levels of influence apparent on tooth development; local level and broader geographic levels may both influence the appearance of teeth. 'Local' levels would be representative of inheritance between parent and offspring and broader levels may be traits present within the wider population. This would then explain why DNA has picked E46 out as an outlier, yet her tooth metrics are not reflective of that pattern as they seem similar to other individuals in the community.

These above three examples are a substantial contribution to this project. The use of mtDNA has helped to validate the methodological approach of using dental metrics to comment on potential biological connections between individuals interred within an archaeological cemetery. These examples demonstrate that it is possible to see consistencies between what is reported in mtDNA analyses with what was discovered in the hierarchical clustering of dental data. Furthermore, these examples highlight the flexibility of dental data to assess biological similarity as it was possible to test potential connections of individuals based on contextual and spatially derived data (i.e. looking within a multiple burial to assess similarity between two individuals), as well as a biodata led approach where the mtDNA results suggested a close relationship which was further supported by tooth data.

6.6 Discussions on Observed Patterns from Dental Analyses

As has been shown in the examples above, and from results presented in Chapter 5, biodata obtained from teeth has enabled the ability to comment on social aspects on population, community and individual levels within the early Anglo-Saxon period. The population level results showed that early Anglo-Saxon residency patterns are overarchingly based on paternal lineages, however, local level differences and variations are evident. Historical sources have documented later Anglo-Saxon laws relating to male-centric practices including land ownership, inheritance and marriage (Lancaster 1958a; 1958b). However, debates regarding the extent to which these ideas are presented or varied within everyday local practice within settlement sites exist in the literature (i.e Murray 1983). For instance, females have also been shown to inherit land, retain rights after deaths of husbands, and achieve elevated statuses

within communities on their own accord (Lancaster 1958a). In this chapter, biological evidence has been presented to support these more fluid notions.

In relation to patrilineal residence patterns, those that have studied this concept in other archaeological populations have commented on the levels of homogeneity among males of a group compared to the higher degree of heterogeneity of females within the population (Kumar *et al.* 2006; Oota *et al.* 2001; Pérez-Lezaun *et al.* 1999). This was inferred to represent the fact that males are residing in home settlements and females come from other places to marry in, contributing to variations in biodata more evident amongst females than males. Montgomery *et al.* (2005) investigated strontium isotope ratios in Neolithic, Bronze Age and early Anglo-Saxon individuals and discovered differences in local and non-local people within their sample. Some female individuals of marriageable ages (Montgomery *et al.* 2005, 132) were found to be non-locals, suggesting female mobility during these time periods. The same general trend was observed at a population level within this project. When looking at combined cemetery samples and the differences between sexes, it was observed in Chapters 5 and 6.1 that females appeared more diverse in their dental metrics compared to males, overall. Dendrograms for females tended to result in greater numbers of clusters and fewer individuals were divided after the first node separation, both markers of lower levels of homogeneity in the sample populations. Additionally, observations based on the application of these dendrograms to spatial aspects within and between cemeteries appeared to support these assertions. One of the strongest examples for support came from the community level investigations at Hatherdene when looking into those who were interred in ring ditches. The individuals interred in ring ditches at Hatherdene were males who showed higher levels of similarity in tooth sizes between themselves and as well as additional strong biological links to other male individuals within the assemblage who could be argued to be of elite

importance to the Hatherdene settlement based on grave structure and artefacts recovered. The fact that it was only decorated males interred in ring ditches and comparisons of biological similarity demonstrated their closest affinity to other males spread throughout the assemblage highlights the concept of patrilocal residence in practice. In effect, this finding, combined with statistical interpretations of cluster data from Chapter 5 regarding male and female patterns, supports the notion that there were not as many females present with close affinity to this group of males due to such residence patterns. It is very likely that similar females did exist at Hatherdene, as evidenced by the one female who did show high levels of similarity to this ring ditch group, see Chapter 6.2.1, but due to the patrilocal patterns of mobility, it is assumed that when these females reached a certain age or life milestone (i.e. age of marriage), most would have married and left their home settlement to reside in that of their new husband, thus the absence of similar females to elite males at Hatherdene.

However, equally as interesting was when this approach was applied to Oakington, Polhill and Eastry, a contrasting pattern was evident. At Oakington, the richly decorated males displayed similarity to an approximate even number of males and females within the cemetery population. Furthermore, there were several richly furnished female graves at Oakington, Polhill and Eastry (also those interred in ring ditches) which showed closer affinity to other females within their corresponding assemblages. This is something that would not be as expected in a society which is thought of being fully patrilocal and based on patrilineal descent. As has been discussed, however, while early Anglo-Saxon societies were said to be male-centric, in practice there does appear to have been a much more fluid approach to the application of later period laws and rights than suggested based on historical documentation. Females were able to own and control land, achieve high status roles in communities and were enabled to certain protections under law (Lancaster 1958a) and Stoodley (2000) found

that female graves were just as likely as males to be elaborately furnished as social age and the lifecycle contribute to grave good inclusions. As such, it would be expected to see examples of this fluidity in place in early Anglo-Saxon societies from this time period, which is what was best observed at Oakington, Polhill and Eastry. The male-centric focus was not found to be strictly applied as it has been interpreted, rather, individual communities reflect much more nuanced and complex social structures at work on various levels. It was also possible to see how age contributed to the female pattern observed within Oakington, Polhill and Eastry as a larger proportion of the females who were buried with elaborate grave goods or in burial structures like ring ditches were classed as young adults, potentially representing teenagers in several cases. In these instances, as it was mostly young females who were buried in such a way, it is possible that they had yet to marry into another family grouping and as such were treated as part of their father's kin within their homestead. Alternatively, as was seen with Polhill and Eastry and the ring ditch analyses, the majority of females buried in ring ditches were found to be most similar to other young females in the wider community rather than males. This could indicate that these females had married into these settlements from elsewhere and their importance was being woven into their new community through use of ring ditches.

This concept of female diversity within an assemblage was further highlighted at Oakington where Grave 109, a triple burial, showed the close and intimate interment of two adult females with a sub adult. The two females spatially and positionally seemed to suggest a close bond but were shown to have low levels of biological similarity in their tooth data. In such cases, the connection between these adults was less likely about biology, as these individuals were less likely to be genetically related, and more about social customs. As their tooth dimensions were very different from one another, it was not likely that these two females

came from the same lineage, but rather were living together at the same settlement site. This could be used to support the notion of wives marrying into patrilineal societies; neither female showed very strong affinity to groups of homogenous males yet were treated similarly in death. Social bonds between these females, such as sisters-in-law or friends, may help to explain their shared interment.

Overall, looking at broader patterns in the data related to residence and patrilineality on population, community and individual levels has shown that teeth can offer valuable insight into discussion of such constructs. By adding a new medium through which to investigate connections between males and females within and between these four early Anglo-Saxon sites, it was possible to find evidence to support the notion of patrilineality in some respects but advocate for a more fluid approach to its understanding within each settlement site. The truth for these discovered patterns is likely a combination of both factors: fluidity within the concept of male-centric focus in early Anglo-Saxon England, and the possibility of life stages affecting the treatment and burial location of individuals within a given population.

6.7 Kinship and Identity: Representation after Death

The investigation of dental metrics from various interments at Hatherdene, Oakington, Polhill and Eastry have provided great insight into the decisions being made regarding burial during the early Anglo-Saxon period, particularly how it relates to identity and kinship. Identity, by definition, is connected to who a person was during life. What is difficult, archaeologically, is interpreting what this could have been based solely on evidence collected from the dead. Within the early Anglo-Saxon period, contextual items like grave goods or burial structures

have helped to comment on areas like family groupings (Lucy 2000; Stoodley 2002), status and occupation (Härke 2000), arguably all aspects that can relate to a person's identity. What has been lacking thus far for this particular time period in South-East England, however, is input from additional robust biological evidence obtained from the skeletal remains to help support or refute these interpretations. The inclusion of dental metric data from these four sites has helped to bridge some of the gap between social theory and biodata support relating to identity.

A main contributor to a person's identity is their relationships to others within the group, and whether this be a biological or social relationship warrants further analysis and discussion. The burials investigated in this chapter highlight a variety of potential relationships between individuals within each cemetery, based on a mix of biological and social connectivity. The burials from these four sites have shown that, within a grave, individuals were just as likely to be buried with someone biologically similar to them as they were to be buried with someone who was less similar. This is not unexpected as many social relationships are not based on a biological foundation. Marriage, for example, would not involve two individuals who were closely related in a genetic sense due to cultural taboos, meaning that the levels of biological similarity in tooth size between two spouses would appear less similar. However, there are other variants of social connections that could be hypothesised from the above discussion. The example of the triple burial at Oakington showcasing the low levels of similarity between two adult females is a prime example of this; the females were close in age and buried in the same interment with body parts overlapping, arguably evidence of a shared connection. However, the tooth data revealed low levels of similarity between the two adult females in this grave, meaning this connection was not based on biology. Due to the shared experience of females during this period, particularly regarding mobility, marriage and childbirth, it is not

unlikely to assume the connection between these two females was based on these shared experiences which, as in modern day, is part of the basis for forming friendships. For argument sake, Stoodley (2002) suggested multiple interments were based on those who died in quick succession of each other, as opposed to any underlying social or biological connection. However, Stoodley (2002) has also put forth that the digging of a larger multiple interment would expend an equitable amount of effort as digging space for two single interments. While a possibility to inter individuals with those that had no social or biological connection, there does appear to be evidence suggesting these connections were important to these groups.

The use of teeth for such interpretations was never meant to exclude the need for additional, more statistically robust analyses of biodata such as DNA testing. Rather, the benefit of using teeth in such a way allows the opportunity to focus interpretations regarding connections between individuals in lieu of or as a precursor to targeted DNA testing. However, using teeth for these investigations has advantages over DNA testing. This method is non-destructive, low cost and can be done by any researcher, anywhere. As such, this method can be widely applied in situations where more expensive, destructive approaches cannot (i.e. museum collections). Furthermore, dental analysis of biological similarity has shown strength and robusticity from preliminary mtDNA work which has shown similar findings. The validation of work with mtDNA and individuals from Oakington and Eastry further helps to support the concepts discussed in this chapter regarding the utility of teeth for helping to identify connections between individuals and interpret potential relationships between these people based on shared levels of dental similarity.

Observations regarding family identity could also be made using the data derived from the four individuals. For instance, later period documentary sources have shown that brothers

and sisters were treated equitably under law in terms of inheritance (i.e. Yorke 2002), though males appeared preferred in a legal sense (Lancaster 1958b), and this was echoed in examples above. Notably Grave 299 from Hatherdene, which had a male and female individual interred together, both of similar ages and displaying high levels of similarity between their tooth dimensions. This was taken to assume a potential brother-sister relationship. Neither of the individuals was interred with any grave furnishings or goods and both were found in the same overall position. This indicates that an approach to burying the male and female was consistent, there did not appear any preferential or status driven treatment related to one or the other here, rather they were presented equitably. Additionally, the lavishly decorated female burials at Oakington, Polhill and Eastry further demonstrate that females were being represented as equally, or more elaborately, than males during this era. Across these four cemetery assemblages there were examples each sex displaying close biological connections to the other, highlighting that male and female identity was treated as equally important.

Grave objects, furnishings and structures have also been cited as being linked to identity and family groupings (Lucy 2000; Sayer 2009). While there were some examples of similarity amongst relative wealth of burials and shared connections, particularly with overlapping connections involving individuals interred in ring ditches, there were not many examples at all of grave goods being definitively linked to biologically connected individuals. The exceptions to this were the spear burials at Oakington and Hatherdene, the cruciform brooch burials at Hatherdene and buckle burials at Polhill. Admittedly, this project did not look in-depth at specific classes or styles of objects which may show greater potential if this was to be undertaken. What can be concluded, however, was that individuals who were ornately decorated were found to share similarity with those that were also decorated in such a way, as well as finding connections to those that were not recovered with any types of goods. The

grave goods that highlighted potential connections to biological relatives demonstrate the multilevel approach to attempting to understand identity. It is not a straightforward association between identity and grave goods within these cemeteries as they do not appear consistent among suggested family groupings, nor across communities.

What appeared to be less important in the organisation of the cemeteries under investigation was the actual location of the graves themselves within the wider cemetery. Individuals who were identified first on biodata for their close affinity were not found to always be buried in close proximity, rather, there appeared more often a spread of similar individuals throughout a cemetery. Furthermore, those that were identified as being outliers, whether it was based on preliminary mtDNA analysis or through tooth metrics, were found to be interred across each cemetery, with or without grave goods and treated as the majority of other individuals within the cemetery. These results dictate that, in terms of identity or kin, burial location within the overall cemetery does not necessarily relate to who a person was when alive. It appears as though, once within a community, the connections among individuals while alive allowed for various burial treatments and socially depicted narratives reflecting identity in death (Sayer 2020).

6.8 Conclusion

Based on these results, evidence from dental biodata has been found to support the notion of patrilocal and patrilineal descent, although fluidity in its application was evident within early Anglo-Saxon populations in England. Tooth analyses also demonstrated their potential to add to discussions regarding social and biological connections between those interred

within these cemeteries. Similar to what has been done with other forms of biodata (i.e. isotopes, DNA and nonmetric skeletal traits), the inclusion of biological data derived from teeth has helped to refine and reinterpret relationships between individuals within these early Anglo-Saxon cemeteries. Burial location, spatial proximity and contextual artefacts all contribute to the interpretation of social relationships within past populations, but do not form a complete picture. The addition of biological data via tooth metric analyses has helped to demonstrate that some assumptions have shown to be too simplistic to completely understand the nature of relationships between individuals as well as the individual identities of those interred. Additionally, the inclusion of biological data to such discussions allows for new possibilities to be explored in regard to relationships between people in skeletal assemblages. As Johnson (2019) has advocated for, the best approaches when investigating past population are ones that are based on holistic evidence where consideration is paid to various types of evidence equally as opposed to focusing on one over another. In this section spatial data, contextual objects, historical documentation, demographic aspects and biological data have all be used in combination to comment on potential connections between individuals within each of the four cemetery sites.

While not explored in its entirety here, the approaches used above are flexible enough to be used to focus on a population or community level, or more narrowly on a particular grave or specific individual. They, arguably, could be employed to investigate any single individual within the cemetery. In doing so, spatial patterning or commonalities between and within communities, grave types or grave goods were assessed which contributed to discussions regarding identity by such authors as Sayer (2009), Thäte (2009) and Stoodley (2002) who discuss the appearance of spatial patterning, burial structures or grave goods as being linked to identity and kinship. The benefit in utilising multiple teeth and various comparative groups

was also demonstrated within this approach. Patterns observed when looking across a combined cemetery sample, representative of a population level, were often not the same as what was observed on a community or individual level. Furthermore, not every tooth presented the same connections as one another, rather, some may have been missing for a particular individual or presenting a different level of similarity with another. However, by using as many teeth as possible from the criteria outlined in Chapter 5.6, it was possible to better observe repeated trends as opposed to one off occurrences. The more teeth that were found to follow the trend, whatever it may have been, the more reliability could be placed behind the results regarding levels of biological similarity.

One of the most significant results discussed in this chapter was in relation to validation of methodological approach and interpretive findings. Preliminary work on mitochondrial DNA from a selection of individuals from Oakington and Eastry was able to support the initial conclusions drawn from dental metric data in the case of Grave 88 (Oakington) and with individuals E45 and E46 (Eastry). The two male individuals interred within Oakington's Grave 88 did not display a convincing level of biological similarity in their teeth to suggest a close genetic relationship. There were some teeth that indicated it was possible there shared a more distant genetic connection, but not enough to suggest immediate blood relatives. The mtDNA supported this assertion in that they appeared not to be similar, however, as mtDNA relates to maternal inheritance as opposed to paternal inheritance, only half the genetic picture is represented here. Therefore, it could still be possible that these two males interred together shared a genetic connection linked through their fathers which would explain the mix of teeth displaying similar and dissimilar distance values. Another strong demonstration of validity of method came in the comparison of two individuals (O1747 and O1370) who were not buried in immediate proximity to one another, but the mtDNA suggested a stronger

connection. When the hierarchical cluster diagrams were reviewed, it was apparent that these two individuals did in fact share a high degree of biological similarity between their tooth measurements. Additionally, at Eastry the mtDNA result suggested a third-degree relationship between E45 and E46, akin to cousins, and this was found to be supported by the moderate level of affinity observed within the corresponding tooth data for these two females. This is solid evidence to support the concept of using teeth as a way to suggest presumptive connections between individuals within larger skeletal assemblages.

The benefit of this type of research relates back to the aims of this project. First, it has been shown that it is possible to use teeth in order to identify various levels of biological similarity among individuals in archaeological skeletal assemblages. Secondly, this chapter has also demonstrated the success in meeting the second and third aims of this study. The results from the identification of similarity can be used to add to interpretations regarding connections between individuals in archaeological assemblages and conclusions could be drawn on individual and group identity, and on broader social aspects like mobility and kinship. By demonstrating the ability to achieve all three aims, the value of collecting metric data from skeletal remains in archaeological populations has been shown to be useful and valuable for broader social level discussions.

7. Conclusion

7.1 Summary of Results

The main aim of this project was to first see if the statistical analysis of metric data obtained from human dentition could be used to identify biological similarity among individuals in early Anglo-Saxon skeletal assemblages. In order to achieve the first aim, four contemporaneous cemeteries from two counties in South-East England, Cambridgeshire and Kent, were chosen for investigation. Choices of cemetery were based on availability, location of sites to one another, dating and size. The four cemeteries consisted of: Hatherdene and Oakington from Cambridgeshire, which were geographically and temporally close to one another, and Polhill and Eastry from Kent, again sharing similarities in occupation period and location. Furthermore, the inclusion of remains from Polhill and Eastry from Kent allowed for testing of this method on partial and fragmentary samples as well as providing additional case studies for the investigation of grave goods and burial structures.

A review of literature on the topics of dental anthropology and tooth formation in Chapter 3 revealed that the expression of final tooth size is dependent on biological sex, environment, genetic and random mutations in any given individual (Alt and Vach 1995; Biggerstaff 1975; Boraas *et al.* 1988; Dempsey *et al.* 1995; Hughes *et al.* 2000; Townsend 1980). Furthermore, nonmetric traits that are usually discussed in relation to genetic inheritance can be classed as part of a dental phenotype, which can then be captured when metric data is recorded from tooth crowns (Brook *et al.* 2014; Moreno Uribe and Miller 2015). As such, the mesiodistal and buccolingual tooth dimensions were recorded from the permanent dentition of males and females aged from 15 +/- 36 months in each of the four cemeteries. Teeth that were too worn or displaying severe pathological conditions (i.e. carious abscesses) were omitted from study.

Through exploratory approaches in statistical analysis, it was shown that while shared local environment and biological sex do have some influence on the size of these tooth dimensions, neither of these factors accounted for the full range in tooth size variation observed across the four sites. As discussed in Chapters 3 and 5, the remaining variation in tooth size was, therefore, attributable to the influence of genetically inherited traits (Hughes and Townsend 2013). Limiting criteria based on normality of data, influence of biological sex and environment and number of available teeth were applied to the dataset to establish a focused list of teeth that could be used to compare between individuals, depending on the level of questions being asked. The tooth data then could be hierarchically sorted using cluster analysis to group together individuals within and across all four cemeteries that shared greater amounts of similarity among tooth sizes. It was these clusters which were used, not to identify distinct family units as a cluster was not interpreted as a family unit, but rather to look for repeats in patterns between individuals who kept appearing in the same clusters across multiple teeth. The clusters were not interpreted as family units because there was no certainty the same individuals would appear in the same clusters each time. This further highlights the complex nature of tooth formation as separate teeth have been cited as being under different genetic control for their formation (Salazar-Cuidad and Jernvall 2002; Huang *et al.* 2012; Townsend *et al.* 2012). The output produced via hierarchical cluster analysis in this study corroborates this notion as two individuals who appeared similar in one tooth's dimensions did not always appear similar in another. If each tooth was under the same genetic control, it would be expected that the same individuals would consistently be clustered together for each tooth, but this was not observed. This finding also highlighted the importance of using as many teeth as possible for an approach like this as the results obtained for one tooth may not show the same connections as another. Therefore, by looking for

similarity across multiple teeth a better idea of which individuals are consistently similar would provide more reliability in results. When individuals were found to share high levels of similarity across multiple teeth, it provided greater support for interpretations regarding the likelihood of close genetic connections between individuals. It was at this stage that contextual information like demographic data, grave location, interment type and grave goods were consulted in order to see if refinements could be made to who these individuals were as a person, and who they may have been to one another. Validation for this approach was discussed in Chapter 6.5 through the use of results from a separate project (Schiffels and Gretzinger, *nd.)* looking at mtDNA analyses from certain individuals within Eastry and Oakington. In these cases, dental analyses were corroborated by the findings with mtDNA demonstrating the value of using teeth for locating biological connections between individuals within archaeological populations.

7.1.1 Conclusions from Population Level Results

When all four cemeteries were combined into one large group, interpretations from the hierarchical cluster analysis showcased interesting patterns related to early Anglo-Saxon populations. Overall, when all four sites were combined and males and females were not separated, the data showed lower levels of similarity present within the whole group. Many clusters of individuals were generated and less of the population were being filtered through the separations together. In contrast the separate results from the four cemetery sites showed fewer clusters being formed with more individuals moving through separations together, see Chapters 5.7 and 6.1 for full results. These findings show that within each cemetery site there were greater amounts of similarity in tooth size compared to when all

sites were combined into one population. This means that each cemetery likely represents the presence of at least one dominant lineage and they are different enough from one another to cause a change in level of similarity expressed when viewed across a whole population. This reiterates what has been discussed by Harke (2011) and Weale et al. (2002) who looked at the possibility of males coming over from the continent during migration movements but also corresponds with the continuous migration theories where it has been postulated that smaller, elite groups had moved over and their culture was adopted by locals.

In order to comment on residence and mobility patterns further, and to see if the basis for these distinct lineages could be identified, differences in the clustering of males and females were investigated separately within each site as well as across a combined group of all four sites. When each cemetery was looked at individually it was found that, overall, male teeth appeared to be more similar than female teeth. Males displayed fewer, larger sized clusters while females displayed more, smaller sized clusters. In terms of similarity, these results translate to males sharing more biological similarity, and therefore likely stronger biological connections within each site than the females present. The results from Hatherdene did present an exception to this as females appeared in fewer cluster than males. It would be erroneous to assume that all females would appear less similar to males in regard to tooth size as sisters or mothers and daughters would be expected to share higher levels of similarity (Townsend and Brown 1978a; 1978b). Therefore, it could be that there were more biologically related females buried at Hatherdene than at the other three cemetery sites. Interestingly, when males and females were investigated separately in a combined cemetery group, the pattern was reversed. When looked at across all four sites, it was females who appeared to be grouped in fewer and larger clusters compared to males. Although a contradiction in pattern, this finding actually further supports the idea of male dominant lineages in each site.

As each cemetery was found to be representative of a distinct lineage, the fact that males become less similar when combined demonstrates that these lineages are centred on the males in each cemetery rather than females. As male data became less similar when all four cemeteries were combined, it shows that male connections are driving the similarity within each cemetery. This finding also supports the notion of female mobility for marriage. If there were smaller pools of females marrying into each community, the differences between females within each site would be more apparent than when looked at across a broader population. This finding is supportive of prior isotopic evidence that suggested female movement for marriage would have occurred during this time period (Hughes et al. 2018).

Sayer (2014), Sayer and Dickinson (2013) and Montgomery *et al.* (2005) discuss the mobility of females during the early Anglo-Saxon period. As communities were based on male lineages, often times females would, through marriage, move into these settlements. Although there are discussions on additional mobility patterns of females for reasons such as childbirth (Sayer 2014), as these women became integral members of these patrilineal communities, when they died, they would be buried in the local cemetery rather than being returned to their homestead for interment. The results from the analysis of tooth data here confirms the notion that females were moving into patrilineal communities, likely after or for marriage, and becoming a part of these communities. These results are also in line with later historical evidence from the Anglo-Saxon era that discussed the male based residence patterns during this time period (Lancaster 1958a; 1958b). However, as will be shown in the next section, fluidity of these patterns was apparent on a community level.

7.1.2 Conclusions from Community Level Results

After looking across all four groups on a population level, the same set of hierarchical cluster outputs could be used to focus more internally within each individual cemetery. Chapter 2 highlighted the various ways researchers have investigated kinship and identity on a community level through the study of spatial organisation in cemeteries (Sayer 2020), the grave goods found in burials (Gowland 2007; Sayer 2009), burial structures (Stoodley 2002, Thäte 2009) and multiple burials (Stoodley 2002).

Even though the analyses presented in Chapters 6.2.1 (ring ditches), 6.2.3 (grave goods), 6.2.4 (weapon burials), 6.2.5 (brooch burials) and 6.2.6 (buckle burials) were done separately, it is important to conclude interpretations through a collective discussion. The community level results demonstrated that decisions made on a community level regarding the burial of the dead varied across each separate site. One of the main results observed related to the use of burial structures and the individuals who were interred within them. Burial structures have been thought to be a visual marker for important individuals in early Anglo-Saxon kin groups (Sayer 2009; 2020; Thäte 2009). Ring ditches were found at Hatherdene, Polhill and Eastry, with the two cemeteries from Kent having higher numbers of such burials compared to Hatherdene. Interesting patterns emerged between these three sites regarding the similarity of individuals interred within ring ditches. At Hatherdene, two individuals were found buried in these structures, both were males aged 26-44 years old at time of death and each buried with an array of grave goods, including knives, spears and buckles. These two males were found to share higher levels of similarity in regard to tooth size, suggesting a likely biological connection between them. Individuals in the wider cemetery who further shared high similarity in tooth size were also identified. Seven additional individuals were found to share

high levels of similarity in tooth size with these two males. Of the seven additional connections, six were also males and four were buried with buckles and spears. When the presence of grave goods was investigated, see Chapter 6.2.4, it was found that individuals at Hatherdene who were buried with spears and shields (although at a slightly lesser extent than spears alone) did appear to share in higher levels of similarity in tooth size. This pattern was also observed strongly at Oakington where the males interred with spears showed high levels of biological similarity in their tooth data. These results align well with Härke (1990) who came to the conclusion that the phenomenon of warrior burials in early Anglo-Saxon cemeteries were less about being warriors, and more about showing connections to family units. Therefore, these findings, in addition to the population level results, demonstrate that at Hatherdene, and in an extent at Oakington, there was a clear centralised group of elite males who shared biological connections amongst one another which were further reflected by interment in burial structure and in the inclusion of certain grave goods.

Interestingly, the ring ditches at Eastry and Polhill provided a different pattern compared to Hatherdene. From the five ring ditches investigated from Eastry and nine from Polhill, there were likely biological connections found between those interred within ring ditches and the wider community, see Chapter 6.2.1 for full results. However, unlike at Hatherdene, when looking at the wider cemetery, most of the connections made that related to high levels of similarity in tooth size were between females, more specifically, young adult females. At Eastry, the additional layer of grave good analysis revealed no strong correlations between grave good and biological connection, but there was strong evidence of this at Polhill. Buckles featured commonly in the grave goods for those interred within ring ditches at Polhill and when buckles were investigated across the wider cemetery separately (Chapter 6.2.6) it was found that buckles did correlate with higher levels of biological similarity. Therefore, at Polhill,

while not all individuals interred in ring ditches had buckles, those that had buckles in the wider cemetery were closely related to those interred in ring ditches. It is clear from the above examples that burial structures and grave goods were being used to signify connections between individuals within each community, but not in a consistent way across all communities.

Cruciform brooches revealed two different patterns between Hatherdene and Oakington. At Oakington cemetery, there were seven females buried with cruciform brooches, but the analysis of connection level between these women revealed that over half of the connections were at the low level of similarity, suggesting biological connection did not correlate to the presence of such a brooch. In contrast, three individuals at Hatherdene were buried with cruciform brooches and over half of the observed connections were at high levels of similarity, strongly suggesting biological connections between these females correlated to the appearance of such a brooch. As Lucy (2000) had argued for, the dichotomy between having or not having a brooch is too simplistic to comment on potential relationships between people. Rather, these findings highlight again the fluid nature in grave expression practised by early Anglo-Saxons (Sayer 2020). Some communities, like Hatherdene, were choosing to highlight biological relationships between some females using brooches, while the same type of brooch was not being used in the same way at Oakington.

While much variation in grave good use was observed across the four sites, it was clear some decisions were linked to community kin networks. In particular, the connections observed in the spear burials at Oakington and Hatherdene and the cruciform brooches at Hatherdene showed that there were specific decisions being made within communities which related to distinct kin groups that would result in certain individuals being interred with particular

objects compared to others. Furthermore, these findings can be related back to skeletal demography and wider interpretations of dental metric data. At Oakington, there were more decorated females found than at Hatherdene, yet it was the male spear burials who showed greater biological similarity in tooth data. At Hatherdene, there were more decorated male individuals than at Oakington, yet there were females with cruciform showing stronger links to biological relationships. Within all these stronger connections, the age of individuals appeared similar. Males with spears tended to be those in the middle adult category (26-44 years) and females with cruciform brooches were either in the middle adult or mature (>45 years) age category. These findings correlate well the age related associations with certain grave goods presented by Stoodley (1999). This could indicate that within the strongly connected male community of Hatherdene, there also appeared a central line of elite females. Similarly, at Oakington where females showed evidence of being generational heads through use of barrows (Sayer 2020, 121-122), males were also being used to convey meanings about connections to the wider community through the inclusion of spears in burial. It would be interesting to explore these ideas in greater depth in future to draw out the details, such as the link to barrows at Oakington to support a full discussion on the idea of lineages and elite groups of males and females.

It is also important to discuss the additional objects investigated in this project. They are important to note as the remaining comparisons of grave goods from Chapters 6.2.4 - 6.2.6 showed that knives, buckles (apart from at Polhill), small long brooches, saucer or disc brooches and annular or penannular brooches revealed no strong correlations to likely biological relationships between those interred with these objects. In these instances, there were fewer connections made between individuals interred with these objects at high and moderate similarity levels compared to low similarity level connections. Therefore, overall,

these results align with Huggett (1996), Gowland (2007) and Stoodley (1999; 2000), regarding the idea that certain objects may be better linked to demography or lifecycle achievements, of which the visual expression of these attributes in death varies between communities.

While the majority of the results above were based on identifying individuals who shared biological similarity to others in a community, it was also found during analysis that there were some who did not share similarity in tooth size and were statistically found to be outliers in the dataset. These outlying individuals were first located in each cemetery in regard to their interment location to comment on how, if at all, the fact that someone was unlikely to share biological connections to the rest of the group would manifest in burial space. Across all four cemeteries, individuals who were found to be very different based on tooth metrics did not appear to be treated any differently to the rest of the group. These individuals were buried in dense and sparse parts of the cemetery, found with and without grave goods, and interred in multiple burials as well as single interments. While it is easy to assume that those that were most dissimilar would be different, akin to the idea of kinless men discussed in the Anglo-Saxon poem The Wanderer (Chambers *et al.* 1933), the results here show that a lack of biological connection to the rest of the community does not render a person kinless. Rather, the decisions made by the living community members regarding burial were afforded to all interred in these cemetery spaces, they were not solely reserved for those that were biologically related to core lineages. Rather, a range of social and biological kinship relationships could be represented simultaneously within the community.

Overall, the results from community level interpretations at Hatherdene, Oakington, Polhill and Eastry reveal diversity in the expression of identity and kin-based connections among the individuals interred within each. It has been shown that burial structures and grave goods do

in fact relate to biological connections between individuals in some communities, but not every artefact type, nor consistently across every community. Therefore, as Sayer (2020) discusses, community level narratives are meant to be shared and understood by members in the group. These findings also relate back to the idea of a phased migration, where new ideas related to identity in death were not being reflected consistently across places. The acculturation of funerary customs was evident in each of the four cemeteries under study here, but these expressions were not the same. How each community decides to evoke social meaning in death is dependent on a multitude of factors which means that simplistic views on burial structures, grave goods and biodata have no place in theoretical discussion on the concepts of identity and kinship in past populations. Rather, it is important to address multifactorial evidence to help build an idea of how each individual community-based decisions relating to funerary and burial rites for its own members.

7.1.3 Conclusions from Individual Level Results

Narrowing the focus from the community level to the individual grave level showcased the flexibility of this method further by being able to target specific graves or specific individuals for further analysis. In Chapter 6.3 it was shown how specific graves and individuals could be investigated further depending on the question of interest. Case studies of unique or particularly wealthy graves were used from Hatherdene and Oakington to show the potential for this type of approach. In such cases, the identity of individuals treated in such ways would be of interest to know, and dental biodata can help to provide some answers relating to how these people may fit into the wider community. The examples of Grave 80 and Grave 57 from Oakington provided two good examples from which to explore biological connections for

targeted individuals in this community. Grave 80 contained a young adult female buried with an articulated cow as well as several other grave goods. She was found to be most similar to two other adult females in the wider community, each of whom were buried with a variety of grave goods. The suggested biological connections between three highly decorated females at Oakington likely reflects their importance within the community, perhaps through marriage as they were not found to be as biologically close to males in the cemetery. In comparison, the case of Grave 57 presented an adult female found with foetal remains, indicative of pregnancy at time of death (Sayer and Dickinson 2013). In the wider cemetery she was found to be most similar to two older adult males and another female (who had been buried in a triple burial). This example can be used to reiterate what has been discussed in relation to females returning home to give birth (Sayer 2014). The high level of similarity between this woman and two older males could be indicative of the fact that she returned home to her father's community for the impending birth of her child. As such, she would be expected to have teeth reflecting more similarity in size to males in this community rather than females, which is what was found in that particular case.

When wealthy burials were investigated within Hatherdene and Oakington, results differed again. At Hatherdene, similar to what was found in relation to the ring ditches, the most decorated individual within the cemetery was a male and those he was found to share greatest amount of similarity in tooth data with were also male individuals. At Oakington, the wealthiest burials reflected a mix of males and females, who were found again to be linked to a relatively equal mix of males and females. These findings further support discoveries made in the community level interpretations regarding Hatherdene and the presence of a core group of males, as well as the fluid approach to identity and gender that varied between all sites. While later Anglo-Saxon laws and certain burial aspects have been shown to be

positively biased towards males (Lancaster 1958a), there are also examples of practices within Anglo-Saxon populations that counter these notions. Murray (1983) suggested, for example, that burial practices related to kin were not static during the whole Anglo-Saxon era. Rather, it is more likely that burial customs adapted to cultural changes in response to how the living viewed the dead (Sayer 2020). Johnson (2019) and Johnson and Paul (2016) advocated for a holistic bioarchaeological approach that incorporates multiple streams of evidence in order to support interpretations of social constructs in past populations. Applying this methodology to understanding kinship patterns at Hatherdene, Oakington, Polhill and Eastry has meant reflecting on current theories related to social mobility and residence while incorporating new data derived from dental biological similarity.

Finally, on an individual grave level, multiple burials were investigated to see if there were biological connections present between individuals interred within the same burial space. There have been multiple examples in archaeology where shared burial space was hypothesised to infer a familial or kin-based connection between interred individuals (i.e. Alt and Vach 1995; Alt *et al.* 1997; Lane and Sublett 1972). Alt *et al.* (1997) highlighted an approach to identifying connections between individuals within the same grave by investigating nonmetric traits recorded from the dentition of a triple burial in the Czech Republic. The nonmetric data revealed that there were many shared traits between these three individuals, and therefore it was determined that those interred together were likely representative of a close family unit due to similarity in dental biodata. For Anglo-Saxon populations, Stoodley (2002) has suggested that multiple burials may be used to discuss group or family membership due to the proximity of individuals within a shared burial space. Despite these suggestions, it is important to recall that definitions of family vary greatly within

populations (Pilloud and Larsen 2011) and that in order to be identified as a member of a particular group in death, more information is needed rather than just burial location alone. Contextual, biological and historical data can all be used in conjunction with one another in order to reach a more holistic interpretation.

Multiple burials were found in all four cemetery sites, though variations in their composition appeared. For instance, Hatherdene had several stacked burials where individuals were interred in multiple layers and Oakington contained a single layered triple burial. Results from all four sites indicated that interment in shared burial space was not solely dependent on biological relationships. There were some who were interred in the same grave that did have tooth evidence to suggest a genetic connection, yet there were also cases where the individuals within the same grave shared very low levels of similarity in regard to tooth size. In such cases, it is important to discuss what this actually shows and what it does not show, echoes of what is and is not kin from Sahlins (2013). The graves that contain individuals who are unlikely to be biologically related, could still be representations of close social relationships. The biodata only suggests that whatever this relationship was, it was not based on blood relations. This is not to say these individuals could not have been 'kin', as has been discussed earlier, there are various interpretations and manifestations of kin across modern and archaeological human populations. Practical kin, adopted family members and ascribed group membership (i.e. through friendship), are but a few examples that have been discussed within the literature (Pilloud and Larsen 2011) and were likely present in early Anglo-Saxon society.

7.2 Limitations of Study

While every attempt was made to be as robust as possible throughout the design, methodological approach, analysis and interpretation sections of this project, there were some limitations that appeared in some areas.

While nonmetric data was attempted to be collected, it became apparent that there were issues with its use for this project. While traits of the ASU (Turner II et al. 1990) were present within each of the four cemetery samples, the numbers were low. As such, it would have been too difficult to generate meaningful statistical analyses when comparing small numbers of individuals. As was shown in Chapter 3, the genes required for the presence of a certain nonmetric trait may be present in an individual, but due to various factors (i.e. extrinsic, intrinsic or random) the trait may not be expressed phenotypically. This then presents problems for researchers trying to locate individuals who may share a biological connection based on the appearance of nonmetric traits alone (i.e. Stojanowski and Hubbard 2017). This limitation of this particular type of data can be avoided by using dental metrics. Every intact and pathologically free tooth that was present in these individuals could have their metrics recorded. This increases the size of the dataset, allows for more comparisons between individuals and generates more robust statistical results. However, the connection between nonmetric traits and metrics should be explored further in future, see Chapter 7.3 for discussion on geometric morphometric analyses.

Preservation of teeth and pathological condition of teeth provided a minor limitation in this study. Most adult individuals within the sample did appear to retain the majority of their dentition and, in most cases, these were better preserved than the skeletal remains, particularly for Polhill and Eastry. However, within each sample there were individuals whose

teeth were not able to be used for a variety of reasons. Pathological lesions such as dental caries, abscesses and large calculus deposits prevented the recording of metric and nonmetric data. In such instances where doubt was present over the level of 'intactness' of a tooth, they were not included for further analysis. Similarly, while the majority of adults had teeth present, not all were recovered. Post-mortem tooth loss was common to observe within the sample which led to missing teeth during data collection. In these cases, it is likely the teeth were lost during excavation and exhumation or over the years in curation. The culminating effect of these variables was limited in Hatherdene and Oakington but became more problematic in Polhill and Eastry due to their already smaller sample sizes. The methodological selection of teeth for hierarchical cluster analysis meant the omission of certain teeth from this part of the statistical analysis, therefore it was not guaranteed that within the sample for each cemetery, each individual present would have all the necessary teeth the HCA was based upon. In cases at Eastry and Polhill this resulted in fewer comparisons across multiple teeth for the individuals under investigation, which meant less certainty in patterns discovered from these observations. Despite this, interpretations were still able to be made from these sites which helped strengthen arguments put forward in the discussion sections of this study. Conversely, this limitation has also highlighted a key benefit of this project's methodological approach. Where some studies have focused on a sole tooth or tooth class, this project allowed for the inclusion of multiple teeth from all tooth classes. This meant that even if an individual was missing a particular tooth or a particular tooth was damaged, it was likely that another tooth could be used, and the individual could remain in the sample. This also helped to counter act issues with sample sizes as it meant more individuals could be retained and included for cluster analysis instead of relying on a single tooth which may have resulted in more omissions. This methodological consideration,

therefore, is important to retain for future work in this area, especially within skeletal assemblages that are small or in poorer states of preservation.

Additional demographic data was an essential aspect to gaining the most robust interpretations from these cemeteries. As sexual dimorphism was found to be statistically significant in some teeth within each cemetery, it was imperative that the biological sex of individuals be accurately estimated in order to understand if the variation in tooth size was attributable to sex or not. Poor preservation of remains meant that not all adult individuals could have their sex determined reliably. In cases where an individual was not classed as either male or female, the individuals could not be used in this project. This was one of the reasons why sub-adult individuals were omitted from use in this current project. A limitation drawn from this is that in many of the cases, again particularly for Polhill and Eastry, the poor skeletal preservation resulted in less certainty around the determinations of sex presented in corresponding reports. Morphological methods to estimate sex from the pelvis report 86-95% accuracy (i.e. Klales *et al.* 2012; Phenice 1969), morphological methods based on cranial morphology estimate sex with reported accuracies of 80-90% and post-cranial sex estimation methods based on metric data can vary dramatically depending on skeletal element available, but have potential to surpass 90% accuracy, depending on the population (Spradley and Jantz 2011). These methods, however, require these areas of the skeleton to be intact and well preserved to use features related to their reported accuracy rates. While this was presented in the skeletal reports and via discussions with anthropologists who conducted the full skeletal analyses, in many cases the resultant sex determinations were left as probable or potential rather than a definitive estimate. Where possible during this project, confirmations of sex estimation were conducted at time of data collection, but due to time constraints, full anthropological analyses were not carried out to always confirm what had been reported

elsewhere. As such, any errors made in sex estimation at time of published reporting for Oakington, Polhill and Eastry, and those available in internal reports for Oakington and Hatherdene may have transferred into the dataset here.

Not including sub-adult remains was also a limiting factor in some respect. While research has suggested there are correlations between deciduous and permanent dentition sizes (i.e. Hughes *et al.* 2000; Kitagawa 2000; Lease and Sciulli 2005; Moorrees *et al.* 1957; Townsend 1980), it was not as well published as correlations between permanent teeth only. As such, they were not chosen to include within this project. Overall this did not detract from the ability to draw conclusions from the data set, but there were quite a few examples of multiple interments containing adults and sub-adults which would have been interesting to explore had deciduous teeth been included. This, however, will be a key area to explore in future research.

7.3 Additional Findings and Future Research

While not within the remit of this project's aims, there were interesting findings relating to dental development and tooth biology overall. The first relates to tooth antimeres, previously it has been suggested that antimeres are not mirror reflections of one another as they are under separate genetic control (İşcan and Kedici 2003). As such, a tooth and its antimere are not presumed to be interchangeable, however, this project did not support those assertions. Here, antimeres overall were found to not differ statistically in size between left and rights of the same tooth. A recent paper by Evans *et al.* (2016) suggested a cascade theory is responsible for how teeth form, and perhaps this cascade is mirrored across left and right

sides of a dental arcade so that the influences of biological sex, genetics and environment are processed in a similar way leading to statistically similar tooth sizes within antimeres. This similarity between antimeres could allow for increasing the sample size where possible to fill in gaps to maximise the number of individuals included within a sample. This will be particularly useful for skeletal assemblages with smaller numbers of interred individuals or those with poor preservation in order to obtain the largest comparative sample possible. The differences in antimere sizes from additional populations apart from Anglo-Saxons would be interesting to research as it may help to refine the reasons for such a trend, perhaps the differences in size were not as pronounced in other geographical locations or in different time periods.

Mesiodistal and buccolingual measurements did not appear to be affected the exact same way for each tooth, rather some factors such as biological sex and cemetery environment appeared to affect one dimension over another, both or neither. Anecdotally, it was observed in this project that the majority of cases where a tooth was found to be statistically different in size between males and females was because of the buccolingual dimension. This dimension, which runs from tongue surface to cheek/lip surface, is not constrained by having teeth positioned approximately to it. Townsend *et al.* (2012) has suggested that there is a chromosomal link to dentition deposition, particularly with the Y chromosome, resultant in larger teeth for males than females. As the differences observed statistically here suggest the buccolingual dimension is more sexually dimorphic it may be a combination of having room to expand when extra dentition is deposited. It would be advantageous to review and expand on this finding in order to help better understand tooth development and the influence that biological sex has on the process, in particular.

Geometric morphometric shape analyses have shown potential to look at subtle changes in species, types and classes of organisms and skeletal elements (Bernal 2007). As such, future work on overall shape analysis may provide a greater level of detail in terms of overall tooth phenotype as it would provide a way to simultaneously incorporate size and shape data reflective of nonmetric traits. Its use may prove more effective in regard to highlighting differences of similarity in overall tooth shape and size at the same time. By approaching the analysis of similarity based on overall shape, it would be possible to include nonmetric trait data from the ASU (Turner II et al. 1990) system with metric traits to see if those with larger teeth for the population are more likely to have 'extra' features and vice versa, a concept that has been discussed by those researching in dental phenomics (Brook *et al.* 2014; Moreno Uribe and Miller 2015). This would also allow for the inclusion of nonmetric data obtained in this project which was not substantial enough across these four cemeteries to explore alone statistically. Geometric shape analysis can be conducted using two dimensional or three-dimensional images of an object or organism, where a series of standardised points are identified and consistently mapped on each individual within the sample (i.e. Cucchi *et al.* 2011). Statistical analyses then are able to identify the amount of variation in the location of each of those standardised points to help identify differences, variation and similarity. While more labour intensive on the part of the researcher compared to the recording of tooth dimensions, if more refinements can be found in the data set, particularly for those individuals this project has discussed as showing moderate levels of similarity, it would be a worthwhile pursuit. Additionally, it may also help to reinforce the notion that metric and nonmetric data are not mutually exclusive, rather, they are inherently linked in the developmental process of tooth formation. However, if results of geometric morphometric shape analysis mirror findings from metric analyses it can be argued that the simpler methodological approach

employed here with the recording of tooth dimensions is sufficient enough to help discover similarity amongst skeletal assemblages.

The decision not to include sub adults in this project was highlighted above as a potential limiting factor, although this methodological choice was based on the need to be able to account for biological sex. However, now that it is clear that this approach is a viable method from which to explore biological similarity and biological connections between adults, it would be advantageous to re-visit these samples and include sub-adult remains. Sub-adults start to develop permanent teeth early in infancy, though they do not start to emerge until around ages four through eight (Ubelaker 1978). Therefore, there is the potential to expand the age of inclusion for research to individuals aged as young as this. Furthermore, some researchers have suggested there is a correlation between deciduous and permanent tooth size (i.e. Townsend and Brown 1978b), wherein those who are predisposed to have larger teeth due to parental inheritance will reflect this trait in both primary and secondary dentition. In order to account for size differences that will be present due to a tooth being a deciduous or permanent form, there would first need to be a standardisation of data between permanent and primary dentition so that size values could be better compared. If this correlation is found, it would be able to repeat the entire process as described here in order to see how similar the sub-adults from Hatherdene, Oakington, Polhill and Eastry are to the adults in these cemeteries, and overall across all four sites. Focusing on the same set of teeth as outlined in Tables 15 and 16 in Chapter 5 (in particular the focus on pole teeth would be important here as they are the earlier developing teeth within a class) would allow for a quicker data collection and stronger comparison to what has already been done within the current study. It would be important to use as many teeth as possible, like the adult comparisons, in order to ensure strength in interpretations.

As some of the multiple burials in these cemeteries contained sub-adult individuals, these cases could be investigated to observe what possible connections the adults may have had to the children they were interred with. The only caveat to come from this approach would be the difficulty in confirming the biological sex of the sub-adult individuals, while DNA testing could confirm this, again it may not be possible. However, newer methods of peptide-based sexing (i.e. Gowland et al. 2021; Stewart et al. 2017) offer a less destructive approach to sampling teeth which can provide reliable estimates of biological sex for sub-adult remains. It would be advantageous to explore this area further for applications for the inclusion of children in the current study.

Alternatively, a way to minimise potential issues arising from not knowing the sex would be to only compare the teeth that were selected for hierarchical cluster analysis that were found not to differ between the males and females of the adult sample. As many of the potential interpretations about connections among the interred adults centre on brothers, sisters and parents, it would be important to look across the age ranges in the cemetery to see if patterns observed among hypothesised relationships of adults could also translate across to younger age categories. Children are often underrepresented in archaeological research due to issues with preservation and lack of grave furnishings (Halcrow and Tayles 2008), so it would be important to try and include them via dental analyses in order to help broaden understandings about how a complete society was structured.

Results discussed in Chapter 6 have also brought to light some questions regarding demographic trends within the biodata and contextual information observed within these communities. These pattern differences were particularly evident amongst females, where there appeared to be commonalities of wealthy or elaborate burials for many younger

females, compared to older adult females. Additionally, there were also some cases where older females were interred with younger adult females but a discrepancy between the presence of grave goods appeared between them. In such instances it would be interesting to approach the question of age with status and biological similarity in order to see if younger females who have appeared more similar in their dental measurements to one another and males of the group represent a group of unwed women who are being acknowledged as part of their father's kin group rather than husband's. In contrast, the older adult females who may be dissimilar and with certain grave goods may indicate a status of life achievement (i.e. motherhood) which echoes findings from Stoodley (1999, 2000) and his discussion on lifecycles, Gilchrist (2012) and Gowland (2006) and their discussions on grave goods reflecting the passing of life milestones. As some of the findings in this study, particularly from Polhill, Oakington and Hatherdene touch on these ideas it would be interesting to explore this concept in more detail in future.

Finally, there are additional avenues to explore that may help with further validation. As this project touched on some preliminary work related to the identity and kinship expressed in early Anglo-Saxon populations through mtDNA analysis, it would be exciting to continue to collaborate with further genomic research on population, community and local levels. Along with this, applying the dental analyses methodology on another archaeological population of known familial groups, such as Spitalfields, would help to corroborate findings from dental metrics to known family connections and relationships. Further corroboration of interpretations made on tooth data through mtDNA and DNA analyses or using known samples of known families would help further validate this methodological approach and contribute more holistically to the study of identity and kinship in the early Anglo-Saxon era. Broader scale questions about mobility, family and identity on the population level could also

be integrated through further genomic and isotopic approaches combined with dental metric analyses.

7.4 Bridging the Gap

It has been long recognised by anthropologists and archaeologists that the concept of kinship needs to move beyond an assumption of biological connections between individuals. Kinship can cover a variety of links between people that are not based on biology, rather, on convenience, social convention and the sharing of life achievements. Schneider (1984) was a main figure arguing for recognition of the dynamic and fluid nature of kinship; adaptations and variations are a common part of human existence and relationships, and the terminology used by those who study human populations needs to reflect this. However, there are still publications (i.e Adachi *et al.* 2003, Deguilloux *et al.* 2014; Haak *et al.* 2008) in recent years that have synonymised kinship with genetically related individuals. This simplistic view of kin prevents the full exploration of how family units are actually identified and interpreted in the archaeological record. Lancaster (1958a) related this notion to later Anglo-Saxon communities as she noted there were many examples of 'kin' that fell into these groupings: semi kin, half relatives resulting from remarriages, quasi kin, fostering or adoption of children, and ritual kin. Arguably, these types of relationships would be found in early Anglo-Saxon communities as well. This is not to say that biology and shared biological affinity has no place in discussions of kinship, rather, its inclusion can provide bountiful evidence for support or refinement of theories. As was highlighted through work of Nolin (2011), even when distinctions between what constitutes biological kinship or social kinship appear, it was evident that there was much overlap between these two 'distinct' areas. To this end, Franklin

and McKinnon (2000, 277) presented an updated definition of how kinship should be defined, describing it as reflective of the worlds that are lived by present and past societies, which pairs well with recent discussion on early Anglo-Saxon identity in death and the narratives established by communities (Sayer 2020).

In order to apply these theoretical concepts to osteoarchaeology and human dentition, what was needed was a way to make it clear exactly how kinship does relate on various levels to the appearance of traits in skeletons that are thought to be linked to genetic inheritance. Biodata obtained from skeletal remains forms an integral part of a person's identity; the physical traits of the skeleton often reflect parental inheritance (i.e. Konigsberg 1988; Lane and Sublett 1972; Schillaci and Stojanowski 2003) which can then be explored to locate presumptive links between individuals. It is important not to completely overlook the 'human' aspect of a person; humans are biological beings, therefore discussions on their identity and personhood should include reference to their biology. Despite this, biology is only one part of identity. Therefore, it is important that the biological data not be used first to assume relationships akin to kin membership, rather, the biological evidence can be used in conjunction with other archaeological aspects such as artefacts or historical documentation to help interpret what this connection between individuals is likely attributable to. Therefore, it was argued in this project that a change in terminology be accepted and implemented as standard for future research, in that, data pertaining to biological similarity between archaeological individuals can, and should, be used to reflect the recording of biodata from skeletal remains that may show affinity to other individuals. Biological similarity does not carry the connotations that kinship does, rather, it allows for a neutral stance to holistically apply this to kinship research. The term biological similarity acknowledges that this type of evidence forms only one part of a person's identity and allows for input from other contextual

aspects. In doing so, accepting that biological connections (or a lack there of) between individuals within skeletal assemblages only form one aspect of that person's identity which may or may not have anything to do with kinship, depending on the society. It is through a combined effort of reviewing as much evidence from as many sources as possible that stronger, more robust notions of who that person is and what may connect them to others around them, that a better idea of identity, kinship and group membership may be discovered (Johnson 2019).

The genetic and environmental influences on tooth development are continuing to be studied, with recent research demonstrating the effects of a variety of these intrinsic and extrinsic factors on tooth size and shape (Townsend *et al.* 2012). While there are still gaps in the current literature in regards to a complete understanding of the developmental process, what has been shown to be consistent is that genetic inheritance is linked, quite strongly, to final determination of size and shape (Biggerstaff 1970; Boraas *et al.* 1988; Brook *et al.* 2014; Townsend *et al.* 2012). Researchers focused on this concept have studied a variety of groups of people ranging from twins, first-degree biological relations, and non-related groups of both sexes in order to demonstrate and validate this concept. Tooth sizes and shapes have been shown to be most similar between identical twins (Hughes and Townsend 2013; Potter and Nance 1976), followed by same sex siblings, mixed sex siblings and then parent and offspring pairs (Hughes and Townsend 2013; Townsend and Brown 1978a; 1978b). Where skeletal preservation was found to be poor, as the cases of Polhill and Eastry helped to highlight, dental preservation was much better. The chemical structure of teeth is well accepted as being more resilient to taphonomic change than the remainder of the skeleton (Galloway 1997) and, as there are up to 32 teeth present in adult skeleton, the potential to recover useable data from which to attempt to locate trends in biological similarity is great. Teeth

have also provided the opportunity to record metric and nonmetric traits that can be used separately, or in combination with one another as has been suggested as practice under the newer area of dental phenomics (Brook *et al.* 2014; Moreno Uribe and Miller 2015). These positive attributes have helped to show that using teeth to assess biological similarity can be advantageous in the study of early Anglo-Saxon populations in South-East England.

One of the main benefits of utilising this methodological approach is in its ability to be flexible enough to be applied to a variety of different research questions involving identity and kinship of past populations. For instance, interpretations were made on population, community and individual levels from the same set of analytical output. There was no need to reanalyse the data once the clustering had been done as the connections between the individuals would remain constant as they were based on metric biodata obtained during data collection. What did vary were the questions being asked of the data. For questions relating to residence patterns and mobility, all individuals needed to be considered and overarching patterns apparent in the data would help to address them. Questions relating to the physical attributes of graves in each cemetery again could be answered from the same series of outputs, but instead of looking across the whole population, outputs were limited to separate sites. Finally, by targeting specific individuals within each site, the same outputs once again could be used to comment on specific connections between targeted people within each community. These interpretations were able to be conducted by approaching questions from either an inductive or deductive viewpoint. Inductively, burial structures or multiple interments were looked at with an *a priori* assumption of a connection between individuals; those who were buried together or in similar elaborate ways were hypothesised as being socially, if not biologically, close. It was then possible to corroborate such hypotheses by comparing the tooth data between those interred and interpreting it along with demographic data. Alternatively, the

approach could be employed deductively by starting with the biodata from the cluster dendrograms to highlight repeat occurrences of strong similarity between individuals, or patterns between males and females. Afterwards, any identified individuals or patterns can be cross referenced with burial locations, grave goods, clustering patterns or historical documents in order to see what could be contributing to such patterns.

Preliminary mtDNA analyses were available for use to help with the validation process of this methodological approach. Two cases from Oakington proved to be extremely useful to help demonstrate the merit of using teeth to identify biological similarity: Grave 88 containing two male individuals who were shown to be maternally distant and an additional connection between two individuals (Graves 56 and 78) who would not have necessarily been connected otherwise, showed that tooth data was corroborated with mtDNA haplogroups (Schiffels and Gretzinger, *nd.*). In addition, a further case from Eastry also helped to validate the methodological approach employed here, with two females (E45 and E46) found to be third-degree relations based on mtDNA haplogroups (Schiffels and Gretzinger, *nd.*) with higher levels of similarity being expressed via their dental metrics. These mirrored findings between mtDNA and dental metrics are very exciting and help demonstrate the sound theoretical underpinning of this project's methodological design. This is particularly important for archaeological research, while DNA comparisons are arguably the more robust method for confirming identification and biological connections between individuals, DNA is not always obtainable, amplifiable or fiscally feasible. Furthermore, sampling teeth for DNA is destructive. As such, knowing that tooth metrics have the potential to reflect the same trends that mtDNA analyses can pick up on demonstrates the utility of dentition as a medium through which to comment on biological connections between archaeological individuals.

In sum, the ways in which early Anglo-Saxons identified kinship through funerary and burial rites appears to be fluid and dynamic. There did not appear to be any real consistent patterns observed regarding connections of individuals within and between these four contemporaneous cemeteries when looking across dental metrics and contextual information. Rather, the results of dental analyses from Hatherdene, Oakington, Polhill and Eastry have demonstrated that not all connections interpreted as being kin-like were based on biological connections and not all factors that have been cited to infer close connections are linked to biology. Rather, it was through the inclusion of both contextual information and dental biodata that better helped to develop interpretations surrounding residence and mobility patterns and ideas regarding personal and group identity. Even in cases where a pattern seemed consistent, such as the abundance of male graves containing wealthy, biologically similar males at Hatherdene, the fluid nature of kinship in early Anglo-Saxon communities quickly became apparent when this was not found to the same extent in the remaining three cemeteries within this sample. To echo Sahlins (2013), kinship within these four early Anglo-Saxon sites, and arguably therefore across the whole early Anglo-Saxon population, *does and does not* appear to be linked to biology. There are multiple factors at work that influence how people connect to one another, and even more so regarding how these connections are displayed after death (Sayer 2020). The utility of teeth for identifying biological similarity among individuals in skeletal assemblages has proven to be invaluable when commenting on constructs such as mobility, residence, identity and connectivity on population, community and individual levels. While this project focused on the early Anglo-Saxon period, the method developed here to study these social aspects via dentition could easily be applied to any other group where it is thought that the population under investigation is representative of familial groupings. These groupings could be from other

archaeological time periods, such as the Neolithic and chambered tombs, or even mass disaster scenarios resulting from modern forensic contexts. The conclusions drawn from this project have proven that teeth have the remarkable ability to bridge the gap between biological data and social constructs. These links define human connections relating to identity on various cultural levels and, because of this, teeth should form an integral part of future bio-cultural research in these areas.

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Appendix 1: Descriptive Statistics

Table 1 – Descriptive statistics from the entire sample (n=145), not separated by sex or site.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 69	6.42	10.78	8.43	0.101	0.839	0.704	8.22 – 8.63
RMxM3	BL = 69	8.17	12.9	10.22	0.107	0.849	0.801	10.01 – 10.44
2	MD = 92	7.03	10.66	9.07	0.071	0.680	0.462	8.93 – 9.21
RMxM2	BL = 92	8.66	12.32	10.67	0.070	0.672	0.452	10.53 – 10.81
3	MD = 87	8.12	11.25	9.97	0.059	0.549	0.301	9.85 – 10.09
RMxM1	BL = 87	9.71	12.29	10.98	0.058	0.538	0.290	10.86 – 11.09
4	MD = 104	4.91	7.47	6.40	0.046	0.467	0.218	6.31- 6.49
RMxP2	BL = 104	7.57	10.15	8.85	0.055	0.558	0.312	8.75 – 8.96
5	MD = 100	5.56	7.49	6.50	0.040	0.405	0.164	6.42 – 6.58
RMxP1	BL = 100	7.37	10.25	8.73	0.059	0.594	0.353	8.61 – 8.85
6	MD = 101	5.35	8.28	7.44	0.044	0.449	0.201	7.35 – 7.53
RMxC	BL = 101	6.92	9.83	8.16	0.050	0.499	0.249	8.06 – 8.26
7	MD = 83	4.43	7.80	6.52	0.064	0.586	0.343	6.40 – 6.65
RMxLI	BL = 83	4.56	7.72	6.37	0.057	0.521	0.271	6.26 – 6.49
8	MD = 66	7.30	9.56	8.34	0.063	0.509	0.259	8.22 – 8.47
RMxCI	BL = 66	5.90	8.30	7.05	0.052	0.426	0.182	6.94 – 7.15
9	MD = 81	7.31	9.30	8.34	0.051	0.462	0.213	8.24 – 8.44
LMxCI	BL = 81	6.00	8.83	7.14	0.051	0.457	0.209	7.04 – 7.24
10	MD = 86	4.43	7.78	6.56	0.061	0.564	0.318	6.44 – 6.68
LMxLI	BL = 86	5.01	7.46	6.23	0.054	0.497	0.247	6.13 – 6.34
11	MD = 98	6.64	8.41	7.44	0.040	0.393	0.155	7.36 – 7.52
LMxC	BL = 98	6.67	9.94	8.14	0.048	0.480	0.230	8.04 – 8.24
12	MD = 94	5.60	7.33	6.49	0.042	0.404	0.163	6.41 – 6.57
LMxP1	BL = 94	7.03	10.14	8.66	0.061	0.593	0.351	8.54 – 8.78
13	MD = 95	5.03	7.40	6.34	0.046	0.445	0.198	6.25 – 6.43

LMxP2	BL = 95	7.66	10.23	8.88	0.058	0.565	0.319	8.77 – 9.00
14	MD = 89	8.44	11.29	10.00	0.055	0.520	0.270	9.89 – 10.11
LMxM1	BL = 89	9.54	12.30	10.96	0.058	0.549	0.301	10.84 – 11.07
15	MD = 90	7.28	11.14	9.19	0.071	0.675	0.455	9.04 – 9.33
LMxM2	BL = 90	9.09	12.08	10.62	0.070	0.667	0.445	10.48 = 10.76
16	MD = 68	6.99	9.78	8.50	0.078	0.645	0.416	8.34 – 8.65
LMxM3	BL = 68	7.67	11.61	10.04	0.099	0.819	0.671	9.85 – 10.24
17	MD = 80	8.36	11.94	10.26	0.088	0.790	0.625	10.09 – 10.44
LMM3	BL = 80	8.08	11.20	9.57	0.072	0.648	0.420	9.42 – 9.71
18	MD = 105	8.11	12.67	10.30	0.067	0.690	0.476	10.16 – 10.43
LMM2	BL = 105	8.28	11.35	9.85	0.054	0.551	0.303	9.74 – 9.95
19	MD = 97	8.91	12.08	10.70	0.063	0.616	0.379	10.58 – 10.83
LMM1	BL = 97	8.79	11.52	10.29	0.051	0.499	0.249	10.19 – 10.39
20	MD = 116	5.44	10.57	6.71	0.055	0.595	0.355	6.60 – 6.82
LMP2	BL = 116	5.41	9.76	7.92	0.054	0.578	0.334	7.82 – 8.03
21	MD = 114	5.45	7.73	6.63	0.038	0.410	0.168	6.55 – 6.70
LMP1	BL = 114	6.44	8.75	7.48	0.044	0.467	0.219	7.40 – 7.57
22	MD = 113	5.57	7.66	6.54	0.037	0.392	0.154	6.47 – 6.61
LMC	BL = 113	6.25	8.90	7.54	0.049	0.526	0.276	7.44 – 7.64
23	MD = 101	4.18	6.77	5.64	0.047	0.476	0.227	5.55 – 5.74
LMLI	BL = 101	5.27	7.30	6.31	0.040	0.404	0.163	6.23 – 6.39
24	MD = 78	3.46	6.04	4.98	0.051	0.448	0.201	4.87 – 5.08
LMCI	BL = 78	5.38	6.88	5.92	0.037	0.328	0.108	5.84 – 5.99
25	MD = 75	3.70	5.98	4.93	0.056	0.485	0.235	4.82 – 5.04
RMCI	BL = 75	5.34	7.00	5.93	0.041	0.357	0.127	5.84 – 6.01
26	MD = 94	4.71	6.63	5.67	0.049	0.472	0.223	5.58 – 5.77
RMLI	BL = 94	5.05	7.39	6.26	0.044	0.430	0.185	6.18 – 6.35
27	MD = 111	5.57	7.73	6.51	0.039	0.412	0.169	6.43 – 6.59
RMC	BL = 111	6.41	9.43	7.54	0.051	0.541	0.292	7.44 – 7.65
28	MD = 117	5.56	7.61	6.66	0.038	0.408	0.166	6.56 – 6.73
RMP1	BL = 117	6.31	8.94	7.51	0.045	0.488	0.238	7.43 – 7.60
29	MD = 109	5.65	8.09	6.70	0.044	0.457	0.209	6.61 – 6.78

RMP2	BL = 109	6.36	9.23	7.91	0.053	0.549	0.301	7.80 – 8.01
30	MD = 101	8.95	12.10	10.66	0.062	0.624	0.390	10.54 – 10.78
RMM1	BL = 101	8.57	11.41	10.30	0.047	0.468	0.219	10.21 – 10.39
31	MD = 103	8.69	11.88	10.28	0.063	0.643	0.413	10.15 – 10.40
RMM2	BL = 103	8.19	11.20	9.77	0.054	0.547	0.299	9.66 – 9.88
32	MD = 77	8.10	11.57	10.10	0.089	0.777	0.604	9.93 – 10.28
RMM3	BL = 77	7.90	10.62	9.41	0.071	0.625	0.390	9.26 – 9.55
Total N	**5988**							

Combined sample, separated by sex.

Table 2 – Descriptive statistics from the combined cemetery sample, males only (n=65).

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 29	6.75	10.32	8.48	0.156	0.840	0.705	8.16 – 8.80
RMxM3	BL = 29	9.50	12.90	10.62	0.152	0.818	0.670	10.31 – 10.93
2	MD = 38	7.78	10.66	9.21	0.117	0.718	0.516	9.98 – 9.45
RMxM2	BL = 38	8.66	12.32	10.90	0.116	0.714	0.509	10.66 – 11.13
3	MD = 36	8.72	11.17	10.04	0.086	0.516	0.266	9.86 – 10.21
RMxM1	BL = 36	10.01	12.29	11.19	0.087	0.521	0.272	11.01 – 11.37
4	MD = 43	5.66	7.39	6.47	0.065	0.429	0.184	6.33 – 6.60
RMxP2	BL = 43	7.77	10.15	9.02	0.087	0.568	0.322	8.84 – 9.19
5	MD = 40	5.90	7.15	6.58	0.058	0.366	0.134	6.46 – 6.69
RMxP1	BL = 40	7.70	10.25	8.92	0.095	0.599	0.359	8.73 – 9.11
6	MD = 43	5.35	8.28	7.52	0.081	0.531	0.282	7.36 – 7.68
RMxC	BL = 43	7.60	9.83	8.38	0.073	0.476	0.227	8.23 – 8.52
7	MD = 36	4.43	7.80	6.53	0.107	0.640	0.409	6.31 – 6.74
RMxLI	BL = 36	4.56	7.72	6.43	0.096	0.574	0.330	6.23 – 6.62
8	MD = 32	7.33	9.29	8.32	0.089	0.503	0.253	8.14 – 8.50
RMxCI	BL = 32	6.52	8.30	7.11	0.069	0.390	0.152	6.97 – 7.25
9	MD = 37	7.31	9.20	8.36	0.075	0.455	0.207	8.21 – 8.52

LMxCl	BL = 37	6.48	8.83	7.19	0.085	0.517	0.267	7.02 – 7.37
10	MD = 38	5.51	7.55	6.58	0.087	0.538	0.289	6.41 – 6.76
LMxLl	BL = 38	5.15	7.46	6.28	0.084	0.520	0.271	6.11 – 6.45
11	MD = 43	7.05	8.41	7.58	0.051	0.333	0.111	7.48 – 7.68
LMxC	BL = 43	6.67	9.94	8.32	0.076	0.498	0.248	8.17 – 8.47
12	MD = 41	5.73	7.33	6.54	0.059	0.381	0.145	6.42 – 6.66
LMxP1	BL = 41	7.86	10.14	8.82	0.082	0.524	0.275	8.65 – 8.98
13	MD = 42	5.08	7.16	6.41	0.067	0.434	0.188	6.27 – 6.54
LMxP2	BL = 42	7.83	10.23	9.05	0.086	0.560	0.314	8.87 – 9.22
14	MD = 36	9.28	11.26	10.18	0.075	0.449	0.202	9.95 – 10.25
LMxM1	BL = 36	10.37	12.30	11.17	0.078	0.467	0.218	11.02 – 11.33
15	MD = 37	7.28	10.48	9.21	0.112	0.684	0.468	8.98 – 9.44
LMxM2	BL = 37	9.09	12.08	10.86	0.120	0.733	0.537	10.62 – 11.10
16	MD = 25	7.05	9.78	8.53	0.114	0.572	0.328	8.30 – 8.77
LMxM3	BL = 25	7.91	11.61	10.37	0.157	0.786	0.618	10.05 – 10.70
17	MD = 40	8.59	11.94	10.44	0.137	0.867	0.752	10.16 – 10.72
LMM3	BL = 40	8.08	11.20	9.75	0.107	0.676	0.457	9.54 – 9.97
18	MD = 50	9.23	11.83	10.48	0.086	0.607	0.369	10.31 – 10.65
LMM2	BL = 50	8.86	11.35	10.06	0.081	0.572	0.327	9.90 – 10.23
19	MD = 43	9.43	12.08	10.84	0.097	0.633	0.401	10.64 – 11.03
LMM1	BL = 43	9.19	11.52	10.42	0.083	0.547	0.299	10.25 – 10.58
20	MD = 56	5.68	8.29	6.76	0.067	0.501	0.251	6.62 – 6.89
LMP2	BL = 56	5.41	9.26	8.01	0.081	0.606	0.368	7.85 – 8.17
21	MD = 51	5.45	7.73	6.66	0.060	0.429	0.184	6.54 – 6.78
LMP1	BL = 51	6.56	8.75	7.57	0.069	0.495	0.245	7.43 – 7.71
22	MD = 50	5.57	7.66	6.71	0.053	0.375	0.141	6.60 – 6.81
LMC	BL = 50	6.81	8.90	7.88	0.065	0.461	0.213	7.75 – 8.01
23	MD = 45	4.72	6.65	5.68	0.070	0.466	0.217	5.54 – 5.82
LMLl	BL = 45	5.38	7.30	6.41	0.063	0.426	0.191	6.28 – 6.53
24	MD = 33	4.24	6.04	4.93	0.080	0.461	0.213	4.77 – 5.09
LMCl	BL = 33	5.39	6.88	5.92	0.062	0.357	0.127	5.79 – 6.05
25	MD = 40	3.70	5.98	4.80	0.081	0.510	0.260	4.64 – 4.96

RMCI	BL = 40	5.36	7.00	5.98	0.061	0.384	0.148	5.86 – 6.11
26	MD = 45	4.71	6.55	5.64	0.074	0.499	0.249	5.49 – 5.79
RMLI	BL = 45	5.59	7.39	6.33	0.067	0.447	0.199	6.20 – 6.46
27	MD = 49	5.92	7.73	6.70	0.052	0.363	0.132	6.59 – 6.80
RMC	BL = 49	6.51	9.43	7.84	0.077	0.540	0.292	7.69 – 8.00
28	MD = 53	5.83	7.61	6.74	0.057	0.418	0.175	6.62 – 6.85
RMP1	BL = 53	6.40	8.94	7.59	0.074	0.538	0.289	7.44 – 7.74
29	MD = 51	5.73	8.09	6.76	0.065	0.467	0.218	6.63 – 6.89
RMP2	BL = 51	6.36	9.23	8.02	0.082	0.582	0.339	7.85 – 8.18
30	MD = 44	8.95	12.03	10.67	0.103	0.684	0.467	10.46 – 10.88
RMM1	BL = 44	9.50	11.41	10.40	0.070	0.465	0.216	10.26 – 10.54
31	MD = 45	9.36	11.81	10.45	0.077	0.518	0.268	10.30 – 10.61
RMM2	BL = 45	8.89	11.20	9.95	0.087	0.586	0.344	9.77 – 10.13
32	MD = 37	8.13	11.57	10.32	0.129	0.784	0.615	10.06 – 10.58
RMM3	BL = 37	8.08	10.62	9.62	0.093	0.567	0.322	9.43 – 9.81
Total N	**2656**							

Table 3 – Descriptive statistics from the combined cemetery sample, female data only (n=80).

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 40	6.42	10.78	8.39	0.134	0.848	0.719	8.12 – 8.66
RMxM3	BL = 40	8.17	11.73	9.94	0.134	0.845	0.714	9.67 – 10.21
2	MD = 54	7.03	10.48	8.97	0.087	0.639	0.408	8.79 – 9.14
RMxM2	BL = 54	9.40	11.53	10.51	0.081	0.598	0.357	10.35 – 10.67
3	MD = 51	8.12	11.25	9.92	0.080	0.571	0.326	9.76 – 10.08
RMxM1	BL = 51	9.71	11.83	10.83	0.070	0.503	0.253	10.69 – 10.97
4	MD = 61	4.91	7.47	6.36	0.063	0.490	0.240	6.23 – 6.48
RMxP2	BL = 61	7.57	9.93	8.74	0.067	0.536	0.277	8.60 – 8.87
5	MD = 60	5.56	7.49	6.46	0.055	0.424	0.180	6.35 – 6.57
RMxP1	BL = 60	7.37	9.83	8.61	0.073	0.562	0.316	8.46 – 8.75
6	MD = 58	6.64	8.16	7.37	0.048	0.368	0.136	7.28 – 7.47

RMxC	BL = 58	6.92	9.06	8.00	0.060	0.457	0.309	7.88 – 8.12
7	MD = 47	5.08	7.56	6.52	0.080	0.548	0.300	6.36 – 6.68
RMxLI	BL = 47	5.51	7.48	6.33	0.070	0.478	0.228	6.20 – 6.48
8	MD = 34	7.30	9.56	8.36	0.089	0.521	0.272	8.18 – 8.54
RMxCI	BL = 34	5.90	7.83	6.98	0.078	0.455	0.207	6.82 – 7.14
9	MD = 44	7.36	9.30	8.32	0.071	0.471	0.222	8.18 – 8.47
LMxCI	BL = 44	6.00	7.76	7.09	0.060	0.400	0.160	6.97 – 7.21
10	MD = 48	4.43	7.78	6.54	0.085	0.589	0.346	6.37 – 6.71
LMxLI	BL = 48	5.01	7.46	6.19	0.069	0.480	0.230	6.06 – 6.33
11	MD = 55	6.64	8.22	7.34	0.055	0.406	0.165	7.23 – 7.45
LMxC	BL= 55	7.25	9.07	8.00	0.056	0.417	0.174	7.89 – 8.11
12	MD = 53	5.60	7.32	6.45	0.058	0.419	0.176	6.33 – 6.56
LMxP1	BL = 53	7.03	9.84	8.54	0.085	0.619	0.383	8.37 – 8.71
13	MD = 53	5.03	7.40	6.28	0.062	0.450	0.203	6.16 – 6.40
LMxP2	BL = 53	7.66	9.79	8.75	0.074	0.538	0.290	8.60 – 8.90
14	MD = 53	8.44	11.29	9.94	0.076	0.557	0.310	9.78 – 10.09
LMxM1	BL = 53	9.54	12.09	10.81	0.076	0.555	0.309	10.66 – 10.96
15	MD = 53	7.62	11.14	9.17	0.093	0.673	0.454	8.98 – 9.36
LMxM2	BL = 53	9.20	11.74	10.46	0.078	0.567	0.321	10.30 – 10.61
16	MD = 43	6.99	9.64	8.48	0.105	0.689	0.475	8.27 – 8.69
LMxM3	BL = 43	7.67	11.33	9.85	0.120	0.786	0.617	9.61 – 10.10
17	MD = 40	8.36	11.46	10.09	0.106	0.672	0.452	9.87 – 10.30
LMM3	BL = 40	8.21	10.33	9.38	0.090	0.567	0.321	9.20 – 9.56
18	MD = 55	8.11	12.67	10.13	0.097	0.721	0.520	9.93 – 10.32
LMM2	BL = 55	8.28	10.53	9.65	0.061	0.452	0.204	9.53 – 9.77
19	MD = 54	8.91	11.73	10.59	0.080	0.585	0.342	10.43 – 10.75
LMM1	BL = 54	8.79	11.10	10.19	0.060	0.438	0.192	10.07 – 10.31
20	MD = 60	5.44	10.57	6.67	0.087	0.673	0.453	6.50 – 6.84
LMP2	BL = 60	6.68	9.76	7.84	0.070	0.542	0.294	7.70 – 7.98
21	MD = 63	5.77	7.51	6.60	0.050	0.397	0.157	6.50 – 6.70
LMP1	BL = 63	6.44	8.22	7.41	0.055	0.436	0.190	7.30 – 7.52
22	MD = 63	5.63	7.30	6.41	0.045	0.357	0.128	6.32 – 6.50

LMC	BL = 63	6.25	8.85	7.27	0.051	0.403	0.163	7.17 – 7.37
23	MD = 56	4.18	6.77	5.61	0.065	0.486	0.237	5.48 – 5.74
LMLI	BL = 56	5.27	7.07	6.23	0.049	0.370	0.137	6.13 – 6.33
24	MD = 45	3.46	5.85	5.01	0.066	0.441	0.194	4.88 – 5.14
LMCI	BL = 45	5.38	6.75	5.92	0.046	0.310	0.096	5.82 – 6.01
25	MD = 35	4.25	5.91	5.07	0.070	0.417	0.174	4.93 – 5.21
RMCI	BL = 35	5.34	6.57	5.86	0.053	0.314	0.098	5.75 – 5.97
26	MD = 49	4.75	6.63	5.71	0.064	0.449	0.202	5.58 – 5.83
RMLI	BL = 49	5.05	7.17	6.21	0.058	0.409	0.167	6.09 – 6.32
27	MD = 62	5.57	7.25	6.36	0.049	0.389	0.152	6.26 – 6.46
RMC	BL = 62	6.41	8.83	7.31	0.052	0.413	0.171	7.20 – 7.41
28	MD = 64	5.56	7.34	6.60	0.049	0.391	0.153	6.50 – 6.69
RMP1	BL = 64	6.31	8.36	7.45	0.055	0.437	0.191	7.34 – 7.56
29	MD = 58	5.65	7.54	6.64	0.058	0.445	0.198	6.52 – 6.75
RMP2	BL = 58	6.66	8.78	7.81	0.066	0.503	0.253	7.68 – 7.94
30	MD = 57	9.42	12.10	10.65	0.077	0.580	0.336	10.49 – 10.80
RMM1	BL = 57	8.57	11.14	10.22	0.061	0.458	0.210	10.10 – 10.34
31	MD = 58	8.69	11.88	10.14	0.092	0.698	0.487	9.95 – 10.32
RMM2	BL = 58	8.19	10.44	9.63	0.062	0.475	0.225	9.51 – 9.76
32	MD = 40	8.10	11.33	9.90	0.114	0.723	0.523	9.67 – 10.13
RMM3	BL = 40	7.90	10.43	9.20	0.097	0.614	0.377	9.01 – 9.40
Total N	**3332**							

Sample divided into cemetery sites, and by sex

Table 4 – Descriptive statistics from Hatherdene, combined sex.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 33	6.75	10.08	8.41	0.154	0.883	0.781	8.10 – 8.72
RMxM3	BL = 33	8.17	12.90	10.18	0.182	1.042	1.088	9.81 – 10.55
2	MD = 40	7.03	10.66	9.13	0.111	0.707	0.500	8.91 – 9.36

RMxM2	BL = 40	9.47	12.32	10.73	0.115	0.728	0.530	10.50 – 10.96
3	MD = 34	8.89	11.17	9.99	0.087	0.504	0.254	9.81 – 10.16
RMxM1	BL = 34	9.74	12.28	11.01	0.096	0.558	0.311	10.82 – 11.20
4	MD = 43	4.91	7.47	6.41	0.077	0.508	0.258	6.26 – 6.57
RMxP2	BL = 43	7.57	9.93	8.87	0.082	0.535	0.286	8.70 – 9.03
5	MD = 43	5.67	7.22	6.50	0.059	0.386	0.149	6.38 – 6.62
RMxP1	BL = 43	7.43	10.24	8.75	0.085	0.558	0.311	8.58 – 8.92
6	MD = 44	6.58	8.20	7.43	0.062	0.411	0.169	7.31 – 7.56
RMxC	BL = 44	7.27	9.83	8.16	0.078	0.513	0.263	8.00 – 8.31
7	MD = 36	5.21	7.57	6.39	0.094	0.564	0.318	6.20 – 6.58
RMxLI	BL = 36	5.51	7.60	6.42	0.085	0.508	0.258	6.25 – 6.59
8	MD = 26	7.30	9.13	8.30	0.094	0.480	0.230	8.11 – 8.49
RMxCI	BL = 26	6.38	7.68	6.97	0.076	0.386	0.149	6.82 – 7.13
9	MD = 29	7.31	9.20	8.31	0.094	0.505	0.255	8.12 – 8.50
LMxCI	BL = 29	6.45	8.83	7.13	0.090	0.485	0.236	6.95 – 7.32
10	MD = 39	4.43	7.55	6.44	0.097	0.608	0.369	6.24 – 6.64
LMxLI	BL = 39	5.01	7.46	6.14	0.079	0.493	0.243	5.98 – 6.30
11	MD = 41	6.64	8.41	7.42	0.059	0.376	0.141	7.30 – 7.54
LMxC	BL = 41	7.31	9.94	8.19	0.075	0.477	0.228	8.04 – 8.34
12	MD = 41	5.80	7.28	6.50	0.057	0.365	0.133	6.38 – 6.61
LMxP1	BL = 41	7.91	10.14	8.69	0.076	0.484	0.234	8.52 – 8.82
13	MD = 42	5.08	7.16	6.34	0.072	0.467	0.218	6.20 – 6.49
LMxP2	BL = 42	7.87	10.15	8.91	0.083	0.535	0.287	8.75 – 9.08
14	MD = 38	8.44	11.26	9.94	0.096	0.595	0.354	9.74 – 10.13
LMxM1	BL = 38	9.54	12.26	10.99	0.091	0.563	0.316	10.80 – 11.17
15	MD = 41	7.80	10.48	9.28	0.094	0.602	0.362	9.09 – 9.47
LMxM2	BL = 41	9.20	12.08	10.68	0.112	0.718	0.516	10.45 – 10.91
16	MD = 34	7.22	9.78	8.49	0.110	0.640	0.409	8.26 – 8.71
LMxM3	BL = 34	7.91	11.61	10.02	0.163	0.953	0.907	9.69 – 10.35
17	MD = 39	8.36	11.94	10.33	0.144	0.896	0.803	10.04 – 10.63
LMM3	BL = 39	8.36	11.20	9.55	0.116	0.727	0.528	9.31 – 9.78
18	MD = 43	8.52	11.75	10.34	0.105	0.691	0.477	10.12 – 10.55

LMM2	BL = 43	8.32	11.35	9.92	0.094	0.614	0.378	9.73 – 10.11
19	MD = 36	8.91	12.08	10.74	0.125	0.748	0.560	10.49 – 10.76
LMM1	BL = 36	8.79	11.41	10.31	0.092	0.555	0.308	10.12 – 10.49
20	MD = 47	5.44	10.57	6.76	0.116	0.795	0.632	6.53 – 7.00
LMP2	BL = 47	5.41	9.76	7.90	0.097	0.666	0.443	7.70 – 8.09
21	MD = 48	5.45	7.73	6.61	0.065	0.447	0.200	6.48 – 6.74
LMP1	BL = 48	6.62	8.53	7.47	0.065	0.451	0.203	7.34 – 7.60
22	MD = 47	5.57	7.39	6.48	0.060	0.409	0.168	6.36 – 6.60
LMC	BL = 47	6.38	8.75	7.55	0.075	0.514	0.264	7.40 – 7.70
23	MD = 43	4.72	6.65	5.63	0.069	0.452	0.205	5.49 – 5.77
LMLI	BL = 43	5.38	7.07	6.31	0.066	0.430	0.185	6.17 – 6.44
24	MD = 32	4.26	6.04	4.93	0.070	0.398	0.159	4.78 – 5.07
LMCI	BL = 32	5.39	6.75	5.92	0.061	0.345	0.119	5.79 – 6.04
25	MD = 30	3.77	5.73	4.82	0.089	0.485	0.236	4.64 – 5.00
RMCI	BL = 30	5.43	6.68	5.94	0.058	0.317	0.101	5.82 – 6.06
26	MD = 36	4.83	6.43	5.62	0.075	0.449	0.202	5.47 – 5.77
RMLI	BL = 36	5.56	7.39	6.28	0.074	0.444	0.197	6.13 – 6.43
27	MD = 44	5.57	7.73	6.47	0.069	0.459	0.211	6.33 – 6.61
RMC	BL = 44	6.46	9.43	7.58	0.085	0.561	0.315	7.41 – 7.75
28	MD = 44	5.56	7.61	6.62	0.070	0.463	0.214	6.48 – 6.76
RMP1	BL = 44	6.31	8.59	7.45	0.073	0.484	0.235	7.29 – 7.58
29	MD = 43	5.65	7.81	6.64	0.073	0.480	0.231	6.49 – 6.78
RMP2	BL = 43	6.36	9.23	7.87	0.083	0.546	0.299	7.70 – 8.04
30	MD = 39	8.95	12.03	10.70	0.117	0.730	0.533	10.46 – 10.94
RMM1	BL = 39	8.57	11.41	10.31	0.081	0.503	0.253	10.15 – 10.48
31	MD = 42	8.84	11.59	10.29	0.105	0.683	0.467	10.08 – 10.50
RMM2	BL = 42	8.19	11.04	9.84	0.091	0.590	0.349	9.66 – 10.03
32	MD = 33	8.13	11.37	10.26	0.139	0.797	0.635	9.97 – 10.54
RMM3	BL = 33	8.08	10.62	9.48	0.119	0.681	0.464	9.24 – 9.72
Total N	**2500**							

Table 5 – Descriptive statistics from Hatherdene, male data only.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 16	6.75	10.08	8.51	0.229	0.915	0.837	8.02 – 8.99
RMxM3	BL = 16	9.82	12.90	10.74	0.221	0.883	0.780	10.27 – 11.21
2	MD = 20	7.89	10.66	9.29	0.158	0.708	0.502	8.96 – 9.62
RMxM2	BL = 20	9.90	12.32	11.05	0.151	0.676	0.457	10.74 – 11.37
3	MD = 18	8.89	11.17	10.09	0.121	0.514	0.264	9.83 – 10.34
RMxM1	BL = 18	10.40	12.28	11.24	0.114	0.485	0.235	11.00 – 11.48
4	MD = 21	5.75	7.39	6.52	0.093	0.425	0.181	6.33 – 6.71
RMxP2	BL = 21	8.20	9.85	9.08	0.102	0.468	0.219	8.87 – 9.30
5	MD = 22	6.07	7.14	6.59	0.071	0.335	0.112	6.44 – 6.73
RMxP1	BL = 22	8.23	10.24	8.94	0.105	0.493	0.243	8.73 – 9.16
6	MD = 23	6.58	8.20	7.55	0.072	0.346	0.120	7.40 – 7.70
RMxC	BL = 23	7.60	9.83	8.33	0.102	0.492	0.242	8.12 – 8.55
7	MD = 18	5.21	7.57	6.50	0.138	0.584	0.341	6.21 – 6.79
RMxLI	BL = 18	6.04	7.60	6.43	0.085	0.361	0.130	6.25 – 6.61
8	MD = 17	7.33	9.13	8.43	0.112	0.461	0.213	8.19 – 8.67
RMxCI	BL = 17	6.52	7.68	7.07	0.085	0.350	0.122	6.89 – 7.25
9	MD = 18	7.31	9.20	8.49	0.109	0.463	0.215	8.26 – 8.71
LMxCI	BL = 18	6.52	8.83	7.19	0.131	0.554	0.307	6.91 – 7.46
10	MD = 21	5.58	7.55	6.57	0.106	0.486	0.237	6.34 – 6.79
LMxLI	BL = 21	5.31	6.67	6.17	0.081	0.370	0.137	6.01 – 6.34
11	MD = 23	7.12	8.41	7.55	0.065	0.312	0.097	7.42 – 7.69
LMxC	BL = 23	7.18	9.94	8.34	0.097	0.463	0.215	8.14 – 8.54
12	MD = 22	6.00	7.23	6.55	0.073	0.342	0.117	6.40 – 6.70
LMxP1	BL = 22	7.92	10.14	8.79	0.108	0.508	0.258	8.57 – 9.02
13	MD = 23	5.08	7.16	6.45	0.102	0.489	0.239	6.24 – 6.66
LMxP2	BL = 23	8.03	10.15	9.08	0.112	0.539	0.290	8.84 – 9.31
14	MD = 21	9.28	11.26	10.13	0.114	0.523	0.273	9.89 – 10.37
LMxM1	BL = 21	10.37	12.26	11.23	0.100	0.460	0.212	11.03 – 11.44

15	MD = 22	8.27	10.48	9.38	0.131	0.617	0.381	9.10 – 9.65
LMxM2	BL = 22	9.67	12.08	10.95	0.157	0.737	0.543	10.62 – 11.27
16	MD = 16	7.53	9.78	8.58	0.128	0.512	0.262	8.30 – 8.85
LMxM3	BL = 16	7.91	11.61	10.36	0.231	0.923	0.851	9.87 – 10.85
17	MD = 21	8.59	11.94	10.66	0.199	0.913	0.834	10.25 – 11.08
LMM3	BL = 21	8.44	11.20	9.83	0.166	0.762	0.528	9.49 – 10.18
18	MD = 25	9.39	11.75	10.59	0.114	0.570	0.325	10.36 – 10.83
LMM2	BL = 25	9.30	11.35	10.14	0.115	0.575	0.330	9.90 – 10.38
19	MD = 21	9.43	12.08	10.95	0.146	0.671	0.450	10.64 – 11.25
LMM1	BL = 21	9.19	11.41	10.46	0.115	0.526	0.276	10.22 – 10.70
20	MD = 27	5.68	8.29	6.82	0.106	0.552	0.305	6.60 – 7.03
LMP2	BL = 27	5.41	9.26	7.94	0.134	0.698	0.487	7.67 – 8.22
21	MD = 26	5.45	7.73	6.61	0.088	0.451	0.203	6.43 – 6.79
LMP1	BL = 26	6.73	8.53	7.55	0.091	0.462	0.214	7.37 – 7.74
22	MD = 22	5.57	7.39	6.68	0.082	0.383	0.147	6.51 – 6.84
LMC	BL = 22	7.16	8.75	7.89	0.090	0.424	0.180	7.70 – 8.08
23	MD = 23	4.72	6.65	5.73	0.100	0.478	0.229	5.53 – 5.94
LMLI	BL = 23	5.38	7.01	6.35	0.091	0.434	0.188	6.16 – 6.54
24	MD = 17	4.28	6.04	4.99	0.108	0.445	0.198	4.76 – 5.21
LMCI	BL = 17	5.40	6.45	5.95	0.082	0.338	0.114	5.78 – 6.12
25	MD = 20	3.77	5.73	4.83	0.119	0.532	0.283	4.58 – 5.08
RMCI	BL = 20	5.44	6.68	5.97	0.078	0.350	0.122	5.80 – 6.13
26	MD = 21	5.00	6.43	5.68	0.103	0.470	0.221	5.47 – 5.90
RMLI	BL = 21	5.59	7.39	6.25	0.098	0.450	0.202	6.05 – 6.46
27	MD = 24	5.92	7.73	6.65	0.080	0.393	0.155	6.48 – 6.82
RMC	BL = 24	6.51	9.43	7.81	0.115	0.564	0.318	7.57 – 8.04
28	MD = 24	5.88	7.61	6.73	0.085	0.418	0.174	6.56 – 6.91
RMP1	BL = 24	6.74	8.59	7.54	0.100	0.489	0.239	7.34 – 7.75
29	MD = 24	5.73	7.81	6.72	0.097	0.474	0.225	6.52 – 6.92
RMP2	BL = 24	6.36	9.23	8.00	0.120	0.590	0.348	7.75 – 8.25
30	MD = 22	8.95	12.03	10.70	0.171	0.801	0.642	10.35 – 11.06
RMM1	BL = 22	9.50	11.41	10.42	0.102	0.480	0.230	10.21 – 10.63

31	MD = 23	9.55	11.59	10.54	0.116	0.556	0.309	10.30 – 10.78
RMM2	BL = 23	9.15	11.04	10.06	0.116	0.557	0.310	9.82 – 10.30
32	MD = 19	8.13	11.37	10.43	0.188	0.819	0.671	10.03 – 10.82
RMM3	BL = 19	8.08	10.62	9.65	0.159	0.691	0.478	9.32 – 9.98
Total N	**1360**							

Table 6 – Descriptive statistics from Hatherdene, female data only.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 17	7.15	9.79	8.32	0.211	0.871	0.759	7.87 – 8.78
RMxM3	BL = 17	8.17	11.36	9.65	0.221	0.909	0.827	9.18 – 10.11
2	MD = 20	7.03	10.48	8.97	0.153	0.687	0.472	8.65 – 9.29
RMxM2	BL = 20	9.47	11.53	10.40	0.143	0.638	0.407	10.10 – 10.70
3	MD = 16	8.98	10.58	9.87	0.121	0.483	0.234	9.61 – 10.13
RMxM1	BL = 16	9.74	11.83	10.75	0.133	0.532	0.283	10.47 – 11.04
4	MD = 22	4.91	7.47	6.31	0.121	0.568	0.322	6.06 – 6.56
RMxP2	BL = 22	7.57	9.93	8.66	0.111	0.522	0.272	8.43 – 8.89
5	MD = 21	5.67	7.22	6.40	0.092	0.421	0.177	6.21 – 6.60
RMxP1	BL = 21	7.43	9.83	8.55	0.122	0.560	0.314	8.29 – 8.80
6	MD = 21	6.64	8.09	7.30	0.097	0.443	0.196	7.10 – 7.50
RMxC	BL = 21	7.27	9.02	7.97	0.104	0.476	0.227	7.75 – 8.19
7	MD = 18	5.40	7.43	6.28	0.126	0.535	0.287	6.01 – 6.54
RMxLI	BL = 18	5.51	7.48	6.40	0.149	0.633	0.401	6.09 – 6.72
8	MD = 9	7.30	8.58	8.06	0.146	0.439	0.193	7.72 – 8.40
RMxCI	BL = 9	6.38	7.56	6.79	0.134	0.403	0.162	6.48 – 7.10
9	MD = 11	7.36	8.75	8.02	0.136	0.450	0.203	7.72 – 8.33
LMxCI	BL = 11	6.45	7.53	7.04	0.106	0.351	0.123	6.80 – 7.28
10	MD = 18	4.43	7.36	6.30	0.168	0.711	0.505	5.94 – 6.65
LMxLI	BL = 18	5.01	7.46	6.09	0.145	0.615	0.378	5.78 – 6.40
11	MD = 18	6.64	7.80	7.25	0.092	0.389	0.151	7.05 – 7.44
LMxC	BL = 18	7.31	9.07	8.00	0.103	0.437	0.191	7.79 – 8.22

12	MD = 19	5.80	7.28	6.43	0.089	0.389	0.151	6.24 – 6.62
LMxP1	BL = 19	7.91	9.60	8.53	0.097	0.424	0.180	8.32 – 8.73
13	MD = 19	5.58	7.02	6.21	0.095	0.415	0.173	6.01 – 6.41
LMxP2	BL = 19	7.87	9.65	8.72	0.108	0.472	0.223	8.49 – 8.94
14	MD = 17	8.44	10.50	9.70	0.147	0.608	0.369	9.39 – 10.01
LMxM1	BL = 17	9.54	11.84	10.69	0.130	0.534	0.285	10.40 – 10.95
15	MD = 19	7.80	9.92	9.16	0.133	0.578	0.334	8.88 – 9.44
LMxM2	BL = 19	9.20	11.41	10.37	0.131	0.570	0.325	10.10 – 10.65
16	MD = 18	7.22	9.59	8.41	0.175	0.741	0.548	8.04 – 8.77
LMxM3	BL = 18	7.95	11.33	9.72	0.211	0.897	0.804	9.27 – 10.16
17	MD = 18	8.36	11.08	9.95	0.171	0.727	0.528	9.59 – 10.31
LMM3	BL = 18	8.36	10.21	9.21	0.123	0.522	0.272	8.95 – 9.47
18	MD = 18	8.52	11.55	9.98	0.164	0.700	0.487	9.63 – 10.32
LMM2	BL = 18	8.32	10.53	9.62	0.129	0.549	0.301	9.35 – 9.90
19	MD = 15	8.91	11.66	10.46	0.201	0.778	0.606	10.02 – 10.89
LMM1	BL = 15	8.79	10.84	10.10	0.140	0.542	0.294	9.80 – 10.40
20	MD = 20	5.44	10.57	6.69	0.235	1.050	1.103	6.20 – 7.18
LMP2	BL = 20	6.92	9.76	7.84	0.142	0.633	0.400	7.54 – 8.14
21	MD = 22	5.96	7.51	6.61	0.097	0.453	0.206	6.41 – 6.82
LMP1	BL = 22	6.62	8.18	7.37	0.091	0.425	0.181	7.18 – 7.55
22	MD = 25	5.63	7.02	6.31	0.071	0.356	0.127	6.16 – 6.45
LMC	BL = 25	6.38	7.82	7.24	0.076	0.379	0.144	7.09 – 7.40
23	MD = 20	4.80	6.22	5.51	0.089	0.398	0.159	5.32 – 5.69
LMLI	BL = 20	5.45	7.07	6.26	0.096	0.430	0.185	6.05 – 6.46
24	MD = 15	4.26	5.43	4.86	0.088	0.342	0.117	4.67 – 5.05
LMCI	BL = 15	5.39	6.75	5.88	0.093	0.360	0.130	5.68 – 6.08
25	MD = 10	4.25	5.67	4.81	0.127	0.403	0.162	4.52 – 5.10
RMCI	BL = 10	5.43	6.24	5.89	0.078	0.248	0.061	5.71 – 6.06
26	MD = 15	4.83	6.28	5.54	0.108	0.419	0.176	5.31 – 5.77
RMLI	BL = 15	5.56	7.17	6.32	0.116	0.447	0.200	6.07 – 6.57
27	MD = 20	5.57	7.13	6.25	0.099	0.444	0.197	6.04 – 6.46
RMC	BL = 20	6.46	8.06	7.31	0.097	0.433	0.188	7.11 – 7.52

28	MD = 20	5.56	7.30	6.49	0.110	0.491	0.241	6.26 – 6.72
RMP1	BL = 20	6.31	8.30	7.31	0.103	0.459	0.211	7.09 – 7.52
29	MD = 19	5.65	7.28	6.53	0.110	0.479	0.229	6.30 – 6.76
RMP2	BL = 19	6.88	8.39	7.70	0.103	0.449	0.202	7.49 – 7.92
30	MD = 17	9.52	11.74	10.70	0.158	0.650	0.422	10.36 – 11.03
RMM1	BL = 17	8.57	10.69	10.18	0.124	0.513	0.263	9.92 – 10.44
31	MD = 19	8.84	11.33	9.99	0.164	0.718	0.514	9.65 – 10.34
RMM2	BL = 19	8.19	10.44	9.58	0.122	0.532	0.283	9.33 – 9.84
32	MD = 14	9.04	11.33	10.03	0.195	0.731	0.535	9.61 – 10.45
RMM3	BL = 14	8.31	10.43	9.25	0.165	0.616	0.379	8.89 – 9.60
Total N	**1140**							

Table 7 – Descriptive statistics from Oakington, combined sex.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 21	6.42	10.78	8.34	0.186	0.854	0.729	7.95 – 8.73
RMxM3	BL = 21	8.89	11.60	10.15	0.144	0.661	0.437	9.85 – 10.46
2	MD = 35	7.78	10.25	8.91	0.108	0.636	0.405	8.69 – 9.13
RMxM2	BL = 35	8.66	11.95	10.50	0.113	0.670	0.449	10.27 – 10.73
3	MD = 33	8.93	11.25	10.04	0.091	0.520	0.271	9.86 – 10.22
RMxM1	BL = 33	9.71	12.29	10.89	0.101	0.582	0.338	10.68 – 11.09
4	MD = 40	5.42	7.38	6.35	0.066	0.420	0.177	6.21 – 6.48
RMxP2	BL = 40	7.77	10.15	8.82	0.094	0.597	0.357	8.63 – 9.01
5	MD = 38	5.56	7.49	6.49	0.072	0.448	0.201	6.34 – 6.64
RMxP1	BL = 38	7.37	10.25	8.71	0.102	0.631	0.398	8.50 – 8.91
6	MD = 35	5.35	8.28	7.43	0.089	0.525	0.276	7.25 – 7.61
RMxC	BL = 25	6.92	9.60	8.16	0.099	0.585	0.342	7.96 – 8.37
7	MD = 33	5.88	7.80	6.71	0.085	0.486	0.236	6.54 – 6.89
RMxLI	BL = 33	5.74	7.72	6.40	0.091	0.522	0.273	6.21 – 6.58
8	MD = 29	7.47	9.56	8.35	0.104	0.559	0.312	8.13 – 8.56
RMxCI	BL = 29	5.90	8.30	7.05	0.086	0.463	0.214	6.88 – 7.23

9	MD = 35	7.51	9.30	8.32	0.077	0.456	0.208	8.16 – 8.47
LMxCI	BL = 35	6.00	8.43	7.12	0.080	0.471	0.222	6.95 – 7.27
10	MD = 32	5.51	7.49	6.62	0.091	0.517	0.267	6.43 – 6.80
LMxLI	BL = 32	5.57	7.46	6.34	0.081	0.457	0.209	6.17 – 6.50
11	MD = 36	6.67	8.20	7.49	0.069	0.414	0.172	7.35 – 7.63
LMxC	BL = 36	6.67	9.18	8.12	0.090	0.541	0.292	7.93 – 8.30
12	MD = 36	5.79	7.32	6.44	0.066	0.398	0.158	6.30 – 6.57
LMxP1	BL = 36	7.03	9.71	8.57	0.101	0.605	0.366	8.37 – 8.78
13	MD = 37	5.03	7.40	6.31	0.072	0.435	0.189	6.16 – 6.45
LMxP2	BL = 37	7.66	10.23	8.84	0.092	0.558	0.311	8.65 – 9.03
14	MD = 32	9.37	11.29	10.13	0.085	0.482	0.232	9.96 – 10.31
LMxM1	BL = 32	9.72	12.30	10.93	0.104	0.588	0.345	10.72 – 11.14
15	MD = 30	7.28	10.41	8.96	0.131	0.715	0.511	8.69 – 9.08
LMxM2	BL = 30	9.09	11.98	10.54	0.120	0.660	0.435	10.30 – 10.79
16	MD = 19	6.99	9.12	8.37	0.142	0.617	0.381	8.07 – 8.67
LMxM3	BL = 19	7.67	11.20	10.08	0.189	0.822	0.676	9.68 – 10.47
17	MD = 26	8.75	11.40	10.01	0.131	0.667	0.446	9.74 – 10.28
LMM3	BL = 26	8.08	10.36	9.54	0.130	0.661	0.437	9.27 – 9.81
18	MD = 38	8.11	11.83	10.12	0.104	0.641	0.410	9.91 – 10.33
LMM2	BL = 38	8.28	11.15	9.80	0.087	0.536	0.288	9.63 – 9.98
19	MD = 35	9.54	11.32	10.59	0.087	0.515	0.265	10.41 – 10.77
LMM1	BL = 35	9.49	11.37	10.25	0.081	0.477	0.228	10.08 – 10.41
20	MD = 42	5.80	7.76	6.65	0.069	0.449	0.201	6.51 – 6.79
LMP2	BL = 42	6.82	9.01	7.97	0.078	0.507	0.257	7.82 – 8.13
21	MD = 39	5.77	7.63	6.60	0.062	0.392	0.154	6.47 – 6.73
LMP1	BL = 39	6.44	8.23	7.46	0.075	0.468	0.219	7.30 – 7.61
22	MD = 39	5.85	7.45	6.62	0.062	0.385	0.148	6.49 – 6.74
LMC	BL = 39	6.25	8.85	7.52	0.090	0.060	0.313	7.33 – 7.70
23	MD = 35	4.18	6.77	5.62	0.099	0.584	0.341	5.42 – 5.82
LMLI	BL = 35	5.27	7.30	6.30	0.066	0.393	0.155	6.17 – 6.44
24	MD = 28	3.46	6.02	4.94	0.110	0.582	0.338	4.71 – 5.17
LMCI	BL = 28	5.38	6.88	5.89	0.068	0.362	0.131	5.75 – 6.03

25	MD = 28	3.70	5.98	5.00	0.108	0.573	0.328	4.78 – 5.22
RMCI	BL = 28	5.34	7.00	5.93	0.082	0.432	0.187	5.77 – 6.10
26	MD = 36	4.71	6.63	5.73	0.082	0.489	0.239	5.57 – 5.90
RMLI	BL = 36	5.35	7.08	6.26	0.063	0.379	0.144	6.13 – 6.38
27	MD = 37	5.92	7.22	6.56	0.063	0.386	0.149	6.43 – 6.69
RMC	BL = 37	6.70	8.83	7.56	0.090	0.545	0.297	7.38 – 7.74
28	MD = 42	6.04	7.42	6.67	0.054	0.351	0.124	6.56 – 6.78
RMP1	BL = 42	6.63	8.94	7.53	0.077	0.502	0.252	7.37 – 7.69
29	MD = 38	5.80	7.46	6.69	0.069	0.427	0.182	6.55 – 6.83
RMP2	BL = 38	6.66	9.10	7.96	0.094	0.583	0.340	7.77 – 8.16
30	MD = 36	9.42	11.35	10.53	0.087	0.522	0.273	10.35 – 10.71
RMM1	BL = 36	9.45	11.23	10.24	0.084	0.506	0.256	10.07 – 10.71
31	MD = 34	8.69	11.81	10.19	0.114	0.666	0.444	9.96 – 10.43
RMM2	BL = 34	8.38	11.20	9.76	0.098	0.572	0.328	9.56 – 9.96
32	MD = 26	8.10	11.24	9.90	0.150	0.763	0.583	9.59 – 10.21
RMM3	BL = 26	7.90	10.39	9.42	0.126	0.642	0.412	9.16 – 9.67
Total N	**2150**							

Table 8 – Descriptive statistics from Oakington, male data only.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 9	7.49	9.21	8.32	0.155	0.464	0.216	7.96 – 8.67
RMxM3	BL = 9	9.65	11.60	10.42	0.224	0.671	0.451	9.90 – 10.94
2	MD = 13	7.78	10.25	8.97	0.187	0.674	0.455	8.56 – 9.38
RMxM2	BL = 13	8.66	11.95	10.59	0.229	0.826	0.682	10.09 – 11.08
3	MD = 11	9.27	10.55	10.05	0.140	0.466	0.217	9.73 – 10.36
RMxM1	BL = 11	10.01	12.29	11.10	0.205	0.679	0.461	10.65 – 11.56
4	MD = 15	5.89	7.03	6.49	0.090	0.349	0.122	6.29 – 6.68
RMxP2	BL = 15	7.77	10.15	9.02	0.167	0.646	0.417	8.66 – 9.38
5	MD = 13	6.04	7.15	6.57	0.106	0.382	0.146	6.34 – 6.80
RMxP1	BL = 13	7.84	10.25	8.93	0.188	0.679	0.461	8.52 – 9.34

6	MD = 14	5.35	8.28	7.54	0.198	0.741	0.550	7.11 – 7.96
RMxC	BL = 14	7.60	9.60	8.47	0.142	0.532	0.283	8.16 – 8.78
7	MD = 14	5.92	7.80	6.65	0.138	0.518	0.268	6.35 – 6.95
RMxLI	BL = 14	5.84	7.72	6.59	0.168	0.628	0.395	6.23 – 6.95
8	MD = 12	7.47	9.29	8.13	0.147	0.509	0.259	7.81 – 8.46
RMxCI	BL = 12	6.55	8.30	7.11	0.129	0.446	0.199	6.83 – 7.40
9	MD = 14	7.59	9.14	8.23	0.111	0.416	0.173	7.99 – 8.47
LMxCI	BL = 14	6.66	8.43	7.24	0.136	0.510	0.261	6.94 – 7.53
10	MD = 12	5.51	7.49	6.47	0.178	0.617	0.381	6.08 – 6.86
LMxLI	BL = 12	5.81	7.46	6.50	0.159	0.550	0.302	6.15 – 6.85
11	MD = 14	7.05	8.15	7.68	0.100	0.375	0.141	7.47 – 7.90
LMxC	BL = 14	6.67	9.18	8.31	0.166	0.621	0.386	7.95 – 8.67
12	MD = 13	6.02	7.12	6.53	0.086	0.310	0.096	6.34 – 6.72
LMxP1	BL = 13	7.86	9.54	8.77	0.150	0.542	0.294	8.44 – 9.10
13	MD = 14	5.85	6.92	6.41	0.086	0.324	0.105	6.22 – 6.59
LMxP2	BL = 14	7.83	10.23	9.02	0.167	0.624	0.389	8.66 – 9.38
14	MD = 11	9.38	10.54	10.11	0.104	0.343	0.118	9.88 – 10.34
LMxM1	BL = 11	10.37	12.30	11.09	0.160	0.530	0.281	10.73 – 11.45
15	MD = 12	7.28	10.41	9.92	0.233	0.808	0.653	8.41 – 9.44
LMxM2	BL = 12	9.09	11.98	10.71	0.234	0.809	0.655	10.20 – 11.23
16	MD = 6	8.06	8.93	8.48	0.166	0.407	0.166	8.05 – 8.90
LMxM3	BL = 6	9.78	11.20	10.46	0.196	0.480	0.230	9.96 – 10.96
17	MD = 11	9.04	11.40	9.96	0.225	0.747	0.558	9.46 – 10.46
LMM3	BL = 11	8.08	10.36	9.54	0.208	0.690	0.476	9.08 – 10.00
18	MD = 17	9.23	11.83	10.36	0.142	0.587	0.345	10.06 – 10.66
LMM2	BL = 17	9.07	11.15	10.05	0.131	0.538	0.290	9.77 – 10.33
19	MD = 15	9.54	11.32	10.60	0.147	0.570	0.325	10.28 – 10.91
LMM1	BL = 15	9.50	11.37	10.36	0.133	0.517	0.267	10.08 – 10.65
20	MD = 19	5.86	7.76	6.73	0.106	0.462	0.214	6.51 – 6.95
LMP2	BL = 19	7.21	9.01	8.11	0.106	0.463	0.215	7.89 – 8.34
21	MD = 16	6.25	7.63	6.67	0.091	0.365	0.133	6.48 – 6.86
LMP1	BL = 16	6.60	8.23	7.54	0.115	0.459	0.211	7.30 – 7.79

22	MD = 18	6.21	7.45	6.79	0.076	0.324	0.105	6.63 – 6.95
LMC	BL = 18	6.81	8.63	7.79	0.118	0.499	0.249	7.55 – 8.04
23	MD = 14	4.79	6.61	5.61	0.136	0.511	0.261	5.32 – 5.90
LMLI	BL = 14	5.84	7.30	6.46	0.109	0.408	0.166	6.22 – 6.69
24	MD = 12	4.24	6.02	4.85	0.160	0.553	0.306	4.50 – 5.20
LMCI	BL = 12	5.39	6.88	5.84	0.121	0.418	0.174	5.58 – 6.11
25	MD = 15	3.70	5.98	4.76	0.146	0.566	0.320	4.45 – 5.08
RMCI	BL = 15	5.36	7.00	6.04	0.120	0.467	0.218	5.78 – 6.29
26	MD = 15	4.71	6.55	5.66	0.125	0.486	0.236	5.39 – 5.93
RMLI	BL = 15	5.83	7.08	6.41	0.099	0.382	0.146	6.20 – 6.62
27	MD = 15	6.37	7.20	6.84	0.068	0.262	0.069	6.69 – 6.98
RMC	BL = 15	6.78	8.75	7.85	0.131	0.509	0.259	7.57 – 8.13
28	MD = 18	6.05	7.42	6.73	0.087	0.370	0.137	6.54 – 6.91
RMP1	BL = 18	6.78	8.95	7.68	0.137	0.580	0.336	7.39 – 7.97
29	MD = 16	6.09	7.46	6.87	0.087	0.348	0.121	6.69 – 7.06
RMP2	BL = 16	7.26	9.10	8.19	0.132	0.527	0.278	7.91 – 8.47
30	MD = 15	9.53	11.27	10.56	0.145	0.561	0.315	10.25 – 10.87
RMM1	BL = 15	9.63	11.23	10.34	0.131	0.506	0.256	10.06 – 10.62
31	MD = 13	10.09	11.81	10.51	0.124	0.446	0.198	10.24 – 10.77
RMM2	BL = 13	8.89	11.20	9.93	0.174	0.626	0.391	9.55 – 10.31
32	MD = 10	9.04	11.03	10.28	0.200	0.633	0.400	9.82 – 10.73
RMM3	BL = 10	8.98	10.39	10.64	0.133	0.419	0.176	9.34 – 9.94
Total N	**872**							

Table 9 – Descriptive statistics from Oakington, female data only.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 12	6.42	10.78	8.36	0.312	1.080	1.168	7.67 – 9.05
RMxM3	BL = 12	8.89	10.88	9.96	0.175	0.604	0.366	9.57 – 10.34
2	MD = 22	7.91	10.12	8.87	0.133	0.626	0.392	8.60 – 8.86
RMxM2	BL = 22	9.40	11.25	10.45	0.122	0.574	0.330	10.20 – 10.70

3	MD = 22	8.93	11.25	10.04	0.119	0.556	0.309	9.79 – 10.28
RMxM1	BL = 22	9.71	11.68	10.78	0.109	0.509	0.259	10.55 – 11.00
4	MD = 25	5.42	7.38	6.26	0.088	0.442	0.196	6.08 – 6.44
RMxP2	BL = 25	7.79	9.83	8.70	0.109	0.546	0.298	8.48 – 8.93
5	MD = 25	5.56	7.49	6.45	0.096	0.481	0.232	6.25 – 6.65
RMxP1	BL = 25	7.37	9.73	8.59	0.117	0.586	0.344	8.35 – 8.83
6	MD = 21	6.85	8.01	7.35	0.068	0.313	0.098	7.21 – 7.50
RMxC	BL = 21	6.92	9.06	7.96	0.117	0.538	0.289	7.72 – 8.21
7	MD = 19	5.88	7.56	6.76	0.108	0.470	0.221	6.53 – 6.99
RMxLI	BL = 19	5.74	6.98	6.26	0.089	0.387	0.150	6.07 – 6.44
8	MD = 17	7.52	9.56	8.50	0.135	0.557	0.310	8.21 – 8.78
RMxCI	BL = 17	5.90	7.83	7.01	0.117	0.483	0.233	6.76 – 7.26
9	MD = 21	7.51	9.30	8.38	0.105	0.482	0.232	8.16 – 8.60
LMxCI	BL = 21	6.00	7.76	7.03	0.095	0.436	0.190	6.84 – 7.23
10	MD = 20	5.97	7.32	6.71	0.098	0.439	0.193	6.50 – 6.91
LMxLI	BL = 20	5.57	7.10	6.24	0.083	0.372	0.138	6.06 – 6.41
11	MD = 22	6.67	8.20	7.37	0.085	0.400	0.160	7.20 – 7.55
LMxC	BL = 22	7.25	8.89	7.99	0.097	0.456	0.208	7.79 – 8.19
12	MD = 23	5.79	7.32	6.39	0.091	0.437	0.191	6.20 – 6.58
LMxP1	BL = 23	7.03	9.71	8.46	0.130	0.621	0.386	8.19 – 8.73
13	MD = 23	5.03	7.40	6.24	0.102	0.487	0.238	6.03 – 6.46
LMxP2	BL = 23	7.66	9.61	8.73	0.103	0.495	0.245	8.52 – 8.94
14	MD = 21	9.37	11.29	10.14	0.120	0.549	0.301	9.89 – 10.39
LMxM1	BL = 21	9.72	12.09	10.84	0.133	0.610	0.372	10.56 – 11.12
15	MD = 18	7.62	9.95	8.98	0.158	0.670	0.448	8.65 – 9.31
LMxM2	BL = 18	9.35	11.12	10.43	0.126	0.534	0.285	10.17 – 10.70
16	MD = 13	6.99	9.12	8.32	0.195	0.703	0.494	7.90 – 8.75
LMxM3	BL = 13	7.67	11.13	9.90	0.250	0.900	0.810	9.36 – 10.44
17	MD = 15	8.75	10.86	10.06	0.162	0.627	0.393	9.71 – 10.40
LMM3	BL = 15	8.21	10.33	9.54	0.171	0.663	0.440	9.18 – 9.91
18	MD = 21	8.11	11.00	9.93	0.137	0.630	0.396	9.64 – 10.21
LMM2	BL = 21	8.28	10.35	9.60	0.099	0.455	0.207	9.40 – 9.81

19	MD = 20	9.58	11.25	10.58	0.108	0.485	0.235	10.35 – 10.81
LMM1	BL = 20	9.49	11.09	10.16	0.098	0.438	0.192	9.95 – 10.36
20	MD = 23	5.80	7.44	6.58	0.091	0.435	0.189	6.39 – 6.77
LMP2	BL = 23	6.82	8.72	7.86	0.109	0.524	0.274	7.63 – 8.09
21	MD = 23	5.77	7.38	6.55	0.086	0.411	0.169	6.38 – 6.73
LMP1	BL = 23	6.44	8.22	7.39	0.099	0.475	0.226	7.19 – 7.60
22	MD = 21	5.85	7.30	6.46	0.082	0.374	0.140	6.29 – 6.63
LMC	BL = 21	6.25	8.85	7.28	0.110	0.504	0.254	7.05 – 7.51
23	MD = 21	4.18	6.77	5.63	0.140	0.640	0.409	5.34 – 5.92
LMLI	BL = 21	5.27	6.68	6.20	0.078	0.357	0.127	6.04 – 6.36
24	MD = 16	3.46	5.85	5.01	0.153	0.612	0.374	4.68 – 5.33
LMCI	BL = 16	5.38	6.51	5.92	0.081	0.324	0.105	5.75 – 6.10
25	MD = 13	4.29	5.91	5.27	0.128	0.460	0.212	5.00 – 5.55
RMCI	BL = 13	5.34	6.57	5.82	0.103	0.372	0.139	5.59 – 6.04
26	MD = 21	4.86	6.63	5.79	0.108	0.496	0.246	5.56 – 6.02
RMLI	BL = 21	5.35	6.69	6.15	0.075	0.345	0.119	5.99 – 6.30
27	MD = 22	5.92	7.22	6.37	0.074	0.346	0.120	6.22 – 6.53
RMC	BL = 22	6.70	8.83	7.36	0.103	0.484	0.235	7.15 – 7.58
28	MD = 24	6.04	7.34	6.63	0.069	0.339	0.115	6.48 – 6.77
RMP1	BL = 24	6.63	8.14	7.42	0.084	0.410	0.168	7.24 – 6.59
29	MD = 22	5.80	7.44	6.56	0.093	0.438	0.192	6.37 – 6.75
RMP2	BL = 22	6.66	8.78	7.80	0.123	0.579	0.335	7.54 – 8.06
30	MD = 21	9.42	11.35	10.51	0.111	0.506	0.256	10.28 – 10.74
RMM1	BL = 21	9.45	11.14	10.17	0.111	0.506	0.256	9.94 – 10.40
31	MD = 21	8.69	11.42	10.00	0.156	0.714	0.510	9.67 – 10.32
RMM2	BL = 21	8.38	10.35	9.65	0.114	0.523	0.273	9.41 – 9.89
32	MD = 16	8.10	11.24	9.67	0.190	0.761	0.579	9.26 – 10.07
RMM3	BL = 16	7.90	10.37	9.27	0.181	0.725	0.526	8.89 – 9.66
Total N	**1288**							

Table 10 – Descriptive statistics from Polhill, combined sex.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 11	7.26	10.32	8.58	0.231	0.766	0.587	8.06 – 9.09
RMxM3	BL = 11	9.00	11.87	10.30	0.273	0.907	0.823	9.69 – 10.91
2	MD = 14	8.14	10.44	9.21	0.176	0.657	0.432	8.83 – 9.59
RMxM2	BL = 14	9.80	11.52	10.87	0.132	0.493	0.243	10.59 – 11.16
3	MD = 15	8.12	10.84	9.69	0.175	0.677	0.458	9.31 – 10.06
RMxM1	BL = 15	10.33	11.66	11.16	0.090	0.348	0.121	10.97 – 11.36
4	MD = 18	5.66	7.18	6.50	0.102	0.432	0.186	6.29 – 6.72
RMxP2	BL = 18	8.19	10.01	8.98	0.124	0.527	0.278	8.72 – 9.25
5	MD = 16	5.90	7.17	6.53	0.093	0.370	0.137	6.33 – 6.73
RMxP1	BL = 16	7.70	9.81	8.72	0.163	0.652	0.426	8.37 – 9.06
6	MD = 17	7.03	8.16	7.54	0.073	0.299	0.090	7.38 – 7.69
RMxC	BL = 17	7.60	8.61	8.15	0.074	0.304	0.092	8.00 – 8.31
7	MD = 12	4.43	7.14	6.44	0.235	0.813	0.661	5.92 – 6.95
RMxLI	BL = 12	4.56	6.76	6.23	0.176	0.608	0.370	5.85 – 6.62
8	MD = 10	7.77	8.81	8.34	0.128	0.405	0.164	8.05 – 8.63
RMxCI	BL = 10	6.59	7.74	7.17	0.132	0.416	0.173	6.87 – 7.47
9	MD = 14	7.68	8.95	8.34	0.094	0.350	0.123	8.13 – 8.54
LMxCI	BL = 14	6.48	7.75	7.18	0.114	0.428	0.183	6.93 – 7.43
10	MD = 12	6.23	7.49	6.71	0.115	0.400	0.160	6.45 – 6.96
LMxLI	BL = 12	5.15	7.45	6.32	0.178	0.618	0.382	5.93 – 6.71
11	MD = 16	6.79	8.22	7.42	0.110	0.440	0.194	7.18 – 7.65
LMxC	BL = 16	7.57	8.82	8.09	0.093	0.371	0.138	7.89 – 8.29
12	MD = 13	5.60	7.33	6.60	0.160	0.577	0.333	6.25 – 6.94
LMxP1	BL = 13	7.10	9.84	8.88	0.230	0.831	0.691	8.38 – 9.38
13	MD = 12	5.52	7.01	6.41	0.134	0.464	0.216	6.12 – 6.71
LMxP2	BL = 12	7.76	9.79	9.05	0.191	0.661	0.437	8.63 – 9.47
14	MD = 15	9.22	10.82	9.91	0.105	0.408	0.166	9.69 – 10.14
LMxM1	BL = 15	10.23	11.53	11.08	0.081	0.315	0.099	10.91 – 11.26

15	MD = 15	8.33	10.41	9.28	0.151	0.584	0.341	8.96 – 9.61
LMxM2	BL = 15	9.58	11.20	10.62	0.117	0.454	0.206	10.37 – 10.88
16	MD = 11	7.05	9.34	8.58	0.205	0.681	0.463	8.13 – 9.04
LMxM3	BL = 11	9.26	10.97	9.98	0.134	0.444	0.197	9.68 – 10.28
17	MD = 12	9.60	11.63	10.60	0.178	0.617	0.381	10.21 – 10.99
LMM3	BL = 12	8.99	10.30	9.69	0.121	0.419	0.175	9.42 – 9.96
18	MD = 19	9.80	12.67	10.66	0.156	0.678	0.460	10.33 – 10.98
LMM2	BL = 19	8.86	10.72	9.82	0.103	0.449	0.202	9.61 – 10.04
19	MD = 20	9.87	11.75	10.83	0.116	0.517	0.267	10.59 – 11.07
LMM1	BL = 20	9.78	11.52	10.39	0.097	0.435	0.189	10.18 – 10.59
20	MD = 21	5.89	7.41	6.75	0.082	0.376	0.141	6.58 – 6.92
LMP2	BL = 21	7.08	9.18	7.97	0.110	0.505	0.255	7.74 – 8.20
21	MD = 20	6.01	7.47	6.72	0.085	0.380	0.144	6.54 – 6.89
LMP1	BL = 20	6.56	8.75	7.58	0.119	0.531	0.282	7.33 – 7.83
22	MD = 20	5.77	7.66	6.54	0.093	0.416	0.173	6.35 – 6.73
LMC	BL = 20	6.63	8.90	7.56	0.125	0.560	0.314	7.30 – 7.82
23	MD = 17	4.75	6.45	5.67	0.091	0.374	0.140	5.47 – 5.86
LMLI	BL = 17	5.67	7.14	6.34	0.096	0.397	0.158	6.14 – 6.54
24	MD = 12	4.62	5.56	5.07	0.068	0.236	0.056	4.92 – 5.22
LMCI	BL = 12	5.54	6.38	5.97	0.072	0.251	0.063	5.81 – 6.13
25	MD = 14	4.54	5.45	4.95	0.074	0.277	0.077	4.79 – 5.10
RMCI	BL = 14	5.34	6.34	5.86	0.080	0.300	0.090	5.68 – 6.03
26	MD = 17	4.71	6.37	5.57	0.127	0.525	0.276	5.30 – 5.84
RMLI	BL = 17	5.05	7.13	6.25	0.130	0.535	0.287	5.97 – 6.52
27	MD = 22	5.76	7.42	6.47	0.084	0.396	0.157	6.29 – 6.64
RMC	BL = 22	6.41	8.95	7.43	0.115	0.541	0.293	7.19 – 7.67
28	MD = 23	5.83	7.51	6.67	0.087	0.417	0.174	6.48 – 6.85
RMP1	BL = 23	6.82	8.48	7.60	0.090	0.431	0.186	7.41 – 7.79
29	MD = 18	6.14	7.63	6.76	0.090	0.384	0.147	6.57 – 6.95
RMP2	BL = 18	6.88	9.20	7.95	0.118	0.500	0.250	7.70 – 8.20
30	MD = 19	9.98	9.80	10.80	0.137	0.599	0.359	10.51 – 11.09
RMM1	BL = 19	12.10	11.10	10.38	0.079	0.347	0.120	10.22 – 10.55

31	MD = 20	9.71	11.88	10.42	0.114	0.512	0.262	10.18 – 10.66
RMM2	BL = 20	8.93	10.27	9.70	0.090	0.400	0.160	9.51 – 9.89
32	MD = 12	9.74	11.57	10.36	0.172	0.595	0.354	9.98 – 10.74
RMM3	BL = 12	8.49	10.08	9.22	0.141	0.490	0.240	8.91 – 9.53
Total N	**1014**							

Table 11 – Descriptive statistics from Polhill, male data only.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 2	7.26	10.32	8.79	1.530	2.163	4.682	--
RMxM3	BL = 2	9.50	11.87	10.69	1.190	1.676	2.808	--
2	MD = 3	8.87	10.44	9.54	0.468	0.810	0.656	7.53 – 11.55
RMxM2	BL = 3	10.97	11.24	11.10	0.078	0.135	0.018	10.78 – 11.44
3	MD = 4	8.72	10.48	9.62	0.360	0.720	0.519	8.47 – 10.76
RMxM1	BL = 4	11.10	11.66	11.35	0.135	0.271	0.073	10.92 – 11.78
4	MD = 5	5.66	7.18	6.40	0.288	0.644	0.415	5.60 – 7.20
RMxP2	BL = 5	8.24	10.01	9.05	0.296	0.662	0.438	8.23 – 9.87
5	MD = 5	5.90	7.11	6.56	0.237	0.529	0.280	5.91 – 7.22
RMxP1	BL = 5	7.70	9.78	8.78	0.403	0.901	0.811	7.67 – 9.90
6	MD = 5	7.27	7.99	7.59	0.138	0.310	0.096	7.20 – 7.97
RMxC	BL = 5	7.88	8.61	8.28	0.122	0.272	0.074	7.94 – 8.62
7	MD = 4	4.43	7.14	6.21	0.606	1.211	1.467	4.28 – 8.14
RMxLI	BL = 4	4.56	6.74	5.86	0.462	0.925	0.855	4.39 – 7.33
8	MD = 2	8.04	8.15	8.10	0.055	0.078	0.006	--
RMxCI	BL = 2	6.90	7.67	7.29	0.385	0.544	0.296	--
9	MD = 4	7.68	8.41	8.12	0.178	0.355	0.126	7.55 – 8.68
LMxCI	BL = 4	6.48	7.65	6.99	0.244	0.488	0.239	6.21 – 7.76
10	MD = 5	6.23	7.49	6.94	0.221	0.495	0.245	6.33 – 7.55
LMxLI	BL = 5	5.15	7.45	6.21	0.395	0.883	0.779	5.12 – 7.31
11	MD = 5	7.11	7.75	7.48	0.147	0.328	0.108	7.08 – 7.89
LMxC	BL = 5	7.80	8.82	8.28	0.179	0.400	0.160	7.78 – 8.77

12	MD = 5	5.73	7.33	6.54	0.331	0.740	0.548	5.62 – 7.46
LMxP1	BL = 5	8.11	9.75	9.08	0.285	0.637	0.406	8.29 – 9.87
13	MD = 4	5.52	6.66	6.24	0.273	0.546	0.298	5.36 – 7.10
LMxP2	BL = 4	8.14	9.32	9.05	0.321	0.642	0.412	8.03 – 10.07
14	MD = 2	9.53	9.89	9.71	0.180	0.255	0.065	--
LMxM1	BL = 2	10.81	11.53	11.17	0.360	0.509	0.259	--
15	MD = 2	9.00	9.12	9.06	0.060	0.085	0.007	--
LMxM2	BL = 2	10.41	10.88	10.65	0.235	0.332	0.110	--
16	MD = 1	--	--	--	--	--	--	--
LMxM3	BL = 1	--	--	--	--	--	--	--
17	MD = 6	9.60	11.63	10.64	0.301	0.738	0.544	9.86 – 11.41
LMM3	BL = 6	9.51	10.30	9.93	0.130	0.318	0.101	9.59 – 10.26
18	MD = 6	9.95	11.57	10.67	0.280	0.687	0.471	9.94 – 11.39
LMM2	BL = 6	8.86	10.72	9.93	0.276	0.676	0.457	9.22 – 10.64
19	MD = 4	11.18	11.75	11.37	0.130	0.260	0.068	10.95 – 11.78
LMM1	BL = 4	10.11	11.52	10.75	0.305	0.610	0.372	9.78 – 11.72
20	MD = 8	5.89	7.41	6.69	0.174	0.493	0.243	6.27 – 7.09
LMP2	BL = 8	7.08	9.18	8.03	0.241	0.682	0.465	7.46 – 8.60
21	MD = 7	6.01	7.47	6.91	0.181	0.479	0.230	6.46 – 7.35
LMP1	BL = 7	6.56	8.75	7.80	0.271	0.716	0.513	7.14 – 8.46
22	MD = 8	5.82	7.66	6.61	0.178	0.504	0.254	6.19 – 7.03
LMC	BL = 8	7.49	8.90	8.02	0.191	0.540	0.291	7.57 – 8.47
23	MD = 7	5.23	6.45	5.62	0.153	0.405	0.164	5.25 – 6.00
LMLI	BL = 7	5.93	7.14	6.43	0.182	0.482	0.232	5.98 – 6.87
24	MD = 3	4.62	5.15	4.90	0.153	0.266	0.071	4.24 – 5.56
LMCI	BL = 3	5.75	6.11	5.94	0.105	0.181	0.033	5.49 – 6.39
25	MD = 4	4.58	4.89	4.69	0.068	0.136	0.018	4.48 – 4.91
RMCI	BL = 4	5.50	5.95	5.81	0.103	0.207	0.043	5.48 – 6.13
26	MD = 8	4.71	6.34	5.43	0.214	0.605	0.367	4.93 – 5.94
RMLI	BL = 8	5.78	7.13	6.31	0.193	0.545	0.297	5.85 – 6.76
27	MD = 8	5.94	7.42	6.55	0.150	0.425	0.181	6.19 – 6.91
RMC	BL = 8	7.16	8.95	7.82	0.220	0.622	0.387	7.30 – 8.34

28 RMP1	MD = 8	5.83	7.51	6.76	0.189	0.533	0.284	6.32 – 7.21
	BL = 8	6.82	8.48	7.73	0.187	0.528	0.279	7.29 – 8.18
29 RMP2	MD = 6	6.29	7.63	6.68	0.199	0.488	0.238	6.17 – 7.20
	BL = 6	7.36	9.20	8.07	0.251	0.615	0.378	7.43 – 8.72
30 RMM1	MD = 5	10.16	11.50	10.95	0.246	0.550	0.303	10.27 – 11.64
	BL = 5	10.21	10.91	10.48	0.126	0.281	0.079	10.13 – 10.83
31 RMM2	MD = 6	9.71	10.64	10.31	0.138	0.338	0.114	9.96 – 10.67
	BL = 6	8.93	10.13	9.71	0.193	0.473	0.224	9.21 – 10.21
32 RMM3	MD = 5	9.74	11.57	10.47	0.303	0.678	0.460	9.63 – 11.31
	BL = 5	9.03	10.08	9.44	0.221	0.494	0.244	8.82 – 11.31
Total N	**314**							

Table 12 – Descriptive statistics from Polhill, female data only.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1 RMxM3	MD = 9	7.98	9.12	8.53	0.123	0.368	0.136	8.25 – 8.82
	BL = 9	9.00	11.32	10.21	0.265	0.795	0.631	9.60 – 10.82
2 RMxM2	MD = 11	8.14	10.32	9.13	0.188	0.624	0.390	8.71 – 9.54
	BL = 11	9.80	11.52	10.81	0.163	0.540	0.292	10.45 – 11.17
3 RMxM1	MD = 11	8.12	10.84	9.72	0.209	0.694	0.482	9.25 – 10.18
	BL = 11	10.33	11.52	11.09	0.108	0.358	0.128	10.85 – 11.33
4 RMxP2	MD = 13	5.71	7.17	6.54	0.096	0.344	0.119	6.33 – 6.75
	BL = 13	8.19	9.63	8.96	0.137	0.495	0.245	8.66 – 9.26
5 RMxP1	MD = 11	6.08	7.17	6.52	0.092	0.305	0.093	6.31 – 6.72
	BL = 11	7.83	9.81	8.68	0.168	0.557	0.311	8.31 – 9.06
6 RMxC	MD = 12	7.03	8.16	7.51	0.088	0.306	0.094	7.32 – 7.71
	BL = 12	7.60	8.60	8.10	0.090	0.311	0.097	7.90 – 8.30
7 RMxLI	MD = 8	5.08	6.95	6.55	0.214	0.605	0.366	6.04 – 7.05
	BL = 8	5.85	6.76	6.42	0.109	0.307	0.094	6.16 – 6.68
8 RMxCI	MD = 8	7.77	8.81	8.40	0.154	0.434	0.189	8.04 – 8.77
	BL = 8	6.59	7.74	7.14	0.148	0.419	0.176	6.79 – 7.49

9	MD = 10	7.94	8.95	8.43	0.102	0.323	0.104	8.19 – 8.66
LMxCl	BL = 10	6.57	7.75	7.25	0.128	0.407	0.163	6.97 – 7.54
10	MD = 7	6.28	6.89	6.54	0.087	0.230	0.053	6.33 – 6.75
LMxLl	BL = 7	5.91	7.19	6.40	0.153	0.405	0.164	6.02 – 6.77
11	MD = 11	6.79	8.22	7.39	0.149	0.495	0.245	7.06 – 7.72
LMxC	BL = 11	7.57	8.50	8.01	0.104	0.343	0.118	7.78 – 8.24
12	MD = 8	5.60	7.32	6.63	0.178	0.504	0.254	6.21 – 7.05
LMxP1	BL = 8	7.10	9.84	8.75	0.336	0.951	0.904	7.96 – 9.55
13	MD = 8	5.86	7.01	6.50	0.152	0.429	0.184	6.14 – 6.86
LMxP2	BL = 8	7.76	9.79	9.05	0.253	0.715	0.511	8.45 – 9.64
14	MD = 13	9.22	10.82	9.94	0.118	0.425	0.181	9.69 – 10.20
LMxM1	BL = 13	10.23	11.37	11.07	0.084	0.304	0.092	10.88 – 11.25
15	MD = 13	8.33	10.41	9.32	0.173	0.622	0.387	8.94 – 9.69
LMxM2	BL = 13	9.58	11.20	10.62	0.133	0.481	0.231	10.33 – 10.91
16	MD = 10	7.74	9.34	8.74	0.151	0.476	0.227	8.40 – 9.08
LMxM3	BL = 10	9.26	10.97	10.02	0.142	0.448	0.201	9.70 – 10.34
17	MD = 6	9.94	11.46	10.56	0.220	0.539	0.290	9.99 – 11.12
LMM3	BL = 6	8.99	10.15	9.46	0.159	0.388	0.151	9.05 – 9.86
18	MD = 13	9.80	12.67	10.65	0.195	0.702	0.493	10.23 – 11.08
LMM2	BL = 13	9.12	10.18	9.77	0.089	0.322	0.104	9.58 – 9.97
19	MD = 16	9.87	11.73	10.70	0.120	0.479	0.229	10.44 – 10.95
LMM1	BL = 16	9.78	11.10	10.29	0.087	0.348	0.121	10.11 – 10.48
20	MD = 13	6.37	7.29	6.80	0.082	0.297	0.088	6.62 – 6.98
LMP2	BL = 13	7.22	8.40	7.93	0.107	0.387	0.150	7.70 – 8.17
21	MD = 13	6.19	7.05	6.61	0.079	0.286	0.082	6.44 – 6.79
LMP1	BL = 13	6.92	8.08	7.46	0.106	0.384	0.147	7.23 – 7.69
22	MD = 12	5.77	7.12	6.49	0.104	0.362	0.131	6.26 – 6.72
LMC	BL = 12	6.63	7.63	7.26	0.093	0.322	0.104	7.05 – 7.46
23	MD = 10	4.75	6.11	5.70	0.117	0.369	0.136	5.43 – 5.96
LMLl	BL = 10	5.67	6.83	6.28	0.107	0.339	0.115	6.03 – 6.52
24	MD = 9	4.91	5.56	5.13	0.070	0.210	0.044	4.97 – 5.29
LMCl	BL = 9	5.54	6.38	5.98	0.093	0.279	0.078	5.76 – 6.19

25	MD = 10	4.54	5.45	5.05	0.080	0.254	0.065	4.86 – 5.23
RMCI	BL = 10	5.34	6.34	5.88	0.107	0.338	0.114	5.64 – 6.12
26	MD = 9	4.75	6.37	5.70	0.147	0.440	0.194	5.36 – 6.04
RMLI	BL = 9	5.05	6.80	6.20	0.185	0.554	0.307	5.77 – 6.62
27	MD = 14	5.76	7.25	6.42	0.103	0.387	0.149	6.19 – 6.64
RMC	BL = 14	6.41	7.67	7.21	0.091	0.341	0.116	7.01 – 7.40
28	MD = 15	6.14	7.26	6.61	0.091	0.351	0.123	6.42 – 6.81
RMP1	BL = 15	7.07	8.36	7.53	0.096	0.371	0.137	7.32 – 7.73
29	MD = 12	6.14	7.40	6.79	0.098	0.339	0.115	6.58 – 7.01
RMP2	BL = 12	6.88	8.54	7.89	0.130	0.451	0.203	7.61 – 8.18
30	MD = 14	9.98	12.10	10.74	0.167	0.625	0.391	10.38 – 11.10
RMM1	BL = 14	9.80	11.10	10.35	0.099	0.370	0.137	10.13 – 10.56
31	MD = 14	9.73	11.88	10.47	0.154	0.575	0.331	10.14 – 10.80
RMM2	BL = 14	9.03	10.27	9.70	0.103	0.385	0.148	9.47 – 9.92
32	MD = 7	9.79	11.12	10.28	0.215	0.570	0.325	9.76 – 10.81
RMM3	BL = 7	8.49	9.86	9.06	0.172	0.456	0.208	8.64 – 9.48
Total N	**700**							

Table 13 – Descriptive statistics from Eastry, combined sex.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 4	7.73	9.50	8.67	0.388	0.775	0.601	7.43 – 9.90
RMxM3	BL = 4	10.39	11.73	10.78	0.318	0.637	0.405	9.77 – 11.79
2	MD = 3	8.67	10.35	9.41	0.496	0.859	0.738	7.27 – 11.54
RMxM2	BL = 3	10.73	11.08	10.94	0.106	0.183	0.034	10.48 – 11.39
3	MD = 5	9.67	10.71	10.23	0.192	0.430	0.185	9.70 – 10.77
RMxM1	BL = 5	10.01	11.39	10.83	0.244	0.545	0.297	10.15 – 11.50
4	MD = 3	5.74	7.23	6/36	0.449	0.777	0.604	4.43 – 8.29
RMxP2	BL = 3	7.88	8.61	8.34	0.233	0.403	0.162	7.34 – 9.34
5	MD = 3	6.20	6.99	6.67	0.241	0.418	0.174	5.64 – 7.71
RMxP1	BL = 3	8.20	9.41	8.23	0.350	0.606	0.367	7.32 – 10.33

6	MD = 5	6.24	7.97	7.21	0.285	0.637	0.405	6.42 – 8.00
RMxC	BL = 5	7.85	8.58	8.19	0.150	0.334	0.112	7.77 – 8.60
7	MD = 2	6.04	6.59	6.32	0.275	0.389	0.151	--
RMxLI	BL = 2	6.08	6.34	6.21	0.130	0.184	0.034	--
8	MD = 1	--	--	--	--	--	--	--
RMxCI	BL = 1	--	--	--	--	--	--	--
9	MD = 3	8.58	9.18	8.93	0.179	0.311	0.097	8.15 – 9.70
LMxCI	BL = 3	6.99	7.51	7.25	0.150	0.260	0.068	6.60 – 7.89
10	MD = 3	5.91	7.78	6.87	0.540	0.936	0.876	4.54 – 9.19
LMxLI	BL = 3	5.74	6.39	6.07	0.188	0.325	0.106	5.25 – 6.87
11	MD = 5	7.08	7.82	7.38	0.121	0.270	0.073	7.05 – 7.72
LMxC	BL = 5	7.55	8.61	8.06	0.189	0.424	0.179	7.53 – 8.59
12	MD = 4	6.32	6.63	6.49	0.065	0.129	0.017	6.28 – 6.70
LMxP1	BL = 4	7.83	9.42	8.67	0.327	0.654	0.428	7.62 – 9.71
13	MD = 4	5.96	6.80	6.35	0.180	0.359	0.129	5.78 – 6.92
LMxP2	BL = 4	7.94	9.11	8.43	0.280	0.560	0.313	7.54 – 9.32
14	MD = 4	9.51	10.30	9.94	0.165	0.331	0.109	9.41 – 10.47
LMxM1	BL = 4	9.68	11.21	10.45	0.338	0.676	0.456	9.37 – 11.52
15	MD = 4	8.56	11.14	9.61	0.551	1.102	1.214	7.85 – 11.36
LMxM2	BL = 4	9.66	11.74	10.59	0.510	1.021	1.042	8.96 – 12.21
16	MD = 4	8.01	9.64	8.95	0.371	0.742	0.551	7.77 – 10.13
LMxM3	BL = 4	9.81	10.86	10.28	0.221	0.443	0.196	9.57 – 10.98
17	MD = 3	9.74	10.53	10.17	0.231	0.400	0.160	9.18 – 11.16
LMM3	BL = 3	9.43	9.73	9.57	0.088	0.152	0.023	9.19 – 9.94
18	MD = 5	9.51	10.95	9.90	0.269	0.602	0.362	9.15 – 10.65
LMM2	BL = 5	9.12	10.20	9.64	0.207	0.462	0.213	9.06 – 10.21
19	MD = 6	10.02	11.49	10.70	0.250	0.612	0.375	10.06 – 11.34
LMM1	BL = 6	9.32	10.70	10.16	0.219	0.536	0.287	9.59 – 10.72
20	MD = 6	6.35	6.97	6.64	0.093	0.228	0.052	6.40 – 6.88
LMP2	BL = 6	6.68	8.09	7.61	0.227	0.555	0.308	7.02 – 8.19
21	MD = 7	6.30	7.34	6.61	0.142	0.376	0.141	6.27 – 6.96
LMP1	BL = 7	6.80	8.15	7.49	0.169	0.446	0.199	7.07 – 7.90

22	MD = 7	6.24	6.77	6.57	0.070	0.186	0.035	6.40 – 6.75
LMC	BL = 7	7.02	8.17	7.56	0.146	0.385	0.148	7.21 – 7.92
23	MD = 6	5.47	5.92	5.77	0.070	0.171	0.029	5.59 – 5.95
LMLI	BL = 6	5.75	6.82	6.25	0.156	0.382	0.146	5.84 – 6.65
24	MD = 6	4.84	5.46	5.20	0.097	0.238	0.056	4.95 – 5.45
LMCI	BL = 6	5.65	6.34	5.96	0.106	0.259	0.067	5.69 – 6.23
25	MD = 3	5.05	5.35	5.19	0.087	0.150	0.023	4.82 – 5.57
RMCI	BL = 3	5.68	6.28	6.00	0.175	0.303	0.092	5.25 – 6.76
26	MD = 5	5.78	6.19	5.96	0.070	0.156	0.024	5.77 – 6.16
RMLI	BL = 5	5.92	6.94	6.27	0.178	0.399	0.159	5.77 – 6.76
27	MD = 8	6.05	6.93	6.63	0.099	0.278	0.078	6.40 – 6.87
RMC	BL = 8	7.14	8.27	7.57	0.159	0.449	0.202	7.19 – 7.94
28	MD = 8	6.26	7/45	6.79	0.133	0.377	0.142	6.48 – 7.10
RMP1	BL = 8	6.40	8.36	7.61	0.215	0.609	0.371	7.10 – 8.12
29	MD = 10	6.18	8.09	6.87	0.186	0.589	0.347	6.45 – 7.29
RMP2	BL = 10	6.65	8.43	7.76	0.174	0.549	0.302	7.37 – 8.15
30	MD = 7	9.97	11.44	10.71	0.199	0.525	0.276	10.22 – 11.19
RMM1	BL = 7	9.74	10.93	10.27	0.143	0.380	0.144	9.92 – 10.62
31	MD = 7	9.36	11.26	10.17	0.247	0.654	0.428	9.56 – 10.77
RMM2	BL = 7	9.13	10.70	9.61	0.210	0.556	0.309	9.10 – 10.13
32	MD = 6	8.29	10.25	9.58	0.304	0.744	0.553	8.80 – 10.36
RMM3	BL = 6	8.67	9.99	9.33	0.203	0.498	0.248	8.81 – 9.86
Total N	**314**							

Table 14 – Descriptive statistics from Eastry, male data only.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 2	8.39	9.06	8.73	0.335	0.474	0.224	--
RMxM3	BL = 2	10.45	10.55	10.50	0.050	0.071	0.005	--
2	MD = 2	8.67	10.35	9.51	0.840	1.188	1.411	--
RMxM2	BL = 2	11.00	11.08	11.04	0.040	0.057	0.003	--

3	MD = 3	10.07	10.62	10.26	0.179	0.309	0.096	9.50 – 11.03
RMxM1	BL = 3	10.57	11.39	10.99	0.237	0.410	0.168	9.97 – 12.01
4	MD = 2	5.74	6.10	5.92	0.180	0.255	0.065	--
RMxP2	BL = 2	7.88	8.61	8.25	0.365	0.516	0.266	--
5	MD = 0	--	--	--	--	--	--	--
RMxP1	BL = 0	--	--	--	--	--	--	--
6	MD = 1	--	--	--	--	--	--	--
RMxC	BL = 1	--	--	--	--	--	--	--
7	MD = 0	--	--	--	--	--	--	--
RMxLI	BL = 0	--	--	--	--	--	--	--
8	MD = 1	--	--	--	--	--	--	--
RMxCI	BL = 1	--	--	--	--	--	--	--
9	MD = 1	--	--	--	--	--	--	--
LMxCI	BL = 1	--	--	--	--	--	--	--
10	MD = 0	--	--	--	--	--	--	--
LMxLI	BL = 0	--	--	--	--	--	--	--
11	MD = 1	--	--	--	--	--	--	--
LMxC	BL = 1	--	--	--	--	--	--	--
12	MD = 1	--	--	--	--	--	--	--
LMxP1	BL = 1	--	--	--	--	--	--	--
13	MD = 1	--	--	--	--	--	--	--
LMxP2	BL = 1	--	--	--	--	--	--	--
14	MD = 2	10.05	10.30	10.18	0.125	0.177	0.031	--
LMxM1	BL = 2	10.76	11.21	10.99	0.225	0.318	0.101	--
15	MD = 1	--	--	--	--	--	--	--
LMxM2	BL = 1	--	--	--	--	--	--	--
16	MD = 2	8.72	9.44	9.08	0.360	0.509	0.259	--
LMxM3	BL = 2	10.33	10.86	10.60	0.265	0.315	0.140	--
17	MD = 2	9.74	10.53	10.14	0.395	0.559	0.312	--
LMM3	BL = 2	9.43	9.73	9.58	0.150	0.212	0.045	--
18	MD = 2	9.51	9.67	9.59	0.080	0.113	0.013	--
LMM2	BL = 2	9.12	10.20	9.66	0.540	0.764	0.583	--

19	MD = 3	10.19	11.21	10.56	0.326	0.565	0.319	9.16 – 11.96
LMM1	BL = 3	9.32	10.70	9.95	0.403	0.699	0.488	8.21 – 11.68
20	MD = 2	6.35	6.68	6.52	0.165	0.233	0.054	--
LMP2	BL = 2	7.70	8.07	7.89	0.185	0.262	0.068	--
21	MD = 2	6.30	6.33	6.32	0.015	0.021	0.000	--
LMP1	BL = 2	7.20	7.20	7.20	0.000	0.000	0.000	--
22	MD = 2	6.59	6.77	6.68	0.090	0.127	0.016	--
LMC	BL = 2	7.81	8.17	7.99	0.180	0.255	0.065	--
23	MD = 1	--	--	--	--	--	--	--
LMLI	BL = 1	--	--	--	--	--	--	--
24	MD = 1	--	--	--	--	--	--	--
LMCI	BL = 1	--	--	--	--	--	--	--
25	MD = 1	--	--	--	--	--	--	--
RMCI	BL = 1	--	--	--	--	--	--	--
26	MD = 1	--	--	--	--	--	--	--
RMLI	BL = 1	--	--	--	--	--	--	--
27	MD = 2	6.68	6.90	6.79	0.110	0.156	0.024	--
RMC	BL = 2	8.22	8.27	8.25	0.025	0.035	0.001	--
28	MD = 3	6.26	7.45	6.75	0.359	0.622	0.387	5.20 – 8.30
RMP1	BL = 3	6.40	7.39	7.05	0.323	0.560	0.314	5.65 – 8.44
29	MD = 5	6.18	8.09	6.72	0.349	0.781	0.611	5.75 – 7.69
RMP2	BL = 5	6.65	8.02	7.50	0.228	0.510	0.260	6.86 – 8.13
30	MD = 2	10.10	10.87	10.49	0.385	0.544	0.296	--
RMM1	BL = 2	9.96	10.93	10.45	0.485	0.686	0.470	--
31	MD = 3	9.36	10.56	9.88	0.355	0.614	0.378	8.36 – 11.41
RMM2	BL = 3	9.13	10.70	9.66	0.518	0.989	0.806	7.43 – 11.89
32	MD = 3	8.29	10.20	9.49	0.603	1.045	1.092	6.98 – 12.09
RMM3	BL = 3	9.34	9.99	9.70	0.190	0.330	0.109	8.88 – 10.52
Total N	**110**							

Table 15 – Descriptive statistics from Eastry, female data only.

Tooth	N	Minimum Value	Maximum Value	Mean	Std. Error	Std. Deviation	Variance	Confidence Interval (95%)
1	MD = 2	7.73	9.50	8.62	0.885	1.251	1.566	--
RMxM3	BL = 2	10.39	11.73	11.06	0.670	0.948	0.898	--
2	MD = 1	--	--	--	--	--	--	--
RMxM2	BL = 1	--	--	--	--	--	--	--
3	MD = 2	9.67	10.71	10.19	0.520	0.735	0.541	--
RMxM1	BL = 2	10.01	11.15	10.58	0.570	0.806	0.650	--
4	MD = 1	--	--	--	--	--	--	--
RMxP2	BL = 1	--	--	--	--	--	--	--
5	MD = 3	6.20	6.99	6.67	0.241	0.418	0.174	5.63 – 7.71
RMxP1	BL = 3	8.20	9.41	8.82	0.350	0.606	0.367	7.32 – 10.33
6	MD = 4	7.09	7.97	7.46	0.190	0.381	0.145	6.85 – 8.06
RMxC	BL = 4	7.85	8.58	8.11	0.162	0.325	0.105	7.59 – 8.62
7	MD = 2	6.04	6.59	6.32	0.275	0.389	0.151	--
RMxLI	BL = 2	6.08	6.34	6.21	0.130	0.184	0.034	--
8	MD = 0	--	--	--	--	--	--	--
RMxCI	BL = 0	--	--	--	--	--	--	--
9	MD = 2	8.58	9.18	8.88	0.300	0.424	0.180	--
LMxCI	BL = 2	6.99	7.24	7.12	0.125	0.177	0.031	--
10	MD = 3	5.91	7.78	6.87	0.540	0.936	0.876	4.54 – 9.19
LMxLI	BL = 3	5.74	6.39	6.07	0.188	0.325	0.106	5.26 – 6.87
11	MD = 4	7.08	7.82	7.39	0.156	0.312	0.097	6.89 – 7.88
LMxC	BL = 4	7.55	8.61	7.99	0.225	0.449	0.202	7.27 – 8.70
12	MD = 3	6.32	6.63	6.49	0.091	0.158	0.025	6.10 – 6.89
LMxP1	BL = 3	7.83	9.42	8.68	0.462	0.801	0.641	6.69 – 10.67
13	MD = 3	5.96	6.80	6.40	0.244	0.422	0.178	5.36 – 7.45
LMxP2	BL = 3	7.94	9.11	8.35	0.380	0.659	0.434	6.71 – 9.99
14	MD = 2	9.51	9.90	9.71	0.195	0.276	0.076	--
LMxM1	BL = 2	9.68	10.13	9.91	0.225	0.318	0.101	--

15	MD = 3	8.56	11.14	9.75	0.751	1.302	1.694	6.52 – 12.98
LMxM2	BL = 3	9.66	11.74	10.40	0.672	1.163	1.352	7.51 – 13.29
16	MD = 2	8.01	9.64	8.83	0.815	1.152	1.328	--
LMxM3	BL = 2	9.81	10.11	9.96	0.150	0.212	0.045	--
17	MD = 1	--	--	--	--	--	--	--
LMM3	BL = 1	--	--	--	--	--	--	--
18	MD = 3	9.53	10.95	10.11	0.431	0.747	0.557	8.25 – 11.96
LMM2	BL = 3	9.20	9.87	9.62	0.211	0.366	0.134	8.71 – 10.53
19	MD = 3	10.02	11.49	10.84	0.432	0.748	0.560	8.98 – 12.70
LMM1	BL = 3	10.08	10.70	10.37	0.180	0.313	0.098	9.59 – 11.14
20	MD = 4	6.47	6.68	6.70	0.115	0.229	0.052	6.34 – 7.07
LMP2	BL = 4	6.97	8.09	7.47	0.321	0.643	0.413	6.44 – 8.49
21	MD = 5	6.36	7.34	6.73	0.173	0.387	0.150	6.25 – 7.21
LMP1	BL = 5	6.80	8.15	7.60	0.220	0.492	0.242	6.99 – 8.21
22	MD = 5	6.24	6.76	6.53	0.090	0.200	0.040	6.28 – 6.78
LMC	BL = 5	7.02	7.68	7.39	0.126	0.282	0.080	7.04 – 7.74
23	MD = 5	5.47	5.92	5.78	0.084	0.188	0.035	5.55 – 6.02
LMLI	BL = 5	5.75	6.47	6.13	0.129	0.288	0.083	5.77 – 6.49
24	MD = 5	4.84	5.46	5.23	0.112	0.251	0.063	4.92 – 5.54
LMCI	BL = 5	5.65	6.09	5.88	0.089	0.199	0.040	5.63 – 6.13
25	MD = 2	5.05	5.35	5.20	0.150	0.212	0.045	--
RMCI	BL = 2	5.68	6.05	5.87	0.285	0.262	0.068	--
26	MD = 4	5.78	6.01	5.91	0.052	0.105	0.011	5.74 – 6.07
RMLI	BL = 4	5.92	6.29	6.10	0.078	0.156	0.024	5.85 – 6.35
27	MD = 6	6.05	6.93	6.58	0.123	0.302	0.091	6.26 – 6.90
RMC	BL = 6	7.14	7.70	7.34	0.079	0.194	0.038	7.14 – 7.55
28	MD = 5	6.59	7.10	6.81	0.103	0.230	0.053	6.53 – 7.10
RMP1	BL = 5	7.53	8.36	7.95	0.146	0.326	0.106	7.55 – 8.36
29	MD = 5	6.66	7.54	7.02	0.152	0.339	0.115	6.60 – 7.44
RMP2	BL = 5	7.27	8.43	8.02	0.221	0.494	0.244	7.41 – 8.64
30	MD = 5	9.97	11.44	10.80	0.247	0.553	0.305	10.11 – 11.48
RMM1	BL = 5	9.74	10.47	10.20	0.124	0.278	0.077	9.86 – 10.54

31	MD = 4	9.60	11.26	10.38	0.341	0.681	0.464	9.29 – 11.46
RMM2	BL = 4	9.30	9.86	9.58	0.138	0.276	0.076	9.14 – 10.01
32	MD = 3	9.27	10.25	9.66	0.299	0.518	0.268	8.38 – 10.95
RMM3	BL = 3	8.67	9.34	8.97	0.197	0.340	0.116	8.12 – 9.82
Total N	**204**							

Appendix 2: Bivariate plots of correlation between MD and BL measurements

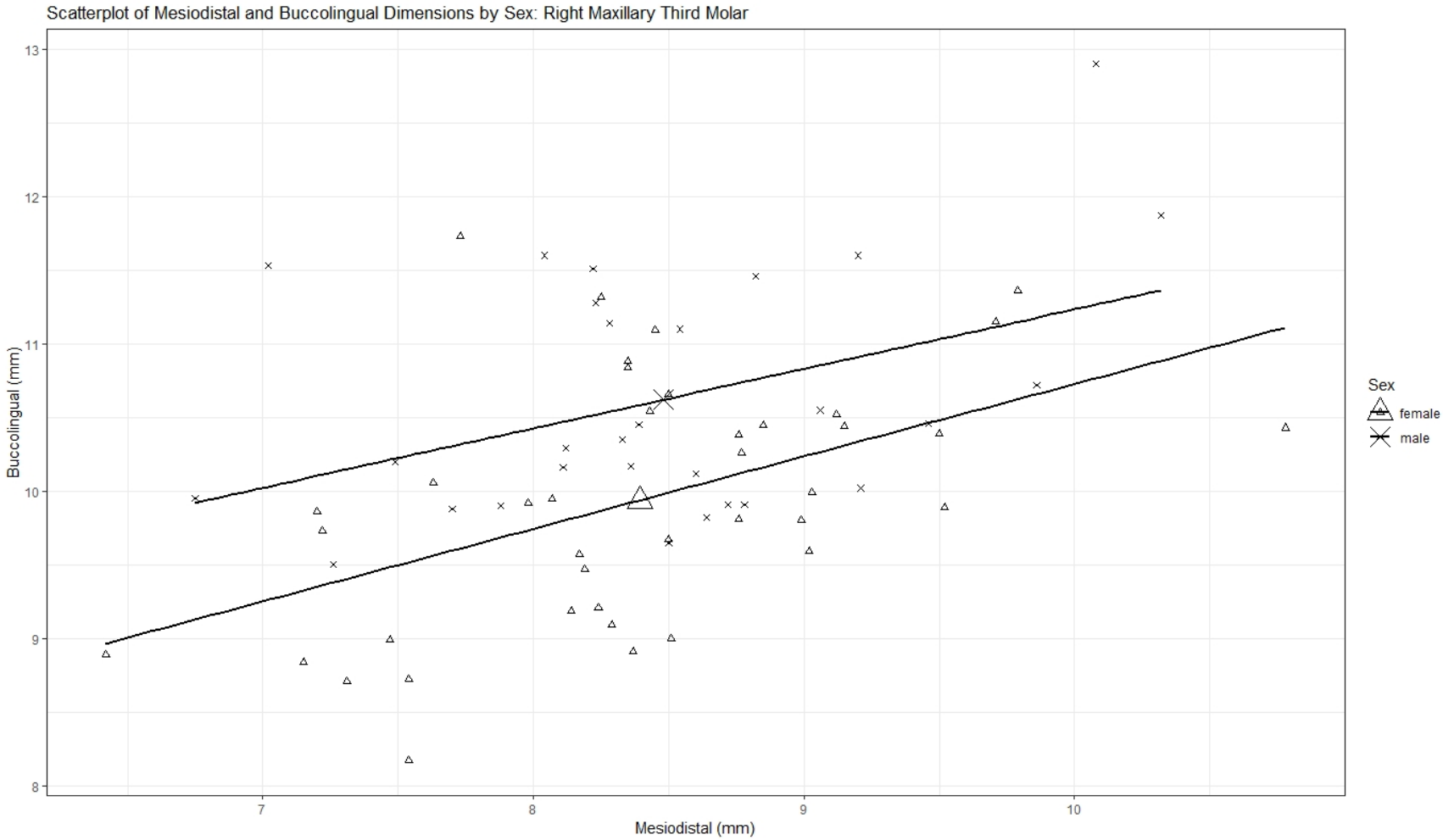

Figure 1 - Correlation of MD and BL measurements of the right maxillary third molar, separated by sex. Regression equation for males: $y=7.2+0.4*x$, $r^2 = 0.172$. Regression equation for females: $y=5.91+0.49*x$, $r^2 = 0.244$.

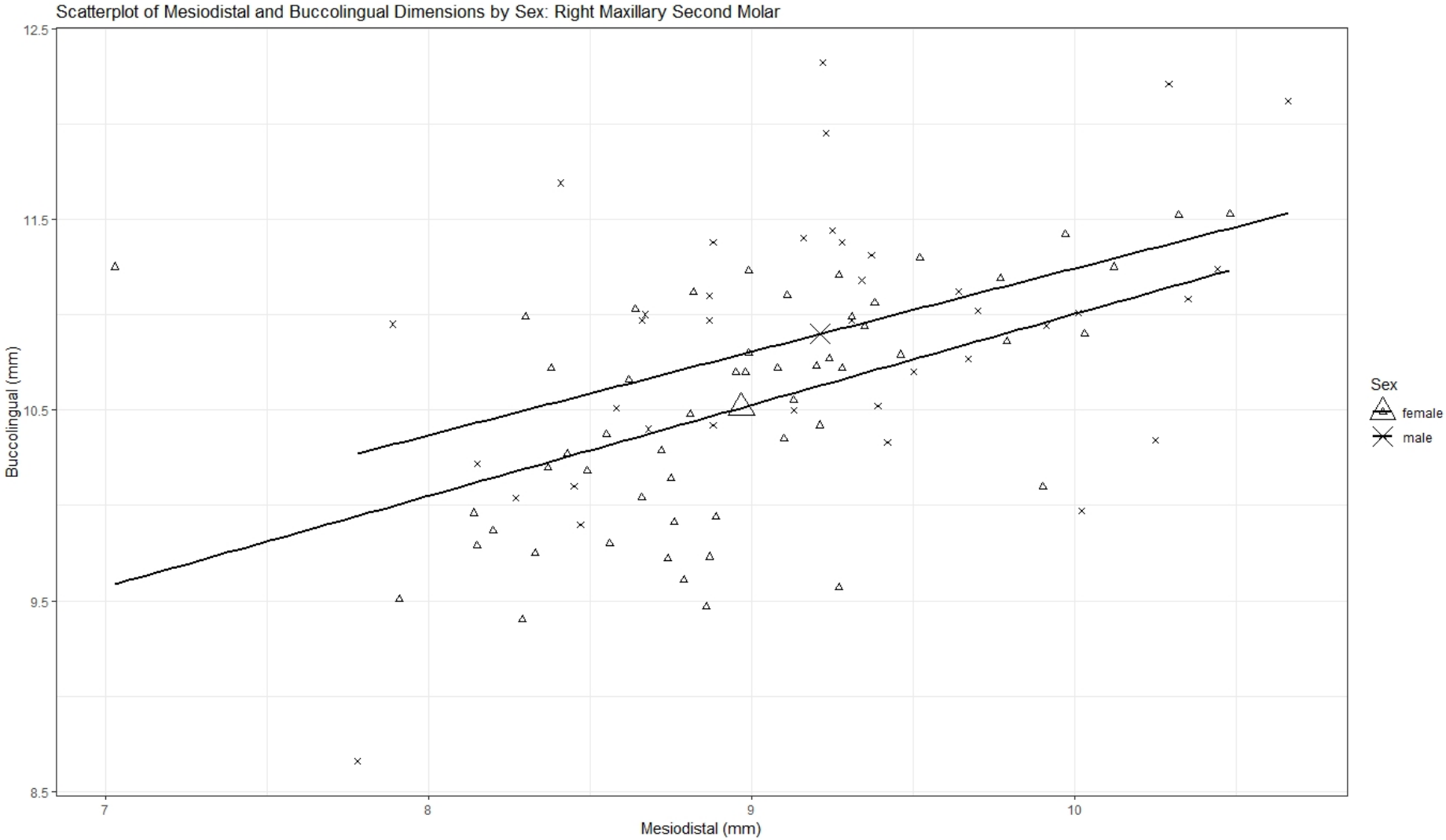

Figure 2 - Correlation of MD and BL measurements for the right maxillary second molar, separated by sex. Regression equation for males: y=6.87+0.44*x, r2 = 0.194. Regression equation for females: y=6.23+0.48*x, r2 = 0.260.

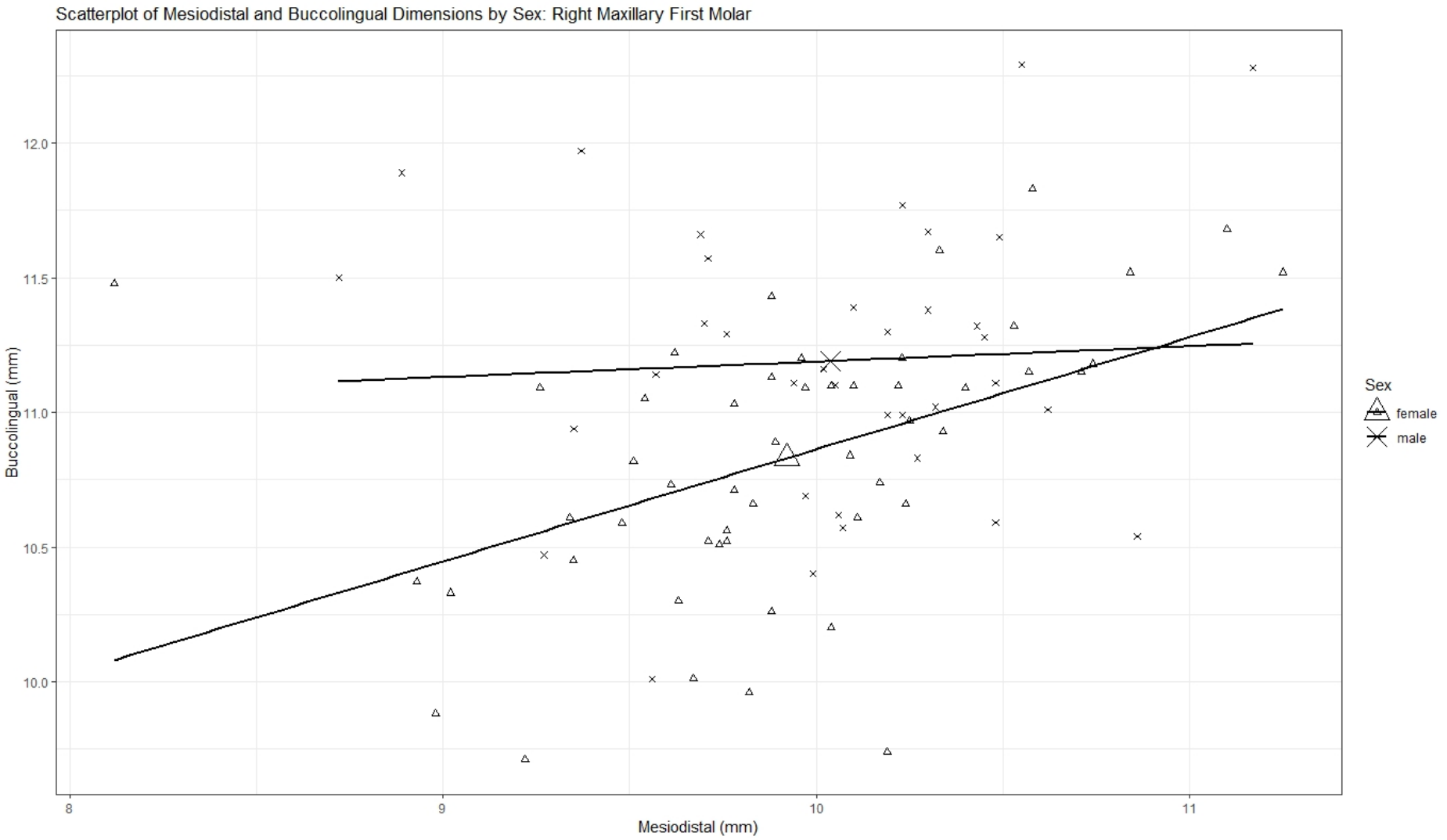

Figure 3 - Correlation of MD and BL measurements for the right maxillary first molar, separated by sex. Regression equation for males: y=10.62+0.06*x, r22 = 0.003. Regression equation for females: y=6.7+0.42*x, r2 = 0.223.

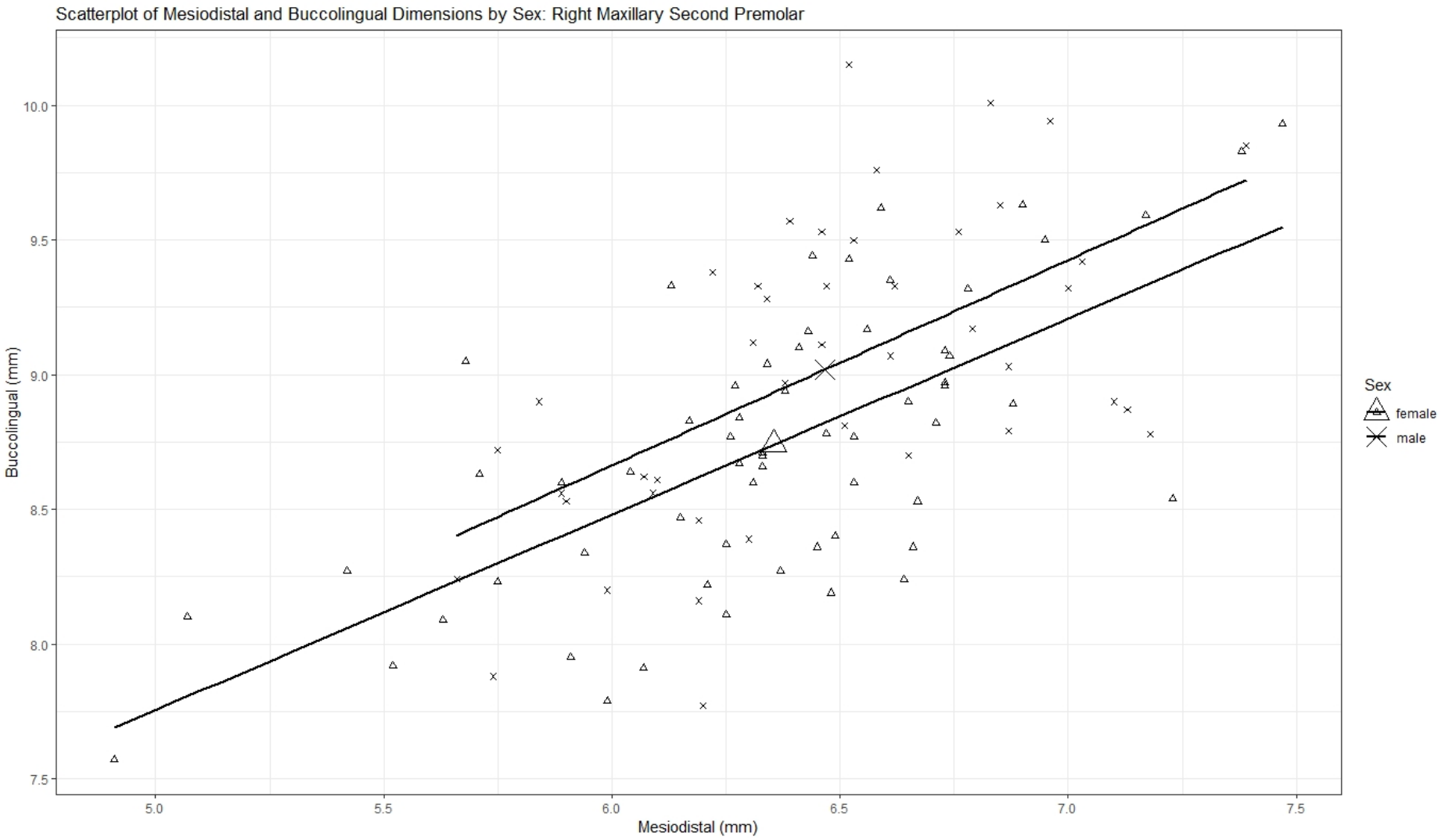

Figure 4 - Correlation between MD and BL measurements for the right maxillary second premolar, separated by sex. Regression equation for males: y= 4.00+0.76*x, r2 = 0.332. Regression equation for females: y=4.12+0.73*x, r2 = 0.457.

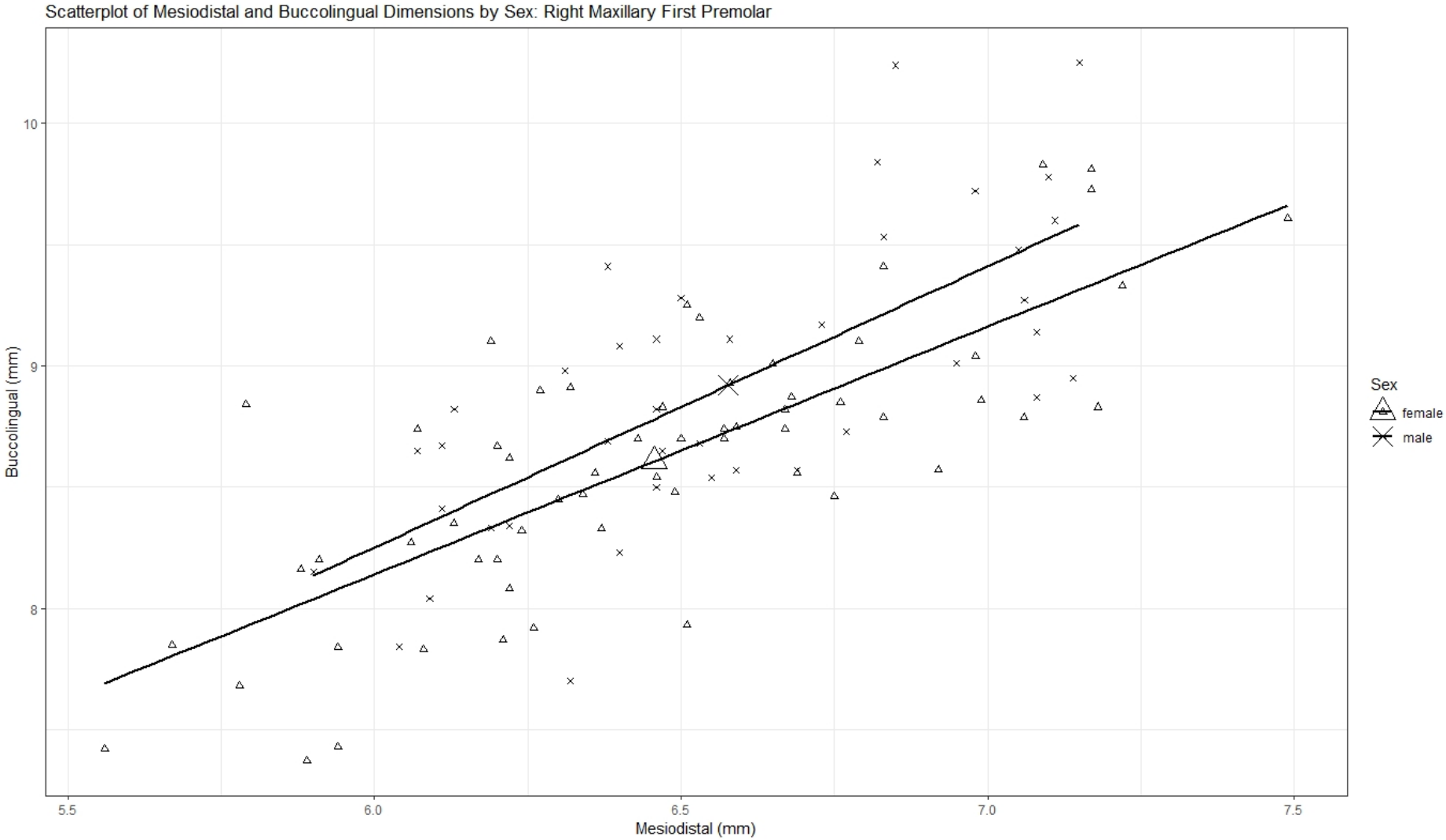

Figure 5 - Correlation between MD and BL measurements for the right maxillary first premolar, separated by sex. Regression equation for males: y=1.29+1.16*x, r2 = 0.503. Regression equation for females: y=2.01+1.02*x, r2 = 0.594.

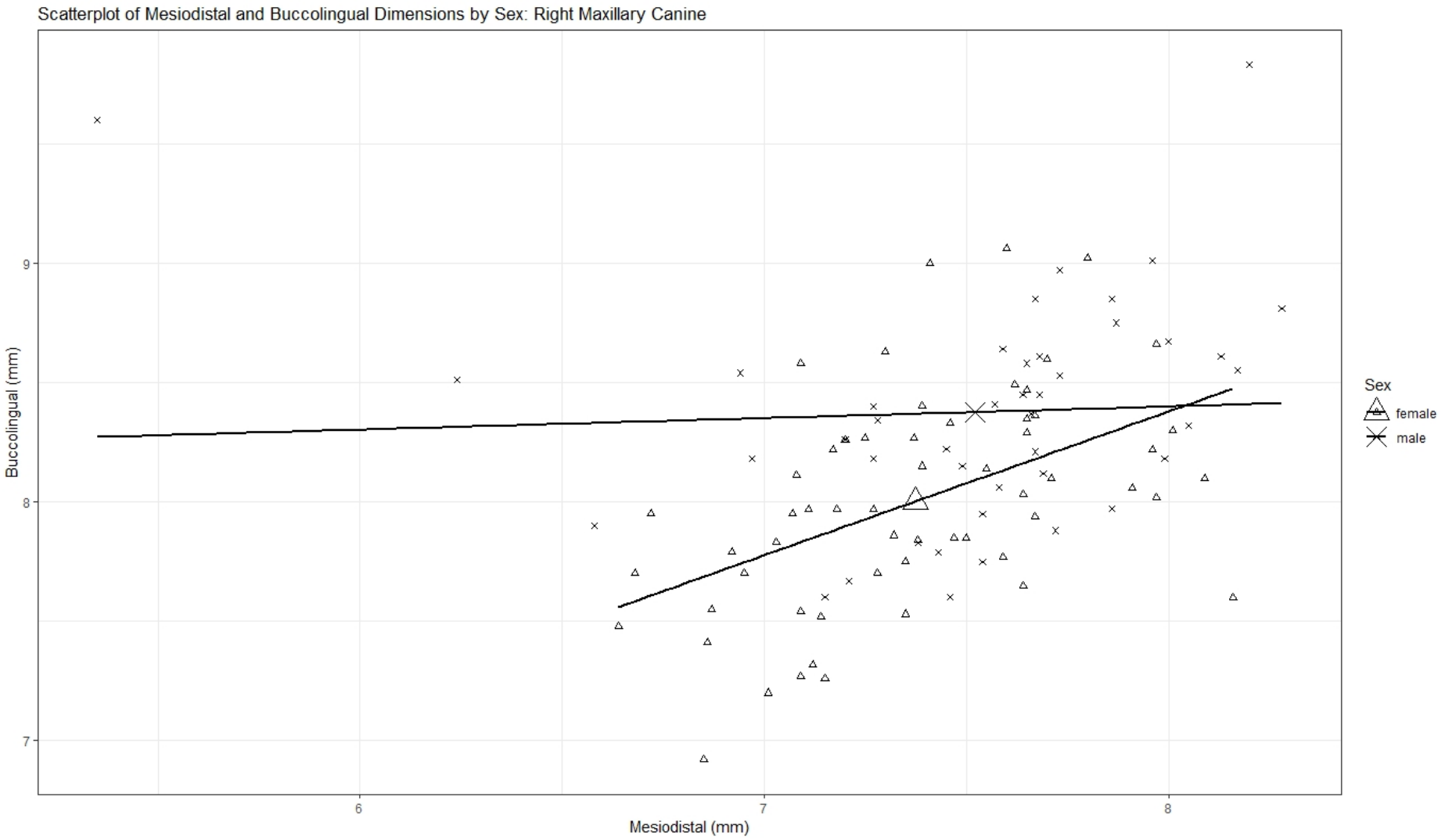

Figure 6 - Correlation between MD and BL measurements of the right maxillary canine, separated by sex. Regression equation for males: y=8.01+0.05*x, r2 = 0.003. Regression equation for females: y=356+0.6*x, r2= 0.235.

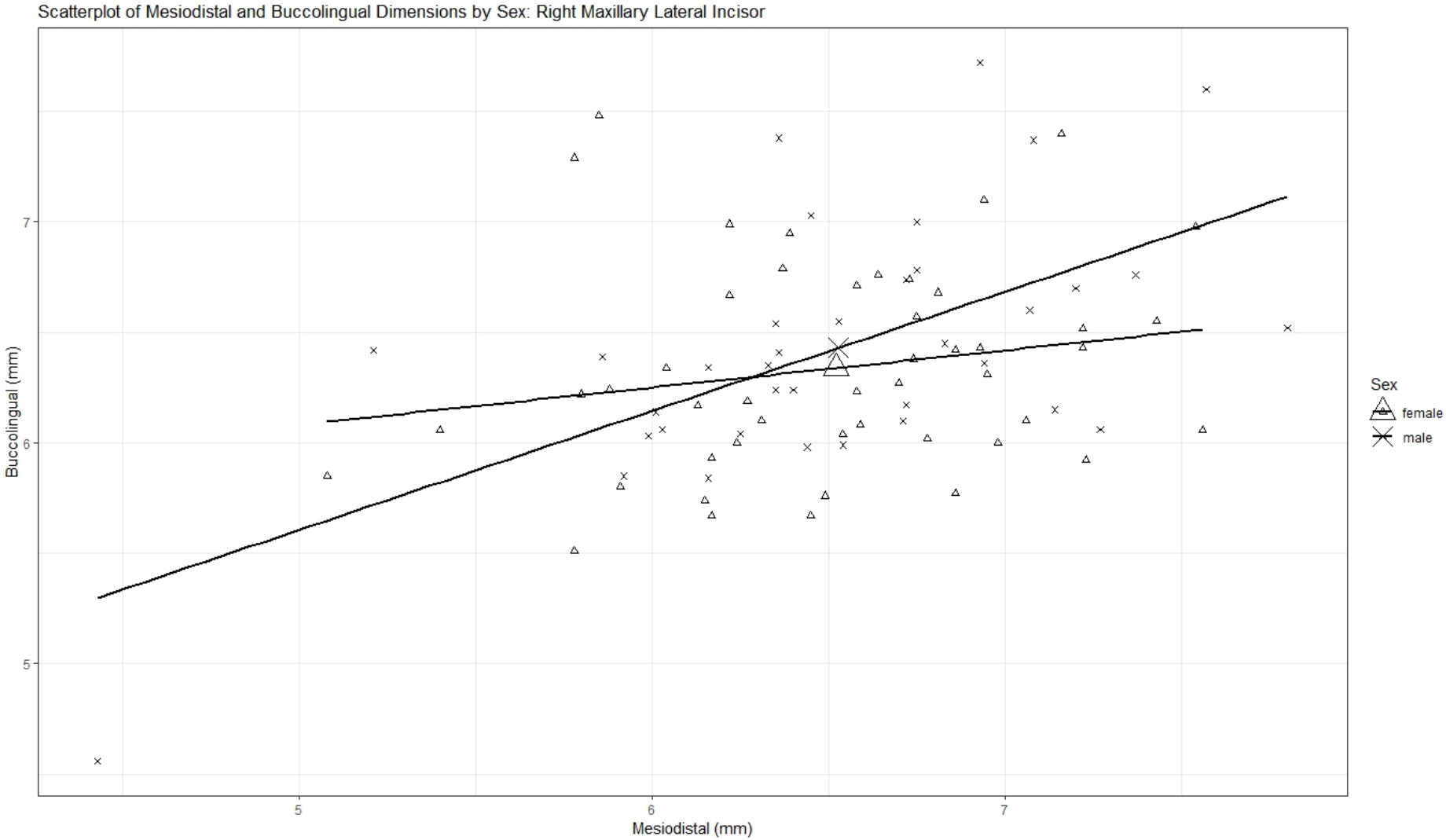

Figure 7 - Correlation between the MD and BL measurements of the right maxillary lateral incisor, separated by sex. Regression equation for males: y=2.91+0.54*x, r2 = 0.360. Regression equation for females: y=5.24+0.17*x, r2 = 0.037.

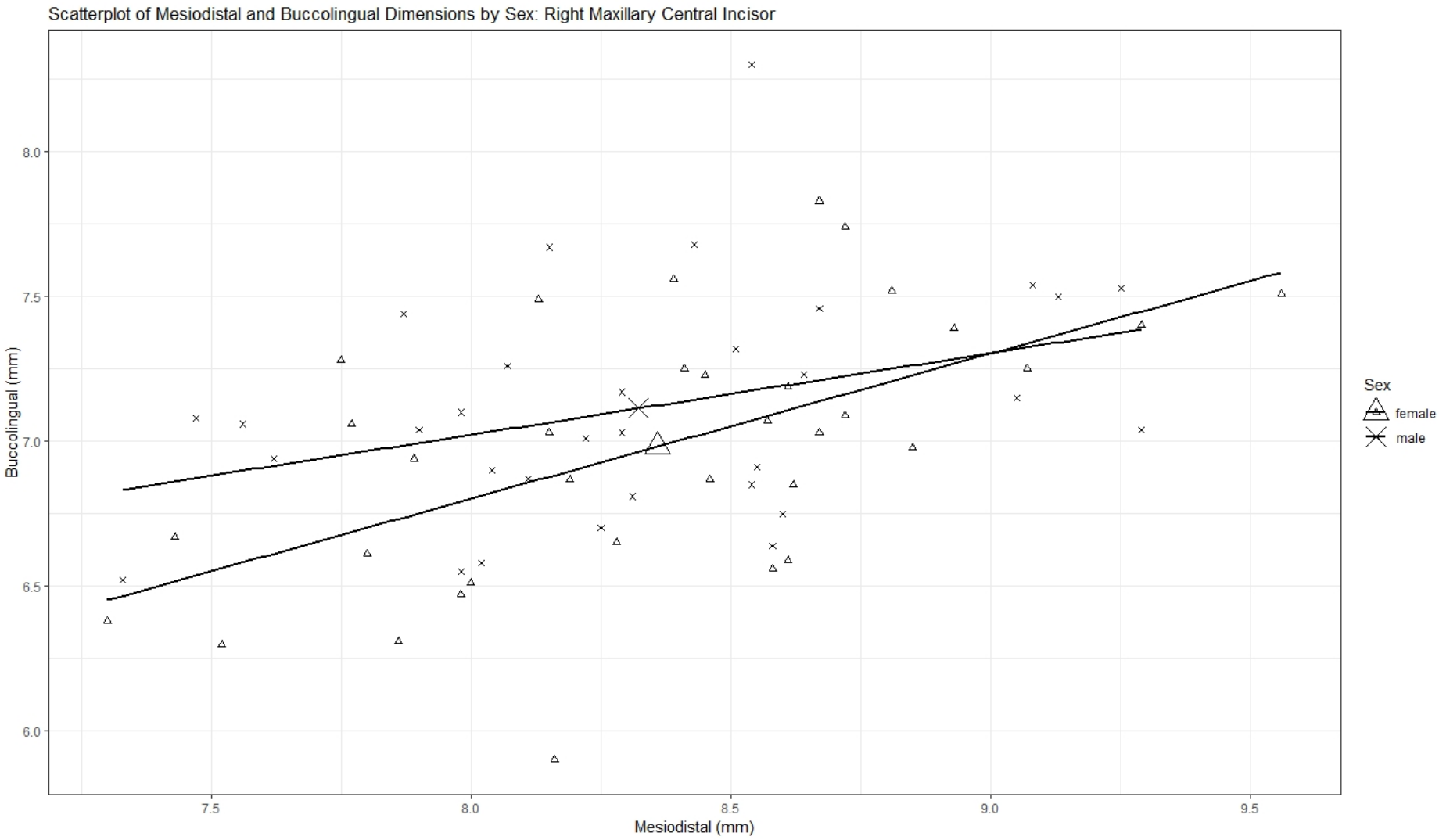

Figure 8 - Correlation between MD and BL measurements of the right maxillary central incisor, separated by sex. Regression equation for males: y=4.77+0.028*x, r2 = 0.133. Regression equation for females: y=2.59+0.5*x, r2 = 0.331.

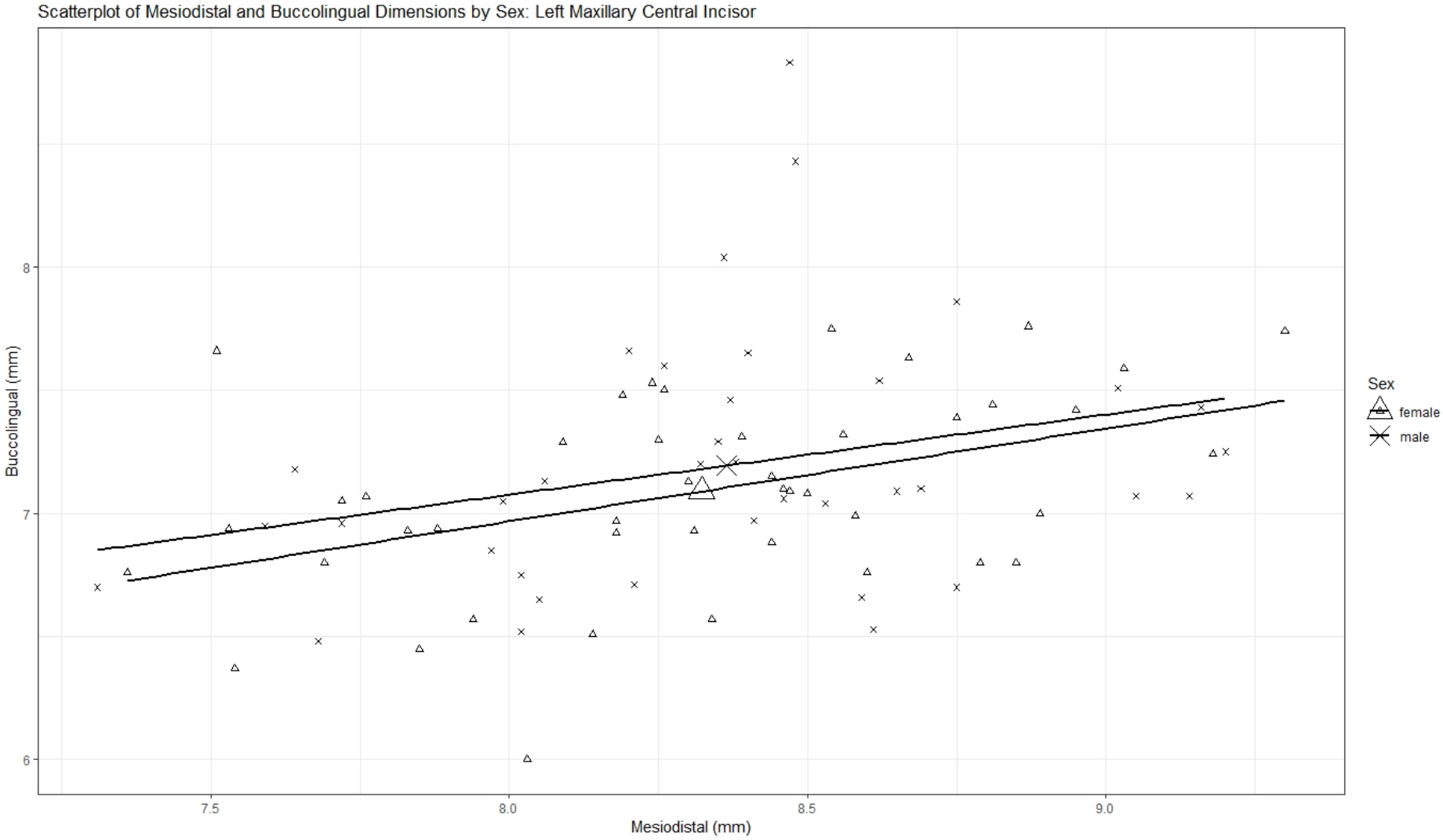

Figure 9 - Correlation between the MD and BL measurements of the left maxillary central incisor, separated by sex. Regression equation for males: y=4.47+0.33*x, r2 = 0.082. Regression equation for females: y=3.95+0.38*x, r2 = 0.197.

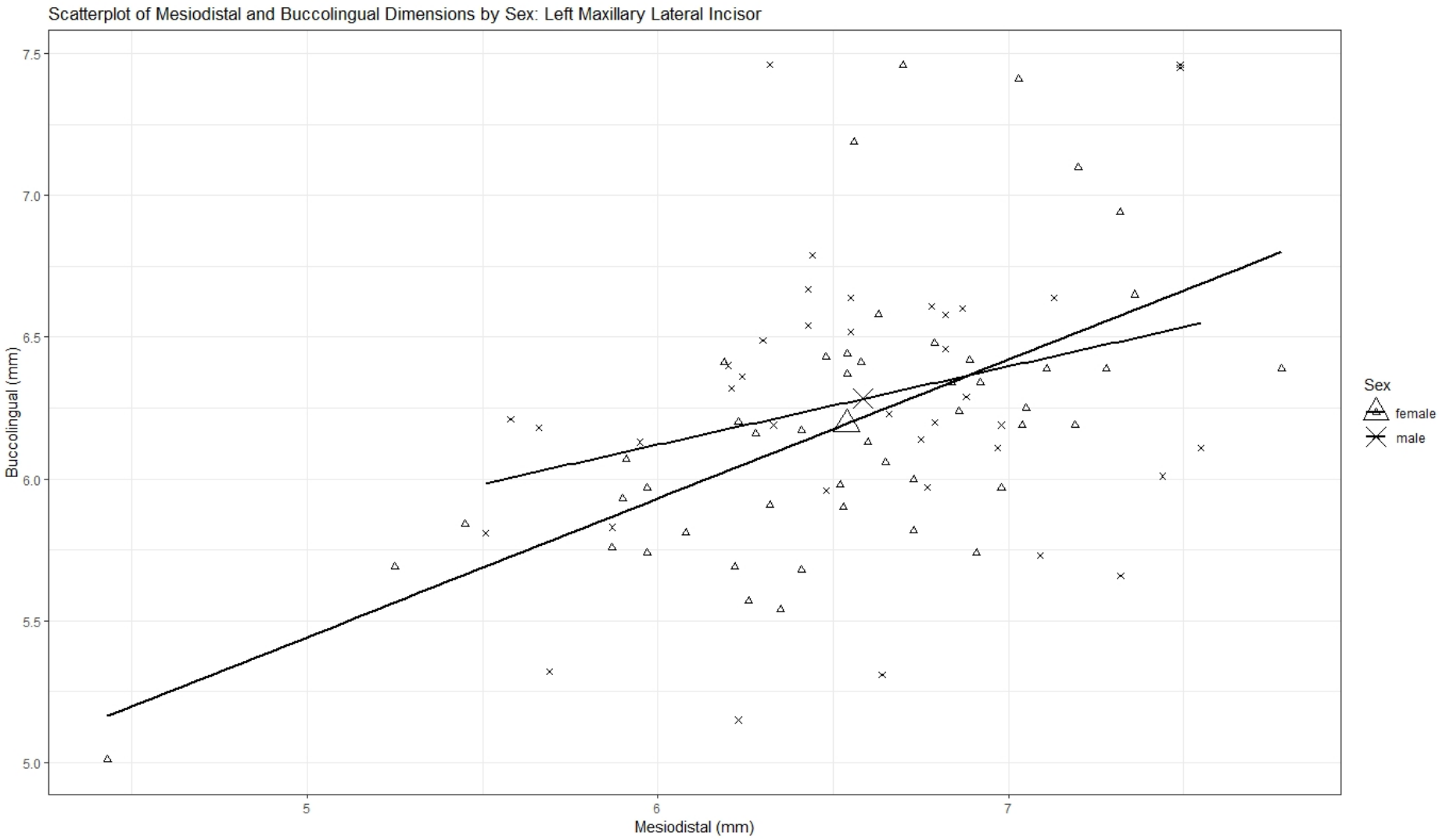

Figure 10 - Correlation between the MD and BL measurements of the left maxillary lateral incisor, separated by sex. Regression equation for males: y=4.46+0.28*x, r2 = 0.082. Regression equation for females: y=3.00+0.49*x, r2 = 0.360.

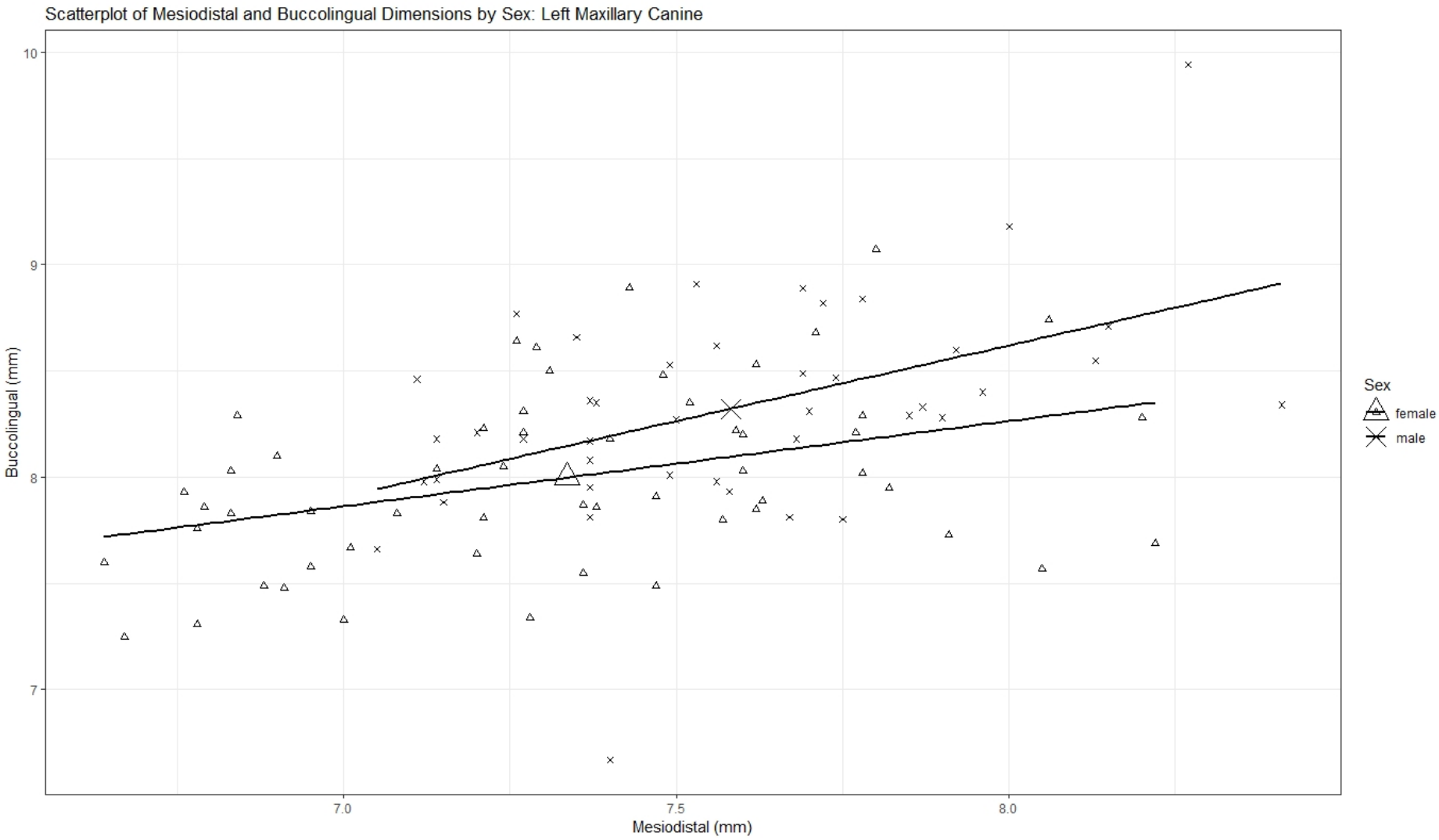

Figure 11 - Correlation between the MD and BL measurements of the left maxillary canine, separated by sex. Regression equation for males: y=2.93+0.71*x, r2 = 0.227. Regression equation for females: y=5.06+0.4*x, r2 = 0.152.

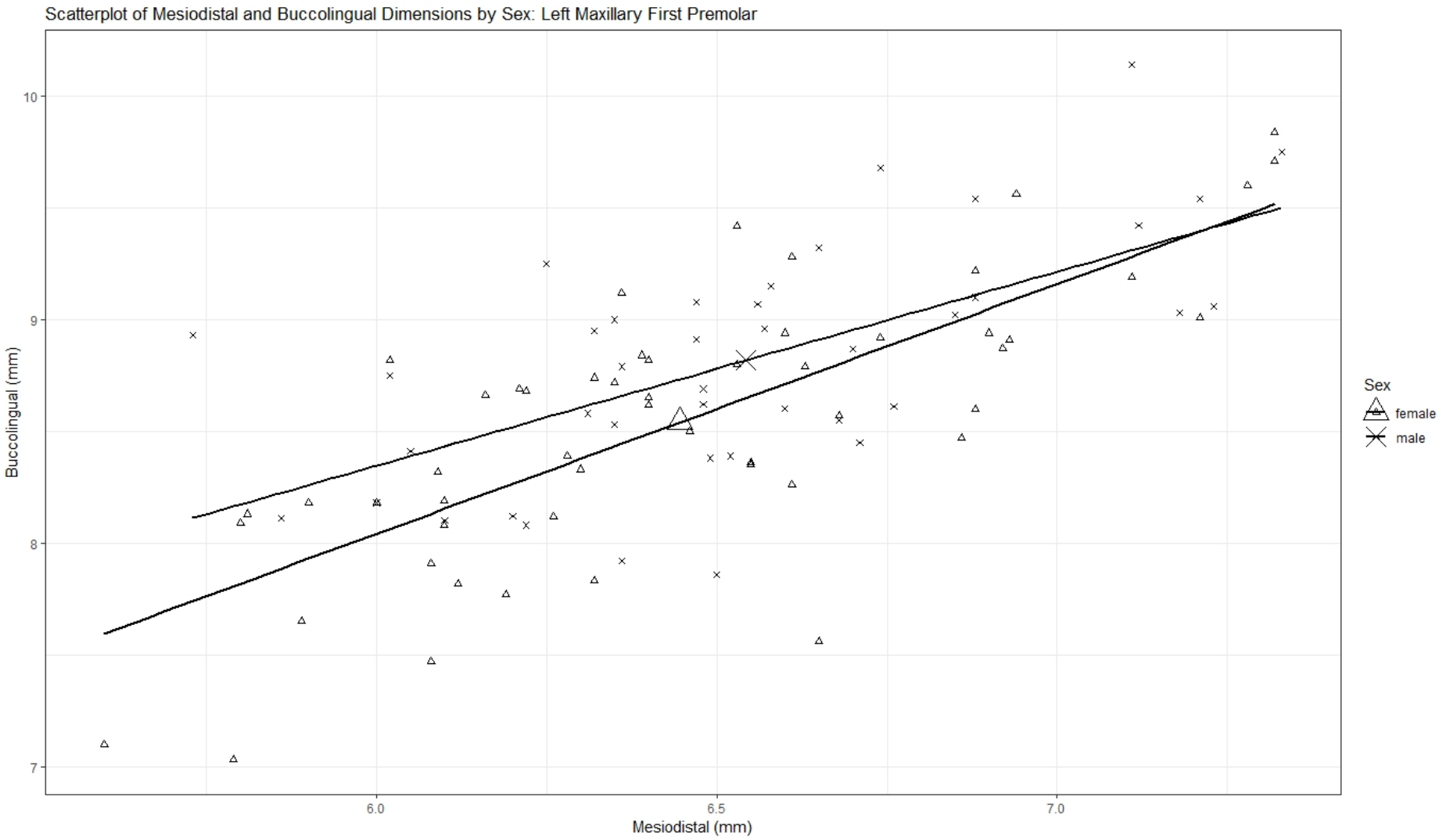

Figure 12 - Correlation between the MD and BL measurements of the left maxillary first premolar, separated by sex. Regression equation for males: y=3.14+0.87*x, r2 = 0.398. Regression equation for females: y=1.33+1.12*x, r2 = 0.573.

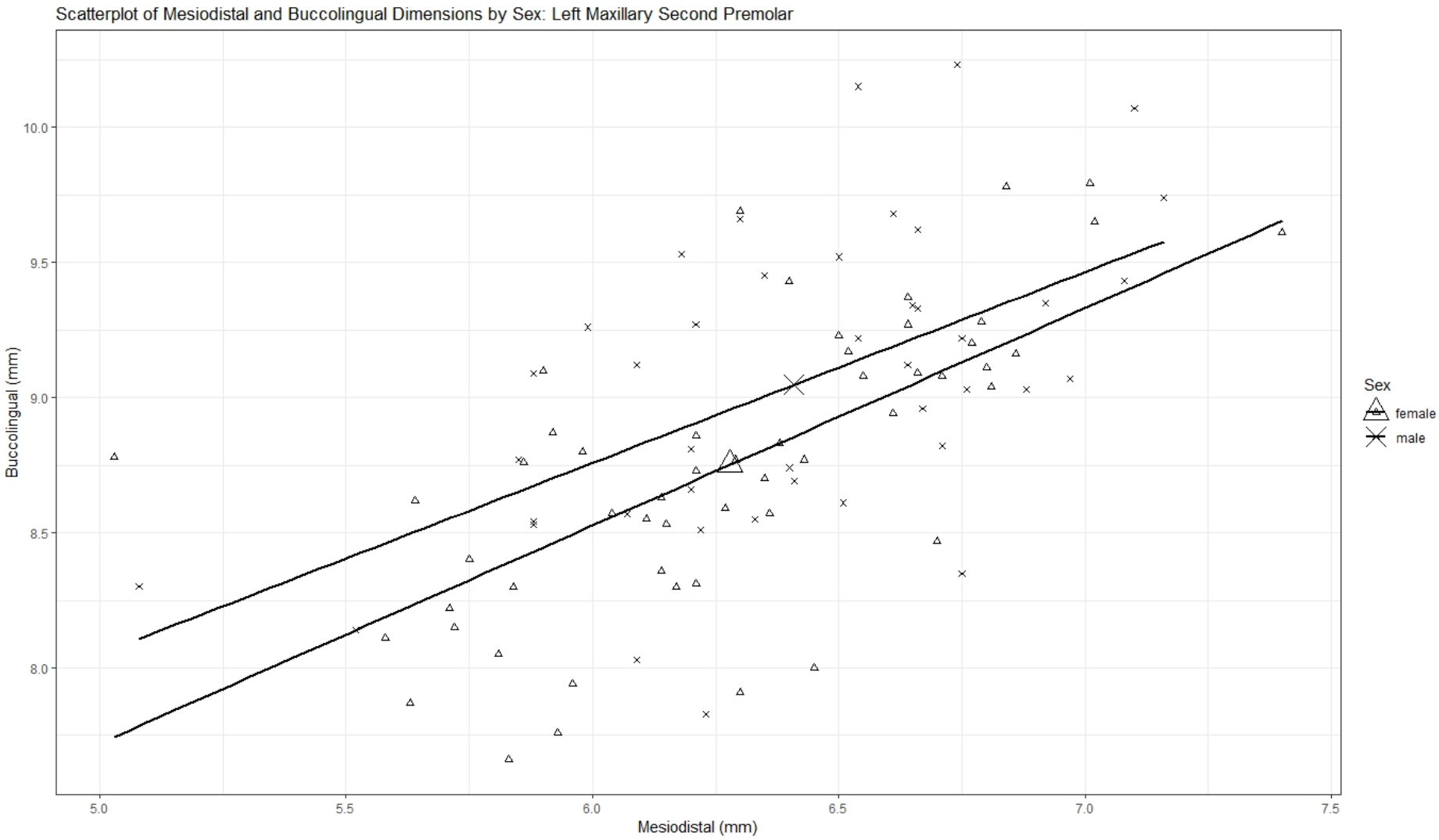

Figure 13 - Correlation between the MD and BL measurements of the left maxillary second premolar, separated by sex. Regression equation for males: y=4.52+0.71*x, r2 = 0.299. Regression equation for females: y=3.7+0.8*x, r2 = 0.453.

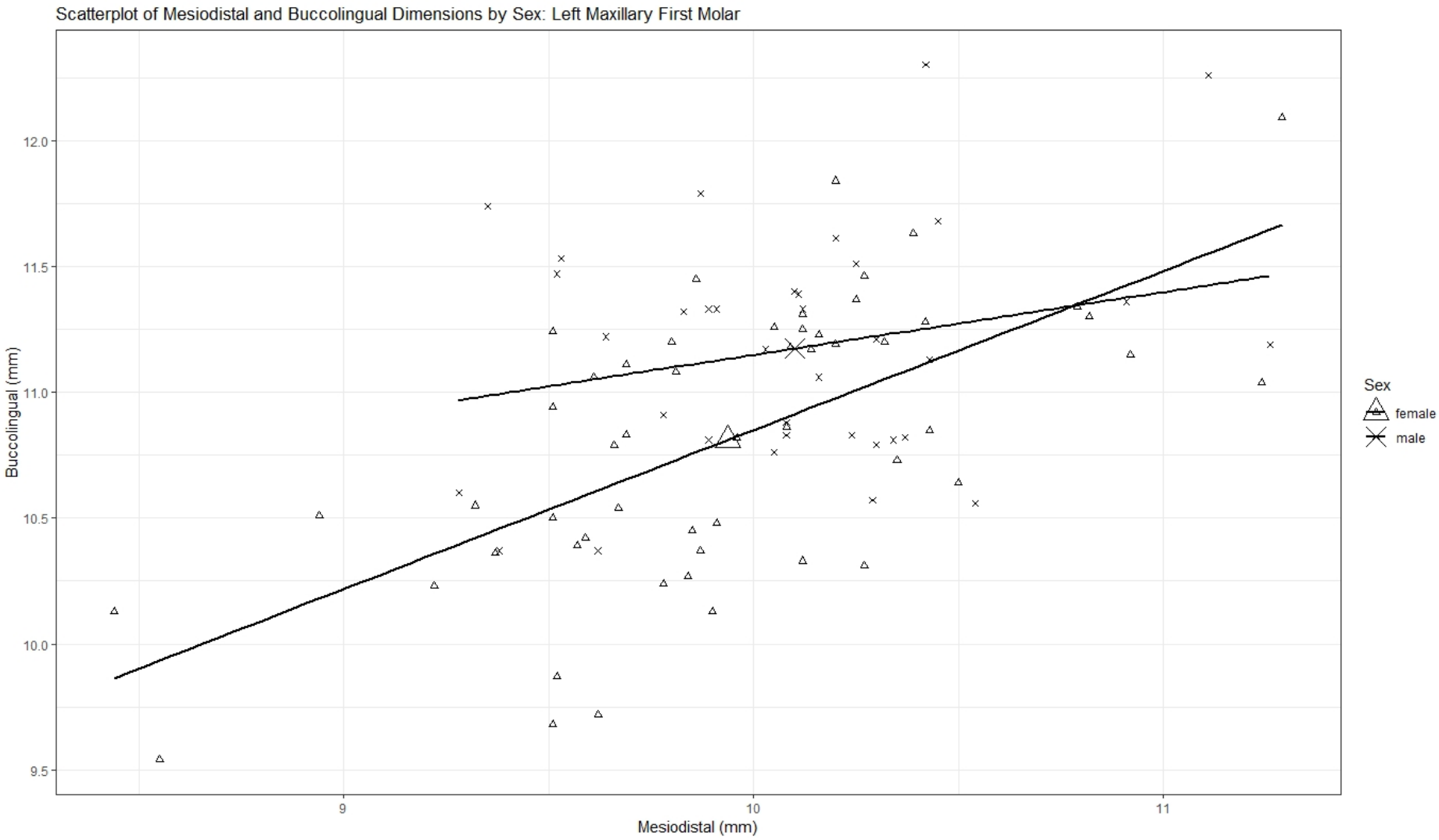

Figure 14 - Correlation between the MD and BL measurements of the left maxillary first molar, separated by sex. Regression equation for males: y=8.66+0.25*x, r2 = 0.058. Regression equation for females: y=4.54+0.63*x, r2 = 0.401.

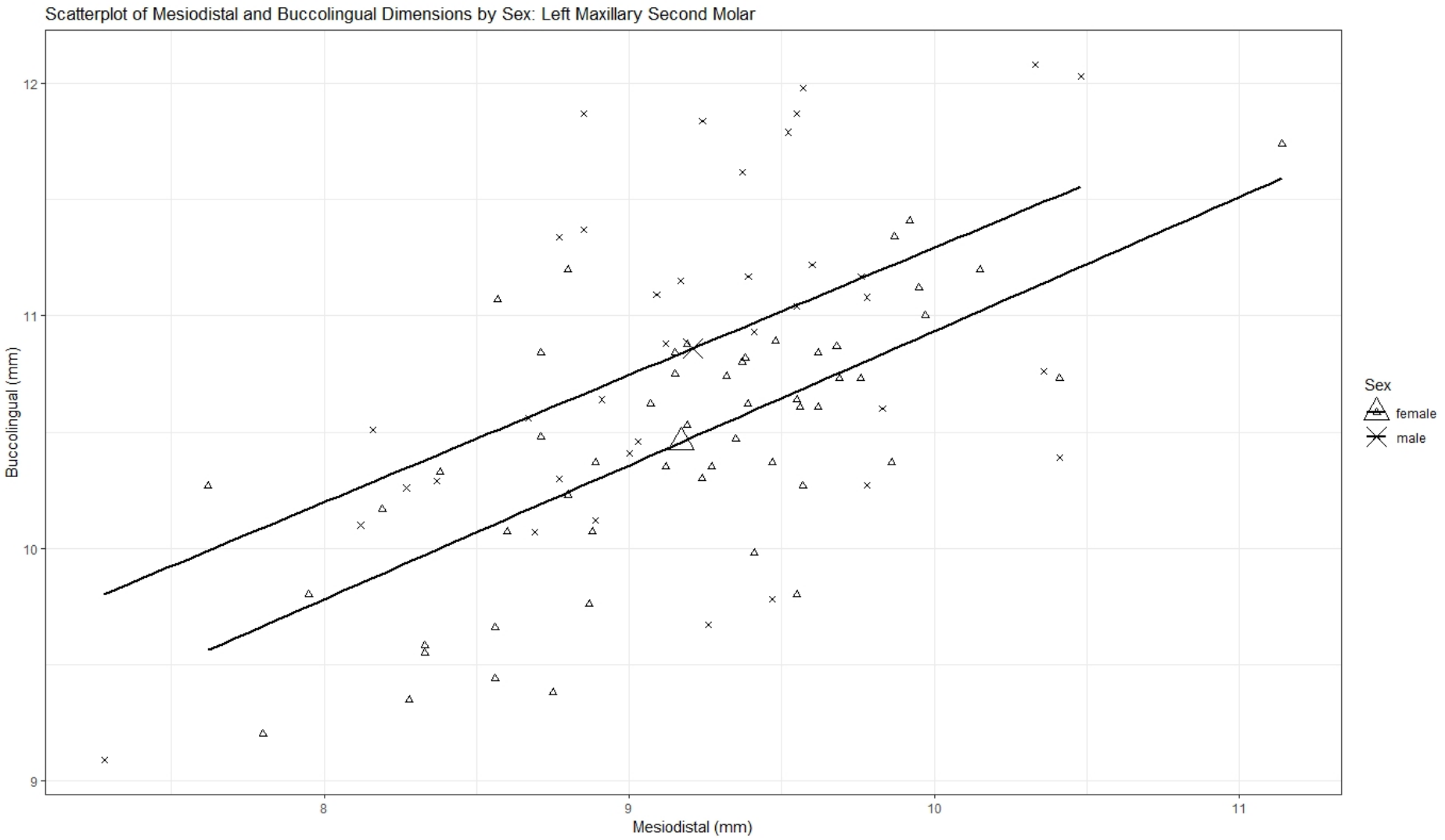

Figure 15 - Correlation between the MD and BL measurements of the left maxillary second molar, separated by sex. Regression equation for males: y=5.81+0.55*x, r2 = 0.262. Regression equation for females: y=5.17+0.58*x, r2 = 0.471.

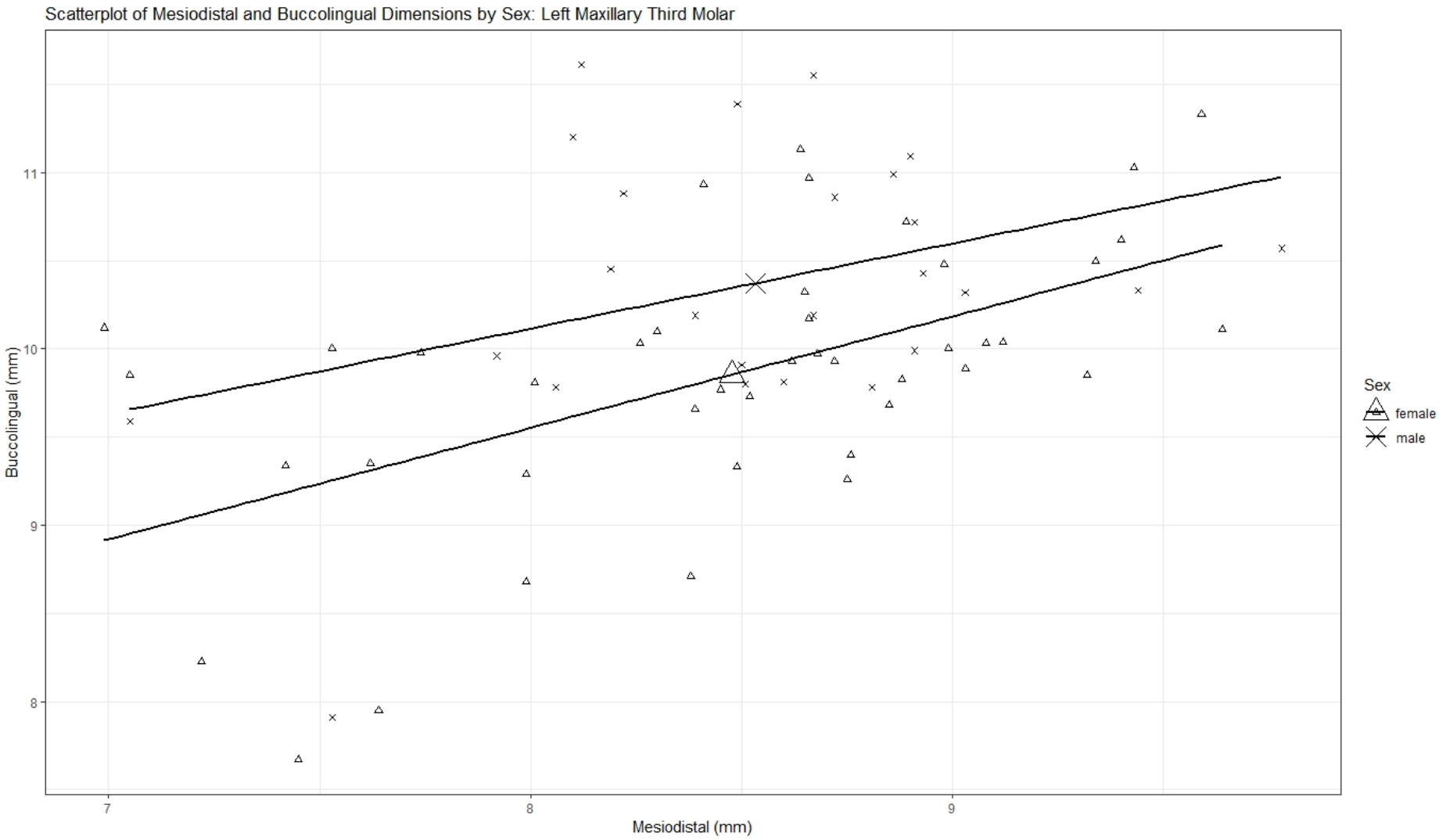

Figure 16 - Correlation between the MD and BL measurements of the left maxillary third molar, separated by sex. Regression equation for males: y=6.25+0.48*x, r2 = 0.124. Regression equation for females: y=4.49+0.63*x, r2 = 0.308.

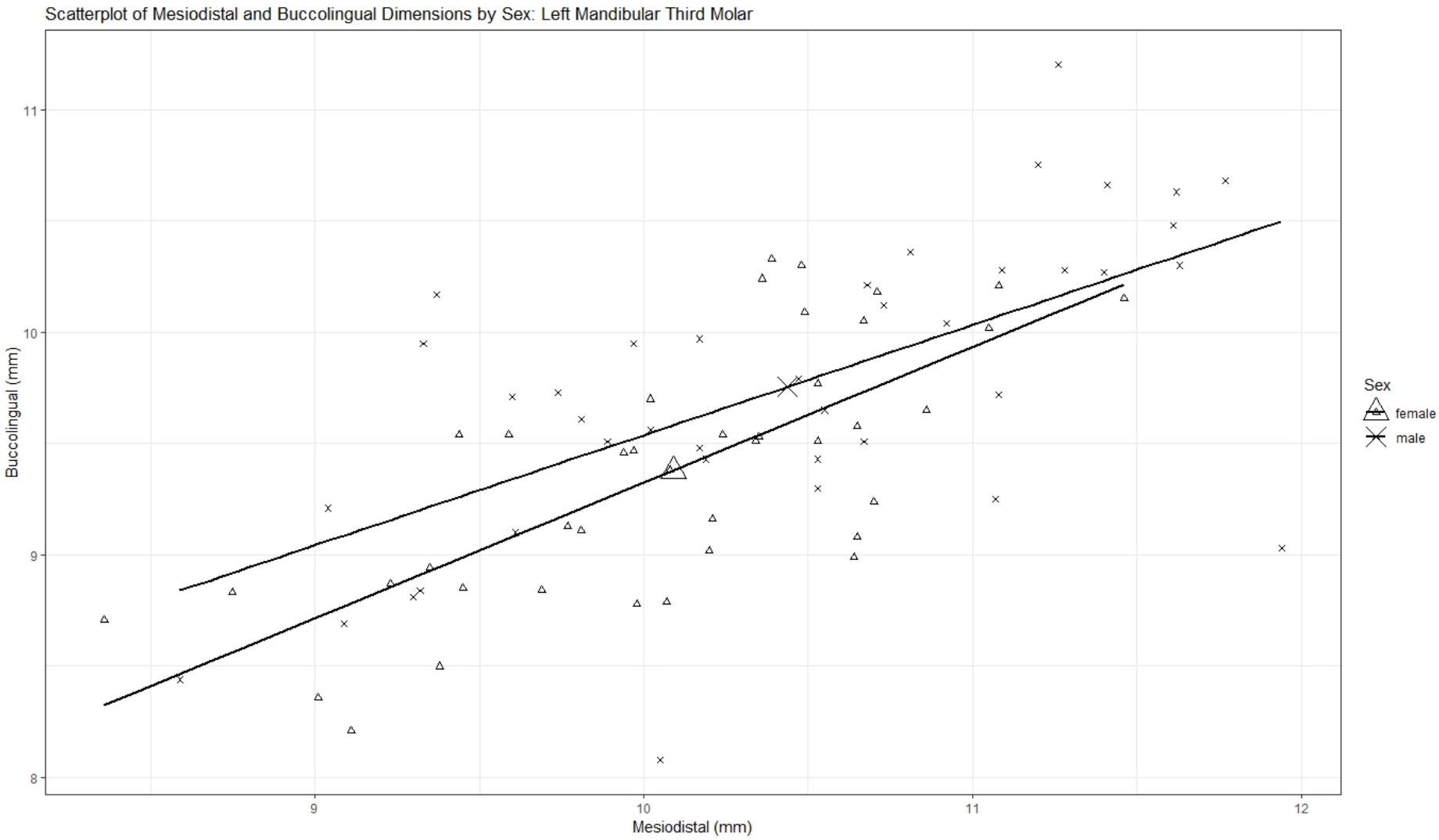

Figure 17 - Correlation between the MD and BL measurements of the left mandibular third molar, separated by sex. Regression equation for males: y=4.59+0.49*x, r2 = 0.403. Regression equation for females: y=3.23+0.61*x, r2 = 0.522.

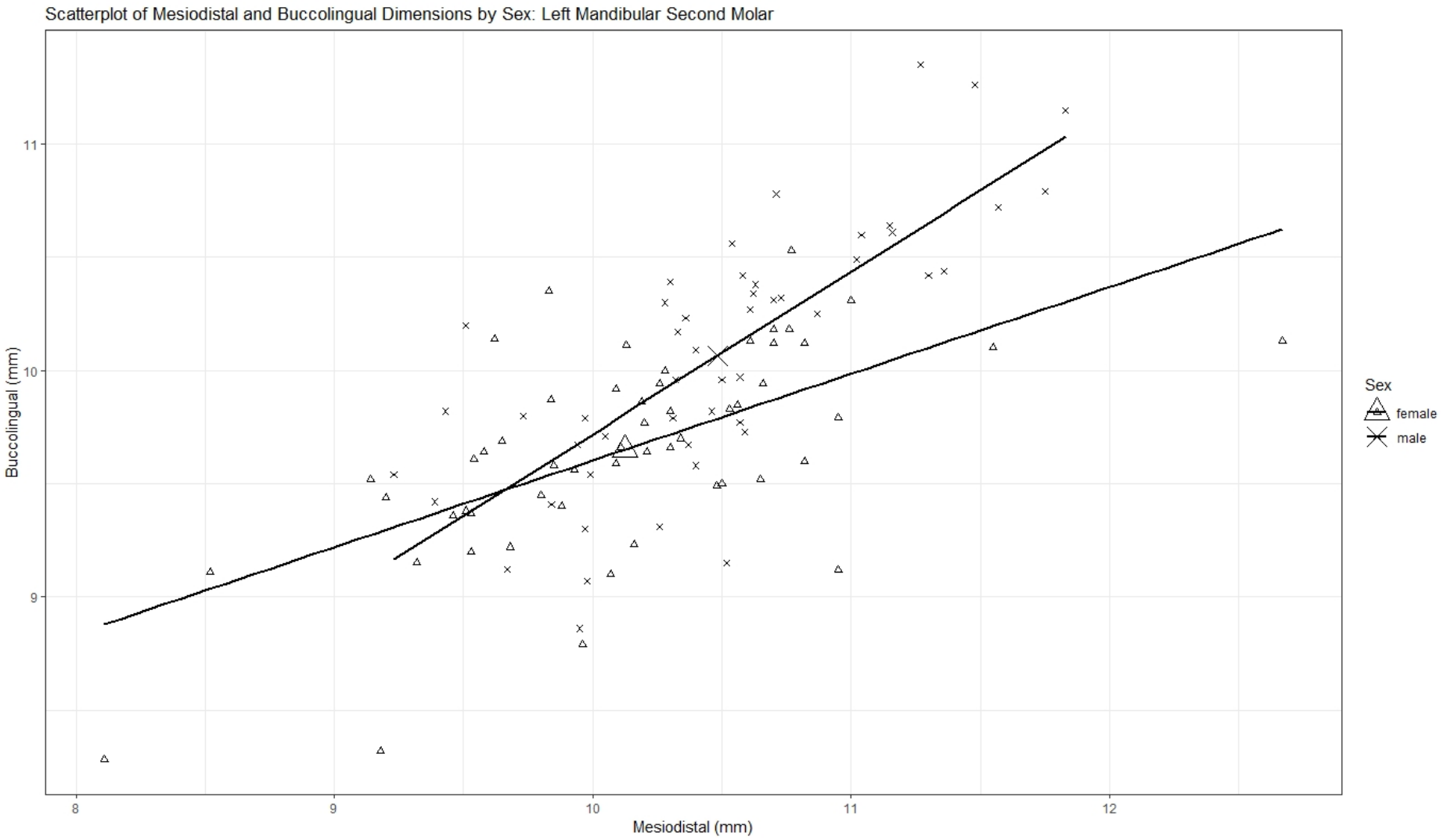

Figure 18 - Correlation between the MD and BL measurement of the left mandibular second molar, separated by sex. Regression equation for males: y=2.54+0.72*x, r2 = 0.582. Regression equation for females: y=5.77+0.38*x, r2 = 0.374.

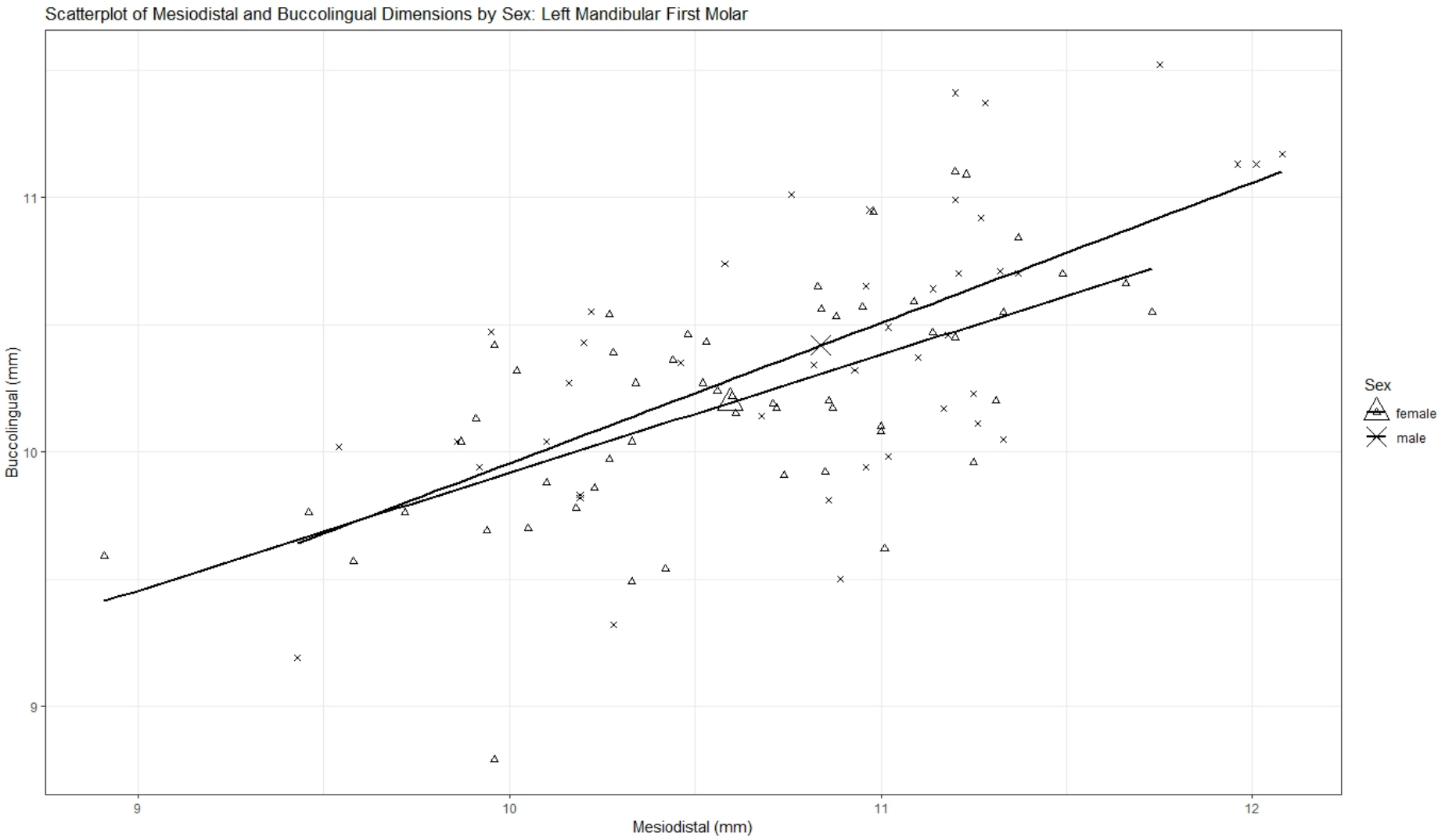

Figure 19 - Correlation between the MD and BL measurements of the left mandibular first molar, separated by sex. Regression equation for males: y=4.44+0.55*x, r2 = 0.409. Regression equation for females: y=5.29+0.46*x, r2 = 0.382.

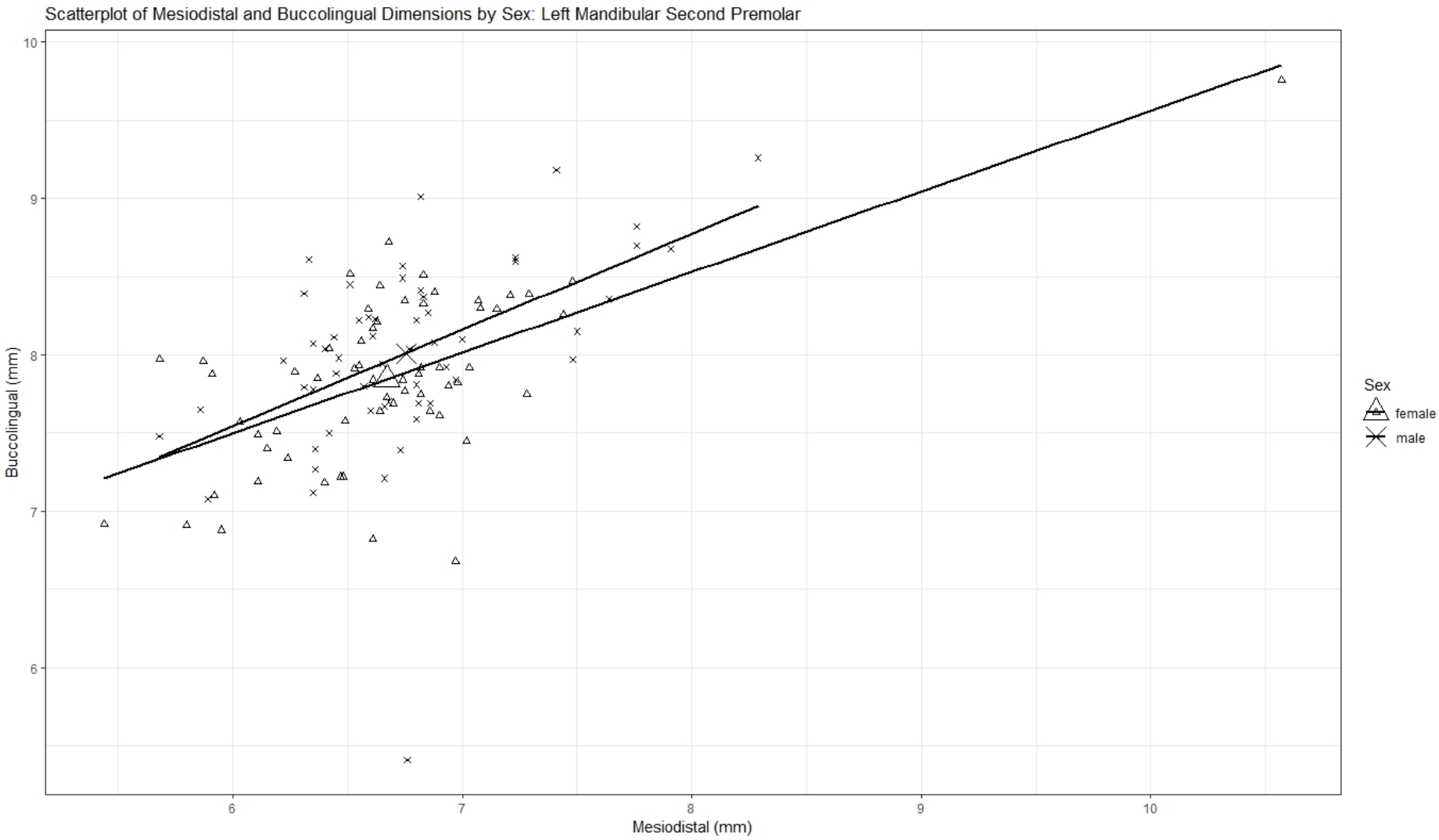

Figure 20 - Correlation between the MD and BL measurements of the left mandibular second premolar, separated by sex. Regression equation for males: y=3.85+0.62*x, r2 = 0.259. Regression equation for females: y=4.41+0.51*x, r2 = 0.410.

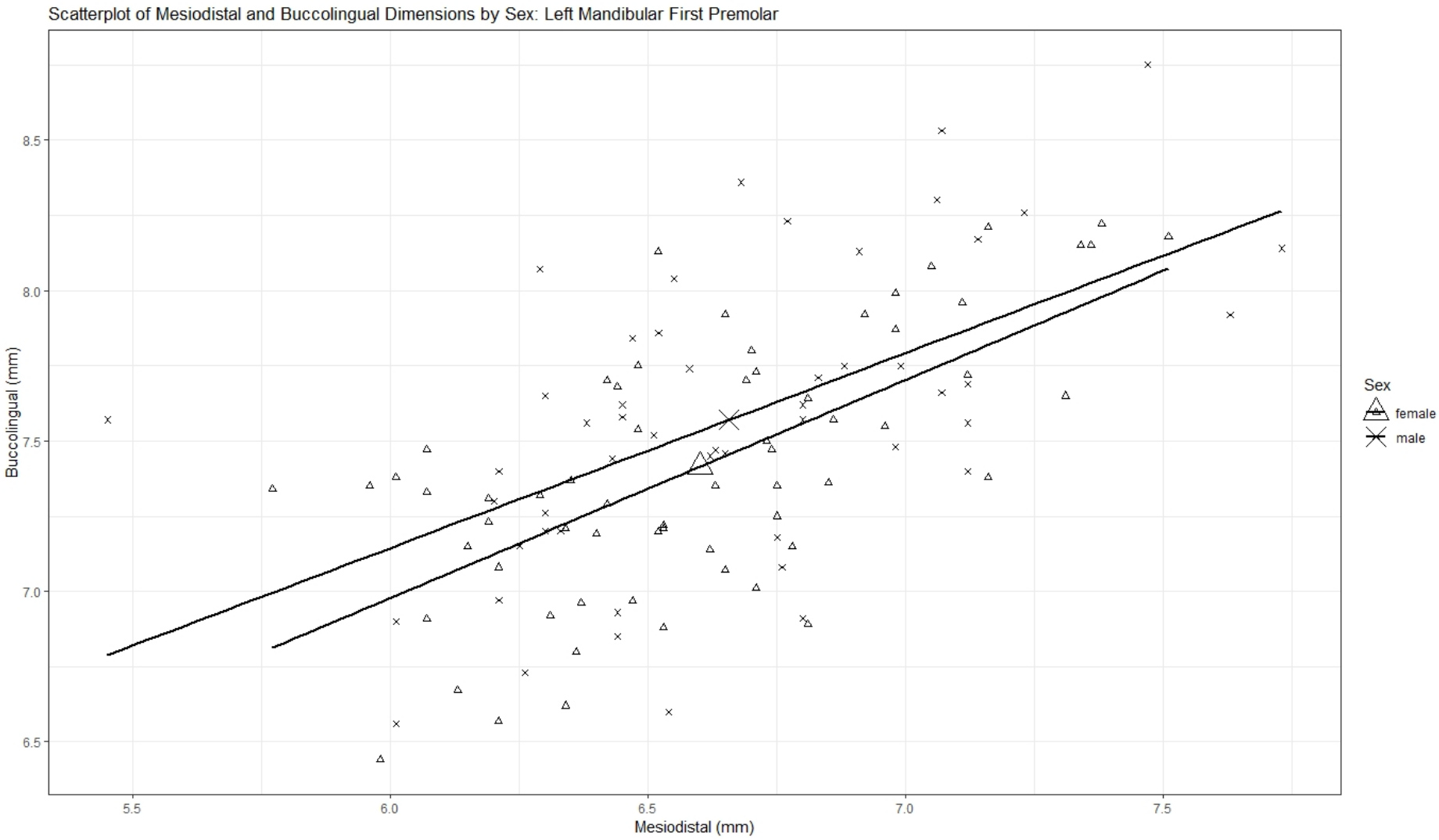

Figure 21 - Correlation between the MD and BL measurement of the left mandibular first premolar, separated by sex. Regression equation for males: y=3.26+0.65*x, r2 = 0.315. Regression equation for females: y=2.63+0.72*x, r2 = 0.436.

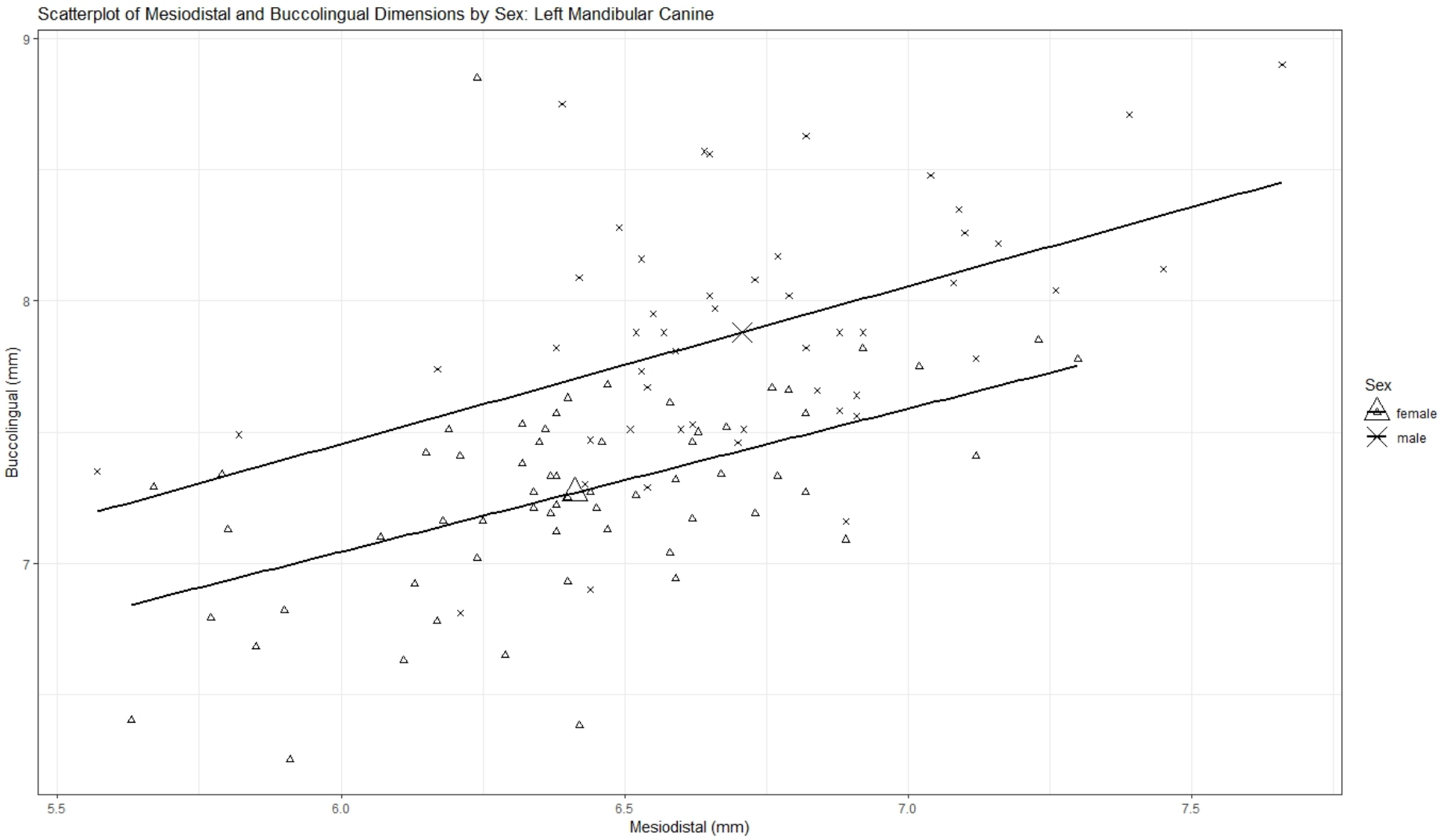

Figure 22 - Correlation between the MD and BL measurements of the left mandibular canine, separated by sex. Regression equation for males: y=3.85+0.6*x, r2 = 0.239. Regression equation for females: y=3.77+0.55*x, r2 = 0.234.

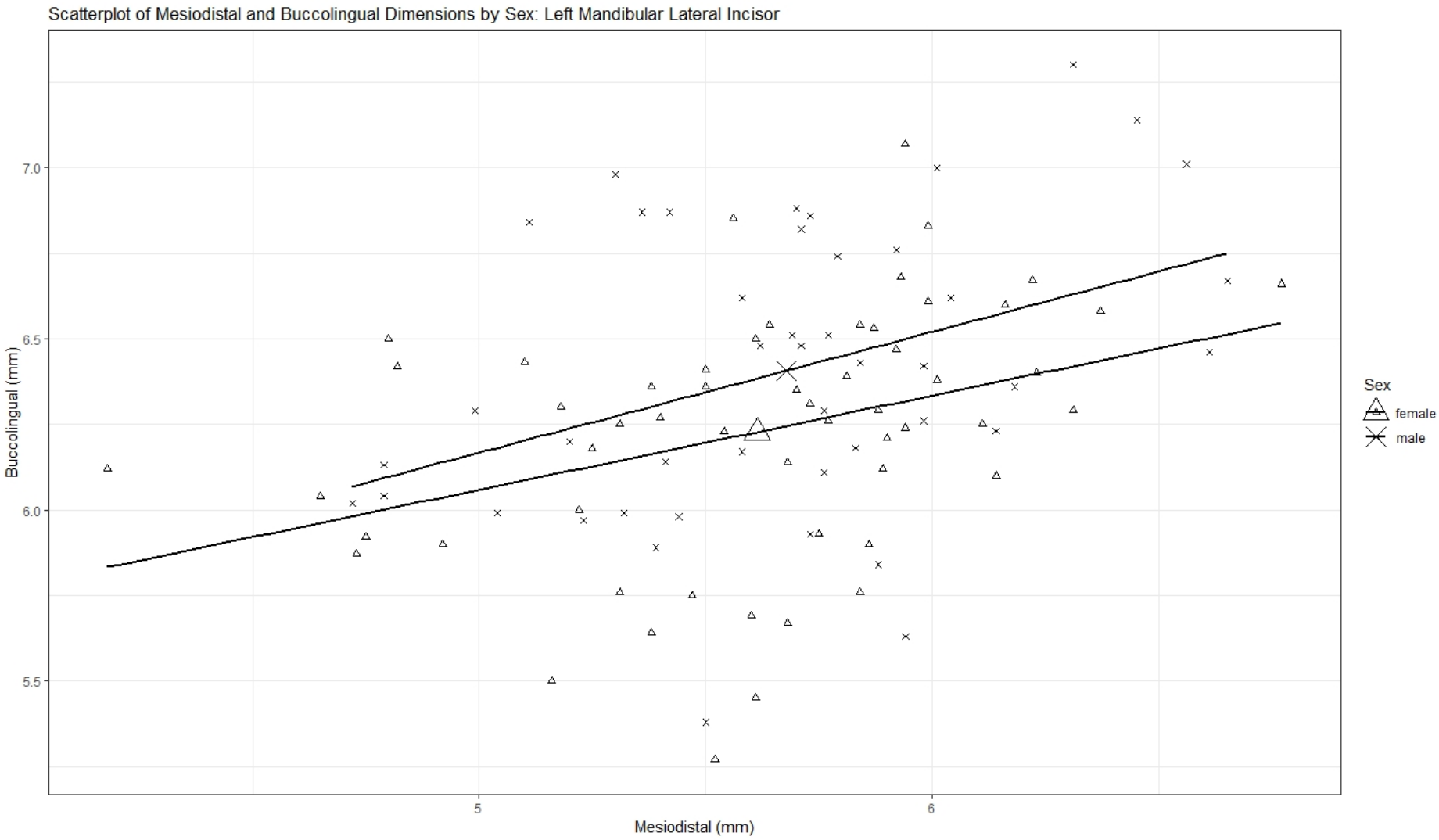

Figure 23 - Correlation between the MD and BL measurements of the left mandibular lateral incisor, separated by sex. Regression equation for males: y=4.4+0.35*x, r2 = 0.150. Regression equation for females: y=4.68+0.28*x, r2 = 0.131.

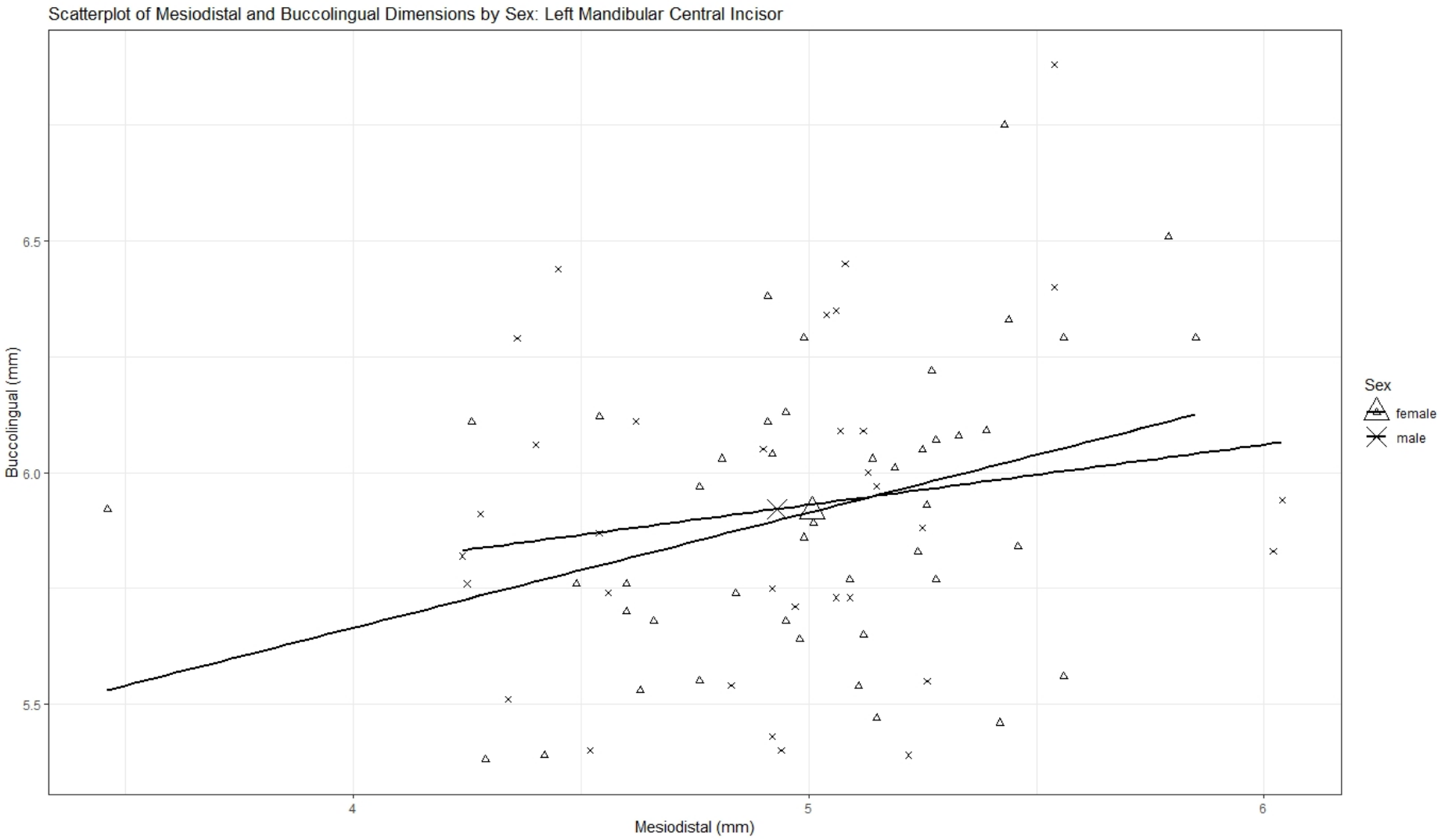

Figure 24 - Correlation between the MD and BL measurements of the left mandibular central incisor, separated by sex. Regression equation for males: y=5.28+0.13*x, r2 = 0.028. Regression equation for females: y=4.67+0.25*x, r2 = 0.125.

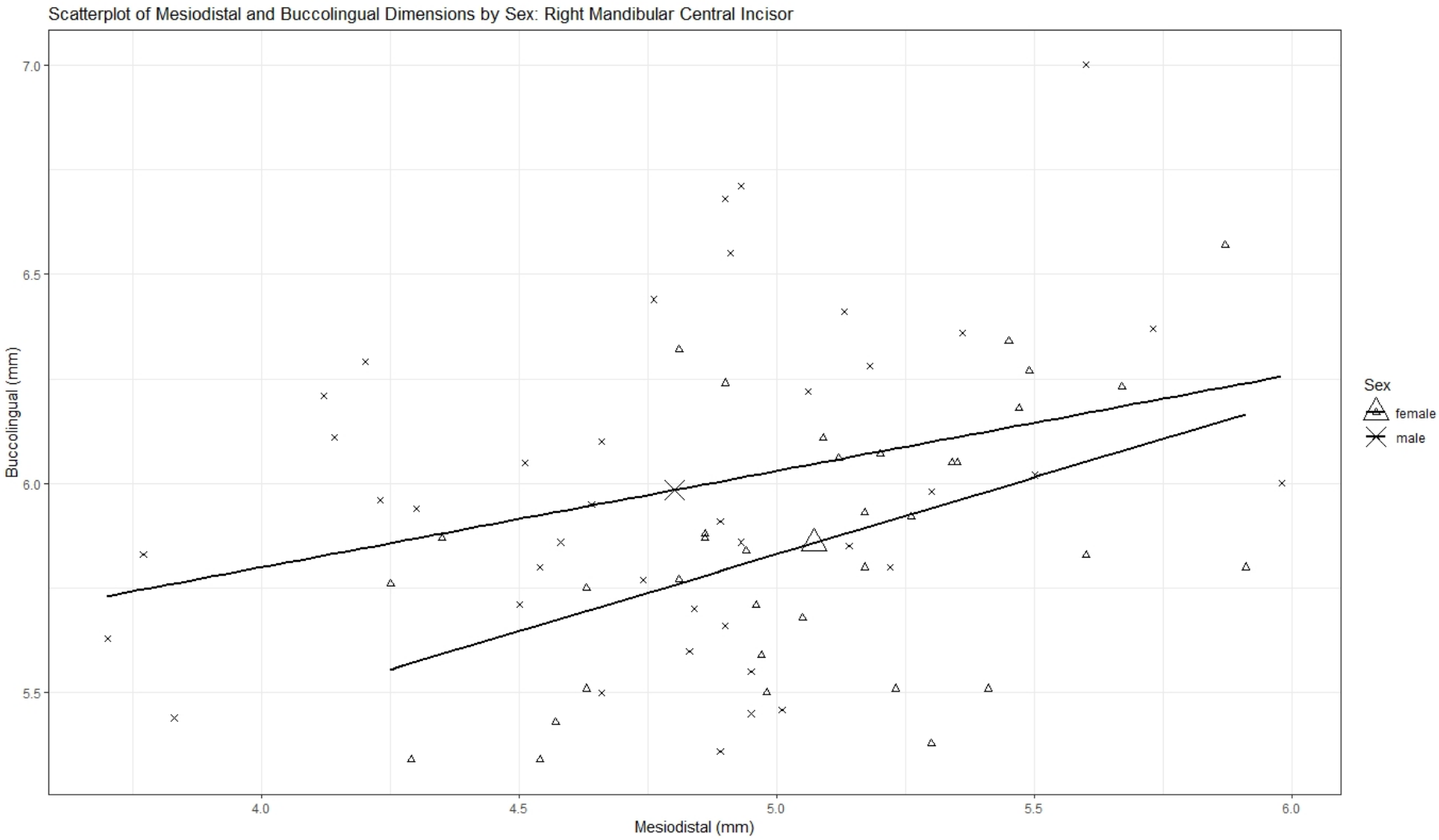

Figure 25 - Correlation between the MD and BL measurements of the right mandibular central incisor, separated by sex. Regression equation for males: y=4.88+0.23*x, r2 = 0.093. Regression equation for females: y=4.00+0.37*x, r2 = 0.238.

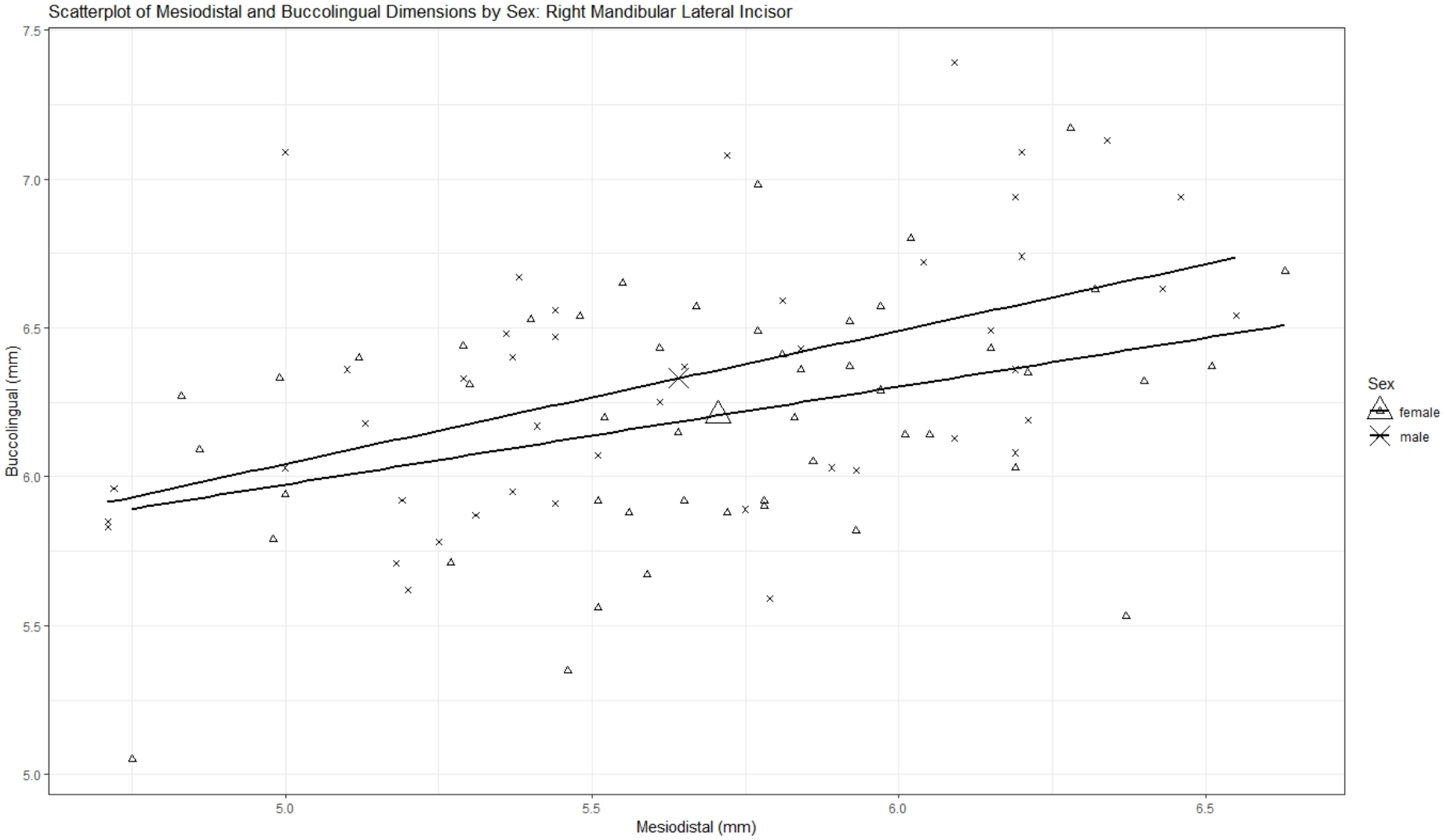

Figure 26 - Correlation between the MD and BL measurements of the right mandibular lateral incisor, separated by sex. Regression equation for males: y=3.81+0.45*x, r2 = 0.250. Regression equation for females: y=4.33+0.33*x, r2 = 0.130.

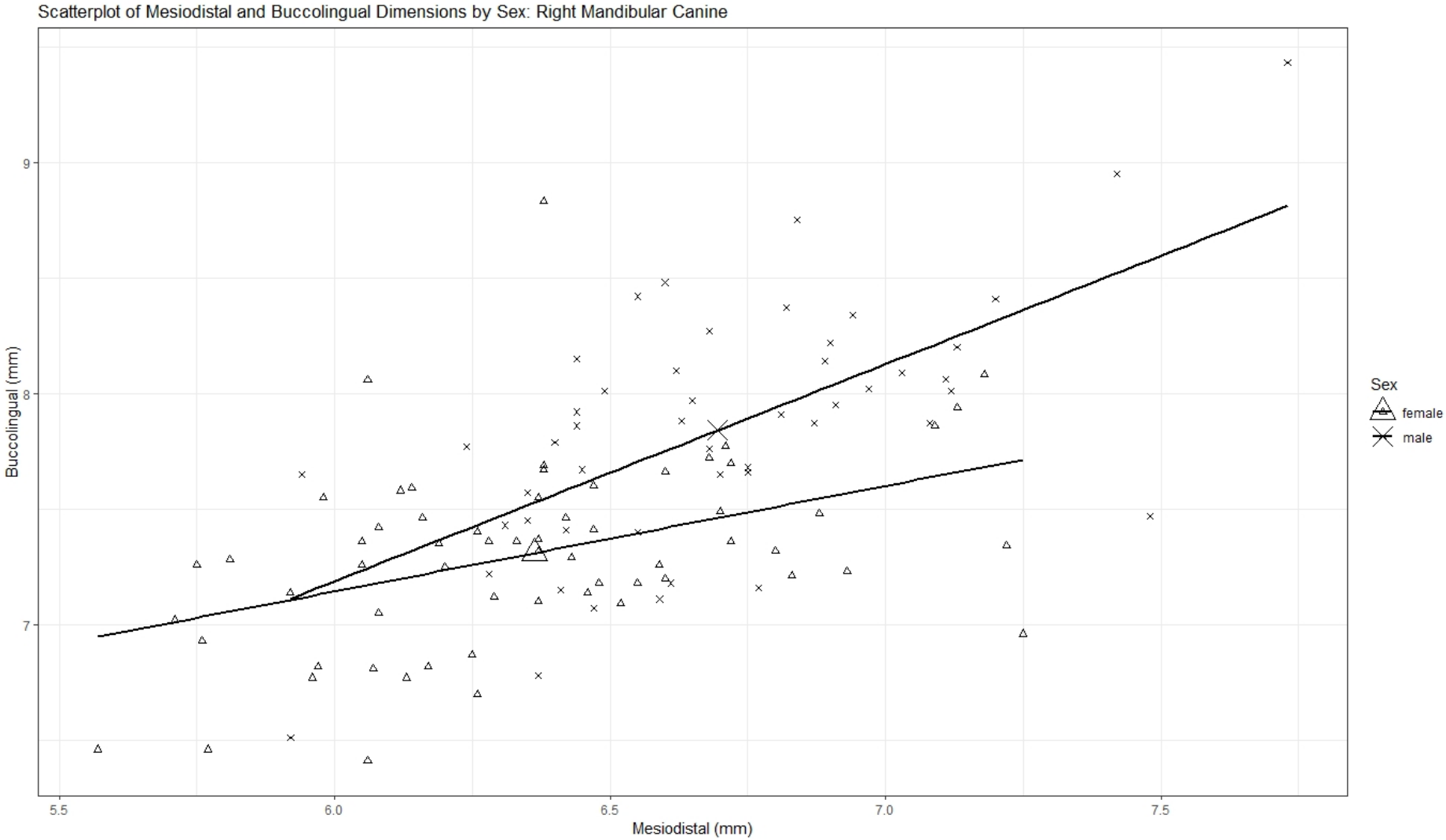

Figure 27 - Correlation between the MD and BL measurements of the right mandibular canine, separated by sex. Regression equation for males: y=1.55+0.94*x, r2 = 0.399. Regression equation for females: y=4.4+0.46*x, r2 = 0.185.

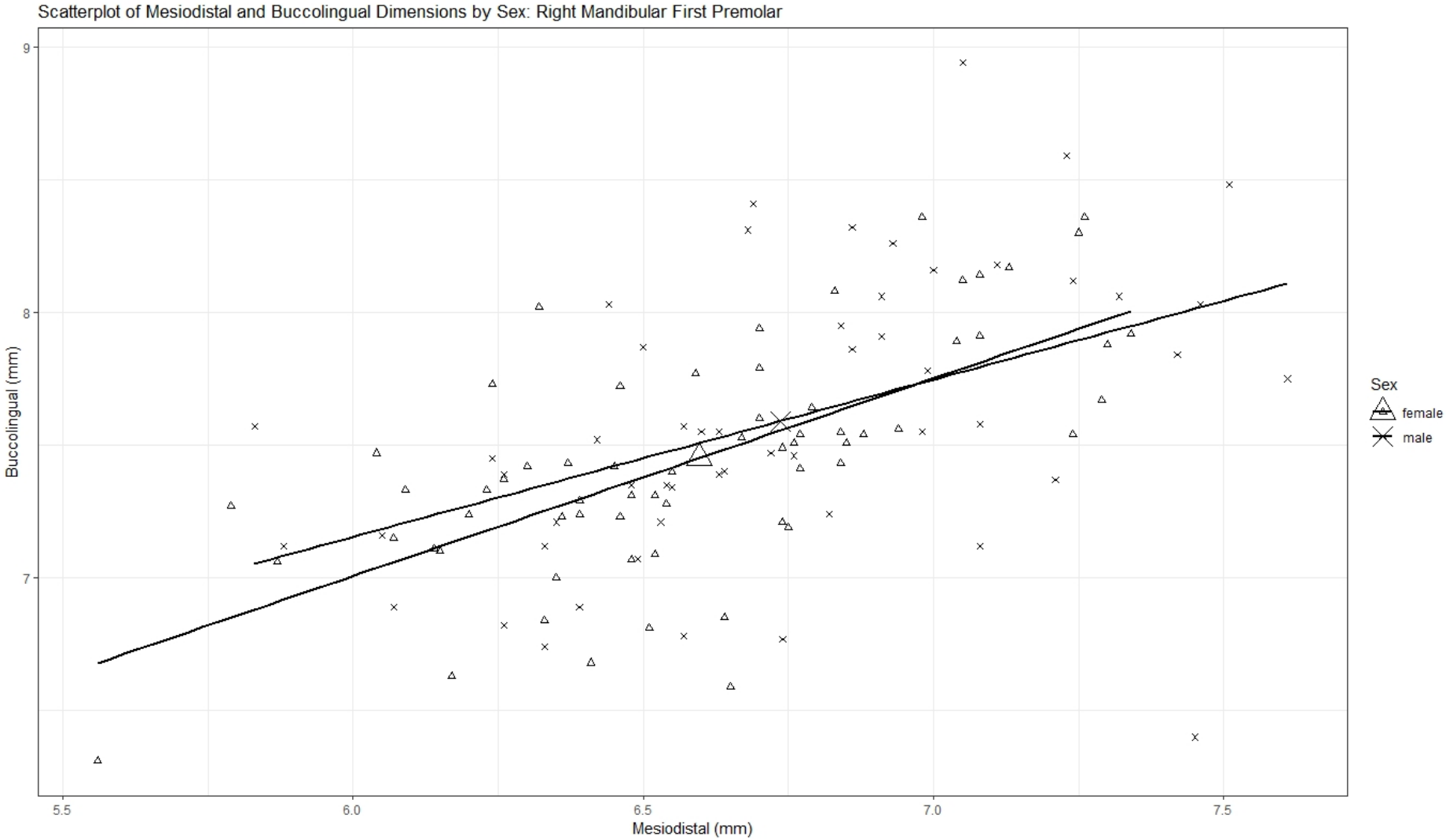

Figure 28 - Correlation between the MD and BL measurements of the right mandibular first premolar, separated by sex. Regression equation for males: y=3.6+0.59*x, r2 = 0.213. Regression equation for females: y=2.54+0.74*x, r2 = 0.445.

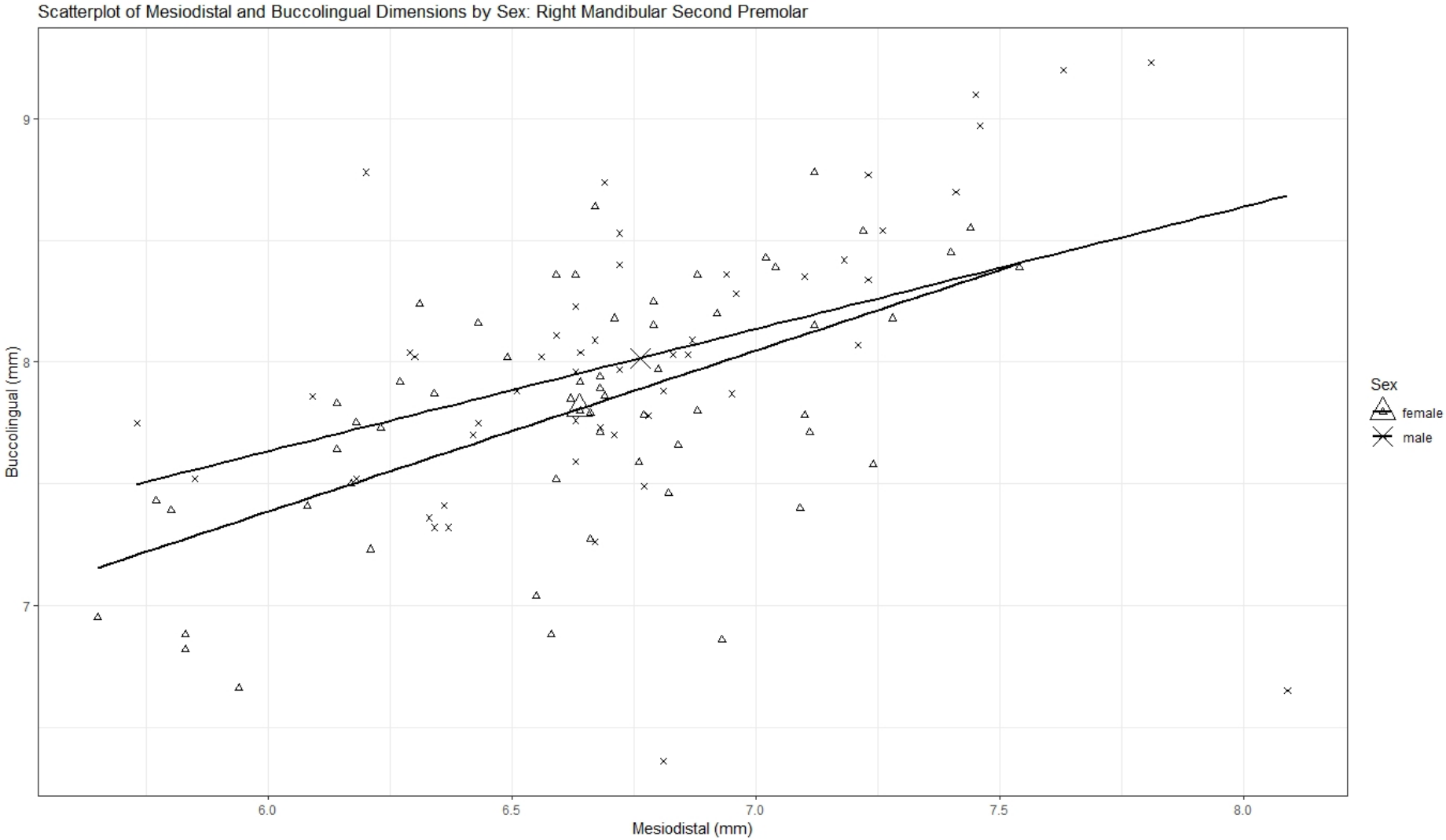

Figure 29 - Correlation between the MD and BL measurements of the right mandibular second premolar, separated by sex. Regression equation for males: y=4.62+0.5*x, r2 = 0.162. Regression equation for females: y=3.42+0.66*x, r2 = 0.342.

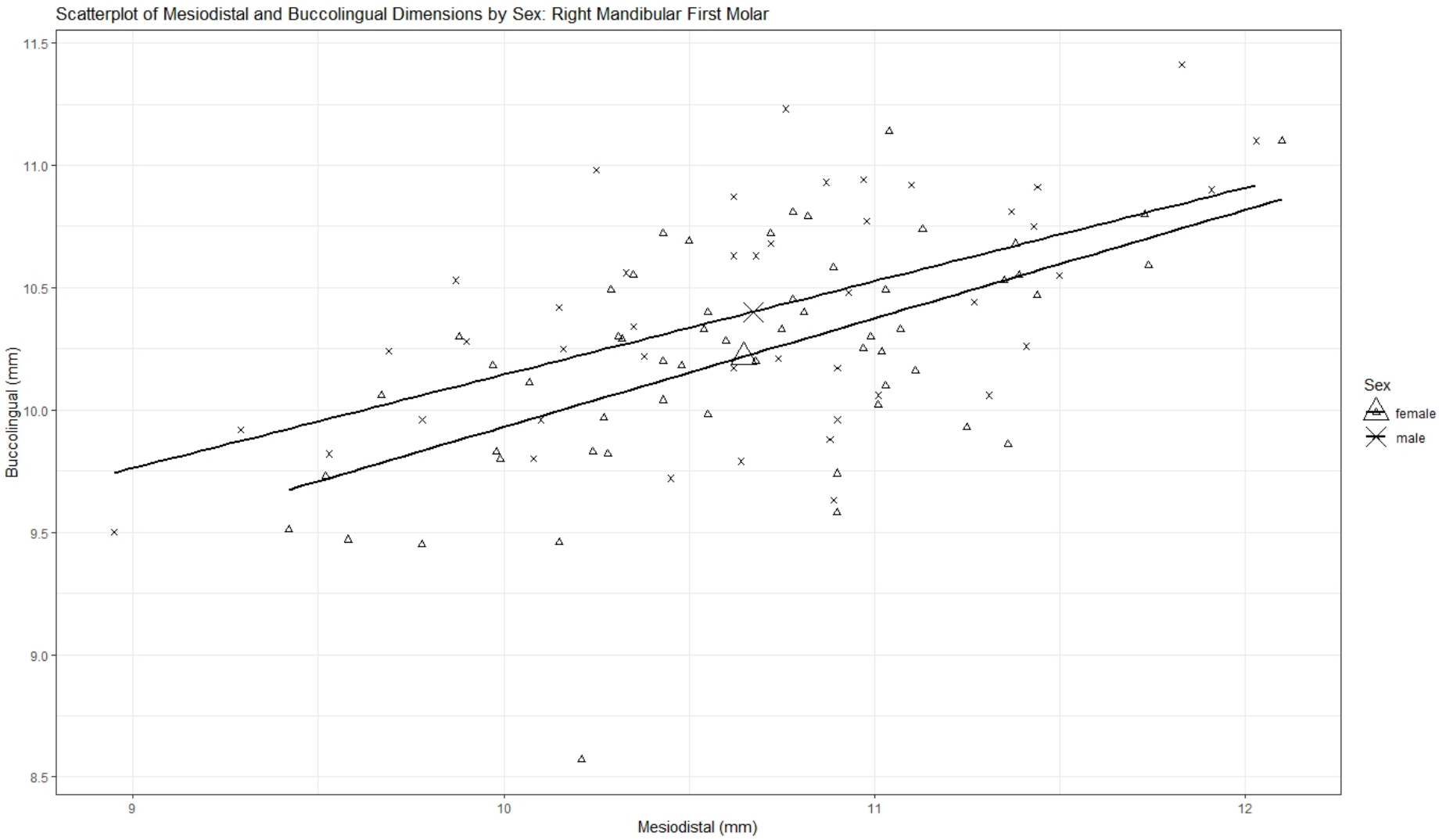

Figure 30 - Correlation between the MD and BL measurements of the right mandibular first molar, separated by sex. Regression equation for males: y=6.33+0.38*x, r2 = 0.315. Regression equation for females: y=5.49+0.44*x, r2 = 0.316.

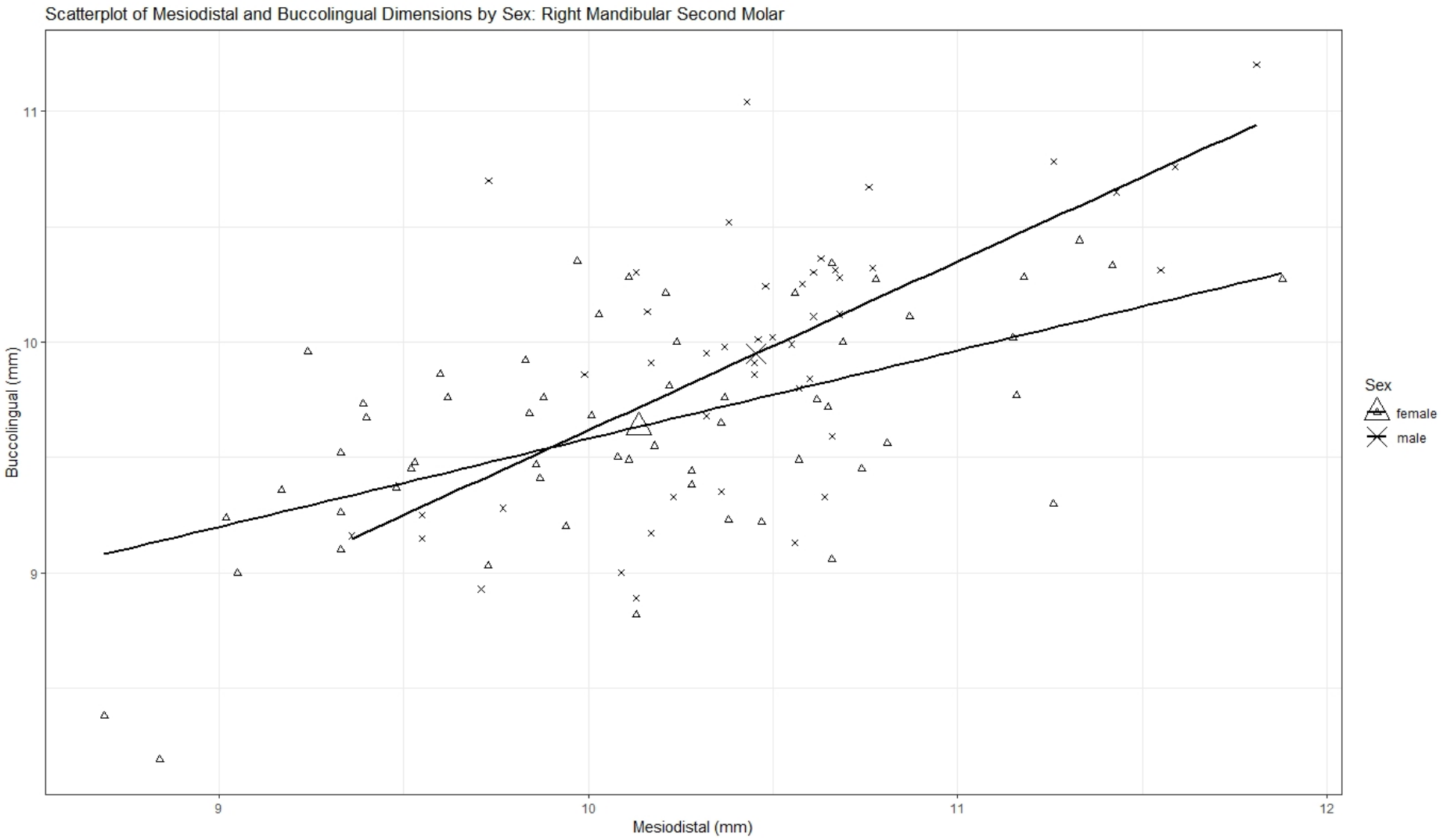

Figure 31 - Correlation between the MD and BL measurements of the right mandibular second molar, separated by sex. Regression equation for males: y=2.29+0.73*x, r2 = 0.418. Regression equation for females: y=5.76+0.38*x, r2 = 0.315.

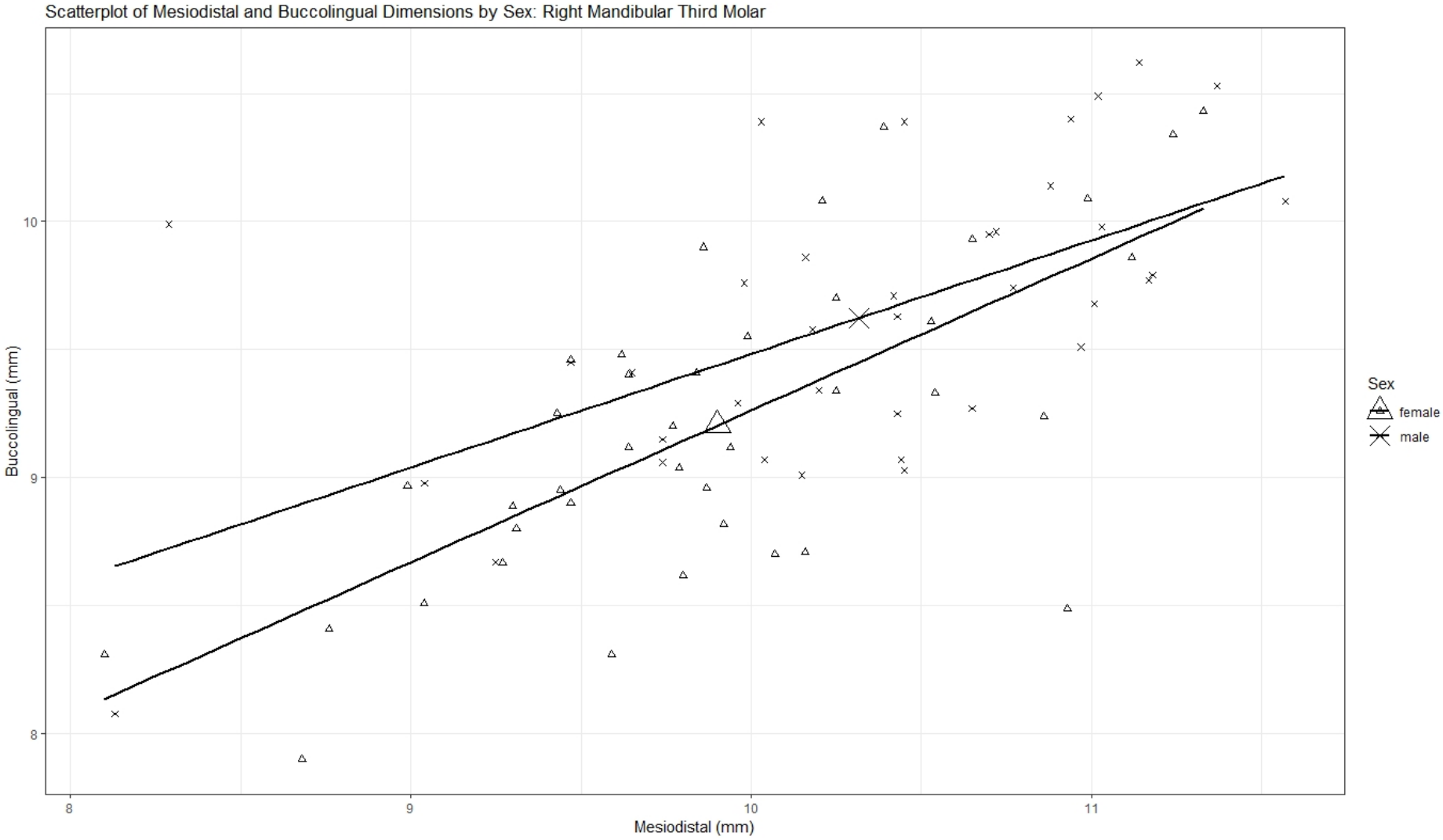

Figure 32 - Correlation between the MD and BL measurements of the right mandibular third molar, separated by sex. Regression equation for males: y=5.05+0.44*x, r2 = 0.375. Regression equation for females: y=3.34+0.59*x, r2 = 0.488.

Appendix 3: Normality Results

Table 1 - Shapiro-Wilk Test for normality for the combined cemetery sample, not separated by cemetery or sex.

Tooth	Measurement	Statistic	df	Significance
1 RMxM3	MD	0.987	69	0.719
	BL	0.984	69	0.515
2 RMxM2	MD	0.986	92	0.448
	BL	0.987	92	0.502
3 RMxM1	MD	0.985	87	0.400
	BL	0.990	87	0.717
4 RMxP2	MD	0.986	104	0.335
	BL	0.992	104	0.809
5 RMxP1	MD	0.986	100	0.374
	BL	0.987	100	0.469
6 RMxC	MD	0.940	101	0.000
	BL	0.986	101	0.383
7 RMxLI	MD	0.975	83	0.112
	BL	0.961	83	0.013
8 RMxCI	MD	0.988	66	0.785
	BL	0.991	66	0.924
9 LMxCI	MD	0.987	81	0.616
	BL	0.965	81	0.026
10 LMxLI	MD	0.973	86	0.066
	BL	0.960	86	0.009
11 LMxC	MD	0.990	98	0.672
	BL	0.981	98	0.167
12 LMxP1	MD	0.982	94	0.232
	BL	0.993	94	0.896
13 LMxP2	MD	0.987	95	0.487
	BL	0.991	95	0.789
14 LMxM1	MD	0.972	89	0.049
	BL	0.984	89	0.359
15 LMxM2	MD	0.991	90	0.830
	BL	0.986	90	0.463
16 LMxM3	MD	0.968	68	0.077
	BL	0.945	68	0.005
17 LMM3	MD	0.991	80	0.853
	BL	0.989	80	0.741
18 LMM2	MD	0.984	105	0.229
	BL	0.989	105	0.529
19 LMM1	MD	0.984	97	0.267
	BL	0.994	97	0.931
20 LMP2	MD	0.830	116	0.000
	BL	0.955	116	0.005
21 LMP1	MD	0.990	114	0.599
	BL	0.992	114	0.734
22	MD	0.987	113	0.361

LMC	BL	0.984	113	0.185
23	MD	0.985	101	0.304
LMLI	BL	0.995	101	0.984
24	MD	0.977	78	0.177
LMCI	BL	0.973	78	0.103
25	MD	0.986	75	0.587
RMCI	BL	0.973	75	0.115
26	MD	0.983	94	0.268
RMLI	BL	0.990	94	0.737
27	MD	0.993	111	0.784
RMC	BL	0.979	111	0.083
28	MD	0.994	117	0.906
RMP1	BL	0.990	117	0.576
29	MD	0.985	109	0.262
RMP2	BL	0.990	109	0.583
30	MD	0.994	101	0.939
RMM1	BL	0.985	101	0.302
31	MD	0.986	103	0.352
RMM2	BL	0.991	103	0.717
32	MD	0.977	77	0.177
RMM3	BL	0.987	77	0.638

Table 2 - Shapiro-Wilk Test for normality for the combined cemetery male data.

Tooth	**Measurement**	**Statistic**	**df**	**Significance**
1	MD	0.979	29	0.811
RMxM3	BL	0.909	29	0.016
2	MD	0.984	38	0.836
RMxM2	BL	0.960	38	0.188
3	MD	0.970	36	0.414
RMxM1	BL	0.986	36	0.928
4	MD	0.985	43	0.831
RMxP2	BL	0.990	43	0.962
5	MD	0.945	40	0.049
RMxP1	BL	0.985	40	0.873
6	MD	0.845	43	0.000
RMxC	BL	0.952	43	0.068
7	MD	0.947	36	0.086
RMxLI	BL	0.920	36	0.012
8	MD	0.973	32	0.585
RMxCI	BL	0.950	32	0.143
9	MD	0.977	37	0.639
LMxCI	BL	0.914	37	0.007
10	MD	0.973	38	0.470
LMxLI	BL	0.948	38	0.077
11	MD	0.967	43	0.249
LMxC	BL	0.932	43	0.013
12	MD	0.979	41	0.638
LMxP1	BL	0.983	41	0.770

13 LMxP2	MD	0.965	42	0.231
	BL	0.989	42	0.952
14 LMxM1	MD	0.962	36	0.251
	BL	0.966	36	0.328
15 LMxM2	MD	0.973	37	0.501
	BL	0.971	37	0.423
16 LMxM3	MD	0.966	25	0.545
	BL	0.919	25	0.050
17 LMM3	MD	0.972	40	0.427
	BL	0.990	40	0.970
18 LMM2	MD	0.980	50	0.551
	BL	0.986	50	0.799
19 LMM1	MD	0.959	43	0.133
	BL	0.986	43	0.868
20 LMP2	MD	0.931	56	0.003
	BL	0.921	56	0.001
21 LMP1	MD	0.977	51	0.415
	BL	0.988	51	0.866
22 LMC	MD	0.965	50	0.144
	BL	0.988	50	0.899
23 LMLI	MD	0.980	45	0.631
	BL	0.983	45	0.759
24 LMCI	MD	0.937	33	0.055
	BL	0.960	33	0.257
25 RMCI	MD	0.979	40	0.635
	BL	0.970	40	0.347
26 RMLI	MD	0.962	45	0.145
	BL	0.965	45	0.187
27 RMC	MD	0.974	49	0.352
	BL	0.983	49	0.713
28 RMP1	MD	0.988	53	0.851
	BL	0.988	53	0.878
29 RMP2	MD	0.972	51	0.268
	BL	0.975	51	0.348
30 RMM1	MD	0.986	44	0.870
	BL	0.980	44	0.626
31 RMM2	MD	0.938	45	0.018
	BL	0.968	45	0.238
32 RMM3	MD	0.933	37	0.027
	BL	0.974	37	0.534

Table 3 - Shapiro-Wilk Test for normality for the combined cemetery sample, female data.

Tooth	Measurement	Statistic	df	Significance
1 RMxM3	MD	0.983	40	0.782
	BL	0.983	40	0.816
2 RMxM2	MD	0.978	54	0.409
	BL	0.958	54	0.054
3	MD	0.981	51	0.574

RMxM1	BL	0.977	51	0.436
4	MD	0.968	61	0.106
RMxP2	BL	0.991	61	0.944
5	MD	0.989	60	0.883
RMxP1	BL	0.978	60	0.336
6	MD	0.982	58	0.564
RMxC	BL	0.990	58	0.918
7	MD	0.987	47	0.861
RMxLI	BL	0.965	47	0.163
8	MD	0.986	34	0.925
RMxCI	BL	0.984	34	0.886
9	MD	0.986	44	0.866
LMxCI	BL	0.977	44	0.516
10	MD	0.946	48	0.028
LMxLI	BL	0.948	48	0.034
11	MD	0.972	55	0.220
LMxC	BL	0.980	55	0.470
12	MD	0.977	53	0.389
LMxP1	BL	0.987	53	0.818
13	MD	0.989	53	0.919
LMxP2	BL	0.983	53	0.659
14	MD	0.971	53	0.213
LMxM1	BL	0.974	53	0.311
15	MD	0.985	53	0.754
LMxM2	BL	0.975	53	0.340
16	MD	0.959	43	0.130
LMxM3	BL	0.939	43	0.023
17	MD	0.977	40	0.591
LMM3	BL	0.964	40	0.228
18	MD	0.958	55	0.052
LMM2	BL	0.952	55	0.028
19	MD	0.985	54	0.753
LMM1	BL	0.979	54	0.445
20	MD	0.741	60	0.000
LMP2	BL	0.962	60	0.057
21	MD	0.984	63	0.577
LMP1	BL	0.979	63	0.357
22	MD	0.981	63	0.423
LMC	BL	0.938	63	0.003
23	MD	0.973	56	0.230
LMLI	BL	0.979	56	0.447
24	MD	0.954	45	0.073
LMCI	BL	0.979	45	0.590
25	MD	0.985	35	0.913
RMCI	BL	0.974	35	0.568
26	MD	0.983	49	0.677
RMLI	BL	0.982	49	0.670
27	MD	0.977	62	0.298
RMC	BL	0.960	62	0.043
28	MD	0.986	64	0.693

RMP1	BL	0.985	64	0.637
29	MD	0.975	58	0.287
RMP2	BL	0.973	58	0.222
30	MD	0.991	57	0.957
RMM1	BL	0.962	57	0.069
31	MD	0.991	58	0.946
RMM2	BL	0.961	58	0.063
32	MD	0.984	40	0.831
RMM3	BL	0.982	40	0.757

Table 4 - Shapiro-Wilk Test for normality for Hatherdene, combined sex.

Tooth	Measurement	Statistic	df	Significance
1	MD	0.977	33	0.689
RMxM3	BL	0.968	33	0.439
2	MD	0.974	40	0.488
RMxM2	BL	0.971	40	0.401
3	MD	0.981	34	0.810
RMxM1	BL	0.989	34	0.978
4	MD	0.957	43	0.112
RMxP2	BL	0.991	43	0.986
5	MD	0.985	43	0.854
RMxP1	BL	0.983	43	0.746
6	MD	0.971	44	0.328
RMxC	BL	0.954	44	0.078
7	MD	0.969	36	0.402
RMxLI	BL	0.953	36	0.128
8	MD	0.949	26	0.224
RMxCI	BL	0.948	26	0.208
9	MD	0.972	29	0.613
LMxCI	BL	0.895	29	0.007
10	MD	0.942	39	0.045
LMxLI	BL	0.962	39	0.205
11	MD	0.973	41	0.419
LMxC	BL	0.932	41	0.017
12	MD	0.966	41	0.247
LMxP1	BL	0.953	41	0.089
13	MD	0.981	42	0.695
LMxP2	BL	0.987	42	0.917
14	MD	0.968	38	0.337
LMxM1	BL	0.986	38	0.916
15	MD	0.981	41	0.720
LMxM2	BL	0.974	41	0.452
16	MD	0.978	34	0.708
LMxM3	BL	0.956	34	0.190
17	MD	0.978	39	0.630
LMM3	BL	0.952	39	0.094
18	MD	0.987	43	0.908
LMM2	BL	0.987	43	0.915

19 LMM1	MD	0.971	36	0.453
	BL	0.980	36	0.736
20 LMP2	MD	0.795	47	0.000
	BL	0.930	47	0.008
21 LMP1	MD	0.981	48	0.637
	BL	0.983	48	0.694
22 LMC	MD	0.978	47	0.516
	BL	0.972	47	0.313
23 LMLI	MD	0.985	43	0.848
	BL	0.977	43	0.549
24 LMCI	MD	0.954	32	0.182
	BL	0.968	32	0.446
25 RMCI	MD	0.947	30	0.665
	BL	0.964	30	0.389
26 RMLI	MD	0.944	36	0.069
	BL	0.963	36	0.267
27 RMC	MD	0.981	44	0.685
	BL	0.961	44	0.143
28 RMP1	MD	0.987	44	0.891
	BL	0.988	44	0.927
29 RMP2	MD	0.981	43	0.671
	BL	0.990	43	0.960
30 RMM1	MD	0.982	39	0.777
	BL	0.953	39	0.108
31 RMM2	MD	0.976	42	0.511
	BL	0.978	42	0.575
32 RMM3	MD	0.941	33	0.071
	BL	0.972	33	0.551

Table 5 - Shapiro-Wilk Test for normality for Hatherdene, males only.

Tooth	Measurement	Statistic	df	Significance
1 RMxM3	MD	0.977	16	0.941
	BL	0.878	16	0.036
2 RMxM2	MD	0.985	20	0.980
	BL	0.956	20	0.460
3 RMxM1	MD	0.953	18	0.470
	BL	0.985	18	0.988
4 RMxP2	MD	0.977	21	0.876
	BL	0.974	21	0.827
5 RMxP1	MD	0.951	22	0.334
	BL	0.941	22	0.206
6 RMxC	MD	0.921	23	0.069
	BL	0.919	23	0.063
7 RMxLI	MD	0.977	18	0.917
	BL	0.814	18	0.002
8 RMxCI	MD	0.953	17	0.503
	BL	0.968	17	0.783
9	MD	0.951	18	0.446

LMxCl	BL	0.872	18	0.019
10	MD	0.982	21	0.950
LMxLl	BL	0.901	21	0.037
11	MD	0.885	23	0.012
LMxC	BL	0.839	23	0.002
12	MD	0.961	22	0.512
LMxP1	BL	0.955	22	0.401
13	MD	0.947	23	0.252
LMxP2	BL	0.984	23	0.959
14	MD	0.956	21	0.433
LMxM1	BL	0.970	21	0.728
15	MD	0.965	22	0.594
LMxM2	BL	0.951	22	0.324
16	MD	0.964	16	0.733
LMxM3	BL	0.899	16	0.077
17	MD	0.944	21	0.256
LMM3	BL	0.969	21	0.712
18	MD	0.977	25	0.831
LMM2	BL	0.953	25	0.279
19	MD	0.955	21	0.413
LMM1	BL	0.962	21	0.559
20	MD	0.884	27	0.010
LMP2	BL	0.871	27	0.003
21	MD	0.969	26	0.594
LMP1	BL	0.969	26	0.606
22	MD	0.941	22	0.211
LMC	BL	0.054	22	0.376
23	MD	0.963	23	0.525
LMLl	BL	0.971	23	0.718
24	MD	0.929	17	0.211
LMCl	BL	0.946	17	0.395
25	MD	0.954	20	0.425
RMCl	BL	0.959	20	0.533
26	MD	0.908	21	0.049
RMLl	BL	0.942	21	0.244
27	MD	0.922	24	0.066
RMC	BL	0.950	24	0.276
28	MD	0.977	24	0.833
RMP1	BL	0.971	24	0.680
29	MD	0.982	24	0.924
RMP2	BL	0.967	24	0.594
30	MD	0.971	22	0.734
RMM1	BL	0.988	22	0.992
31	MD	0.946	23	0.237
RMM2	BL	0.955	23	0.374
32	MD	0.879	19	0.020
RMM3	BL	0.956	19	0.503

Table 6 - Shapiro-Wilk Test for normality for Hatherdene, females only.

Tooth	Measurement	Statistic	df	Significance
1 RMxM3	MD	0.933	17	0.246
	BL	0.956	17	0.559
2 RMxM2	MD	0.910	20	0.065
	BL	0.949	20	0.357
3 RMxM1	MD	0.962	16	0.701
	BL	0.977	16	0.938
4 RMxP2	MD	0.912	22	0.052
	BL	0.985	22	0.975
5 RMxP1	MD	0.975	21	0.840
	BL	0.983	21	0.964
6 RMxC	MD	0.954	21	0.400
	BL	0.927	21	0.122
7 RMxLI	MD	0.933	18	0.221
	BL	0.931	18	0.204
8 RMxCI	MD	0.901	9	0.259
	BL	0.868	9	0.116
9 LMxCI	MD	0.954	11	0.699
	BL	0.938	11	0.500
10 LMxLI	MD	0.924	18	0.152
	BL	0.896	18	0.050
11 LMxC	MD	0.919	18	0.126
	BL	0.961	18	0.628
12 LMxP1	MD	0.960	19	0.569
	BL	0.940	19	0.269
13 LMxP2	MD	0.963	19	0.634
	BL	0.988	19	0.995
14 LMxM1	MD	0.924	17	0.174
	BL	0.972	17	0.859
15 LMxM2	MD	0.939	19	0.258
	BL	0.944	19	0.305
16 LMxM3	MD	0.954	18	0.497
	BL	0.970	18	0.801
17 LMM3	MD	0.976	18	0.903
	BL	0.924	18	0.154
18 LMM2	MD	0.980	18	0.946
	BL	0.959	18	0.576
19 LMM1	MD	0.966	15	0.795
	BL	0.938	15	0.355
20 LMP2	MD	0.725	20	<.001
	BL	0.899	20	0.039
21 LMP1	MD	0.943	22	0.228
	BL	0.973	22	0.780
22 LMC	MD	0.963	25	0.480
	BL	0.915	25	0.040
23 LMLI	MD	0.977	20	0.894
	BL	0.963	20	0.604
24 LMCI	MD	0.972	15	0.893
	BL	0.946	15	0.461
25	MD	0.941	10	0.568

RMCI	BL	0.916	10	0.323
26	MD	0.968	15	0.834
RMLI	BL	0.954	15	0.594
27	MD	0.947	20	0.321
RMC	BL	0.939	20	0.234
28	MD	0.968	20	0.722
RMP1	BL	0.988	20	0.994
29	MD	0.964	19	0.650
RMP2	BL	0.952	19	0.420
30	MD	0.956	17	0.562
RMM1	BL	0.812	17	0.003
31	MD	0.963	19	0.628
RMM2	BL	0.950	19	0.390
32	MD	0.932	14	0.328
RMM3	BL	0.972	14	0.897

Table 7 - Shapiro-Wilk Test for normality for Oakington, combined sex.

Tooth	Measurement	Statistic	df	Significance
1	MD	0.920	21	0.087
RMxM3	BL	0.952	21	0.369
2	MD	0.967	35	0.360
RMxM2	BL	0.983	35	0.858
3	MD	0.989	33	0.976
RMxM1	BL	0.985	33	0.921
4	MD	0.985	40	0.879
RMxP2	BL	0.983	40	0.805
5	MD	0.977	38	0.603
RMxP1	BL	0.974	38	0.515
6	MD	0.872	35	0.001
RMxC	BL	0.990	35	0.986
7	MD	0.980	33	0.780
RMxLI	BL	0.921	33	0.019
8	MD	0.970	29	0.565
RMxCI	BL	0.959	29	0.303
9	MD	0.976	35	0.631
LMxCI	BL	0.957	25	0.182
10	MD	0.981	32	0.815
LMxLI	BL	0.937	32	0.063
11	MD	0.975	36	0.573
LMxC	BL	0.985	36	0.892
12	MD	0.966	36	0.316
LMxP1	BL	0.983	36	0.835
13	MD	0.969	37	0.380
LMxP2	BL	0.986	37	0.924
14	MD	0.955	32	0.204
LMxM1	BL	0.971	32	0.540
15	MD	0.976	30	0.705
LMxM2	BL	0.978	30	0.775

16 LMxM3	MD	0.865	19	0.012
	BL	0.881	19	0.023
17 LMM3	MD	0.970	26	0.617
	BL	0.924	26	0.055
18 LMM2	MD	0.953	38	0.115
	BL	0.981	38	0.745
19 LMM1	MD	0.940	35	0.056
	BL	0.973	35	0.530
20 LMP2	MD	0.971	42	0.346
	BL	0.976	42	0.520
21 LMP1	MD	0.988	39	0.950
	BL	0.971	39	0.392
22 LMC	MD	0.972	39	0.431
	BL	0.980	39	0.707
23 LMLI	MD	0.986	35	0.916
	BL	0.987	35	0.951
24 LMCI	MD	0.980	28	0.850
	BL	0.952	28	0.217
25 RMCI	MD	0.981	28	0.877
	BL	0.952	28	0.218
26 RMLI	MD	0.981	36	0.788
	BL	0.963	36	0.270
27 RMC	MD	0.954	37	0.125
	BL	0.963	37	0.245
28 RMP1	MD	0.976	42	0.519
	BL	0.967	42	0.258
29 RMP2	MD	0.954	38	0.117
	BL	0.982	38	0.803
30 RMM1	MD	0.943	36	0.064
	BL	0.964	36	0.293
31 RMM2	MD	0.965	34	0.343
	BL	0.966	34	0.364
32 RMM3	MD	0.976	26	0.780
	BL	0.965	26	0.491

Table 8 - Shapiro-Wilk Test for normality for Oakington, male data.

Tooth	Measurement	Statistic	df	Significance
1 RMxM3	MD	0.956	9	0.758
	BL	0.783	9	0.013
2 RMxM2	MD	0.977	13	0.963
	BL	0.932	13	0.361
3 RMxM1	MD	0.885	11	0.119
	BL	0.976	11	0.940
4 RMxP2	MD	0.963	15	0.751
	BL	0.986	15	0.995
5 RMxP1	MD	0.882	13	0.076
	BL	0.984	13	0.994
6	MD	0.784	14	0.003

RMxC	BL	0.956	14	0.658
7	MD	0.960	14	0.731
RMxLI	BL	0.921	14	0.231
8	MD	0.937	12	0.462
RMxCI	BL	0.841	12	0.028
9	MD	0.952	14	0.592
LMxCI	BL	0.893	14	0.088
10	MD	0.948	12	0.604
LMxLI	BL	0.913	12	0.234
11	MD	0.905	14	0.132
LMxC	BL	0.905	14	0.134
12	MD	0.985	13	0.996
LMxP1	BL	0.954	13	0.665
13	MD	0.958	14	0.691
LMxP2	BL	0.983	14	0.990
14	MD	0.906	11	0.221
LMxM1	BL	0.919	11	0.313
15	MD	0.970	12	0.912
LMxM2	BL	0.968	12	0.886
16	MD	0.830	6	0.107
LMxM3	BL	0.982	6	0.963
17	MD	0.949	11	0.636
LMM3	BL	0.927	11	0.386
18	MD	0.898	17	0.064
LMM2	BL	0.978	17	0.937
19	MD	0.913	15	0.150
LMM1	BL	0.979	15	0.961
20	MD	0.948	19	0.370
LMP2	BL	0.981	19	0.953
21	MD	0.904	16	0.093
LMP1	BL	0.976	16	0.926
22	MD	0.964	18	0.685
LMC	BL	0.969	18	0.786
23	MD	0.977	14	0.952
LMLI	BL	0.950	14	0.565
24	MD	0.920	12	0.282
LMCI	BL	0.870	12	0.066
25	MD	0.960	15	0.690
RMCI	BL	0.968	15	0.820
26	MD	0.970	15	0.864
RMLI	BL	0.955	15	0.611
27	MD	0.948	15	0.492
RMC	BL	0.925	15	0.226
28	MD	0.971	18	0.815
RMP1	BL	0.968	18	0.769
29	MD	0.930	16	0.240
RMP2	BL	0.976	16	0.921
30	MD	0.878	15	0.044
RMM1	BL	0.950	15	0.518
31	MD	0.753	13	0.002

RMM2	BL	0.919	13	0.245
32	MD	0.922	10	0.378
RMM3	BL	0.962	10	0.812

Table 9 - Shapiro-Wilk Test for normality for Oakington, female data.

Tooth	Measurement	Statistic	df	Significance
1	MD	0.951	12	0.659
RMxM3	BL	0.968	12	0.884
2	MD	0.936	22	0.166
RMxM2	BL	0.944	22	0.241
3	MD	0.971	22	0.740
RMxM1	BL	0.983	22	0.952
4	MD	0.962	25	0.447
RMxP2	BL	0.978	25	0.847
5	MD	0.977	25	0.815
RMxP1	BL	0.933	25	0.101
6	MD	0.958	21	0.482
RMxC	BL	0.987	21	0.990
7	MD	0.978	19	0.921
RMxLI	BL	0.933	19	0.194
8	MD	0.982	17	0.976
RMxCI	BL	0.939	17	0.312
9	MD	0.977	21	0.881
LMxCI	BL	0.944	21	0.258
10	MD	0.938	20	0.217
LMxLI	BL	0.937	20	0.207
11	MD	0.980	22	0.918
LMxC	BL	0.968	22	0.659
12	MD	0.933	23	0.125
LMxP1	BL	0.974	23	0.780
13	MD	0.966	23	0.591
LMxP2	BL	0.982	23	0.944
14	MD	0.928	21	0.125
LMxM1	BL	0.970	21	0.737
15	MD	0.947	18	0.383
LMxM2	BL	0.907	18	0.075
16	MD	0.823	13	0.013
LMxM3	BL	0.892	13	0.103
17	MD	0.909	15	0.131
LMM3	BL	0.928	15	0.256
18	MD	0.936	21	0.178
LMM2	BL	0.925	21	0.111
19	MD	0.951	20	0.381
LMM1	BL	0.965	20	0.644
20	MD	0.962	23	0.514
LMP2	BL	0.948	23	0.269
21	MD	0.978	23	0.875
LMP1	BL	0.956	23	0.395

22 LMC	MD	0.932	21	0.148
	BL	0.882	21	0.016
23 LMLI	MD	0.966	21	0.640
	BL	0.939	21	0.207
24 LMCI	MD	0.944	16	0.396
	BL	0.980	16	0.967
25 RMCI	MD	0.940	13	0.458
	BL	0.941	13	0.464
26 RMLI	MD	0.972	21	0.770
	BL	0.944	21	0.266
27 RMC	MD	0.900	22	0.030
	BL	0.910	22	0.047
28 RMP1	MD	0.966	24	0.575
	BL	0.954	24	0.329
29 RMP2	MD	0.963	22	0.550
	BL	0.967	22	0.640
30 RMM1	MD	0.963	21	0.570
	BL	0.951	21	0.355
31 RMM2	MD	0.976	21	0.865
	BL	0.954	21	0.397
32 RMM3	MD	0.967	16	0.779
	BL	0.972	16	0.875

Table 10 - Shapiro-Wilk Test for normality for Polhill, combined sex.

Tooth	Measurement	Statistic	df	Significance
1 RMxM3	MD	0.931	11	0.418
	BL	0.974	11	0.927
2 RMxM2	MD	0.945	14	0.493
	BL	0.891	14	0.083
3 RMxM1	MD	0.948	15	0.499
	BL	0.924	15	0.223
4 RMxP2	MD	0.933	18	0.219
	BL	0.961	18	0.612
5 RMxP1	MD	0.950	16	0.486
	BL	0.951	16	0.502
6 RMxC	MD	0.953	17	0.511
	BL	0.964	17	0.702
7 RMxLI	MD	0.681	12	0.001
	BL	0.779	12	0.006
8 RMxCI	MD	0.864	10	0.084
	BL	0.921	10	0.367
9 LMxCI	MD	0.991	14	1.000
	BL	0.921	14	0.225
10 LMxLI	MD	0.920	12	0.286
	BL	0.965	12	0.848
11 LMxC	MD	0.943	16	0.391
	BL	0.948	16	0.462
12	MD	0.919	13	0.246

LMxP1	BL	0.891	13	0.101
13	MD	0.925	12	0.329
LMxP2	BL	0.923	12	0.312
14	MD	0.967	15	0.805
LMxM1	BL	0.896	15	0.082
15	MD	0.963	15	0.738
LMxM2	BL	0.919	15	0.183
16	MD	0.878	11	0.099
LMxM3	BL	0.895	11	0.159
17	MD	0.958	12	0.759
LMM3	BL	0.955	12	0.712
18	MD	0.887	19	0.028
LMM2	BL	0.983	19	0.969
19	MD	0.970	20	0.760
LMM1	BL	0.937	20	0.212
20	MD	0.973	21	0.802
LMP2	BL	0.976	21	0.864
21	MD	0.985	20	0.980
LMP1	BL	0.987	20	0.990
22	MD	0.919	20	0.096
LMC	BL	0.925	20	0.124
23	MD	0.957	17	0.583
LMLI	BL	0.970	17	0.821
24	MD	0.964	12	0.843
LMCI	BL	0.981	12	0.986
25	MD	0.962	14	0.749
RMCI	BL	0.955	14	0.642
26	MD	0.943	17	0.356
RMLI	BL	0.971	17	0.832
27	MD	0.957	22	0.438
RMC	BL	0.908	22	0.042
28	MD	0.987	23	0.985
RMP1	BL	0.963	23	0.532
29	MD	0.947	18	0.387
RMP2	BL	0.951	18	0.440
30	MD	0.957	19	0.518
RMM1	BL	0.978	19	0.918
31	MD	0.923	20	0.115
RMM2	BL	0.961	20	0.555
32	MD	0.899	12	0.156
RMM3	BL	0.915	12	0.246

Table 11 - Shapiro-Wilk Test for normality for Polhill, male data.

Tooth	Measurement	Statistic	df	Significance
1	MD	--	2	--
RMxM3	BL	--	2	--
2	MD	0.940	3	0.525
RMxM2	BL	1.000	3	0.959

3	MD	0.971	4	0.848
RMxM1	BL	0.870	4	0.299
4	MD	0.940	5	0.669
RMxP2	BL	0.979	5	0.927
5	MD	0.880	5	0.308
RMxP1	BL	0.925	5	0.564
6	MD	0.892	5	0.365
RMxC	BL	0.976	5	0.912
7	MD	0.814	4	0.129
RMxLI	BL	0.906	4	0.463
8	MD	--	2	--
RMxCI	BL	--	2	--
9	MD	0.868	4	0.290
LMxCI	BL	0.949	4	0.709
10	MD	0.953	5	0.755
LMxLI	BL	0.989	5	0.976
11	MD	0.741	5	0.025
LMxC	BL	0.980	5	0.932
12	MD	0.881	5	0.312
LMxP1	BL	0.943	5	0.684
13	MD	0.863	4	0.272
LMxP2	BL	0.895	4	0.408
14	MD	--	2	--
LMxM1	BL	--	2	--
15	MD	--	2	--
LMxM2	BL	--	2	--
16	MD	--	1	--
LMxM3	BL	--	1	--
17	MD	0.981	6	0.959
LMM3	BL	0.925	6	0.545
18	MD	0.903	6	0.391
LMM2	BL	0.964	6	0.850
19	MD	0.764	4	0.052
LMM1	BL	0.980	4	0.902
20	MD	0.963	8	0.839
LMP2	BL	0.982	8	0.974
21	MD	0.931	7	0.561
LMP1	BL	0.956	7	0.784
22	MD	0.821	8	0.048
LMC	BL	0.887	8	0.218
23	MD	0.846	7	0.113
LMLI	BL	0.894	7	0.298
24	MD	0.994	3	0.855
LMCI	BL	0.984	3	0.756
25	MD	0.844	4	0.207
RMCI	BL	0.787	4	0.081
26	MD	0.923	8	0.452
RMLI	BL	0.841	8	0.077
27	MD	0.906	8	0.325
RMC	BL	0.885	8	0.210

28 RMP1	MD	0.978	8	0.954
	BL	0.971	8	0.907
29 RMP2	MD	0.757	6	0.023
	BL	0.877	6	0.258
30 RMM1	MD	0.927	5	0.576
	BL	0.916	5	0.504
31 RMM2	MD	0.892	6	0.330
	BL	0.828	6	0.103
32 RMM3	MD	0.899	5	0.405
	BL	0.810	5	0.097

Table 12 - Shapiro-Wilk Test for normality for Polhill, female data.

Tooth	Measurement	Statistic	df	Significance
1 RMxM3	MD	0.961	9	0.806
	BL	0.961	9	0.807
2 RMxM2	MD	0.967	11	0.858
	BL	0.922	11	0.340
3 RMxM1	MD	0.911	11	0.253
	BL	0.919	11	0.310
4 RMxP2	MD	0.936	13	0.411
	BL	0.919	13	0.241
5 RMxP1	MD	0.952	11	0.675
	BL	0.961	11	0.786
6 RMxC	MD	0.934	12	0.422
	BL	0.973	12	0.942
7 RMxLI	MD	0.610	8	<0.000
	BL	0.919	8	0.422
8 RMxCI	MD	0.799	8	0.028
	BL	0.923	8	0.452
9 LMxCI	MD	0.981	10	0.969
	BL	0.875	10	0.113
10 LMxLI	MD	0.929	7	0.540
	BL	0.885	7	0.249
11 LMxC	MD	0.913	11	0.264
	BL	0.907	11	0.227
12 LMxP1	MD	0.910	8	0.351
	BL	0.889	8	0.231
13 LMxP2	MD	0.907	8	0.336
	BL	0.914	8	0.383
14 LMxM1	MD	0.967	13	0.855
	BL	0.812	13	0.009
15 LMxM2	MD	0.966	13	0.847
	BL	0.916	13	0.218
16 LMxM3	MD	0.922	10	0.373
	BL	0.870	10	0.099
17 LMM3	MD	0.929	6	0.570
	BL	0.911	6	0.440
18	MD	0.783	13	0.004

LMM2	BL	0.936	13	0.401
19	MD	0.979	16	0.958
LMM1	BL	0.959	16	0.635
20	MD	0.962	13	0.778
LMP2	BL	0.932	13	0.360
21	MD	0.933	13	0.370
LMP1	BL	0.943	13	0.491
22	MD	0.970	12	0.916
LMC	BL	0.901	12	0.165
23	MD	0.786	10	0.010
LMLI	BL	0.975	10	0.932
24	MD	0.908	9	0.299
LMCI	BL	0.971	9	0.902
25	MD	0.970	10	0.887
RMCI	BL	0.954	10	0.716
26	MD	0.914	9	0.346
RMLI	BL	0.835	9	0.050
27	MD	0.983	14	0.987
RMC	BL	0.945	14	0.481
28	MD	0.949	15	0.514
RMP1	BL	0.928	15	0.253
29	MD	0.976	12	0.965
RMP2	BL	0.930	12	0.378
30	MD	0.930	14	0.306
RMM1	BL	0.975	14	0.937
31	MD	0.925	14	0.258
RMM2	BL	0.951	14	0.573
32	MD	0.822	7	0.067
RMM3	BL	0.956	7	0.787

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Table 13 - Shapiro-Wilk Test for normality for Eastry, combined sex.

Tooth	Measurement	Statistic	df	Significance
1	MD	0.978	4	0.890
RMxM3	BL	0.723	4	0.021
2	MD	0.957	3	0.599
RMxM2	BL	0.911	3	0.420
3	MD	0.919	5	0.526
RMxM1	BL	0.941	5	0.670
4	MD	0.918	3	0.446
RMxP2	BL	0.821	3	0.166
5	MD	0.894	3	0.368
RMxP1	BL	0.997	3	0.900
6	MD	0.962	5	0.824
RMxC	BL	0.847	5	0.185
7	MD	--	2	--
RMxLI	BL	--	2	--
8	MD	--	1	--
RMxCI	BL	--	1	--

9	MD	0.932	3	0.497
LMxCl	BL	1.000	3	0.958
10	MD	0.998	3	0.923
LMxLl	BL	1.000	3	0.983
11	MD	0.894	5	0.380
LMxC	BL	0.966	5	0.847
12	MD	0.976	4	0.879
LMxP1	BL	0.978	4	0.891
13	MD	0.990	4	0.955
LMxP2	BL	0.888	4	0.375
14	MD	0.983	4	0.917
LMxM1	BL	0.977	4	0.883
15	MD	0.926	4	0.573
LMxM2	BL	0.875	4	0.320
16	MD	0.930	4	0.597
LMxM3	BL	0.977	4	0.882
17	MD	0.977	3	0.709
LMM3	BL	0.977	3	0.708
18	MD	0.735	5	0.022
LMM2	BL	0.907	5	0.449
19	MD	0.895	6	0.347
LMM1	BL	0.930	6	0.577
20	MD	0.984	6	0.970
LMP2	BL	0.875	6	0.249
21	MD	0.837	7	0.093
LMP1	BL	0.956	7	0.788
22	MD	0.929	7	0.541
LMC	BL	0.973	7	0.921
23	MD	0.862	6	0.196
LMLI	BL	0.984	6	0.968
24	MD	0.942	6	0.672
LMCI	BL	0.948	6	0.722
25	MD	0.994	3	0.853
RMCI	BL	0.982	3	0.744
26	MD	0.974	5	0.898
RMLI	BL	0.850	5	0.194
27	MD	0.885	8	0.209
RMC	BL	0.816	8	0.042
28	MD	0.960	8	0.813
RMP1	BL	0.931	8	0.528
29	MD	0.928	10	0.427
RMP2	BL	0.945	10	0.610
30	MD	0.947	7	0.702
RMM1	BL	0.973	7	0.921
31	MD	0.954	7	0.769
RMM2	BL	0.850	7	0.122
32	MD	0.887	6	0.303
RMM3	BL	0.958	6	0.800

Table 14 - Shapiro-Wilk Test for normality for Eastry, males only.

Tooth	Measurement	Statistic	df	Significance
1 RMxM3	MD	--	2	--
	BL	--	2	--
2 RMxM2	MD	--	2	--
	BL	--	2	--
3 RMxM1	MD	0.791	3	0.093
	BL	0.998	3	0.919
4 RMxP2	MD	--	2	--
	BL	--	2	--
5 RMxP1	MD	--	0	--
	BL	--	0	--
6 RMxC	MD	--	1	--
	BL	--	1	--
7 RMxLI	MD	--	0	--
	BL	--	0	--
8 RMxCI	MD	--	1	--
	BL	--	1	--
9 LMxCI	MD	--	1	--
	BL	--	1	--
10 LMxLI	MD	--	0	--
	BL	--	0	--
11 LMxC	MD	--	1	--
	BL	--	1	--
12 LMxP1	MD	--	1	--
	BL	--	1	--
13 LMxP2	MD	--	1	--
	BL	--	1	--
14 LMxM1	MD	--	2	--
	BL	--	2	--
15 LMxM2	MD	--	1	--
	BL	--	1	--
16 LMxM3	MD	--	2	--
	BL	--	2	--
17 LMM3	MD	--	2	--
	BL	--	2	--
18 LMM2	MD	--	2	--
	BL	--	2	--
19 LMM1	MD	0.816	3	0.152
	BL	0.975	3	0.699
20 LMP2	MD	--	2	--
	BL	--	2	--
21 LMP1	MD	--	2	--
	BL	--	2	--
22 LMC	MD	--	2	--
	BL	--	2	--
23 LMLI	MD	--	1	--
	BL	--	1	--
24	MD	--	1	--

LMCI	BL	--	1	--
25	MD	--	1	--
RMCI	BL	--	1	--
26	MD	--	1	--
RMLI	BL	--	1	--
27	MD	--	2	--
RMC	BL	--	2	--
28	MD	0.915	3	0.433
RMP1	BL	0.780	3	0.068
29	MD	0.745	5	0.027
RMP2	BL	0.874	5	0.283
30	MD	--	2	--
RMM1	BL	--	2	--
31	MD	0.953	3	0.584
RMM2	BL	0.764	3	0.032
32	MD	0.835	3	0.201
RMM3	BL	0.972	3	0.681

Table 15 - Shapiro-Wilk Test for normality for Eastry, females only.

Tooth	Measurement	Statistic	df	Significance
1	MD	--	2	--
RMxM3	BL	--	2	--
2	MD	--	1	--
RMxM2	BL	--	1	--
3	MD	--	2	--
RMxM1	BL	--	2	--
4	MD	--	1	--
RMxP2	BL	--	1	--
5	MD	0.894	3	0.368
RMxP1	BL	0.997	3	0.900
6	MD	0.951	4	0.724
RMxC	BL	0.823	4	0.150
7	MD	--	2	--
RMxLI	BL	--	2	--
8	MD	--	0	--
RMxCI	BL	--	0	--
9	MD	--	2	--
LMxCI	BL	--	2	--
10	MD	0.998	3	0.923
LMxLI	BL	1.000	3	0.983
11	MD	0.927	4	0.578
LMxC	BL	0.926	4	0.570
12	MD	0.960	3	0.614
LMxP1	BL	0.986	3	0.772
13	MD	0.991	3	0.817
LMxP2	BL	0.788	3	0.087
14	MD	--	2	--
LMxM1	BL	--	2	--

15 LMxM2	MD	0.982	3	0.745
	BL	0.800	3	0.115
16 LMxM3	MD	--	2	--
	BL	--	2	--
17 LMM3	MD	--	1	--
	BL	--	1	--
18 LMM2	MD	0.904	3	0.399
	BL	0.838	3	0.209
19 LMM1	MD	0.964	3	0.637
	BL	0.983	3	0.752
20 LMP2	MD	0.942	4	0.669
	BL	0.939	4	0.650
21 LMP1	MD	0.914	5	0.495
	BL	0.873	5	0.279
22 LMC	MD	0.968	5	0.962
	BL	0.907	5	0.449
23 LMLI	MD	0.798	5	0.078
	BL	0.963	5	0.829
24 LMCI	MD	0.901	5	0.418
	BL	0.887	5	0.340
25 RMCI	MD	--	2	--
	BL	--	2	--
26 RMLI	MD	0.945	4	0.688
	BL	0.999	4	0.996
27 RMC	MD	0.925	6	0.543
	BL	0.870	6	0.226
28 RMP1	MD	0.890	5	0.358
	BL	0.988	5	0.972
29 RMP2	MD	0.948	5	0.720
	BL	0.862	5	0.236
30 RMM1	MD	0.974	5	0.898
	BL	0.882	5	0.319
31 RMM2	MD	0.959	4	0.773
	BL	0.876	4	0.323
32 RMM3	MD	0.895	3	0.371
	BL	0.968	3	0.658

Appendix 4: Outliers by Tooth Size

Table 1 – Outliers identified from the combined sample, not separated by site or sex.

Tooth	Outlier	Notes (than mean)
1	O1709	MD Larger
	P4	MD Larger
	H241	MD Larger
	H259	MD Smaller
	O1376	MD Smaller
	H241	BL Larger
	H1272	BL Smaller
2	H241	MD Larger
	H956	MD Smaller
	O1618	BL Smaller
3	O1709	MD Larger
	P5	MD Smaller
	P32	MD Smaller
4	H443	MD Smaller
	H205	MD Smaller
5	H1293	BL Larger
	O1616	BL Larger
6	E50	MD Smaller
	O1616	MD Smaller – extreme
	H241	BL Larger
	O1616	BL Larger
7	P41	MD Smaller
	O1424	BL Larger
	P41	BL Smaller
8	O1424	BL Larger
9	H373	BL Larger
	O1424	BL Larger
10	H220	MD Smaller
	H493	BL Larger
	P50	BL Larger
	O1441	BL Larger
	O1424	BL Larger
	H1300	BL Larger
	H220	BL Smaller
11	H241	BL Larger
	O1631	BL Smaller
12	O1376	BL Smaller
	P2	BL Smaller
13	O1785	MD Smaller
	H373	MD Smaller
14	H228	MD Larger
	O1636	MD Larger
	O1709	MD Larger
	H300	MD Smaller
	H443	MD Smaller

15	E12 O1618	MD Larger MD Smaller
16	H205 H856 H526 O841	BL Smaller BL Smaller BL Smaller BL Smaller
17	N/A	
18	P42 H225 O2165 H241 H560 H956 O2165	MD Larger MD Smaller MD Smaller BL Larger BL Larger BL Smaller BL Smaller
19	P5 H999	BL Larger BL Smaller
20	H999 H560 H241 O731 O1424 H705 H325 H1178 H205 H999 H1293	MD Larger extreme MD Larger MD Larger MD Larger MD Larger MD Larger MD Smaller MD Smaller MD Smaller BL Larger BL Smaller extreme
21	H560 H964 P50	MD Larger MD Smaller BL Larger
22	P50 H225 H205 P50 O1615 H274 O2154	MD Larger MD Smaller MD Smaller BL Larger BL Larger BL Larger BL Smaller
23	O1636 O1772 O1424 O2165	MD Larger MD Smaller BL Larger BL Smaller
24	O1772 O1424 H493	MD Smaller BL Larger BL Larger
25	O1441 O1424	MD Smaller BL Larger
26	N/A	
27	H241 H241 P50	MD Larger BL Larger BL Larger
28	H205	MD Smaller

	O1862	BL Larger
29	E5 H241 H259	MD Larger MD Larger BL Smaller
30	H1178 H956	MD Smaller BL Smaller
31	P13 O2165	MD Larger MD Smaller
32	N/A	

Table 2 - Outliers identified from the combined cemetery male data.

Tooth	Outliers	Notes (above mean)
1	P4 H241 H1293 H259	MD L MD L MD S MD S
2	O1618	BL S
3	N/A	
4	N/A	
5	N/A	
6	H353 E50 O1616 H241 O1616	MD S MD S MD S extreme BL L BL L
7	P41 O1424 P41	MD S BL L BL S
8	O1424	BL L
9	H373 O1424	BL L BL L
10	O1424 O1441 P50 P40	BL L BL L BL L BL S
11	H506 H241 O1631	MD L BL L BL S
12	H1293	BL L
13	H373	MD S
14	H228 H241	MD L MD L
15	O1618	MD S
16	P36 H526	MD S BL S
17	N/A	
18	N/A	
19	N/A	
20	H560	MD L extreme

	H241 H705 O1424 O731 H1178 H1293	MD L MD L MD L MD L MD S BL S extreme
21	H964	MD S
22	P50 P27 H361	MD L MD S MD S
23	N/A	
24	O1631 H560 O1424	MD L MD L BL L
25	O1631	MD L
26	N/A	
27	H241 H241	MD L BL L
28	N/A	
29	E5 H241 H201 E5 H259	MD L MD L MD S BL S BL S
30	N/A	
31	O1862 H241 H361 H506 E28	MD L MD L MD L MD L MD S
32	E5 H353 H353	MD S MD S BL S

Table 3 - Outliers identified from the combined female data.

Tooth	Outliers	Notes (above mean)
1	O1709	MD L
2	H637 H956	MD L MD S
3	O1709 P32	MD L MD S
4	H637 H443 H205	MD L MD S MD S
5	N/A	
6	N/A	
7	P2	MD S
8	N/A	
9	N/A	

10	H220 H493 H1300 H220	MD S BL L BL L BL S
11	N/A	
12	O1376	BL S
13	N/A	
14	O1636 O1709 H300 H443	MD L MD L MD S MD S
15	E12	MD L
16	H493 H1202 H205 H856 O841	BL L BL L BL S BL S BL S extreme
17	N/A	
18	P42 O2165 O2165 H956	MD L MD S BL S BL S
19	H1127 H999	MD S BL S
20	H999 H205 H999	MD L extreme MD S BL L
21	N/A	
22	O1709 O1636 H205 O1615 H637 H205 O2154	MD L MD L MD S BL L extreme BL S BL S BL S
23	O1772	MD S
24	O1772	MD S
25	N/A	
26	P2	BL S
27	O1615 P3	BL L BL S
28	H205 H205	MD S BL S
29	N/A	
30	H956	BL S
31	O2165 H956	BL S BL S
32	O2165	MD S

Table 4 - Outliers identified from Hatherdene, combined sex.

Tooth	Outlier	Notes (than mean)
1	N/A	
2	H956	MD smaller
3	N/A	
4	H443	MD smaller
	H205	MD smaller
5	H1293	BL larger
	H225	BL smaller
6	H241	BL larger
7	H1293	BL larger
8	N/A	
9	H373	BL larger
10	H325	MD smaller
	H220	MD smaller extreme
	H493	BL larger
	H1300	BL larger
	H220	BL smaller
11	H506	MD larger
	H241	BL larger extreme
	H493	BL larger
12	H1293	BL larger
13	N/A	
14	H443	MD smaller
	H300	MD smaller
15	N/A	
16	N/A	
17	N/A	
18	H225	MD smaller
	H956	BL smaller
19	H999	BL smaller
20	H999	MD larger extreme
	H560	MD larger
	H241	MD larger
	H705	MD larger
	H205	MD smaller
	H999	BL larger
	H1293	BL smaller
21	N/A	
22	H560	MD larger
	H225	MD smaller
	H205	MD smaller
	H361	MD smaller
	H274	BL larger
	H560	BL larger
	H205	BL smaller
	H637	BL smaller
23	N/A	
24	H560	MD larger
	H493	BL larger

25	N/A	
26	H1275	BL larger
27	H241 H241	MD larger BL larger
28	H964	BL larger
29	H241 H241 H259	MD larger BL larger BL smaller
30	H956	BL smaller
31	N/A	
32	N/A	

Table 5 - Outliers identified from Hatherdene, males only.

Tooth	Outlier	Notes (regarding mean)
1	N/A	
2	N/A	
3	H241 H1149	MD larger MD smaller
4	N/A	
5	H1293	BL larger
6	H506 H241 H1178 H353 H241	MD larger MD larger MD smaller MD smaller extreme BL larger
7	H1293	BL larger
8	N/A	
9	H422 H373	MD smaller BL larger
10	H1165 H640	BL smaller BL smaller
11	H506 H241 H241	MD larger MD larger BL larger
12	H1293	BL larger
13	H373	MD smaller
14	H228 H241	MD larger MD larger
15	N/A	
16	H1275 H526	MD larger BL smaller
17	N/A	
18	N/A	
19	H1178 H1178	MD smaller BL smaller
20	H560 H241 H705 H1275	MD larger extreme MD larger MD larger MD larger

	H228 H1178 H560 H1293	MD larger MD smaller BL larger BL smaller extreme
21	H560 H964 H241	MD larger MD smaller BL larger
22	H361	MD smaller
23	N/A	
24	H560	MD larger
25	N/A	
26	H1275 H964	BL larger BL larger
27	H241 H1275 H241 H964	MD larger MD larger BL larger BL smaller
28	N/A	
29	H241 H259	MD larger BL smaller
30	N/A	
31	H361 H241 H506 H422 H201	MD larger MD larger MD larger MD smaller MD smaller
32	H353	MD smaller

Table 6 - Outliers identified from Hatherdene, females only.

Tooth	Outlier	Notes (regarding mean)
1	N/A	
2	H637 H956	MD larger MD smaller extreme
3	N/A	
4	H443 H205	MD smaller MD smaller
5	N/A	
6	N/A	
7	H603	MD larger
8	H225	MD smaller
9	N/A	
10	H220 H1300 H493	MD smaller BL larger BL larger
11	N/A	
12	N/A	
13	N/A	
14	H300 H443	MD smaller MD smaller

15	H1127 H493 H637 H1092 H1127	MD smaller BL larger BL larger BL smaller BL smaller
16	H493 H856	BL larger BL smaller
17	N/A	
18	H603	MD larger
19	N/A	
20	H999 H999	MD larger extreme BL larger
21	N/A	
22	H999 H225 H205 H637 H205	MD larger MD smaller MD smaller BL smaller BL smaller
23	N/A	
24	N/A	
25	H999	MD larger
26	H493 H1272	BL larger BL smaller
27	H1272 H205	BL smaller BL smaller
28	N/A	
29	N/A	
30	H956	BL smaller
31	H956	BL smaller
32	N/A	

Table 7 - Outliers identified from Oakington, combined sex.

Tooth	Outlier	Notes (than mean)
1	O1709 O820 O1376 O794 O1616 O1376	MD larger extreme MD smaller MD smaller extreme BL larger BL larger BL smaller
2	O1618	BL smaller
3	O1709 O1424	MD larger BL larger
4	O1709 O1376 O841	MD larger MD smaller MD smaller
5	O1616	BL larger
6	O1616	MD smaller
7	N/A	
8	O1424	BL larger

	O1782	BL smaller
9	O1636 O1424 O1370 O1782	MD larger BL larger BL larger BL smaller
10	O1441 O1424	BL larger BL larger
11	O1631	BL smaller
12	N/A	
13	O1709 O1785	MD larger MD smaller
14	O1636	MD larger
15	O808	BL larger
16	O1782 O820 O1626 O841	MD smaller MD smaller BL smaller BL smaller extreme
17	N/A	
18	O1862 O2165 O2165	MD larger MD smaller BL smaller
19	N/A	
20	O1424	MD larger
21	O1424	MD larger
22	N/A	
23	O1772 O1424 O2165	MD smaller BL larger BL smaller
24	O1424	BL larger
25	N/A	
26	N/A	
27	N/A	
28	N/A	
29	O1862 O1709 O1424 O2165 O1782 O1807	MD larger MD larger MD larger MD smaller MD smaller MD smaller
30	N/A	
31	O1862 O2165	MD larger MD smaller
32	N/A	

Table 8 - Outliers identified from Oakington, male data.

Tooth	Outliers	Notes
1	O869 O1424 O794	MD larger MD smaller BL larger extreme

	O1616 O1618	BL larger extreme BL smaller
2	N/A	
3	N/A	
4	N/A	
5	N/A	
6	O1616	MD smaller
7	N/A	
8	O1424	BL larger extreme
9	O1424	BL larger
10	N/A	
11	O1631	BL smaller
12	N/A	
13	N/A	
14	O1870 O1424	MD smaller BL larger
15	N/A	
16	N/A	
17	O1321	BL smaller
18	O1862 O1862	MD larger BL larger
19	N/A	
20	O1424 O731	MD larger MD larger
21	O1424	MD larger
22	N/A	
23	N/A	
24	O1424	BL larger
25	O1631	MD larger
26	N/A	
27	O1370 O1631 O1622 O1870	BL larger BL smaller BL smaller BL smaller extreme
28	N/A	
29	N/A	
30	N/A	
31	O1862 O1862 O1631 O1321	MD larger BL larger BL smaller BL smaller
32	O1616	MD smaller

Table 9 - Outliers identified from Oakington, female data.

Tooth	Outliers	Notes
1	O1709	MD larger
2	N/A	
3	O1709 O1636	MD larger MD larger

	O1782	MD smaller
4	O1709 O841	MD larger MD smaller
5	O1450 O2165	BL larger BL smaller
6	N/A	
7	N/A	
8	O1782	BL smaller
9	O1709 O1636 O1411 O1843 O1376 O1782	BL larger BL larger BL larger BL larger BL smaller BL smaller extreme
10	O1709	BL larger
11	N/A	
12	O1376	BL smaller
13	O1709 O1785	MD larger MD smaller
14	O1636	MD larger
15	N/A	
16	O1636 O841 O1782 O820 O1626 O841	MD larger MD smaller extreme MD smaller extreme MD smaller extreme BL smaller BL smaller extreme
17	N/A	
18	O2165 O2165	MD smaller BL smaller
19	N/A	
20	N/A	
21	N/A	
22	O1709 O1636 O1615 O2154	MD larger MD larger BL larger extreme BL smaller
23	O1772 O2165	MD smaller BL smaller
24	O1772	MD smaller
25	O820 O1376	MD smaller MD smaller
26	N/A	
27	O1709 O1636 O1615	MD larger MD larger BL larger
28	N/A	
29	N/A	
30	O820	MD smaller
31	N/A	

32	N/A	

Table 10 - Outliers identified from Polhill, combined sex.

Tooth	Outlier	Notes (than mean)
1	P4 P36	MD larger MD smaller
2	P4 P42 P20 P3	MD larger MD larger BL smaller BL smaller
3	P13 P5 P32 P3	MD larger MD smaller MD smaller extreme BL smaller
4	P40 P19	MD smaller MD smaller
5	N/A	
6	N/A	
7	P2 P41 P41	MD smaller extreme MD smaller extreme BL smaller
8	N/A	
9	N/A	
10	P50 P40	BL larger BL smaller
11	N/A	
12	P42 P2	BL smaller BL smaller
13	N/A	
14	P3	BL smaller
15	N/A	
16	P36 P30 P9 P36 P3	MD smaller BL larger extreme BL larger extreme BL smaller BL smaller extreme
17	N/A	
18	P42	MD larger extreme
19	P5	BL larger
20	N/A	
21	N/A	
22	P50 P42 P27 P2 P50 P5 P3	MD larger extreme MD larger MD smaller MD smaller BL larger BL larger BL smaller
23	P50	MD larger

	P2	MD smaller extreme
24	N/A	
25	N/A	
26	P2	BL smaller
27	P50 P42 P50 P5 P3	MD larger MD larger BL larger BL larger BL smaller
28	N/A	
29	P50 P18 P50 P2	MD larger MD larger BL larger extreme BL smaller
30	P13	BL larger
31	P13	MD larger
32	N/A	

Table 11 - Outliers identified from Polhill, male data.

Tooth	Outliers	Notes
1	N/A	
2	N/A	
3	N/A	
4	N/A	
5	N/A	
6	N/A	
7	N/A	
8	N/A	
9	N/A	
10	N/A	
11	N/A	
12	N/A	
13	N/A	
14	N/A	
15	N/A	
16	N/A	
17	N/A	
18	N/A	
19	N/A	
20	N/A	
21	P40	MD smaller
22	P50 P27	MD larger extreme MD smaller extreme
23	P50	MD larger
24	N/A	
25	N/A	
26	N/A	
27	P50	MD larger
28	N/A	

29	P50 P50	MD larger extreme BL larger extreme
30	N/A	
31	N/A	
32	P4	MD larger extreme

Table 12 - Outliers identified from Polhill, female data.

Tooth	Outliers	Notes
1	N/A	
2	P42 P3	MD larger BL smaller
3	P13 P32 P3	MD larger MD smaller extreme BL smaller
4	P19	MD smaller
5	P20 P20	MD larger BL larger
6	N/A	
7	P2	MD smaller extreme
8	N/A	
9	N/A	
10	P13	BL larger
11	N/A	
12	P2	MD smaller
13	N/A	
14	P3	BL smaller
15	N/A	
16	P20 P30 P9 P3	MD smaller BL larger extreme BL larger BL smaller
17	P19	BL larger
18	P42	MD larger extreme
19	N/A	
20	N/A	
21	N/A	
22	N/A	
23	P2	MD smaller extreme
24	N/A	
25	P2	MD smaller
26	P42 P2 P42 P2	MD larger MD smaller extreme BL smaller BL smaller extreme
27	N/A	
28	P13	BL larger
29	P2	BL smaller
30	P13	MD larger
31	P13	MD larger

32	N/A	

Table 13 - Outliers identified from Eastry, combined sex.

Tooth	Outlier	Notes (than mean)
1	N/A	
2	N/A	
3	N/A	
4	N/A	
5	N/A	
6	E50	MD smaller
7	N/A	
8	N/A	
9	N/A	
10	N/A	
11	E54 E20	MD larger extreme MD smaller
12	N/A	
13	N/A	
14	N/A	
15	N/A	
16	N/A	
17	N/A	
18	E45	MD larger extreme
19	N/A	
20	N/A	
21	N/A	
22	N/A	
23	N/A	
24	N/A	
25	N/A	
26	E50	BL larger
27	E20	MD smaller
28	N/A	
29	N/A	
30	E50	BL larger
31	E50	BL larger
32	N/A	

Table 14 - Outliers identified from Eastry, males only.

Tooth	Outliers	Notes
1	N/A	
2	N/A	
3	N/A	
4	N/A	
5	--	No teeth
6	N/A	
7	--	No teeth

8	N/A	
9	N/A	
10	--	No teeth
11	N/A	
12	N/A	
13	N/A	
14	N/A	
15	N/A	
16	N/A	
17	N/A	
18	N/A	
19	N/A	
20	N/A	
21	N/A	
22	N/A	
23	N/A	
24	N/A	
25	N/A	
26	N/A	
27	N/A	
28	N/A	
29	E5 E50 E5	MD larger extreme BL larger BL smaller extreme
30	N/A	
31	N/A	
32	N/A	

Table 15 - Outliers identified from Eastry, females only.

Tooth	Outliers	Notes
1	N/A	
2	N/A	
3	N/A	
4	N/A	
5	N/A	
6	N/A	
7	N/A	
8	--	No teeth
9	N/A	
10	N/A	
11	N/A	
12	N/A	
13	N/A	
14	N/A	
15	N/A	
16	N/A	
17	N/A	
18	N/A	

19	N/A	
20	N/A	
21	E45 E40	BL larger extreme BL smaller extreme
22	N/A	
23	E46	MD smaller
24	N/A	
25	N/A	
26	N/A	
27	E20 E9	MD smaller BL larger
28	N/A	
29	N/A	
30	E40	BL smaller
31	N/A	
32	N/A	

Appendix 5: Inter-cemetery variation

Table 1 – Results from the ANOVA/Kruskal-Wallis tests for influence of cemetery on tooth size, combined sex.

Tooth	Measurement	Test Used	Result	Interpretation
1 RMxM3	MD	ANOVA	Df=3. F = 0.249, p = 0.862	Not significant
	BL	ANOVA	Df=3, F = 0.601, p = 0.616	Not significant
2 RMxM2	MD	ANOVA	Df=3, F = 1.031, p = 0.383	Not significant
	BL	ANOVA	Df=3, F = 1.457. p = 0.232	Not significant
3 RMxM1	MD	ANOVA	Df=3, F = 2.066, p = 0.111	Not significant
	BL	ANOVA	Df=3, F = 0.987, p = 0.403	Not significant
4 RMxP2	MD	ANOVA	Df=3, F = 0.505, p = 0.680	Not significant
	BL	ANOVA	Df=3, F = 1.221, p = 0.306	Not significant
5 RMxP1	MD	ANOVA	Df=3, F = 0.290, p = 0.832	Not significant
	BL	ANOVA	Df=3, F = 0.033, p = 0.992	Not significant
6 RMxC	MD	Kruskal Wallis	p = 0.664	Not significant
	BL	ANOVA	Df=3, F = 0.008, p = 0.999	Not significant
7 RMxLI	MD	ANOVA	Df=3, F = 2.989, p = 0.036	Significant
	BL	Kruskal Wallis	p = 0.929	Not significant
8 RMxCI	MD	ANOVA	Df=3, F = 0.039, p = 0.990	Not significant
	BL	ANOVA	Df=3, F = 0.982, p = 0.407	Not significant
9 LMxCI	MD	ANOVA	Df=3, F = 1.722, p = 0.169	Not significant
	BL	Kruskal Wallis	p = 0.783	Not significant
10 LMxLI	MD	ANOVA	Df=3, F = 1.298, p = 0.280	Not significant
	BL	ANOVA	Df=3, F = 1.324, p = 0.272	Not significant
11 LMxC	MD	ANOVA	Df=3, F = 0.196, p = 0.899	Not significant
	BL	ANOVA	Df=3, F = 0.283, p = 0.838	Not significant
12 LMxP1	MD	ANOVA	Df=3, F = 0.483, p = 0.695	Not significant
	BL	ANOVA	Df=3, F = 0.842, p = 0.475	Not significant
13 LMxP2	MD	ANOVA	Df=3, F = 0.215, p = 0.886	Not significant
	BL	ANOVA	Df=3, F = 1.335, p = 0.268	Not significant
14 LMxM1	MD	Kruskal Wallis	p = 0.631	Not significant
	BL	ANOVA	Df=3, F = 1.507, p = 0.218	Not significant
15 LMxM2	MD	ANOVA	Df=3, F = 2.546, p = 0.061	Not significant
	BL	ANOVA	Df=3, F = 0.237, p = 0.870	Not significant
16 LMxM3	MD	ANOVA	Df=3, F = 0.788, p = 0.505	Not significant
	BL	Kruskal Wallis	p = 0.716	Not significant
17 LMM3	MD	ANOVA	Df=3, F = 1.546, p = 0.209	Not significant
	BL	ANOVA	Df=3, F = 0.164, p = 0.920	Not significant
18 LMM2	MD	ANOVA	Df=3, F = 3.376, p = 0.021	Significant
	BL	ANOVA	Df=3, F = 0.838, p = 0.476	Not significant
19 LMM1	MD	ANOVA	Df=3, F = 0.709, p = 0.549	Not significant
	BL	ANOVA	Df=3, F = 0.437, p = 0.727	Not significant
20 LMP2	MD	Kruskal Wallis	p = 0.797	Not significant
	BL	Kruskal Wallis	p = 0.575	Not significant
21 LMP1	MD	ANOVA	Df=3, F = 0.500, p = 0.683	Not significant
	BL	ANOVA	Df=3, F = 0.317, p = 0.813	Not significant
22	MD	ANOVA	Df=3, F = 0.698, p = 0.555	Not significant

LMC	BL	ANOVA	Df=3, F = 0.078, p = 0.972	Not significant
23	MD	ANOVA	Df=3, F = 0.197, p = 0.898	Not significant
LMLI	BL	ANOVA	Df=3, F = 0.093, p = 0.964	Not significant
24	MD	ANOVA	Df=3, F = 0.832, p = 0.481	Not significant
LMCI	BL	ANOVA	Df=3, F = 0.266, p = 0.850	Not significant
25	MD	ANOVA	Df=3, F = 1.122, p = 0.346	Not significant
RMCI	BL	ANOVA	Df=3, F = 0.241, p = 0.867	Not significant
26	MD	ANOVA	Df=3, F = 1.174, p = 0.324	Not significant
RMLI	BL	ANOVA	Df=3, F = 0.023, p = 0.995	Not significant
27	MD	ANOVA	Df=3, F = 0.968, p = 0.411	Not significant
RMC	BL	ANOVA	Df=3, F = 0.411, p = 0.745	Not significant
28	MD	ANOVA	Df=3, F = 0.379, p = 0.768	Not significant
RMP1	BL	ANOVA	Df=3, F = 0.703, p = 0.552	Not significant
29	MD	ANOVA	Df=3, F = 1.077, p = 0.362	Not significant
RMP2	BL	ANOVA	Df=3, F = 0.419, p = 0.739	Not significant
30	MD	ANOVA	Df=3, F = 0.753, p = 0.523	Not significant
RMM1	BL	ANOVA	Df=3, F = 0.334, p = 0.801	Not significant
31	MD	ANOVA	Df=3, F = 0.700, p = 0.554	Not significant
RMM2	BL	ANOVA	Df=3, F = 0.571, p = 0.636	Not significant
32	MD	ANOVA	Df=3, F = 2.454, p = 0.070	Not significant
RMM3	BL	ANOVA	Df=3, F = 0.565, p = 0.639	Not significant

Table 2 - Results from the ANOVA/Kruskal-Wallis tests for influence of cemetery on tooth size, males only.

Tooth	Measurement	Test Used	Result	Interpretation
1	MD	ANOVA	Df= 3, F = 0.243, p = 0.866	Not significant
RMxM3	BL	Kruskal Wallis	p = 0.933	Not significant
2	MD	ANOVA	Df=3, F = 0.857, p = 0.472	Not significant
RMxM2	BL	ANOVA	Df=3, F = 1.300, p = 0.290	Not significant
3	MD	ANOVA	Df=3, F = 1.194, p = 0.327	Not significant
RMxM1	BL	ANOVA	Df=3, F = 0.364, p = 0.779	Not significant
4	MD	ANOVA	Df=3, F = 1.268, p = 0.299	Not significant
RMxP2	BL	ANOVA	Df=3, F = 1.371, p = 0.266	Not significant
5	MD	Kruskal Wallis	p = 0.976	Not significant
RMxP1	BL	ANOVA	Df=3, F = 0.204, p = 0.816	Not significant
6	MD	Kruskal Wallis	p = 0.315	Not significant
RMxC	BL	ANOVA	Df=3, F = 0.365, p = 0.778	Not significant
7	MD	ANOVA	Df=2, F = 0.792, p = 0.461	Not significant
RMxLI	BL	Kruskal Wallis	p = 0.358	Not significant
8	MD	ANOVA	Df=3, F = 2.361, p = 0.093	Not significant
RMxCI	BL	ANOVA	Df=3, F = 0.588, p = 0.647	Not significant
9	MD	ANOVA	DF=3, F = 2.075, p = 0.122	Not significant
LMxCI	BL	Kruskal Wallis	p = 0.617	Not significant
10	MD	ANOVA	Df=2, F = 1.409, p = 0.258	Not significant
LMxLI	BL	ANOVA	Df=2, F = 1.909, p = 0.163	Not significant
11	MD	ANOVA	Df=3, F = 0.755, p = 0.526	Not significant
LMxC	BL	Kruskal Wallis	p = 0.914	Not significant
12	MD	ANOVA	Df=3, F = 0.016, p = 0.997	Not significant

LMxP1	BL	ANOVA	Df= 3, F = 0.495, p = 0.688	Not significant
13	MD	ANOVA	Df=3, F = 0.346, p = 0.792	Not significant
LMxP2	BL	ANOVA	Df=3, F = 0.177, p = 0.911	Not significant
14	MD	ANOVA	Df=3, F = 0.526, p = 0.668	Not significant
LMxM1	BL	ANOVA	Df=3, F = 0.324, p 0 0.808	Not significant
15	MD	ANOVA	Df=3, F = 1.207, p = 0.322	Not significant
LMxM2	BL	ANOVA	Df=3, F = 0.352, p = 0.788	Not significant
16	MD	ANOVA	Df=3, F = 4.176, p = 0.017	Significant
LMxM3	BL	ANOVA	Df=3, F = 0.379, p = 0.769	Not significant
17	MD	ANOVA	Df=3, F = 1.902, p = 0.147	Not significant
LMM3	BL	ANOVA	Df=3, F = 0.618, p = 0.607	Not significant
18	MD	ANOVA	Df=3, F = 2.318, p = 0.088	Not significant
LMM2	BL	ANOVA	Df=3, F = 1.133, p = 0.345	Not significant
19	MD	ANOVA	Df=3, F = 2.219, p = 0.101	Not significant
LMM1	BL	ANOVA	Df=3, F = 1.459, p = 0.239	Not significant
20	MD	Kruskal Wallis	p = 0.813	Not significant
LMP2	BL	Kruskal Wallis	p = 0.855	Not significant
21	MD	ANOVA	Df=3, F = 1.333, p = 0.275	Not significant
LMP1	BL	ANOVA	Df=3, F = 0.892, p = 0.452	Not significant
22	MD	ANOVA	Df=3, F = 0.525, p = 0.668	Not significant
LMC	BL	ANOVA	Df=3, F = 0.469, p = 0.705	Not significant
23	MD	ANOVA	Df=3, F = 0.283, p = 0.837	Not significant
LMLI	BL	ANOVA	Df=3, F = 0.434, p = 0.729	Not significant
24	MD	ANOVA	Df=3, F = 0.206, p = 0.891	Not significant
LMCI	BL	ANOVA	Df=3, F = 0.980, p = 0.458	Not significant
25	MD	ANOVA	Df=3, F = 0.250, p = 0.861	Not significant
RMCI	BL	ANOVA	Df=3, F = 0.426, p = 0.710	Not significant
26	MD	ANOVA	Df=3, f = 0.943, p = 0.428	Not significant
RMLI	BL	ANOVA	Df=3, F = 1.135, p = 0.345	Not significant
27	MD	ANOVA	Df=3, F = 1.719, p = 0.176	Not significant
RMC	BL	ANOVA	Df=3, F = 0.395, p = 0.757	Not significant
28	MD	ANOVA	Df=3, F = 0.014, p = 0.998	Not significant
RMP1	BL	ANOVA	Df=3, F = 1.494, p = 0.228	Not significant
29	MD	ANOVA	Df=3, F = 0.415, p = 0.743	Not significant
RMP2	BL	ANOVA	Df=3, F = 1.876, p = 0.146	Not significant
30	MD	ANOVA	Df=3, F = 0.405, p = 0.750	Not significant
RMM1	BL	ANOVA	Df=3, F = 0.149, p = 0.930	Not significant
31	MD	Kruskal Wallis	p = 0.153	Not significant
RMM2	BL	ANOVA	Df=3, F = 0.892, p = 0.453	Not significant
32	MD	Kruskal Wallis	p = 0.342	Not significant
RMM3	BL	ANOVA	Df=3, F = 0.200, p = 0.896	Not significant

Table 3 - Results from the ANOVA/Kruskal-Wallis tests for influence of cemetery on tooth size, females only.

Tooth	**Measurement**	**Test Used**	**Result**	**Interpretation**
1	MD	ANOVA	Df= 3, F = 0.159, p = 0.923	Not significant
RMxM3	BL	ANOVA	Df= 3. F = 2.398, p= 0.084	Not significant
2	MD	ANOVA	Df=3, F = 0.380, p = 0.768	Not significant

RMxM2	BL	ANOVA	Df=3, F = 1.280, p = 0.291	Not significant
3	MD	ANOVA	Df=3, F = 1.091, p = 0.362	Not significant
RMxM1	BL	ANOVA	Df=3, F = 1.419, p = 0.249	Not significant
4	MD	ANOVA	Df=3, F = 2.245, p = 0.093	Not significant
RMxP2	BL	ANOVA	Df=3, F = 0.984, p = 0.407	Not significant
5	MD	ANOVA	Df= 3, F = 0.464, p = 0.708	Not significant
RMxP1	BL	ANOVA	Df= 3, F = 0.285, p = 0.836	Not significant
6	MD	ANOVA	Df=3, F = 0.944, p = 0.426	Not significant
RMxC	BL	ANOVA	Df=3, F = 0.351, p = 0.789	Not significant
7	MD	ANOVA	Df=3, F = 3.723, p = 0.018	Significant
RMxLI	BL	ANOVA	Df=3, F = 0.413, p = 0.745	Not significant
8	MD	ANOVA	Df=3, F = 2.782, p = 0.057	Not significant
RMxCI	BL	ANOVA	Df=3, F = 1.391, p = 0.264	Not significant
9	MD	ANOVA	Df=3, F = 3.034, p = 0.040	Significant
LMxCI	BL	ANOVA	DF=3, F = 0.763, p = 0.522	Not significant
10	MD	Kruskal Wallis	p = 0.218	Not significant
LMxLI	BL	Kruskal Wallis	p = 0.204	Not significant
11	MD	ANOVA	Df=3, F = 0.592, p = 0.623	Not significant
LMxC	BL	ANOVA	Df=3, F = 0.005, p = 0.999	Not significant
12	MD	ANOVA	Df=3, F = 0.683, p = 0.567	Not significant
LMxP1	BL	ANOVA	Df=3, F = 0.478, p = 0.699	Not significant
13	MD	ANOVA	Df=3, F = 1.074, p= 0.369	Not significant
LMxP2	BL	ANOVA	Df=3, F = 1.430, p = 0.245	Not significant
14	MD	ANOVA	Df=3, F = 1.081, p = 0.365	Not significant
LMxM1	BL	ANOVA	Df=3, F = 3.481, p = 0.023	Significant
15	MD	ANOVA	Df=3, F = 1.929, p = 0.137	Not significant
LMxM2	BL	ANOVA	Df=3, F = 0.512, p = 0.676	Not significant
16	MD	ANOVA	Df=3, F = 0.779, p = 0.512	Not significant
LMxM3	BL	Kruskal Wallis	p = 0.733	Not significant
17	MD	ANOVA	Df=3, F = 1.238, p = 0.310	Not significant
LMM3	BL	ANOVA	Df=3, F = 1.025, p = 0.393	Not significant
18	MD	ANOVA	Df=3, F = 3.542, p = 0.021	Significant
LMM2	BL	Kruskal Wallis	p = 0.698	Not significant
19	MD	ANOVA	Df=3, F = 0.612, p = 0.610	Not significant
LMM1	BL	ANOVA	Df=3, F = 0.678, p = 0.570	Not significant
20	MD	Kruskal Wallis	p = 0.465	Not significant
LMP2	BL	ANOVA	Df=3, F = 0.776, p = 0.512	Not significant
21	MD	ANOVA	Df=3, F = 0.278, p = 0.841	Not significant
LMP1	BL	ANOVA	Df=3, F = 0.452, p = 0.717	Not significant
22	MD	ANOVA	Df=3, F = 1.261, p = 0.295	Not significant
LMC	BL	Kruskal Wallis	p = 0.664	Not significant
23	MD	ANOVA	Df=3, F = 0.691, p = 0.562	Not significant
LMLI	BL	ANOVA	Df=3, F = 0.240, p = 0.868	Not significant
24	MD	ANOVA	Df=3, F = 1.188, p = 0.326	Not significant
LMCI	BL	ANOVA	Df=3, F = 0.195, p = 0.899	Not significant
25	MD	ANOVA	Df=3, F = 2.846, p = 0.054	Not significant
RMCI	BL	ANOVA	Df=3, F = 0.161, p = 0.922	Not significant
26	MD	ANOVA	Df=3, F = 1.206, p = 0.318	Not significant
RMLI	BL	ANOVA	Df=3, F = 0.635, p = 0.596	Not significant
27	MD	ANOVA	Df=3, F = 1.301, p = 0.282	Not significant

RMC	BL	Kruskal Wallis	p = 0.786	Not significant
28	MD	ANOVA	Df=3, F = 1.007, p = 0.396	Not significant
RMP1	BL	ANOVA	Df=3, F = 3.528, p = 0.020	Significant
29	MD	ANOVA	Df=3, F = 3.006, p = 0.038	Significant
RMP2	BL	ANOVA	Df=3, F = 0.695, p = 0.559	Not significant
30	MD	ANOVA	Df=3, F = 0.526, p = 0.666	Not significant
RMM1	BL	ANOVA	Df=3, F = 0.433, p = 0.730	Not significant
31	MD	ANOVA	Df=3, F = 1.920, p = 0.137	Not significant
RMM2	BL	ANOVA	Df=3, F = 0.172, p = 0.915	Not significant
32	MD	ANOVA	Df=3, F = 1.520, p = 0.226	Not significant
RMM3	BL	ANOVA	Df=3, F = 0.502, p = 0.683	Not significant

Table 4 - Results from the ANOVA/Kruskal-Wallis tests for influence of sex on tooth size, combined cemetery sample.

Tooth	Measurement	Test Used	Result	Interpretation
1	MD	ANOVA	Df=1, F = 0.114, p = 0.737	Not significant
RMxM3	BL	ANOVA	Df=1, F = 11.307, p = 0.001	Significant
2	MD	ANOVA	Df=1, F = 2.336, p = 0.071	Not significant
RMxM2	BL	ANOVA	Df=1, F = 7.946, p = 0.006	Significant
3	MD	ANOVA	Df=1, F = 0.823, p = 0.367	Not significant
RMxM1	BL	ANOVA	Df=1, F = 11.122, p = 0.001	Significant
4	MD	ANOVA	Df=1, F = 1.458, p = 0.230	Not significant
RMxP2	BL	ANOVA	Df=1, F = 6.614, p = 0.012	Significant
5	MD	ANOVA	Df=1, F = 2.586, p = 0.111	Not significant
RMxP1	BL	ANOVA	Df=1, F = 8.091, p = 0.005	Significant
6	MD	Kruskal Wallis	Df=1, F = 2.659, p = 0.106	Not significant
RMxC	BL	ANOVA	Df=1, F=17.089, p <0.001	Significant
7	MD	ANOVA	Df=1, F = 0.036, p = 0.850	Not significant
RMxLI	BL	Kruskal Wallis	p = 0.293	Not significant
8	MD	ANOVA	Df=1, F = 0.004, p = 0.950	Not significant
RMxCI	BL	ANOVA	Df=1, F = 1.782, p = 0.187	Not significant
9	MD	ANOVA	Df=1, F = 0.163, p = 0.687	Not significant
LMxCI	BL	Kruskal Wallis	p = 0.628	Not significant
10	MD	ANOVA	Df=1, F = 0.133, p = 0.716	Not significant
LMxLI	BL	ANOVA	Df=1, F = 0.858, p = 0.357	Significant
11	MD	ANOVA	Df=1, F = 10.066, p = 0.002	Significant
LMxC	BL	ANOVA	Df=1, F = 12.273, p = 0.001	Significant
12	MD	ANOVA	Df=1, F = 1.322, p = 0.253	Not significant
LMxP1	BL	ANOVA	Df=1, F = 5.278, p = 0.024	Significant
13	MD	ANOVA	Df=1, F = 1.1789, p = 0.184	Not significant
LMxP2	BL	ANOVA	Df=1, F = 6.793, p = 0.011	Significant
14	MD	Kruskal Wallis	p = 0.175	Not significant
LMxM1	BL	ANOVA	Df=1, F = 10.422, p = 0.002	Significant
15	MD	ANOVA	Df=1, F = 0.069, p = 0.794	Not significant
LMxM2	BL	ANOVA	Df=1, F = 8.688, p = 0.004	Significant
16	MD	ANOVA	Df=1, F = 0.043, p = 0.837	Not significant
LMxM3	BL	Kruskal Wallis	p = 0.009	Significant
17	MD	ANOVA	Df=1, F = 3.629, p = 0.060	Not significant

LMM3	BL	ANOVA	Df=1, F = 7.401, p = 0.008	Significant
18	MD	ANOVA	Df=1, F = 7.434, p = 0.008	Significant
LMM2	BL	ANOVA	Df=1, F = 16.011, p <0.001	Significant
19	MD	ANOVA	Df=1, F = 3.807, p = 0.054	Not significant
LMM1	BL	ANOVA	Df=1, F = 5.059, p = 0.027	Significant
20	MD	Kruskal Wallis	p = 0.485	Not significant
LMP2	BL	Kruskal Wallis	p = 0.064	Not significant
21	MD	ANOVA	Df=1, F = 0.536, p = 0.466	Not significant
LMP1	BL	ANOVA	Df=1, F = 3.520, p = 0.063	Not significant
22	MD	ANOVA	Df=1, F = 19.623, p <0.001	Significant
LMC	BL	ANOVA	Df=1, F = 57.943, p <0.001	Significant
23	MD	ANOVA	Df=1, F = 0.487, p = 0.487	Not significant
LMLI	BL	ANOVA	Df=1, F = 4.646, p = 0.033	Significant
24	MD	ANOVA	Df=1, F = 0.558, p = 0.457	Not significant
LMCI	BL	ANOVA	Df=1, F = 0.030, p = 0.863	Not significant
25	MD	ANOVA	Df=1, F = 6.091, p = 0.016	Significant
RMCI	BL	ANOVA	Df=1, F = 2.314, p = 0.132	Not significant
26	MD	ANOVA	Df=1, F = 0.397, p = 0.530	Not significant
RMLI	BL	ANOVA	Df=1, F = 2.369, p = 0.127	Not significant
27	MD	ANOVA	Df=1, F = 24.014, p <0.001	Significant
RMC	BL	ANOVA	Df=1, F = 34.547, p <0.001	Significant
28	MD	ANOVA	Df=1, F = 3.741, p = 0.056	Not significant
RMP1	BL	ANOVA	Df=1, F = 2.755, p = 0.100	Not significant
29	MD	ANOVA	Df=1, F = 1.461, p = 0.229	Not significant
RMP2	BL	ANOVA	Df=1, F = 4.351, p = 0.039	Significant
30	MD	ANOVA	Df=1, F = 0.135, p = 714	Not significant
RMM1	BL	ANOVA	Df=1, F = 3.496, p = 0.064	Not significant
31	MD	ANOVA	Df=1, F = 6.482, p = 0.012	Significant
RMM2	BL	ANOVA	Df=1, F = 8.612, p = 0.004	Significant
32	MD	ANOVA	Df=1, F = 4.923, p = 0.029	Significant
RMM3	BL	ANOVA	Df=1, F = 7.896, p = 0.006	Significant

Table 5 - Results from the ANOVA/Kruskal-Wallis tests for influence of sex on tooth size from Hatherdene only.

Tooth	Measurement	Test Used	Result	Interpretation
1	MD	ANOVA	Df=1, F = 0.359, p = 0.554	Not significant
RMxM3	BL	ANOVA	Df=1, F = 12.268, p = 0.001	Significant
2	MD	ANOVA	Df=1, F = 2.665, p = 0.111	Not significant
RMxM2	BL	ANOVA	Df=1, F = 9.872, p = 0.003	Significant
3	MD	ANOVA	Df=1, F = 1.598, p = 0.215	Not significant
RMxM1	BL	ANOVA	Df=1, F = 7.769, p = 0.009	Significant
4	MD	ANOVA	Df=1, F = 1.798, p = 0.187	Not significant
RMxP2	BL	ANOVA	Df=1, F = 7.731, p = 0.008	Significant
5	MD	ANOVA	Df=1, F = 2.425, p = 0.127	Not significant
RMxP1	BL	ANOVA	Df=1, F = 6.052, p = 0.018	Significant
6	MD	ANOVA	Df=1, F = 4.466, p = 0.041	Significant
RMxC	BL	ANOVA	Df=1, F = 6.205, p = 0.017	Significant
7	MD	ANOVA	Df=1, F = 1.313, p = 0.260	Not significant

RMxLI	BL	ANOVA	Df=1, F = 0.028, p = 0.867	Not significant
8	MD	ANOVA	Df=1, F = 3.916, p = 0.059	Not significant
RMxCI	BL	ANOVA	Df=1, F = 3.472, p = 0.075	Not significant
9	MD	ANOVA	Df=1, F = 6.925, p = 0.014	Significant
LMxCI	BL	Kruskal Wallis	p = 0.014	Significant
10	MD	Kruskal Wallis	p = 0.574	Not significant
LMxLI	BL	ANOVA	Df=1, F = 0.281, p = 0.599	Not significant
11	MD	ANOVA	Df=1, F = 7.789, p = 0.008	Significant
LMxC	BL	Kruskal Wallis	p = 0.025	Significant
12	MD	ANOVA	Df=1, F = 1.109, p = 0.299	Not significant
LMxP1	BL	ANOVA	Df=1, F = 3.280, p = 0.078	Not significant
13	MD	ANOVA	Df=1, F = 2.833, p = 0.100	Not significant
LMxP2	BL	ANOVA	Df=1, F = 5.178, p = 0.028	Significant
14	MD	ANOVA	Df=1, F = 4.189, p = 0.048	Significant
LMxM1	BL	ANOVA	Df=1, F = 11.904, p = 0.001	Significant
15	MD	ANOVA	Df=1, F = 1.371, p = 0.249	Not significant
LMxM2	BL	ANOVA	Df=1, F = 7.566, p = 0.009	Significant
16	MD	ANOVA	Df=1, F = 0.601, p = 0.444	Not significant
LMxM3	BL	ANOVA	Df=1, F = 4.234, p = 0.048	Significant
17	MD	ANOVA	Df=1, F = 7.006, p = 0.012	Significant
LMM3	BL	ANOVA	Df=1, F = 8.652, p = 0.006	Significant
18	MD	ANOVA	Df=1, F = 10.149, p = 0.003	Significant
LMM2	BL	ANOVA	Df=1, F = 8.830, p = 0.005	Significant
19	MD	ANOVA	Df=1, F = 4.133, p = 0.050	Not significant
LMM1	BL	ANOVA	Df=1, F = 4.025, p = 0.053	Not significant
20	MD	Kruskal Wallis	p = 0.224	Not significant
LMP2	BL	Kruskal Wallis	p = 0.229	Not significant
21	MD	ANOVA	Df=1, F = 0.070, p = 0.792	Not significant
LMP1	BL	ANOVA	Df=1, F = 2.102, p = 0.154	Not significant
22	MD	ANOVA	Df=1, F = 10.092, p = 0.003	Significant
LMC	BL	ANOVA	Df=1, F = 11.259, p = 0.002	Significant
23	MD	ANOVA	Df=1, F = 3.162. p = 0.083	Not significant
LMLI	BL	ANOVA	Df=1, F = 0.530, p = 0.471	Not significant
24	MD	ANOVA	Df=1, F = 0.748, p = 0.394	Not significant
LMCI	BL	ANOVA	Df=1, F = 0.292, p = 0.593	Not significant
25	MD	ANOVA	Df=1, F = 0.009, p = 0.927	Not significant
RMCI	BL	ANOVA	Df=1, F = 0.415, p = 0.525	Not significant
26	MD	ANOVA	Df=1, F = 0.909, p = 0.347	Not significant
RMLI	BL	ANOVA	Df=1, F = 0.223, p = 0.640	Not significant
27	MD	ANOVA	Df=1, F = 10.143, p = 0.003	Significant
RMC	BL	ANOVA	Df=1, F = 10.281, p = 0.003	Significant
28	MD	ANOVA	Df=1, F = 3.035, p = 0.089	Not significant
RMP1	BL	ANOVA	Df=1, F = 2.608, p = 0.114	Not significant
29	MD	ANOVA	Df=1, F = 1.691, p = 0.201	Not significant
RMP2	BL	ANOVA	Df=1, F = 3.214, p = 0.080	Not significant
30	MD	ANOVA	Df=1, F = 0.001, p = 0.972	Not significant
RMM1	BL	ANOVA	Df=1, F = 2.282, p = 0.139	Not significant
31	MD	ANOVA	Df=1, F = 7.771, p = 0.008	Significant
RMM2	BL	ANOVA	Df=1, F = 7.930, p = 0.008	Significant
32	MD	ANOVA	Df=1, F = 2.113, p = 0.156	Not significant

RMM3	BL	ANOVA	Df=1, F = 3.010, p = 0.093	Not significant

Table 6 - Results from the ANOVA/Kruskal-Wallis tests for influence of sex on tooth size Oakington only.

Tooth	Measurement	Test Used	Result	Interpretation
1 RMxM3	MD	ANOVA	Df=1, F = 0.074, p = 0.788	Not significant
	BL	ANOVA	Df=1, F = 2.768, p = 0.113	Not significant
2 RMxM2	MD	ANOVA	Df=1, F = 0.212, p = 0.648	Not significant
	BL	ANOVA	Df=1, F = 0.327, p = 0.571	Not significant
3 RMxM1	MD	ANOVA	Df=1, F = 0.001, p = 0.978	Not significant
	BL	ANOVA	Df=1, F = 3.089, p = 0.088	Not significant
4 RMxP2	MD	ANOVA	Df=1, F = 2.963, p = 0.093	Not significant
	BL	ANOVA	Df=1, F = 2.737, p = 0.106	Not significant
5 RMxP1	MD	ANOVA	Df=1, F = 0.925, p = 0.342	Not significant
	BL	ANOVA	Df=1, F = 3.612, p = 0.065	Not significant
6 RMxC	MD	Kruskal Wallis	p = 0.042	Significant
	BL	ANOVA	Df=1, F = 8.875, p = 0.005	Significant
7 RMxLI	MD	ANOVA	Df=1, F = 0.423, p = 0.520	Not significant
	BL	Kruskal Wallis	p = 0.150	Not significant
8 RMxCI	MD	ANOVA	Df=1, F = 3.219. p = 0.084	Not significant
	BL	ANOVA	Df=1, F = 0.453, p = 0.506	Not significant
9 LMxCI	MD	ANOVA	Df=1, F = 0.837, p = 0.367	Not significant
	BL	ANOVA	Df=1, F = 1.667, p = 0.205	Not significant
10 LMxLI	MD	ANOVA	Df=1, F = 1.632, p = 0.211	Not significant
	BL	ANOVA	Df=1, F = 3.189, p = 0.084	Not significant
11 LMxC	MD	ANOVA	Df=1, F = 6.008, p = 0.019	Significant
	BL	ANOVA	Df=1, F = 3.127, p = 0.086	Not significant
12 LMxP1	MD	ANOVA	Df=1, F = 1.108, p = 0.300	Not significant
	BL	ANOVA	Df=1, F = 2.287, p = 0.140	Not significant
13 LMxP2	MD	ANOVA	Df=1, F = 1.225, p = 0.276	Not significant
	BL	ANOVA	Df=1, F = 2.506, p = 0.122	Not significant
14 LMxM1	MD	ANOVA	Df=1, F = 0.022, p = 0.883	Not significant
	BL	ANOVA	Df=1, F = 1.304, p = 0.263	Not significant
15 LMxM2	MD	ANOVA	Df=1, F = 0.019, p = 0.891	Not significant
	BL	ANOVA	Df=1, F = 1.314, p = 0.261	Not significant
16 LMxM3	MD	Kruskal Wallis	p = 0.789	Not significant
	BL	Kruskal Wallis	p = 0.114	Not significant
17 LMM3	MD	ANOVA	Df=1, F = 0.316, p = 0.579	Not significant
	BL	ANOVA	Df=1, F = 0.002, p = 0.962	Not significant
18 LMM2	MD	ANOVA	Df=1, F = 4.641, p = 0.038	Significant
	BL	ANOVA	Df=1, F = 7.925, p = 0.008	Significant
19 LMM1	MD	ANOVA	Df=1, F = 0.002, p = 0.965	Not significant
	BL	ANOVA	Df=1, F = 1.739, p = 0.195	Not significant
20 LMP2	MD	ANOVA	Df=1, F = 1.225, p = 0.275	Not significant
	BL	ANOVA	Df=1, F = 2.774, p = 0.103	Not significant
21 LMP1	MD	ANOVA	Df=1, F = 0.360, p = 0.552	Not significant
	BL	ANOVA	Df=1, F = 1.330. p = 0.256	Not significant
22	MD	ANOVA	Df=1, F = 10.092, p = 0.003	Significant

LMC	BL	ANOVA	Df=1, F = 11.259, p = 0.002	Significant
23	MD	ANOVA	Df=1, F = 0.013, p = 0.912	Not significant
LMLI	BL	ANOVA	Df=1, F = 3.043, p = 0.090	Not significant
24	MD	ANOVA	Df=1, F = 0.479, p = 0.495	Not significant
LMCI	BL	ANOVA	Df=1, F = 0.873, p = 0.358	Not significant
25	MD	ANOVA	Df=1, F = 6.184, p = 0.019	Significant
RMCI	BL	ANOVA	Df=1, F = 1.680, p = 0.205	Not significant
26	MD	ANOVA	Df=1, F = 0.469, p = 0.498	Not significant
RMLI	BL	ANOVA	Df=1, F = 5.786, p = 0.021	Significant
27	MD	ANOVA	Df=1, F = 22.841, p <0.001	Significant
RMC	BL	ANOVA	Df=1, F = 8.737, p = 0.006	Significant
28	MD	ANOVA	Df=1, F = 1.101, p = 0.300	Not significant
RMP1	BL	ANOVA	Df=1, F = 3.655, p = 0.063	Not significant
29	MD	ANOVA	Df=1, F = 5.583, p = 0.024	Significant
RMP2	BL	ANOVA	Df=1, F = 4.828, p = 0.034	Significant
30	MD	ANOVA	Df=1, F = 0.269, p = 0.607	Not significant
RMM1	BL	ANOVA	Df=1, F = 0.845, p = 0.364	Not significant
31	MD	ANOVA	Df=1, F = 5.463, p = 0.025	Significant
RMM2	BL	ANOVA	Df=1, F = 1.634, p = 0.210	Not significant
32	MD	ANOVA	Df=1, F = 3.803, p = 0.062	Not significant
RMM3	BL	ANOVA	Df=1, F = 1.242, p = 0.276	Not significant

Table 7 - Results from the ANOVA/Kruskal-Wallis tests for influence of sex on tooth size, Polhill only.

Tooth	Measurement	Test Used	Result	Interpretation
1	MD	ANOVA	Df=1, F = 0.168, p = 0.691	Not significant
RMxM3	BL	ANOVA	Df=1, F = 0.421, p = 0.533	Not significant
2	MD	ANOVA	Df=1, F = 0.953, p = 0.353	Not significant
RMxM2	BL	ANOVA	Df=1, F = 0.819, p = 0.383	Not significant
3	MD	ANOVA	Df=1, F = 0.060, p = 0.810	Not significant
RMxM1	BL	ANOVA	Df=1, F = 1.693, p = 0.216	Not significant
4	MD	ANOVA	Df=1, F = 0.414, p = 0.529	Not significant
RMxP2	BL	ANOVA	Df=1, F = 0.111, p = 0.743	Not significant
5	MD	ANOVA	Df=1, F = 0.049, p = 0.828	Not significant
RMxP1	BL	ANOVA	Df=1, F = 0.76, p = 0.786	Not significant
6	MD	ANOVA	Df=1, F = 0.209, p = 0.654	Not significant
RMxC	BL	ANOVA	Df=1, F = 1.300, p = 0.272	Not significant
7	MD	Kruskal Wallis	p = 0.497	Not significant
RMxLI	BL	Kruskal Wallis	p = 0.202	Not significant
8	MD	ANOVA	Df=1, F = 0.920, p = 0.365	Not significant
RMxCI	BL	ANOVA	Df=1, F = 0.173, p = 0.688	Not significant
9	MD	ANOVA	Df=1, F = 2.500, p = 0.140	Not significant
LMxCI	BL	ANOVA	Df=1, F = 1.116, p = 0.312	Not significant
10	MD	ANOVA	Df=1, F = 3.573, p = 0.088	Not significant
LMxLI	BL	ANOVA	Df=1, F = 0.240, p = 0.635	Not significant
11	MD	ANOVA	Df=1, F = 0.151, p = 0.704	Not significant
LMxC	BL	ANOVA	Df=1, F = 1.922, p = 0.187	Not significant
12	MD	ANOVA	Df=1, F = 0.074, p = 0.790	Not significant
LMxP1	BL	ANOVA	Df=1, F = 0.460, p = 0.512	Not significant

13 LMxP2	MD	ANOVA	Df=1, F = 0.874, p = 0.372	Not significant
	BL	ANOVA	Df=1, F = 0.000, p = 0.989	Not significant
14 LMxM1	MD	ANOVA	Df=1, F = 0.552, p = 0.471	Not significant
	BL	ANOVA	Df=1, F = 0.172, p = 0.685	Not significant
15 LMxM2	MD	ANOVA	Df=1, F = 0.318, p = 0.583	Not significant
	BL	ANOVA	Df=1, F = 0.004, p = 0.949	Not significant
16 LMxM3	MD	ANOVA	Df=1, F = 11.422, p = 0.008	Significant
	BL	ANOVA	Df=1, F = 0.842, p = 0.383	Not significant
17 LMM3	MD	ANOVA	Df=1, F = 0.044, p = 0.838	Not significant
	BL	ANOVA	Df=1, F = 5.299, p = 0.044	Significant
18 LMM2	MD	Kruskal Wallis	p = 0.726	Not significant
	BL	ANOVA	Df=1, F = 0.496, p = 0.491	Not significant
19 LMM1	MD	ANOVA	Df=1, F = 7.081, p = 0.016	Significant
	BL	ANOVA	Df=1, F = 4.130, p = 0.057	Not significant
20 LMP2	MD	ANOVA	Df=1, F = 0.464, p = 0.504	Not significant
	BL	ANOVA	Df=1, F = 0.169, p = 0.685	Not significant
21 LMP1	MD	ANOVA	Df=1, F = 2.975, p = 0.102	Not significant
	BL	ANOVA	Df=1, F = 1.945, p = 0.180	Not significant
22 LMC	MD	ANOVA	Df=1, F = 0.480, p = 0.496	Not significant
	BL	ANOVA	Df=1, F = 15.727, p = 0.001	Significant
23 LMLI	MD	ANOVA	Df=1, F = 0.273, p = 0.608	Not significant
	BL	ANOVA	Df=1, F = 0.585, p = 0.456	Not significant
24 LMCI	MD	ANOVA	Df=1, F = 2.405, p = 0.152	Not significant
	BL	ANOVA	Df=1, F = 0.034, p = 0.858	Not significant
25 RMCI	MD	ANOVA	Df=1, F = 6.712, p = 0.024	Significant
	BL	ANOVA	Df=1, F = 0.158, p = 0.698	Not significant
26 RMLI	MD	ANOVA	Df=1, F = 1.380, p = 0.257	Not significant
	BL	ANOVA	Df=1, F = 0.172, p = 0.684	Not significant
27 RMC	MD	ANOVA	Df=1, F = 0.794, p = 0.383	Not significant
	BL	Kruskal Wallis	p = 0.029	Significant
28 RMP1	MD	ANOVA	Df=1, F = 0.656. p = 0.427	Not significant
	BL	ANOVA	Df=1, F = 1.189, p = 0.288	Not significant
29 RMP2	MD	ANOVA	Df=1, F = 0.706, p = 0.412	Not significant
	BL	ANOVA	Df=1, F = 0.498, p = 0.491	Not significant
30 RMM1	MD	ANOVA	Df=1, F = 0.446, p = 0.513	Not significant
	BL	ANOVA	Df=1, F = 0.516, p = 0.482	Not significant
31 RMM2	MD	ANOVA	Df=1, F = 0.388, p = 0.541	Not significant
	BL	ANOVA	Df=1, F = 0.007, p = 0.935	Not significant
32 RMM3	MD	ANOVA	Df=1, F = 0.005, p = 0.944	Not significant
	BL	ANOVA	Df=1, F = 1.877, p = 0.201	Not significant

Table 8 - Results from the ANOVA/Kruskal-Wallis tests for influence of sex on tooth size, Eastry only.

Tooth	Measurement	Test Used	Result	Interpretation
1 RMxM3	MD	ANOVA	Df=1, F = 0.014, p = 0.918	Not significant
	BL	Kruskal Wallis	p = 1.000	Not significant
2 RMxM2	MD	ANOVA	Df=1, F = 0.045, p = 0.866	Not significant
	BL	ANOVA	Df=1, F = 20.021, p = 0.140	Not significant
3	MD	ANOVA	Df=1, F = 0.026, p = 0.881	Not significant

RMxM1	BL	ANOVA	Df=1, F = 0.613, p = 0.491	Not significant
4	MD	ANOVA	Df=1, F = 17.655, p = 0.149	Not significant
RMxP2	BL	ANOVA	Df=1, F = 0.218, p = 0.722	Not significant
5	MD	--	--	
RMxP1	BL	--	--	
6	MD	ANOVA	Df=1, F = 8.184, p = 0.065	Not significant
RMxC	BL	ANOVA	Df=1, F = 1.245, p = 0.346	Not significant
7	MD	--	--	
RMxLI	BL	--	--	
8	MD	--	--	
RMxCI	BL	--	--	
9	MD	ANOVA	Df=1, F = 0.073, p = 0.832	Not significant
LMxCI	BL	ANOVA	Df=1, F = 3.329, p = 0.319	Not significant
10	MD	--	--	
LMxLI	BL	--	--	
11	MD	ANOVA	Df=1, F = 0.092, p = 0.776	Not significant
LMxC	BL	ANOVA	Df=1, F = 0.558, p = 0.509	Not significant
12	MD	ANOVA	Df=1, F = 0.005, p = 0.948	Not significant
LMxP1	BL	ANOVA	Df=1, F = 0.004, p = 0.954	Not significant
13	MD	ANOVA	Df=1, F = 0.424, p = 0.562	Not significant
LMxP2	BL	ANOVA	Df=1, F = 0.166, p = 0.723	Not significant
14	MD	ANOVA	Df=1, F = 0.040, p = 0.854	Not significant
LMxM1	BL	ANOVA	Df=1, F = 11.520, p = 0.077	Not significant
15	MD	ANOVA	Df=1, F = 0.238, p = 0.659	Not significant
LMxM2	BL	ANOVA	Df=1, F = 0.312, p = 0.633	Not significant
16	MD	ANOVA	Df=1, F = 0.287, p = 0.630	Not significant
LMxM3	BL	ANOVA	Df=1, F = 4.349, p = 0.172	Not significant
17	MD	ANOVA	Df=1, F = 0.024, p = 0.903	Not significant
LMM3	BL	ANOVA	Df=1, F = 0.024, p = 0.903	Not significant
18	MD	ANOVA	Df=1, F = 0.852, p = 0.424	Not significant
LMM2	BL	ANOVA	Df=1, F = 0.051, p = 0.832	Not significant
19	MD	ANOVA	Df=1, F = 0.261, p = 0.636	Not significant
LMM1	BL	ANOVA	Df=1, F = 0.903, p = 0.396	Not significant
20	MD	ANOVA	Df=1, F = 0.885, p = 0.400	Not significant
LMP2	BL	ANOVA	Df=1, F = 0.711, p = 0.447	Not significant
21	MD	ANOVA	Df=1, F = 2.069, p = 0.210	Not significant
LMP1	BL	ANOVA	Df=1, F = 1.181, p = 0.327	Not significant
22	MD	ANOVA	Df=1, F = 0.887, p = 0.390	Not significant
LMC	BL	ANOVA	Df=1, F = 6.616, p = 0.050	Not significant
23	MD	ANOVA	Df=1, F = 0.130, p = 0.737	Not significant
LMLI	BL	ANOVA	Df=1, F = 4.780, p = 0.094	Not significant
24	MD	ANOVA	Df=1, F = 0.466, p = 0.532	Not significant
LMCI	BL	ANOVA	Df=1, F = 4.458, p = 0.102	Not significant
25	MD	ANOVA	Df=1, F = 0.006, p = 0.951	Not significant
RMCI	BL	ANOVA	Df=1, F = 1.677, p = 0.419	Not significant
26	MD	ANOVA	Df=1, F = 5.925, p = 0.093	Not significant
RMLI	BL	ANOVA	Df=1, F = 23.326, p = 0.017	Significant
27	MD	ANOVA	Df=1, F = 0.838, p = 0.395	Not significant
RMC	BL	Kruskal Wallis	p = 0.044	Significant
28	MD	ANOVA	Df=1, F = 0.047, p = 0.836	Not significant

RMP1	BL	ANOVA	Df=1, F = 8.792, p = 0.025	Significant
29	MD	ANOVA	Df=1, F = 0.612, p = 0.457	Not significant
RMP2	BL	ANOVA	Df=1, F = 2.761, p = 0.135	Not significant
30	MD	ANOVA	Df=1, F = 0.166, p = 0.698	Not significant
RMM1	BL	ANOVA	Df=1, F = 0.410, p = 0.546	Not significant
31	MD	ANOVA	Df=1, F = 1.133, p = 0.328	Not significant
RMM2	BL	ANOVA	Df=1, F = 0.036, p = 0.856	Not significant
32	MD	ANOVA	Df=1. F = 0.066, p = 0.810	Not significant
RMM3	BL	ANOVA	Df=1, F = 7.055, p = 0.057	Not significant

Appendix 6: Worked example of statistical process for dental metrics

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 regression analysis in order to be used for identifying potential biological connections between individuals.

Step 1:

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

Tooth	Measurement	Statistic	df	Significance	Interpretation
RMxM1	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.

Step 2:

Determine if a shared environment (cemetery site) influences the size of the tooth significantly using an ANOVA test. Post-hoc Tukey tests used if necessary.

Tooth	Measurement	Test Used	Result	Interpretation
RMxM1	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 affected by shared environment. Therefore, this tooth can be included in Step 3.

Step 3:

Determine if biological sex influences the size of the tooth significantly using an ANOVA test.

Tooth	Measurement	Test Used	Result	Interpretation
RMxM1	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 together in further analyses.

Step 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 RMXM1 meet this?**
Normally distributed?	Yes
Both measurements not affected by shared environment?	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.

Appendix 7: Hierarchical Cluster Dendrograms

Combined sampled, pooled sex

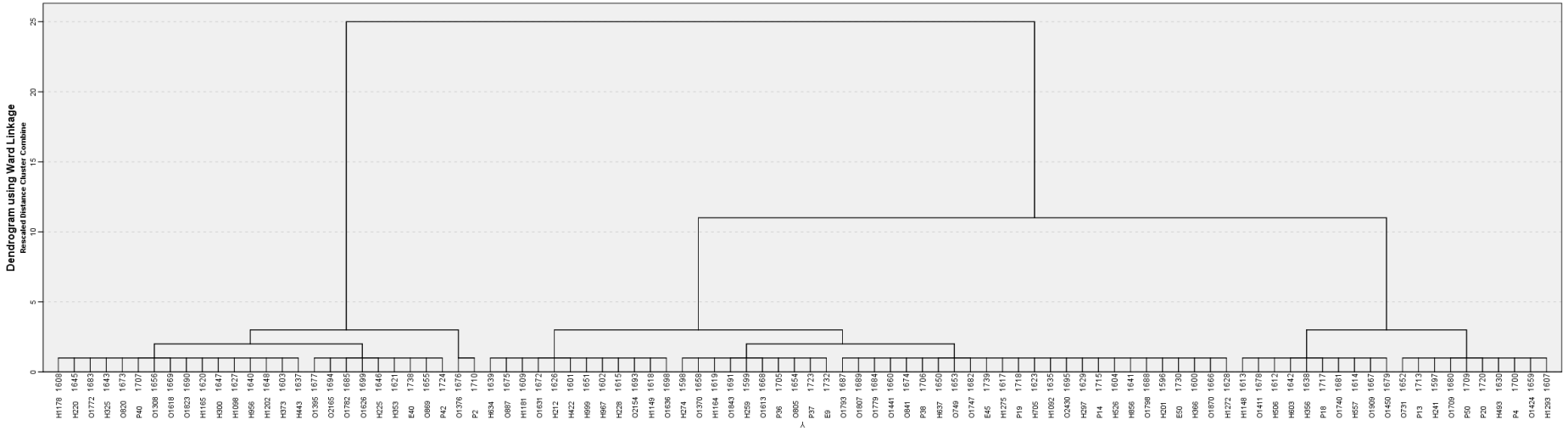

Figure 1 - Dendrogram output from hierarchical cluster analysis for the left maxillary first premolar for the combined cemetery and pooled sex sample.

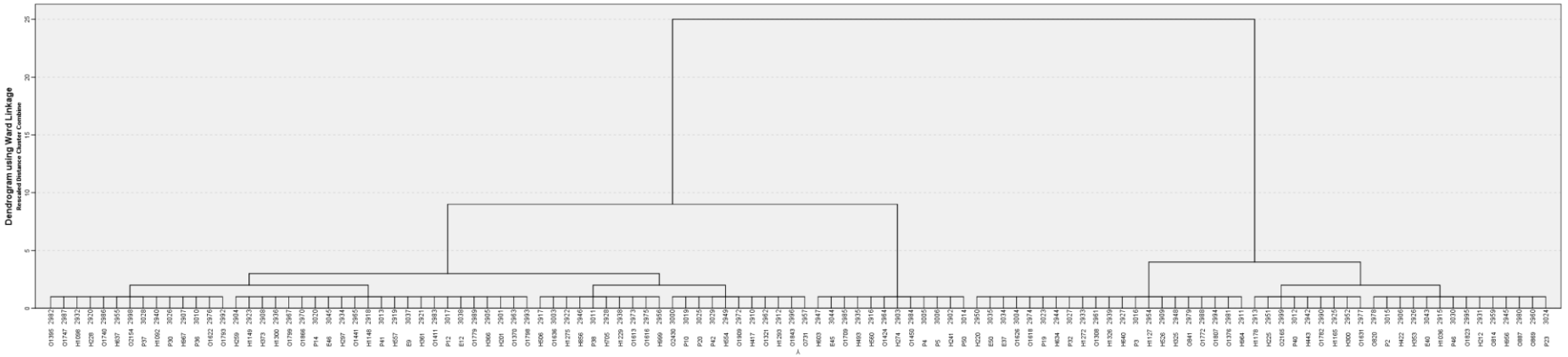

Figure 2 - Dendrogram output from hierarchical cluster analysis for the left mandibular first premolar for the combined cemetery and pooled sex sample.

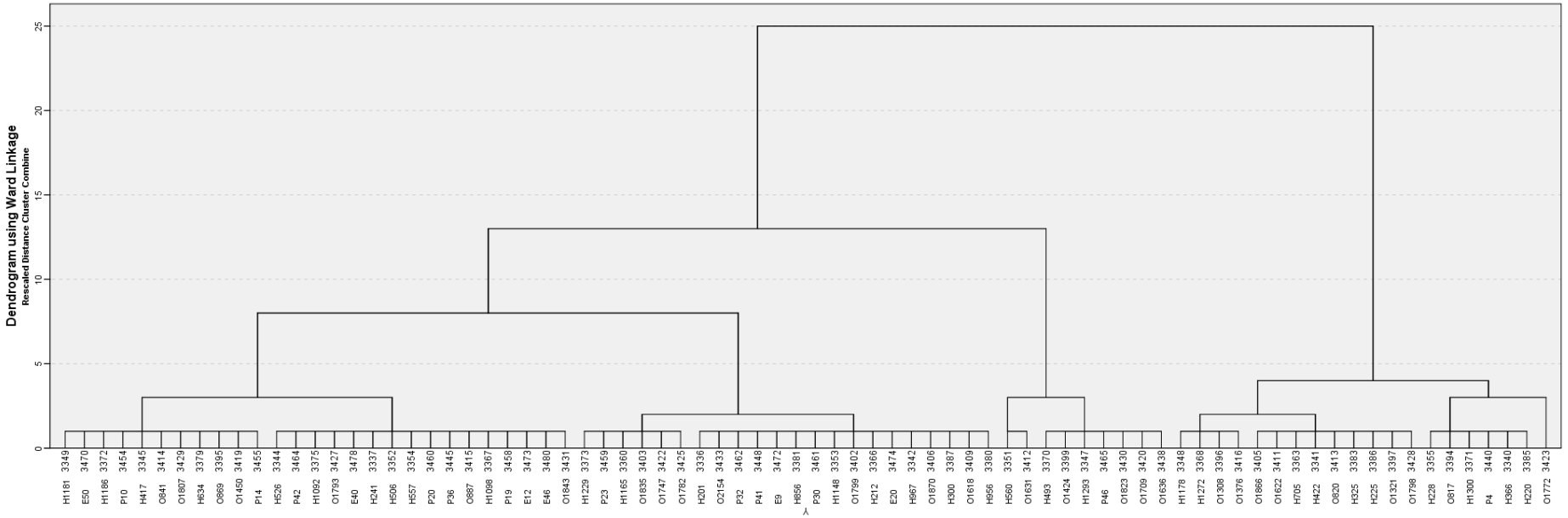

Figure 3 - Dendrogram output from hierarchical cluster analysis for the left mandibular central incisor for the combined cemetery and pooled sex sample.

Combined cemetery, male only comparisons

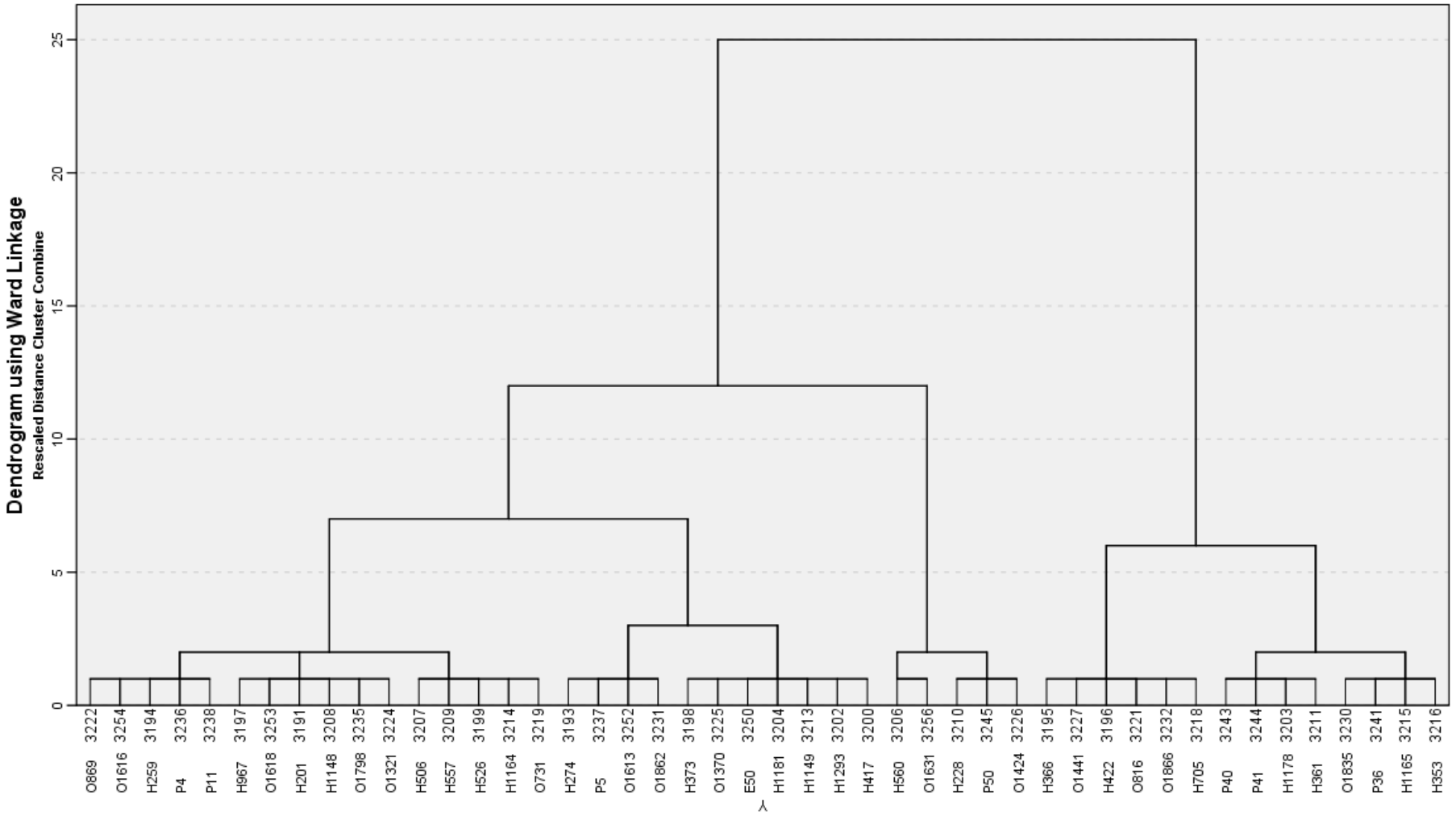

Figure 4 - Dendrogram output from hierarchical cluster analysis for the left mandibular lateral incisor for males from the combined cemetery sample.

Combined cemetery, female only comparisons

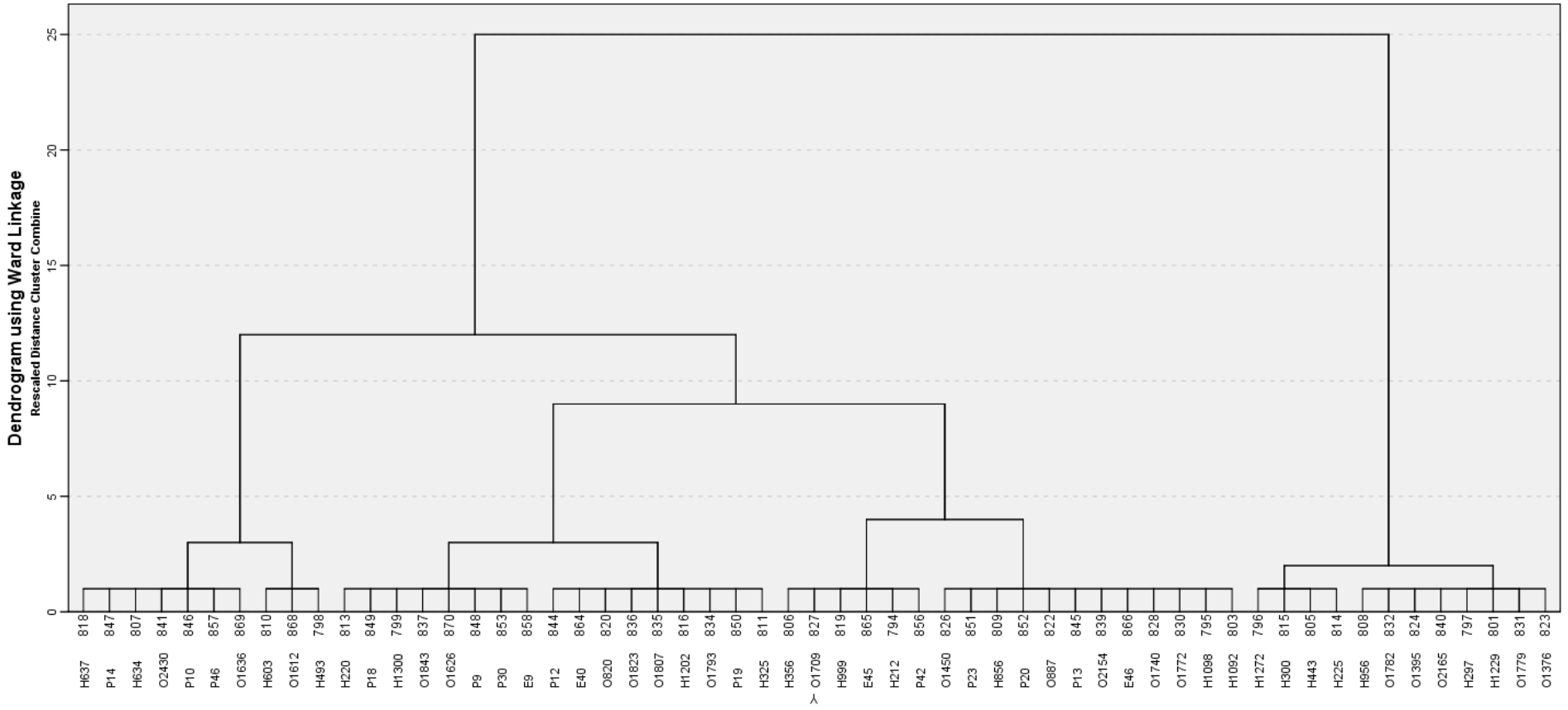

Figure 5 - Dendrogram output from hierarchical cluster analysis for the right maxillary canine for females from the combined cemetery sample.

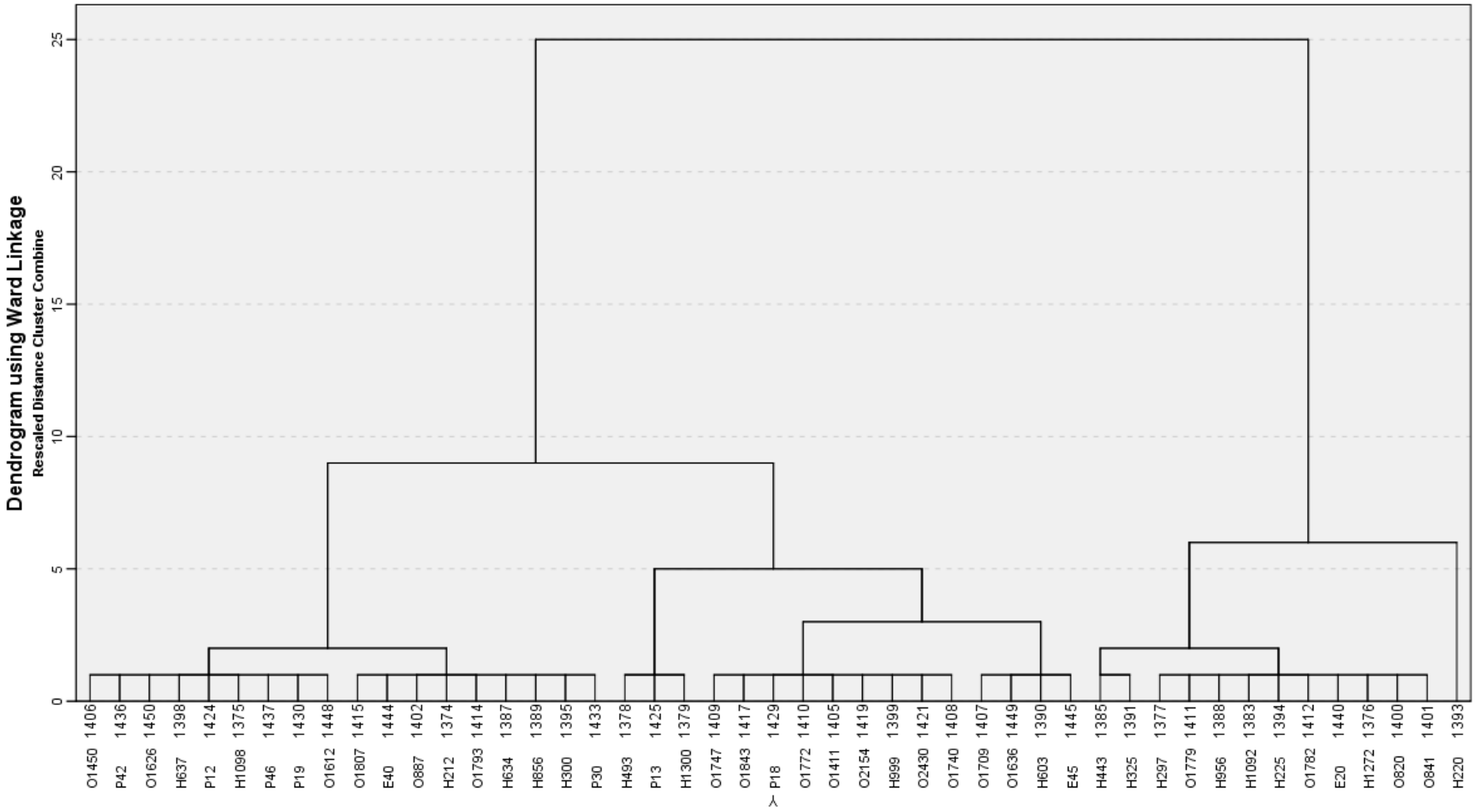

Figure 6 - Dendrogram output from hierarchical cluster analysis for the left maxillary lateral incisor for females from the combined cemetery sample.

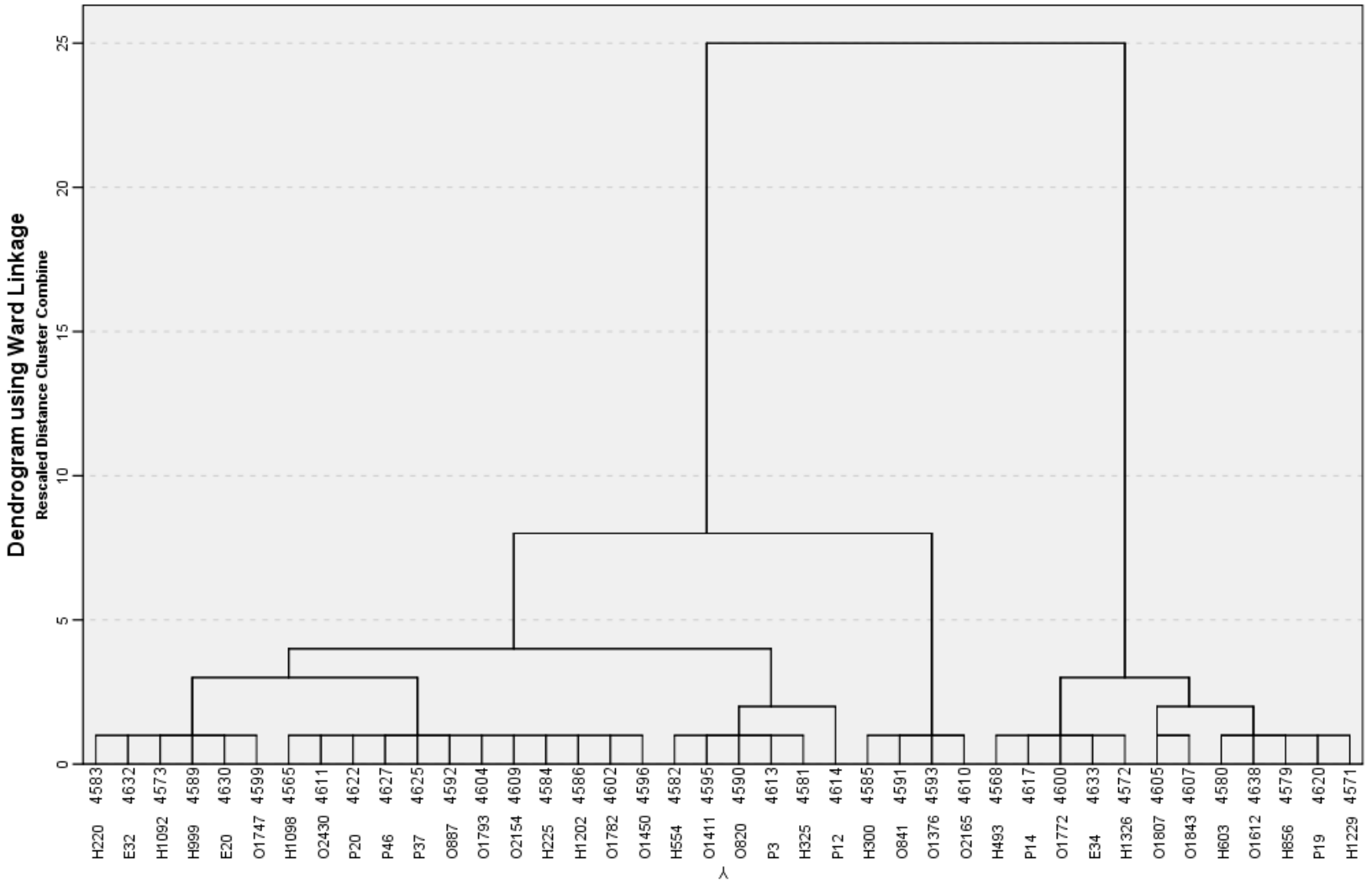

Figure 7 - Dendrogram output from hierarchical cluster analysis for the right mandibular third molar for females from the combined cemetery sample.

Hatherdene, pooled sex comparisons

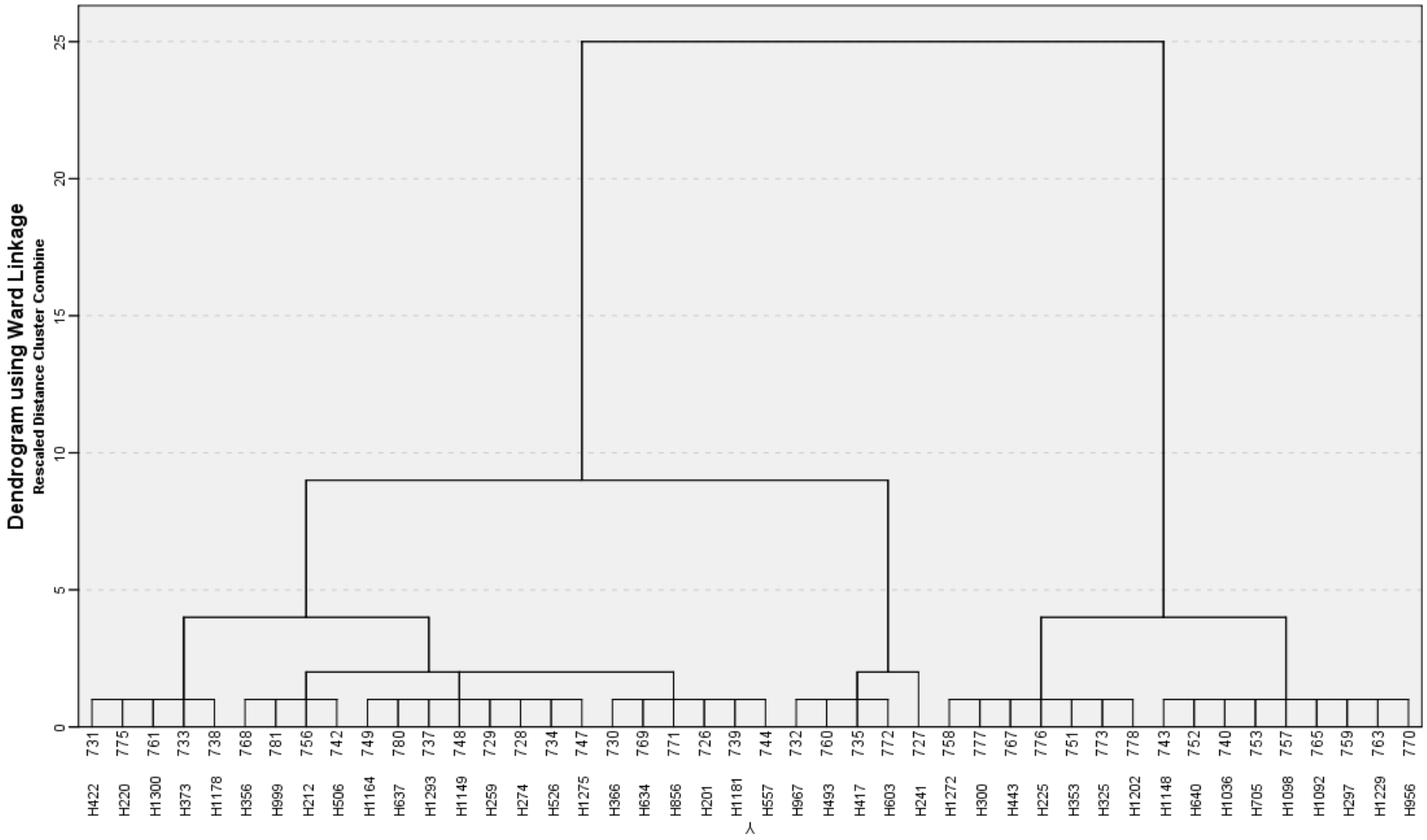

Figure 8 - Dendrogram output from hierarchical cluster analysis for the right maxillary canine for the pooled sex sample at Hatherdene.

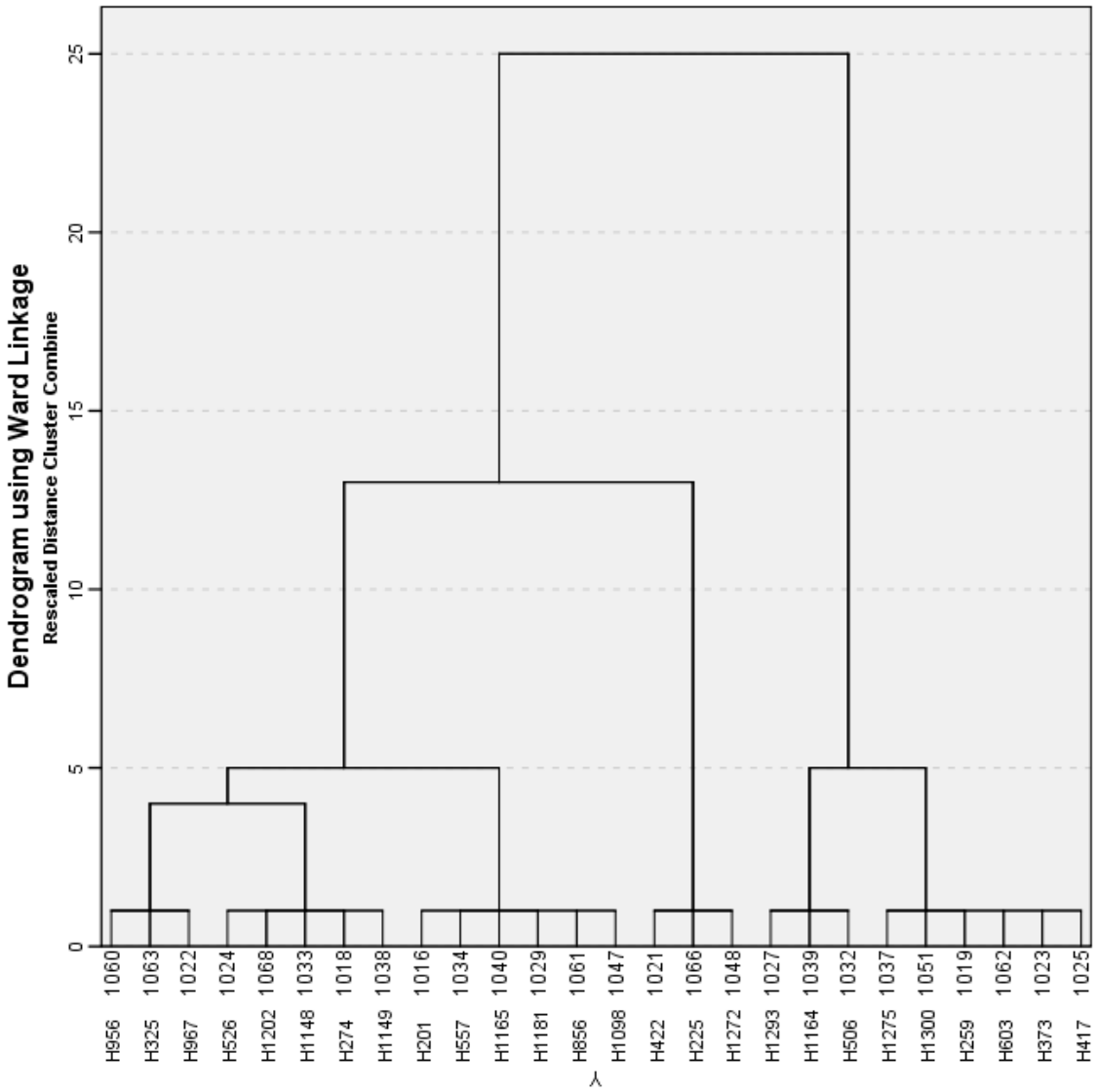

Figure 9 - Dendrogram output from hierarchical cluster analysis for the right maxillary central incisor for the pooled sex sample at Hatherdene.

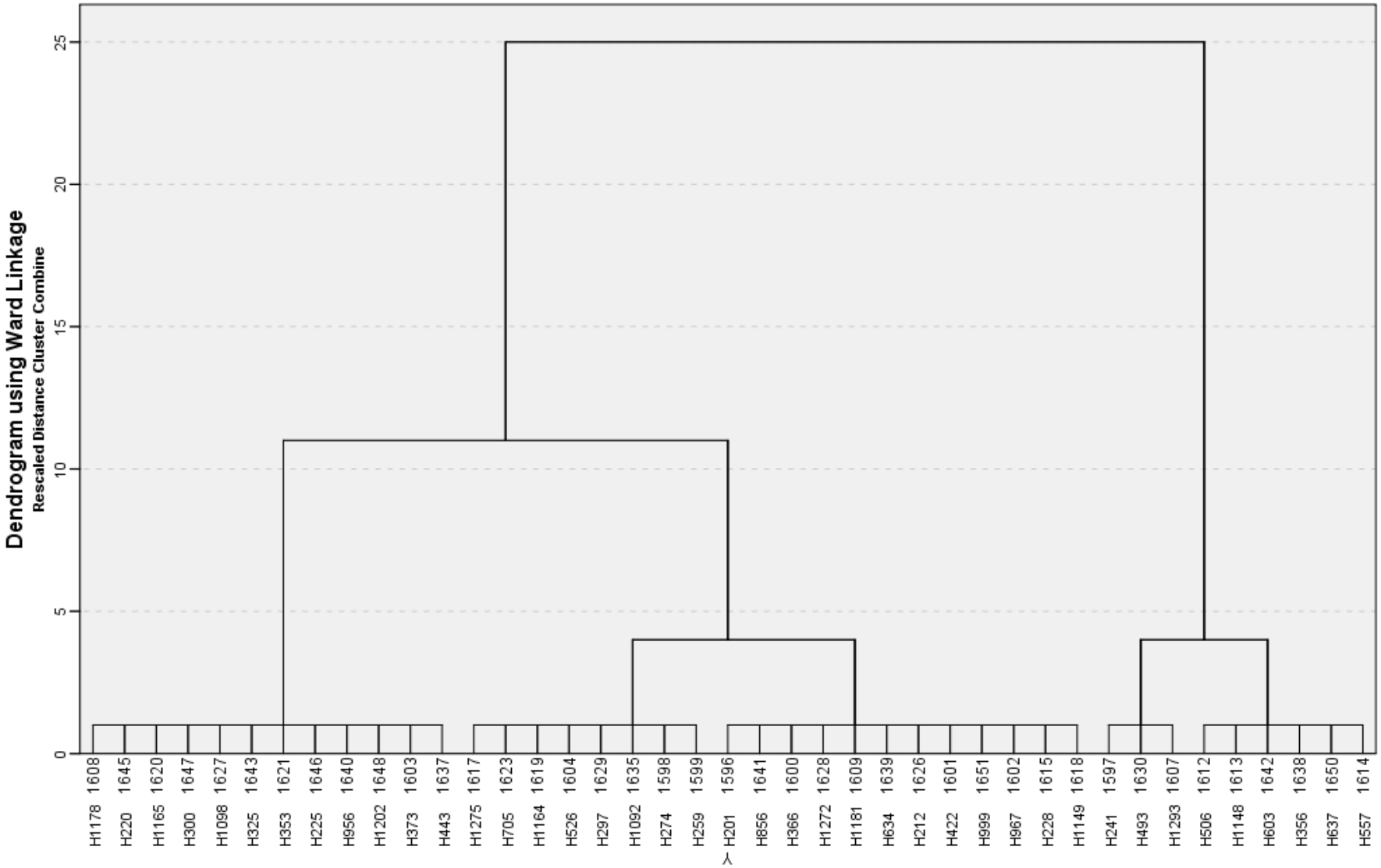

Figure 10 - Dendrogram output from hierarchical cluster analysis for the left maxillary first premolar for the pooled sex sample at Hatherdene.

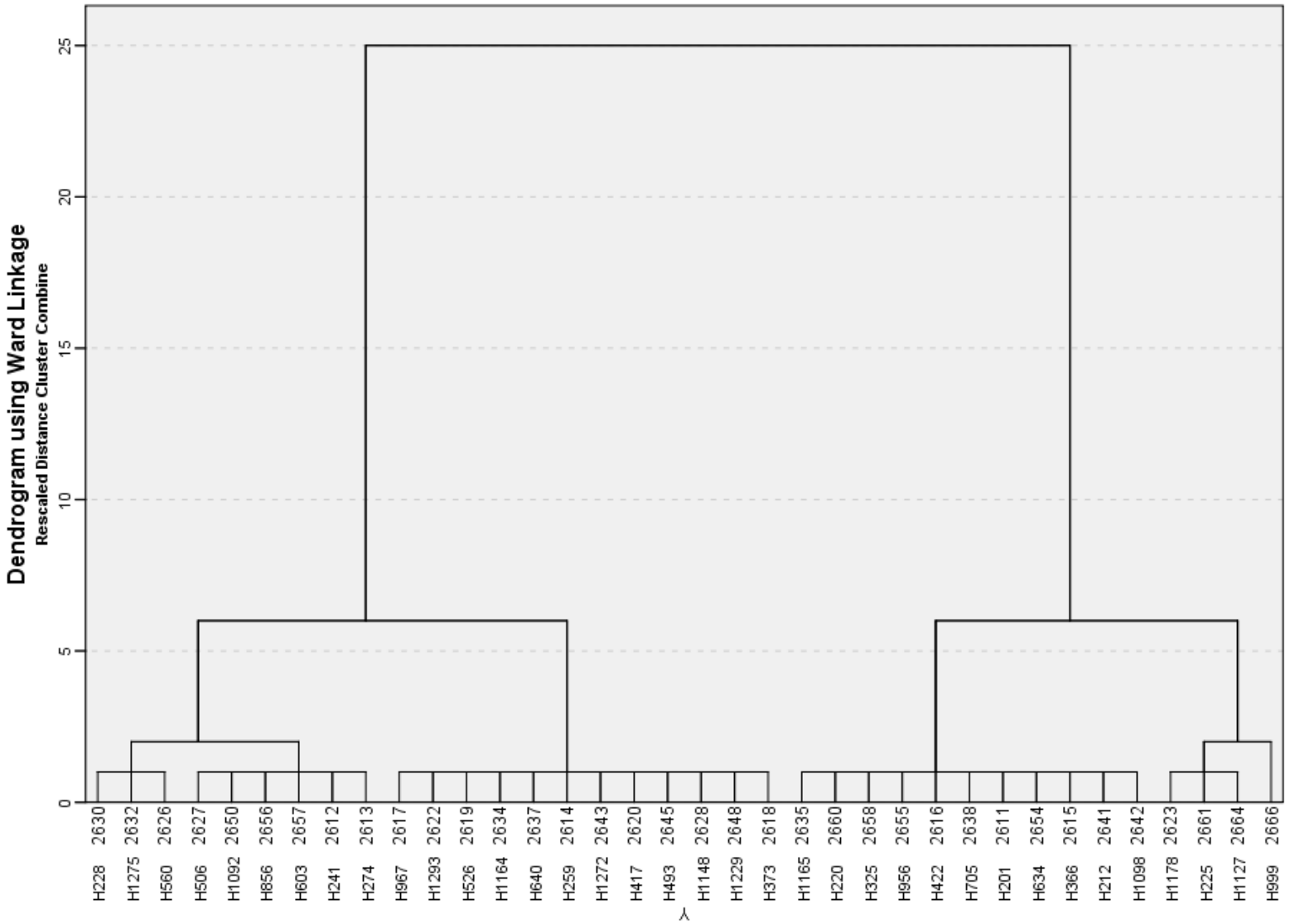

Figure 11 - Dendrogram output from hierarchical cluster analysis for the left mandibular first molar for the pooled sex sample at Hatherdene.

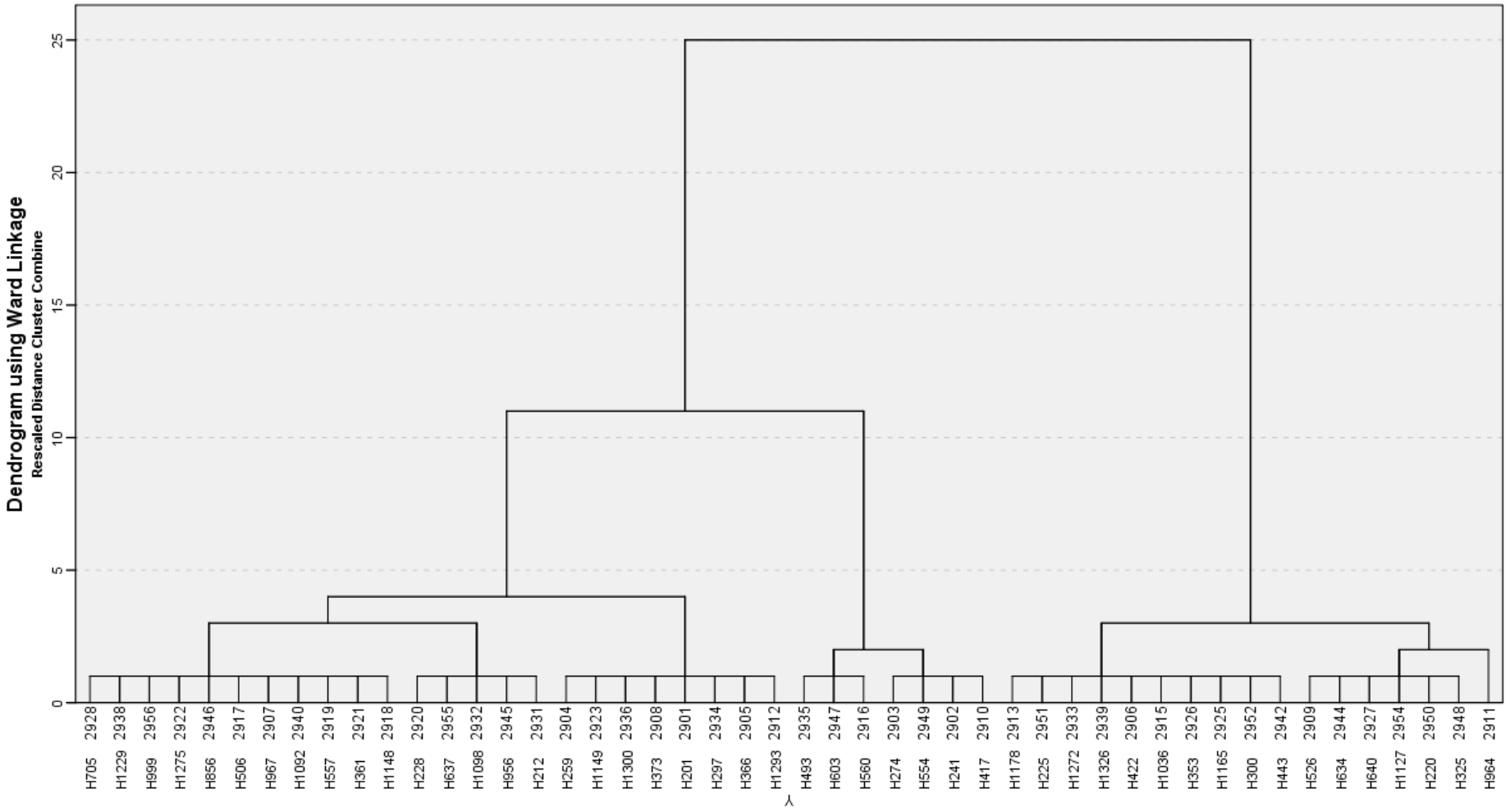

Figure 12 - Dendrogram output from hierarchical cluster analysis for the left mandibular first premolar for the pooled sex sample at Hatherdene.

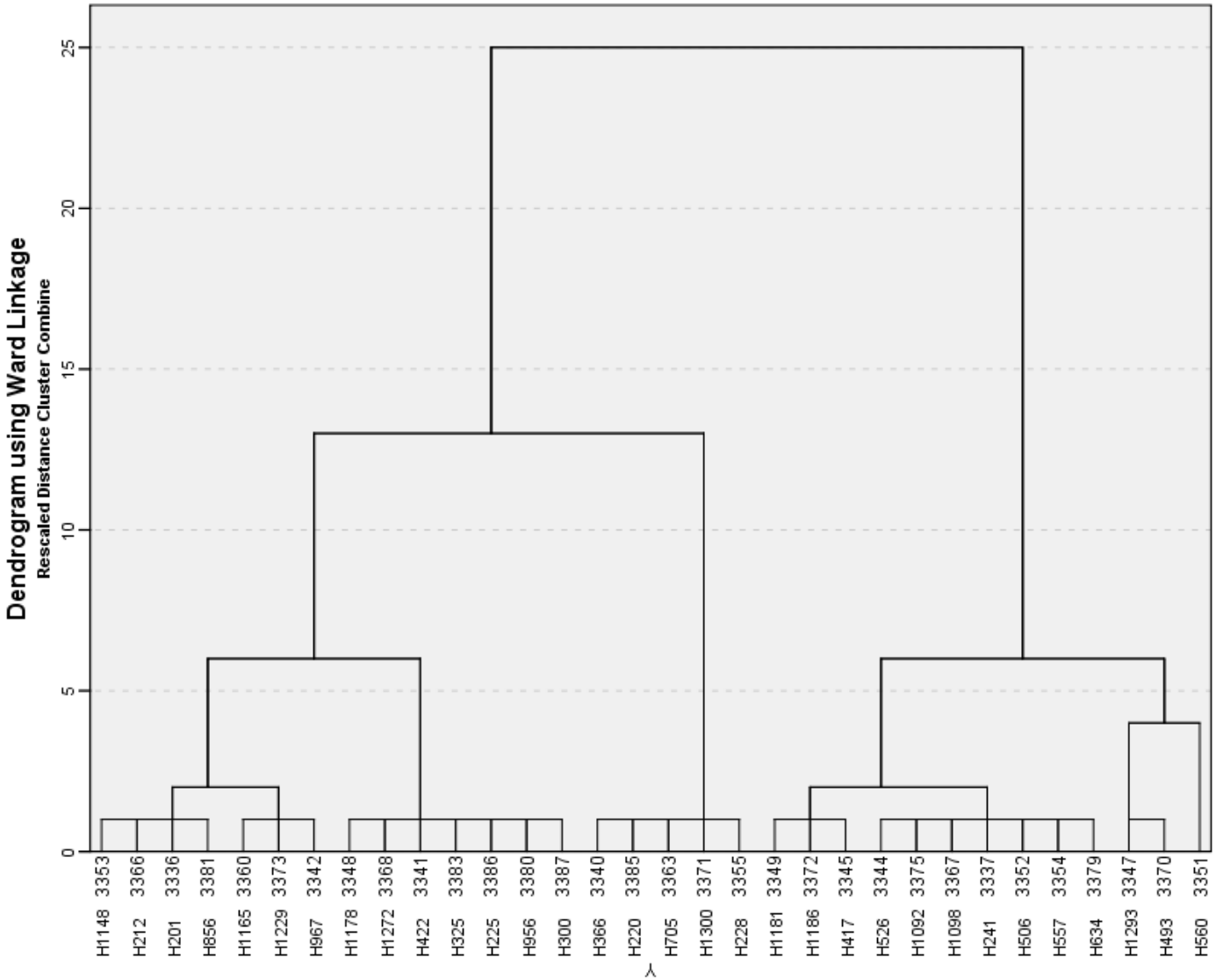

Figure 13 - Dendrogram output from hierarchical cluster analysis for the left mandibular central incisor for the pooled sex sample at Hatherdene.

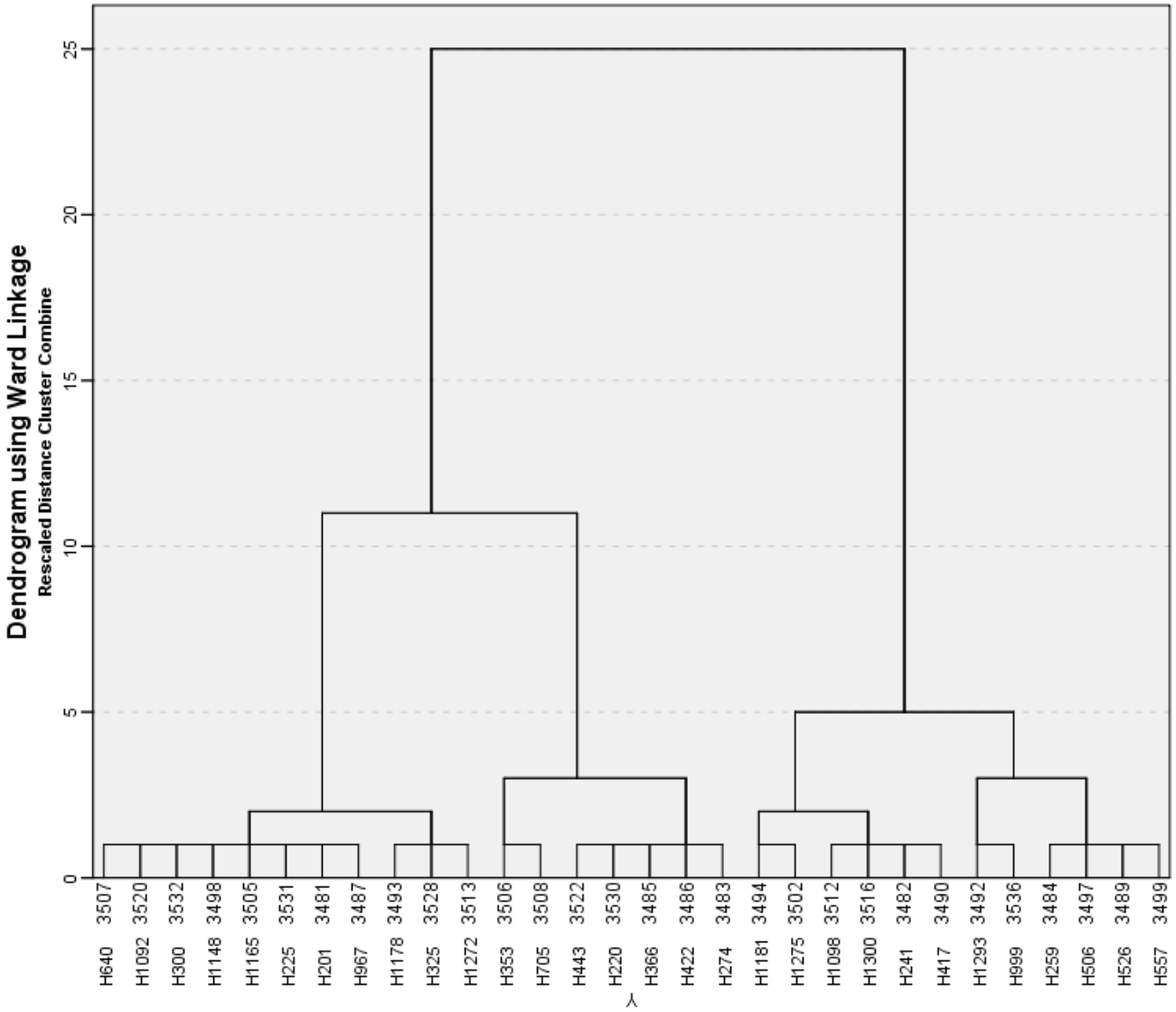

Figure 14 - Dendrogram output from hierarchical cluster analysis for the right mandibular central incisor for the pooled sex sample at Hatherdene.

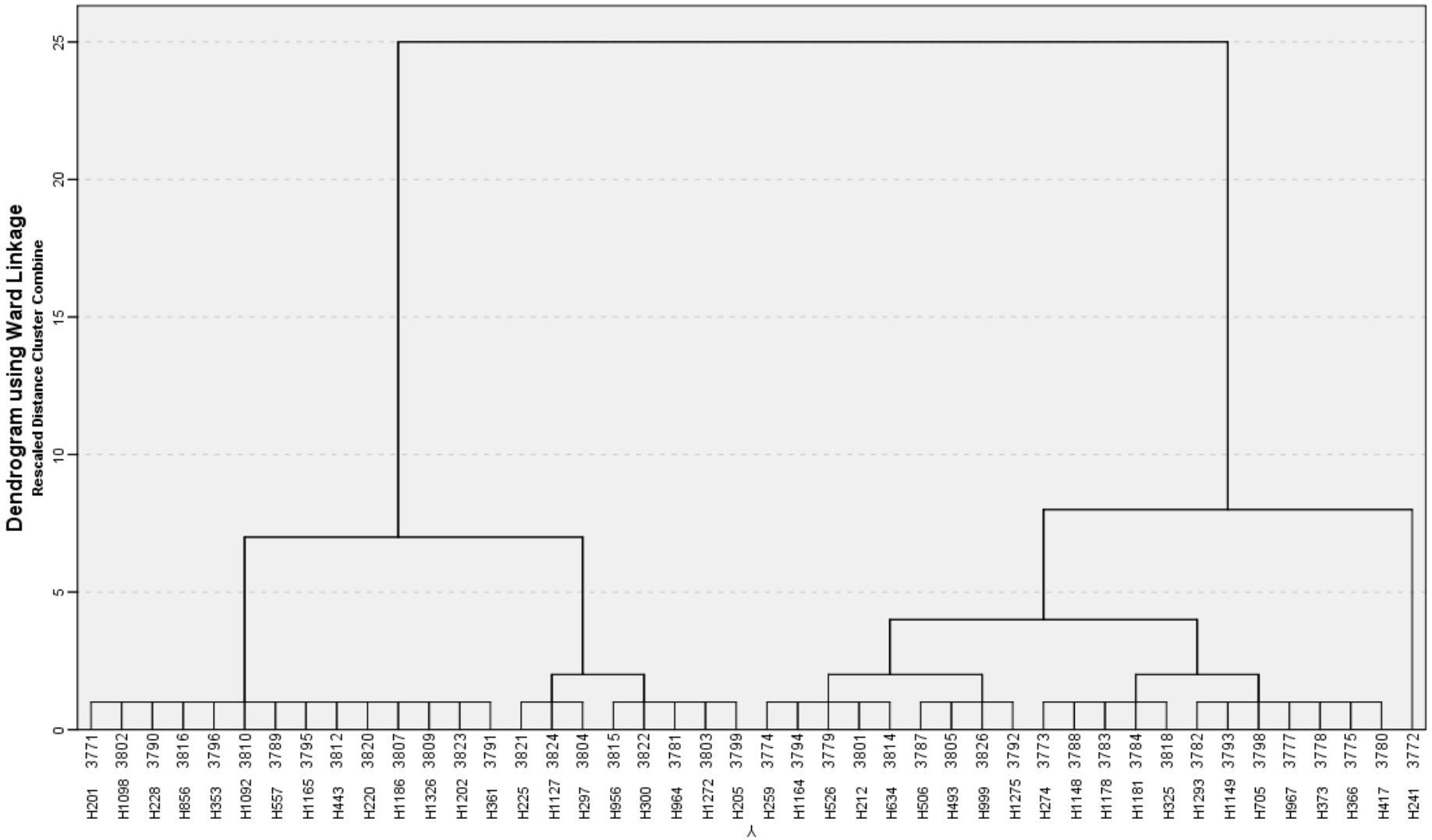

Figure 15 - Dendrogram output from hierarchical cluster analysis for the right mandibular canine for the pooled sex sample at Hatherdene.

Hatherdene, male comparisons only

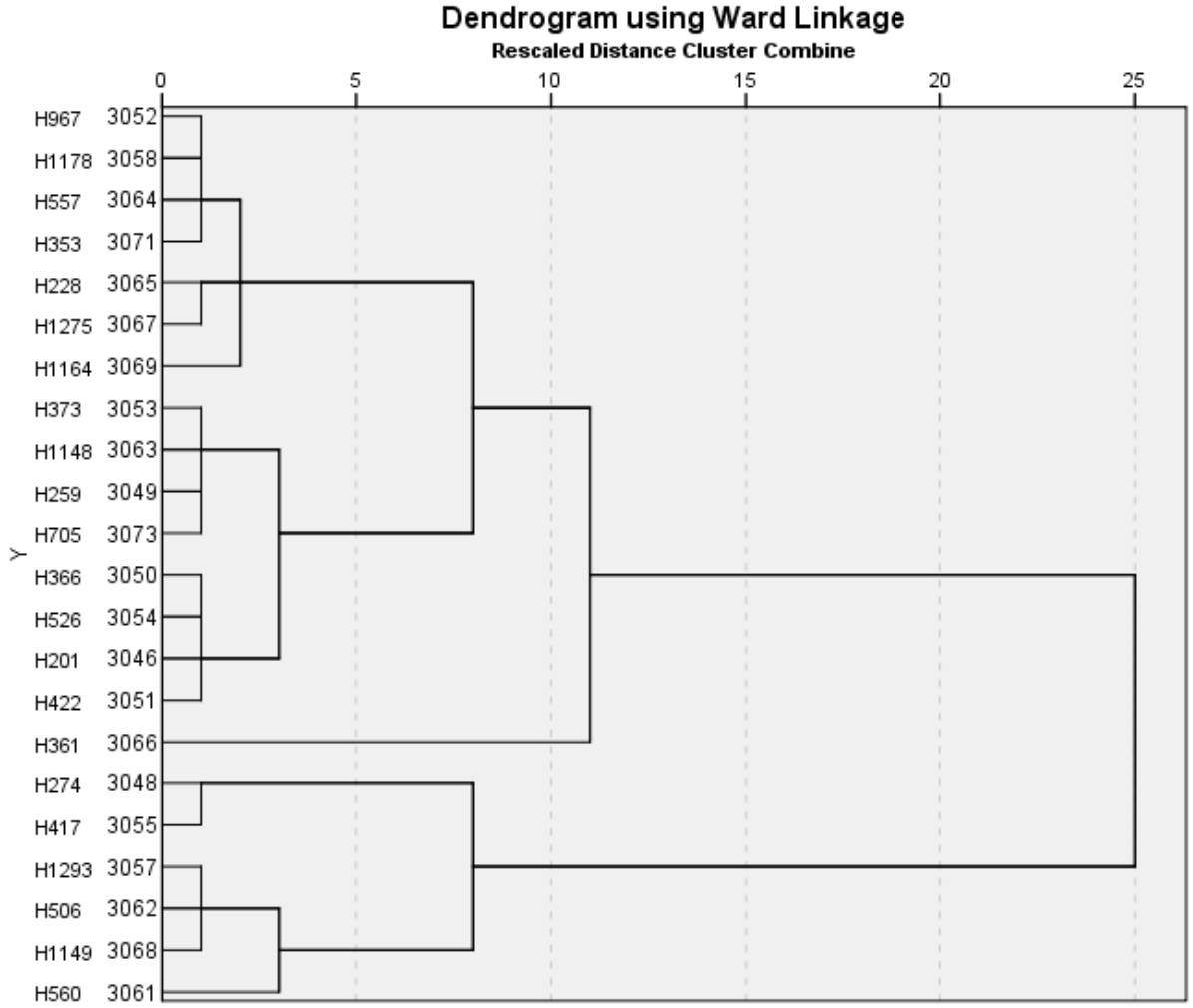

Figure 16 - Dendrogram output from hierarchical cluster analysis for the left mandibular canine for the male sample at Hatherdene.

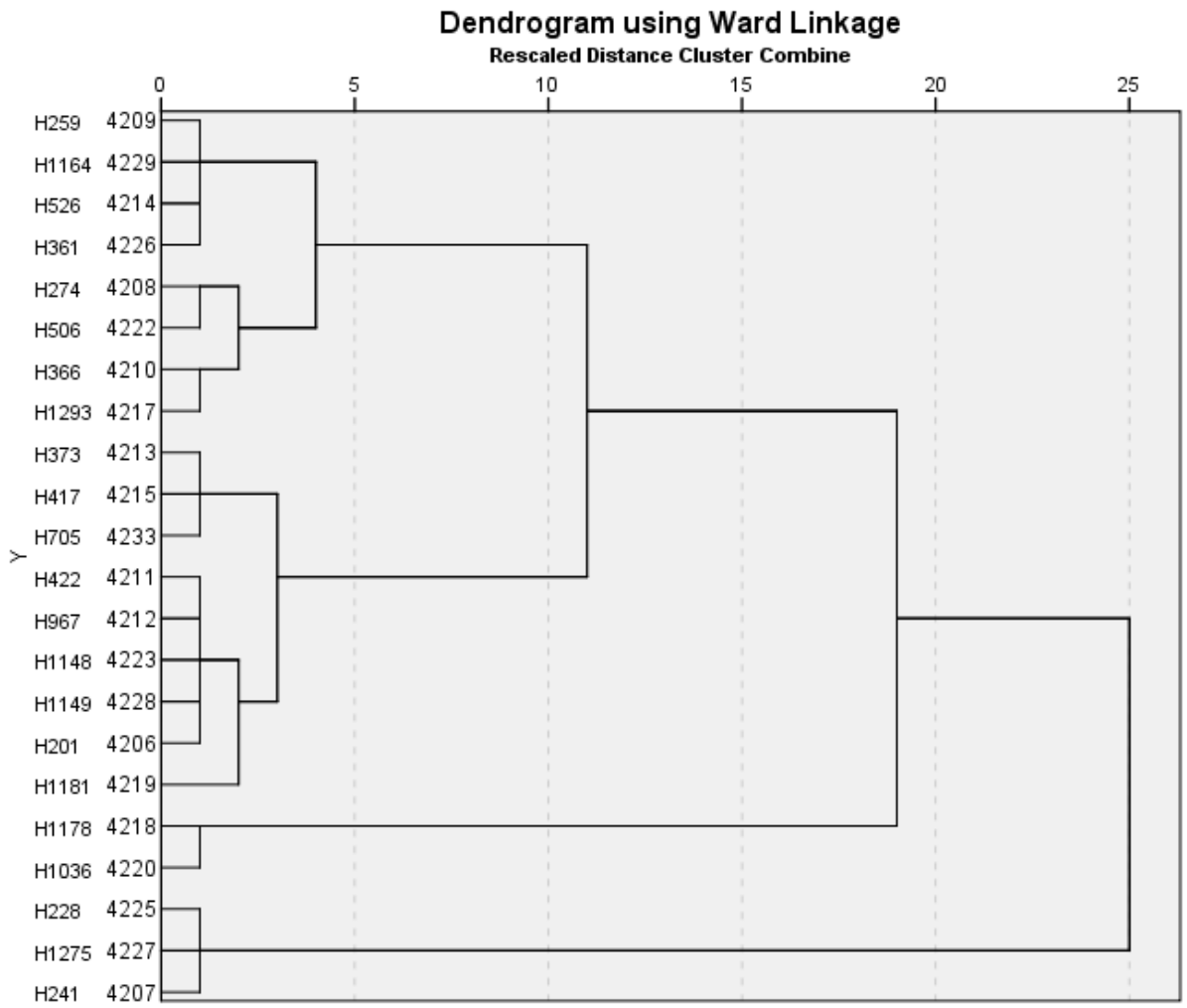

Figure 17 - Dendrogram output from hierarchical cluster analysis for the right mandibular first molar for the male sample at Hatherdene.

Hatherdene, female comparisons only

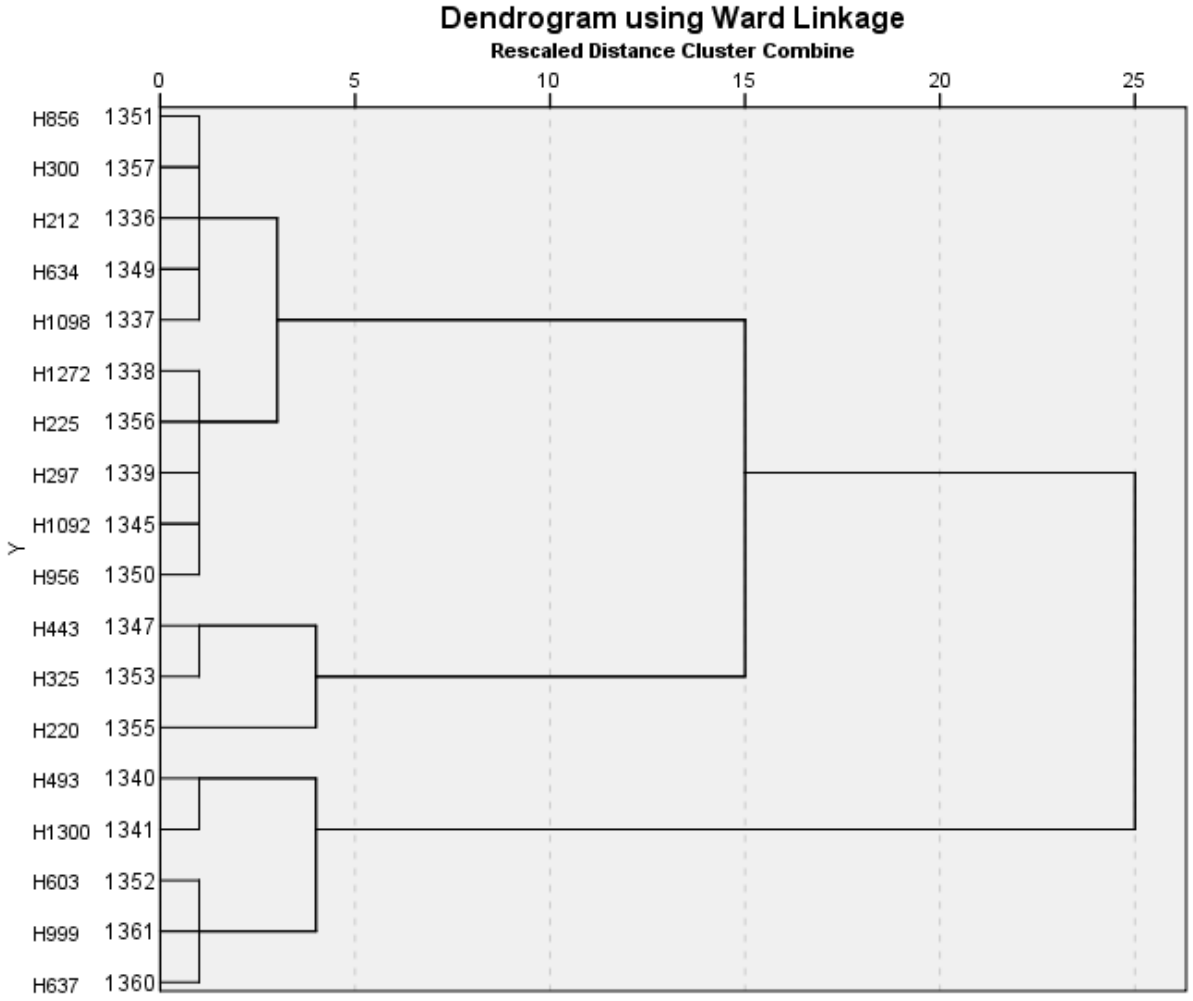

Figure 18 - Dendrogram output from hierarchical cluster analysis for the left maxillary lateral incisor for the female sample at Hatherdene.

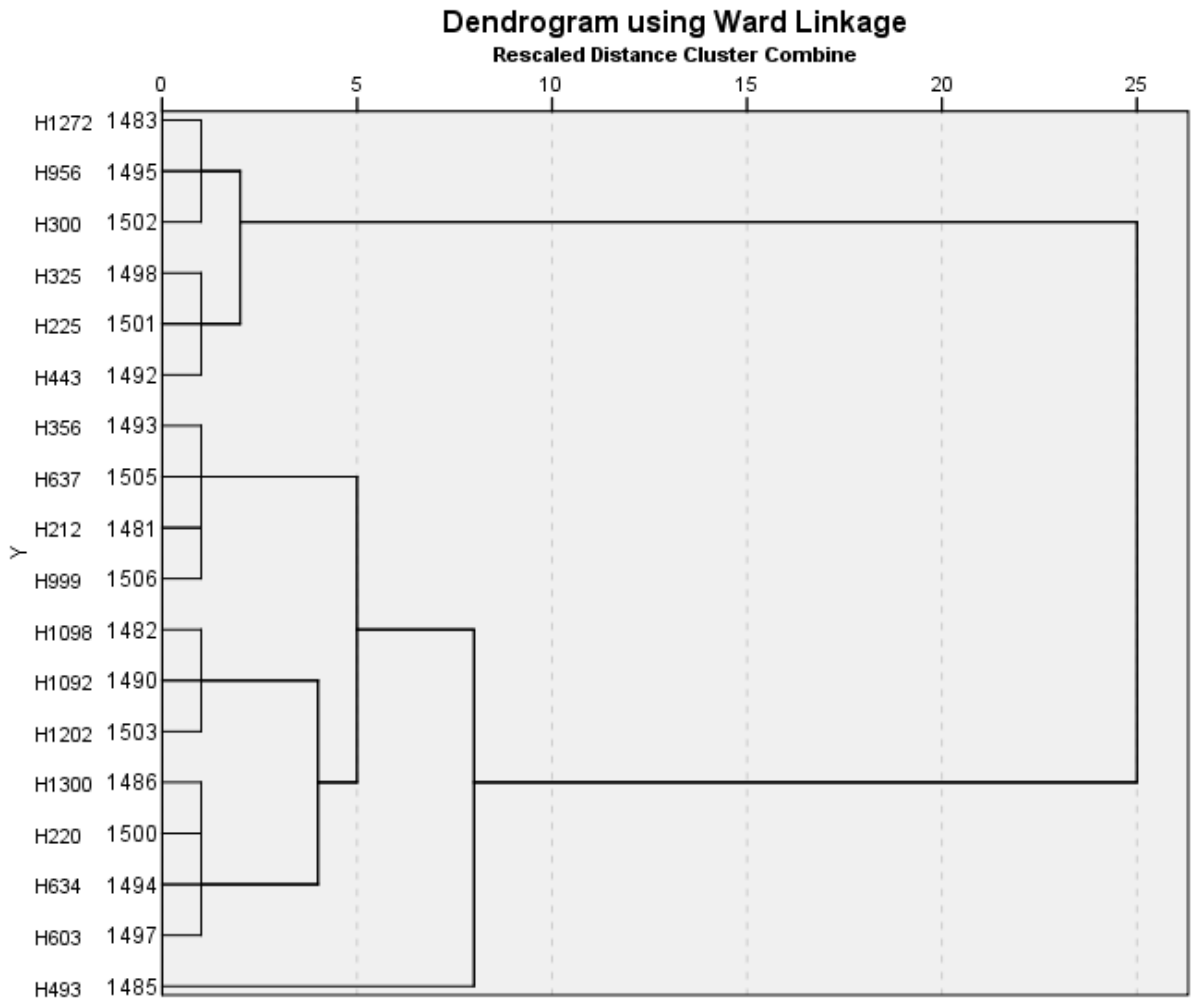

Figure 19 - Dendrogram output from hierarchical cluster analysis for the left maxillary canine for the female sample at Hatherdene.

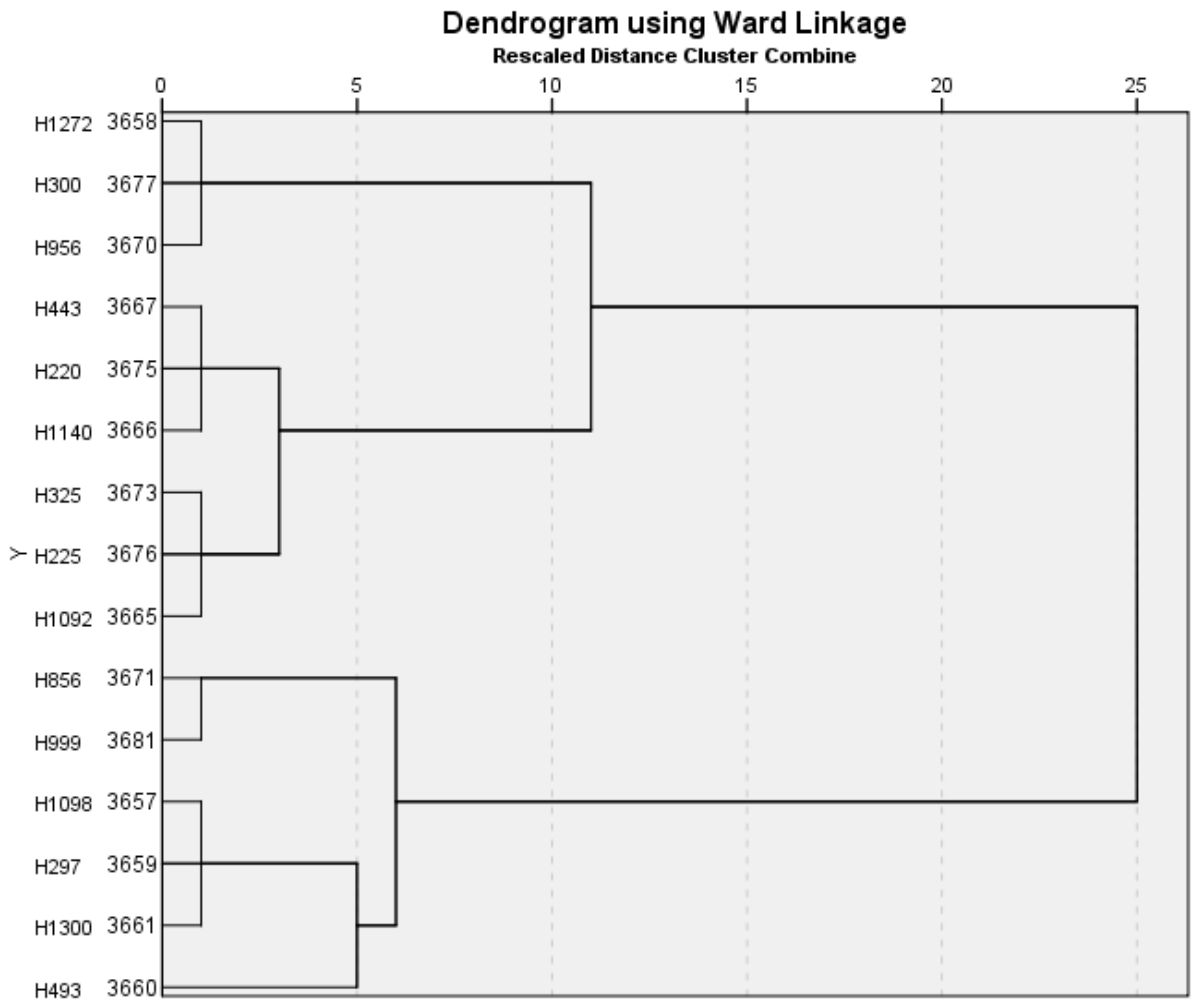

Figure 20 - Dendrogram output from hierarchical cluster analysis for the right mandibular lateral incisor for the female sample at Hatherdene.

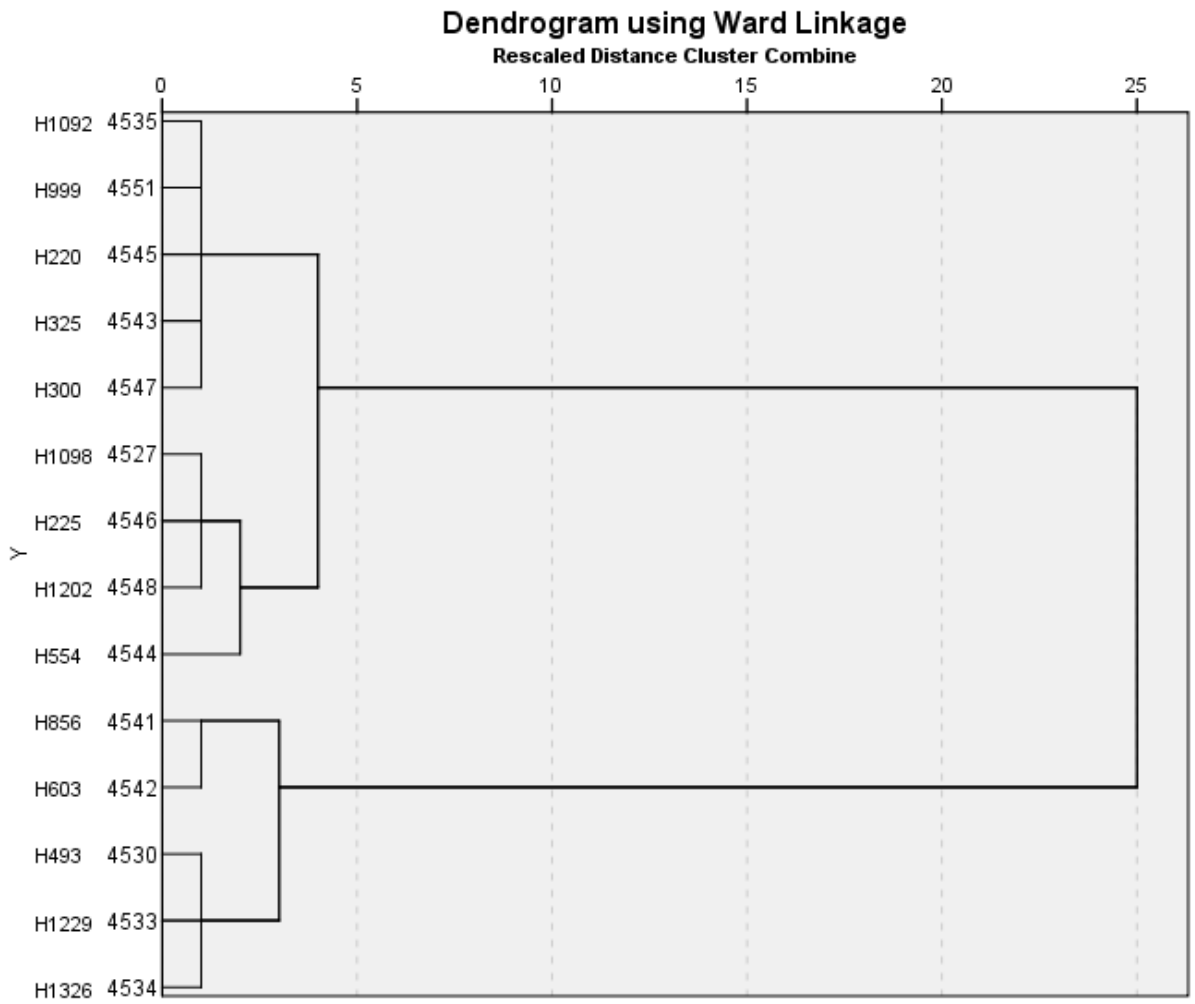

Figure 21 - Dendrogram output from hierarchical cluster analysis for the right mandibular third molar for the female sample at Hatherdene.

Oakington, pooled sex comparisons

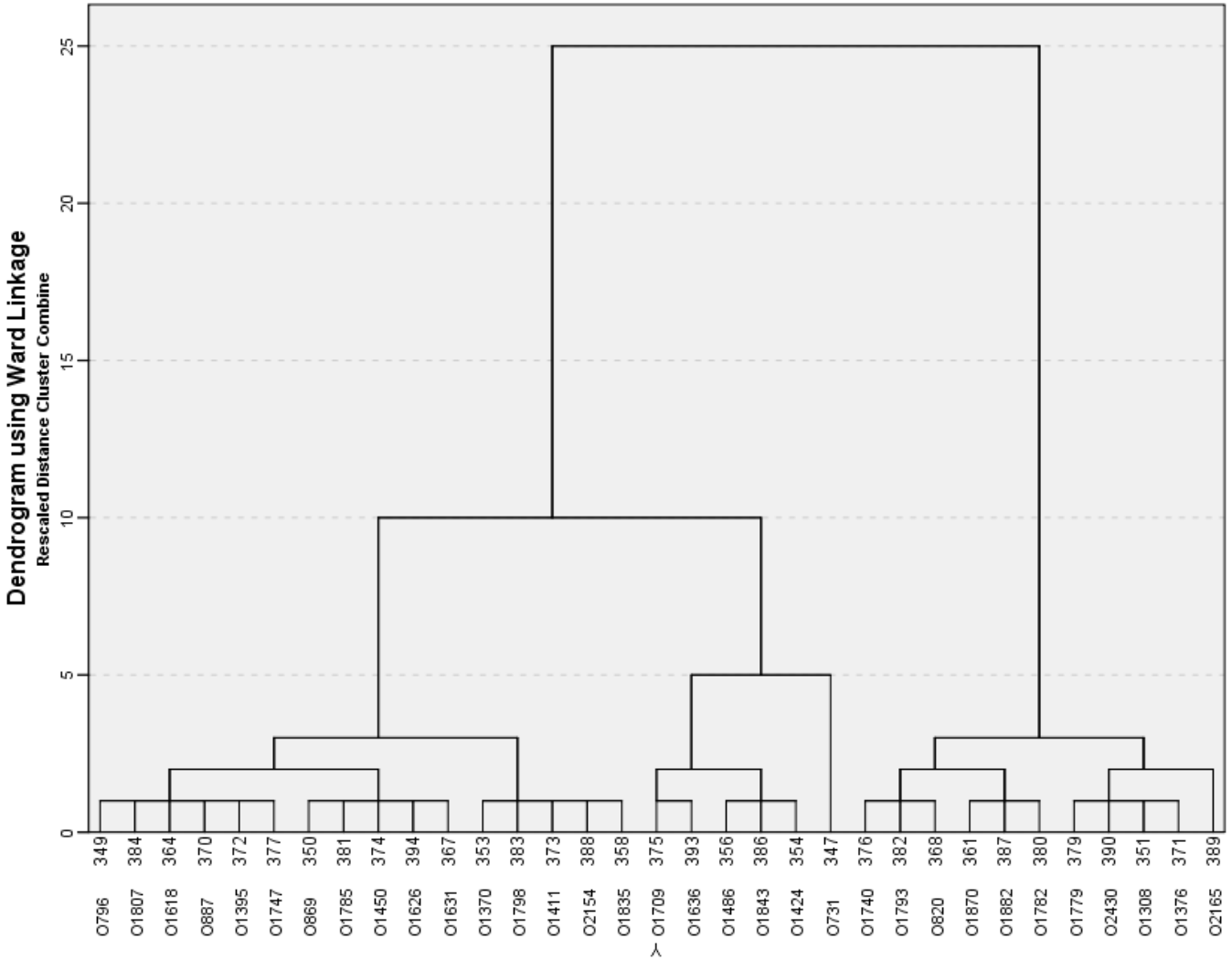

Figure 22 - Dendrogram output from hierarchical cluster analysis for the right maxillary first molar for the pooled sex sample at Oakington.

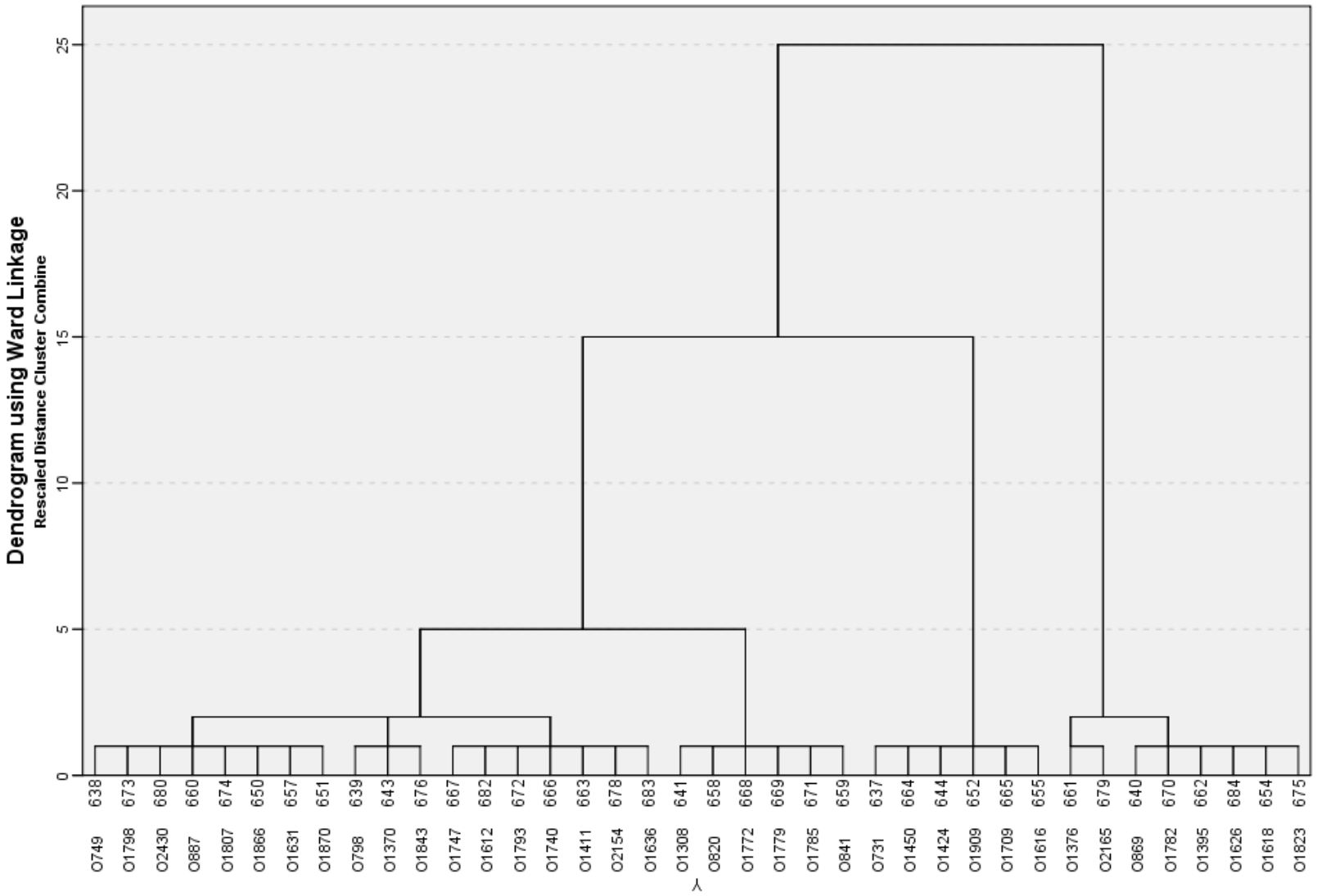

Figure 23 - Dendrogram output from hierarchical cluster analysis for the right maxillary first premolar for the pooled sex sample at Oakington.

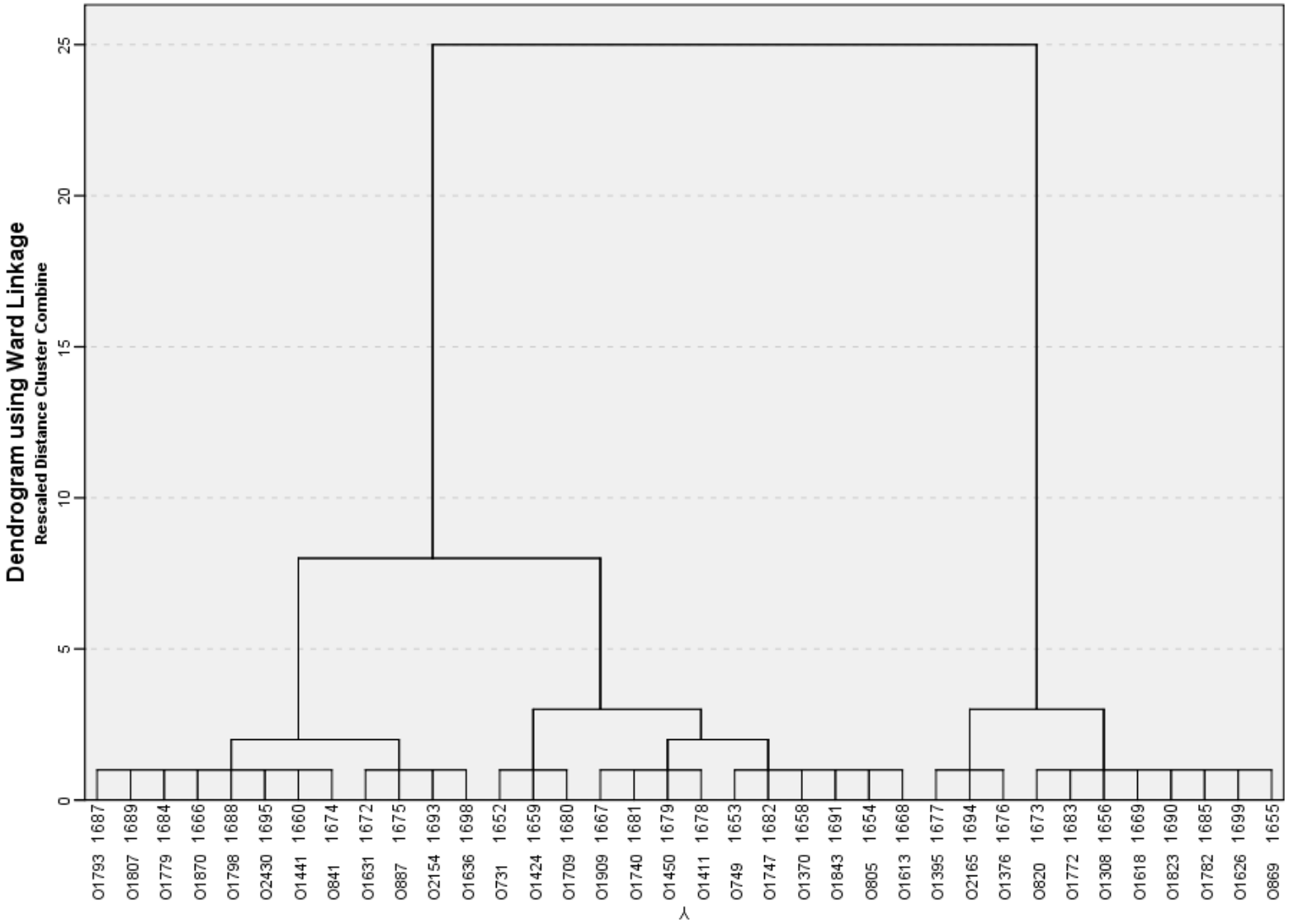

Figure 24 - Dendrogram output from hierarchical cluster analysis for the left maxillary first premolar for the pooled sex sample at Oakington.

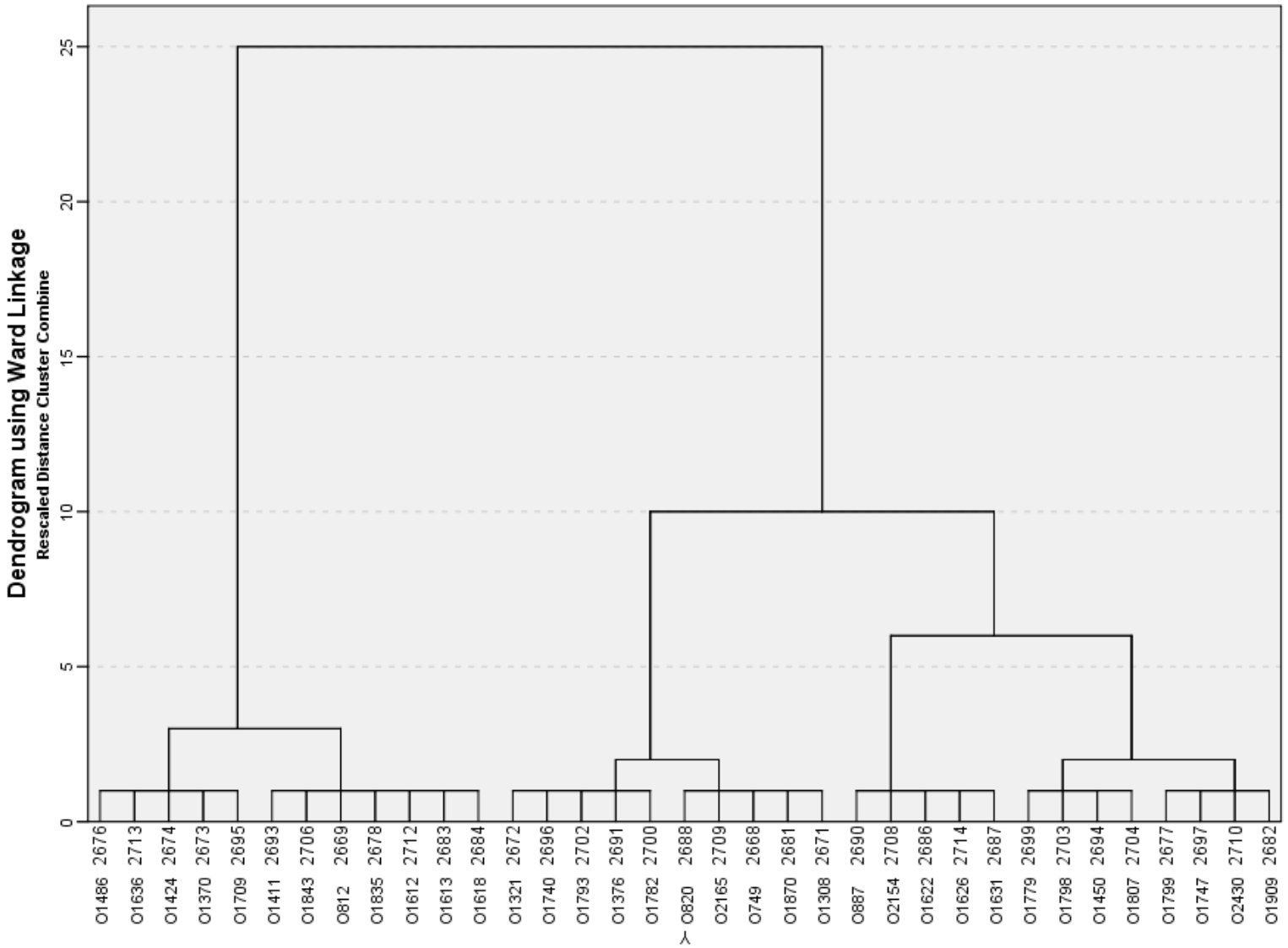

Figure 25 - Dendrogram output from hierarchical cluster analysis for the left mandibular first molar for the pooled sex sample at Oakington.

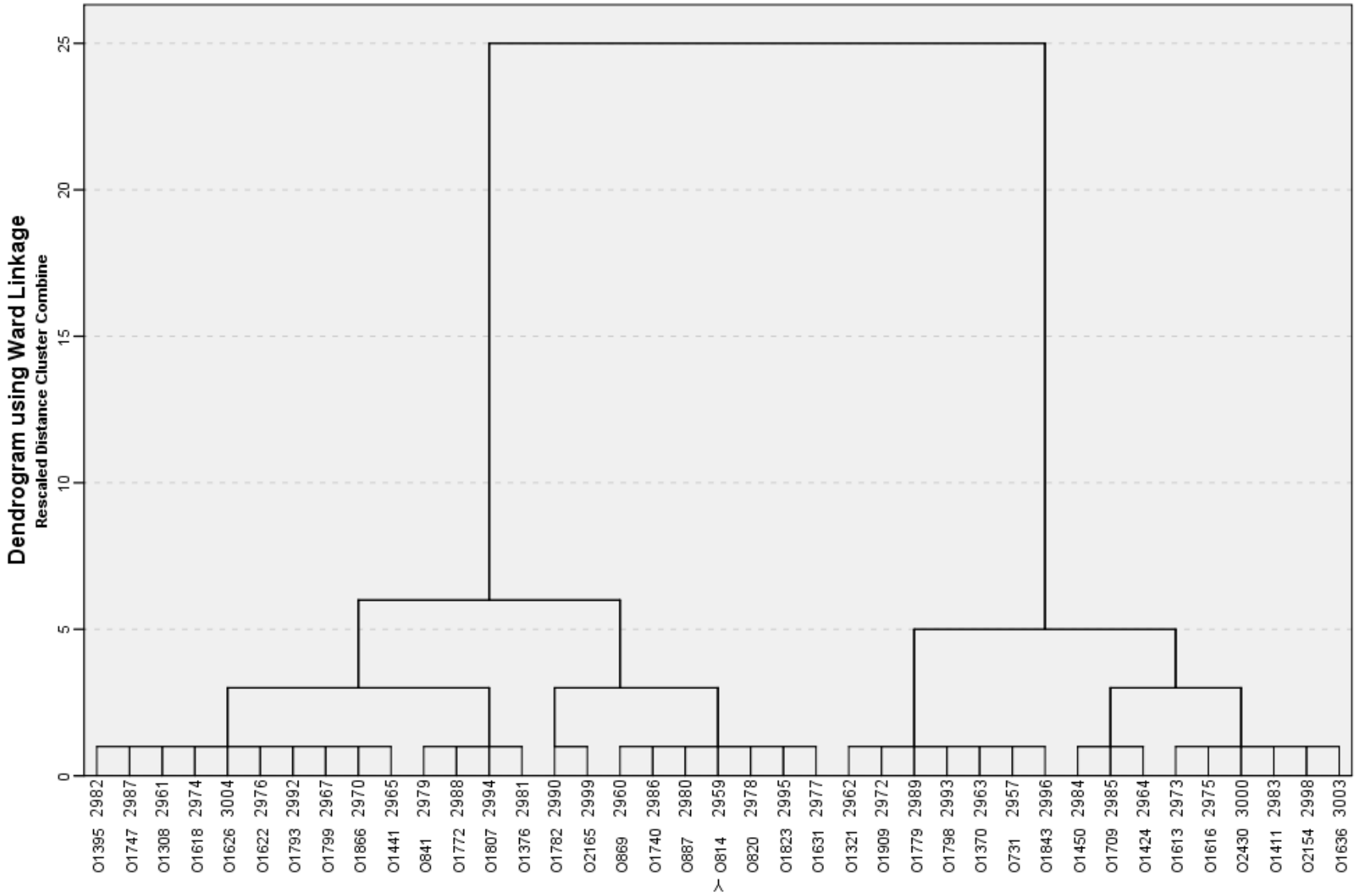

Figure 26 - Dendrogram output from hierarchical cluster analysis for the left mandibular first premolar for the pooled sex sample at Oakington.

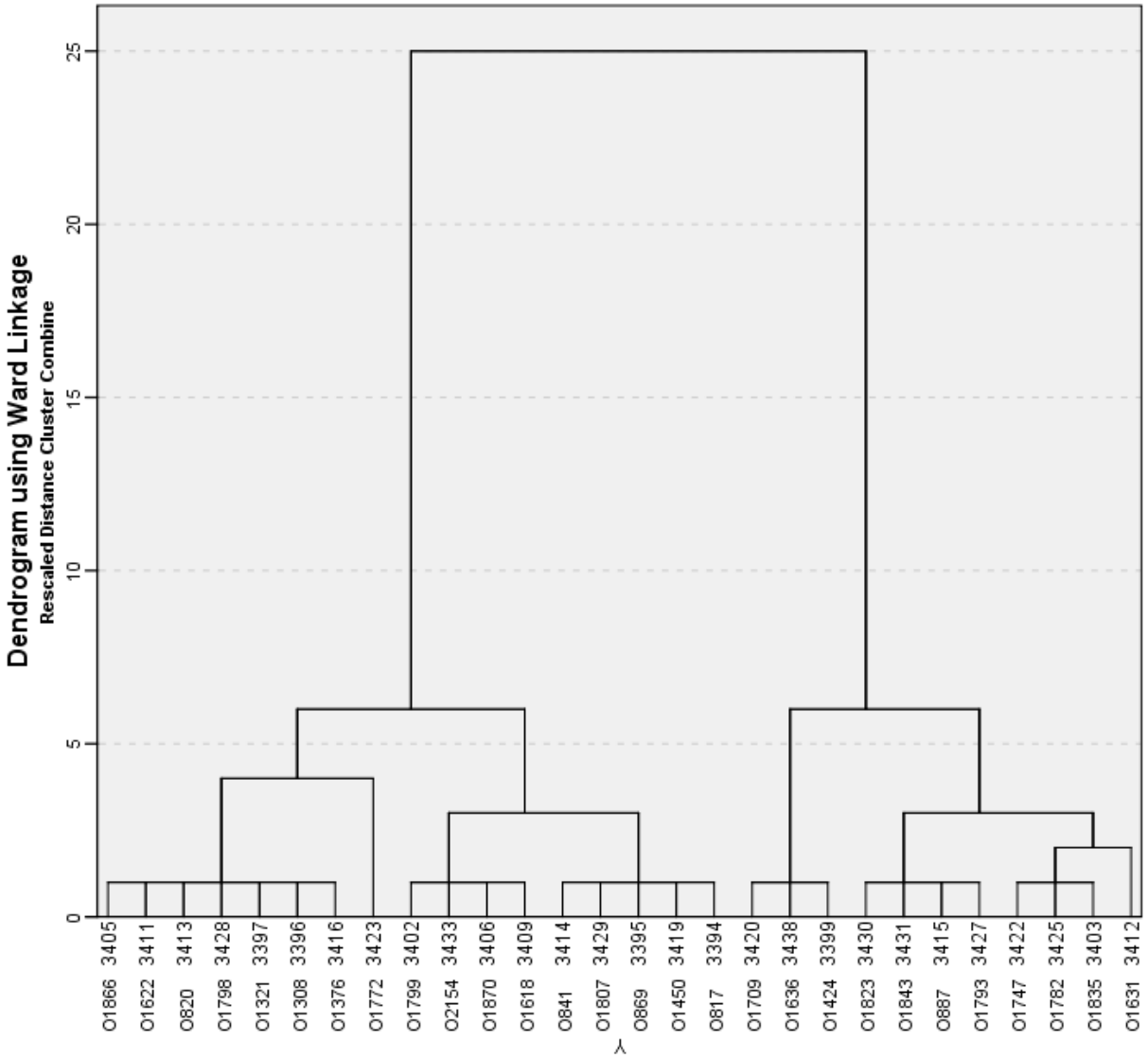

Figure 27 - Dendrogram output from hierarchical cluster analysis for the left mandibular central incisor for the pooled sex sample at Oakington.

Oakington, male comparisons only

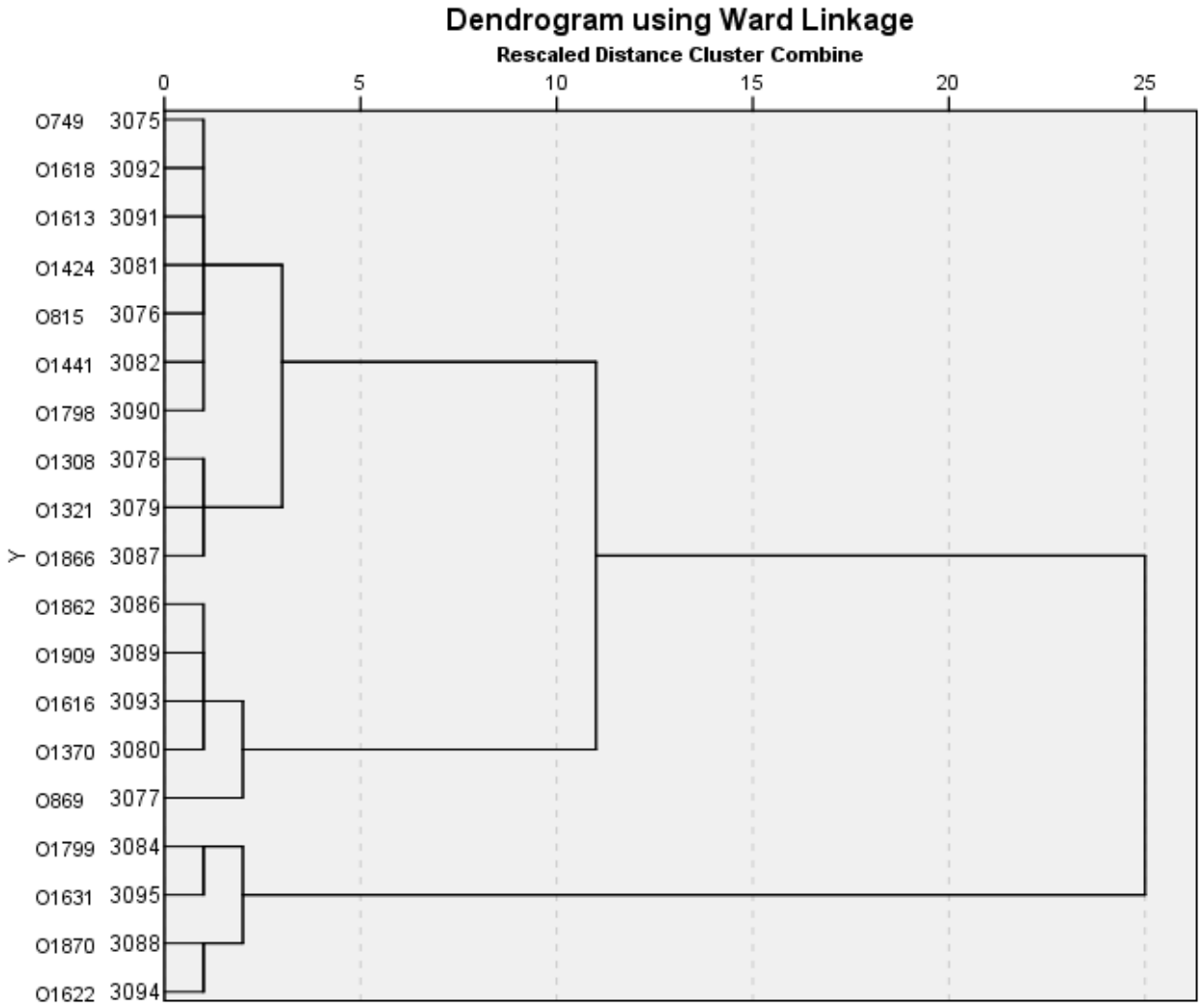

Figure 28 - Dendrogram output from hierarchical cluster analysis for the left mandibular canine for the male sample at Oakington.

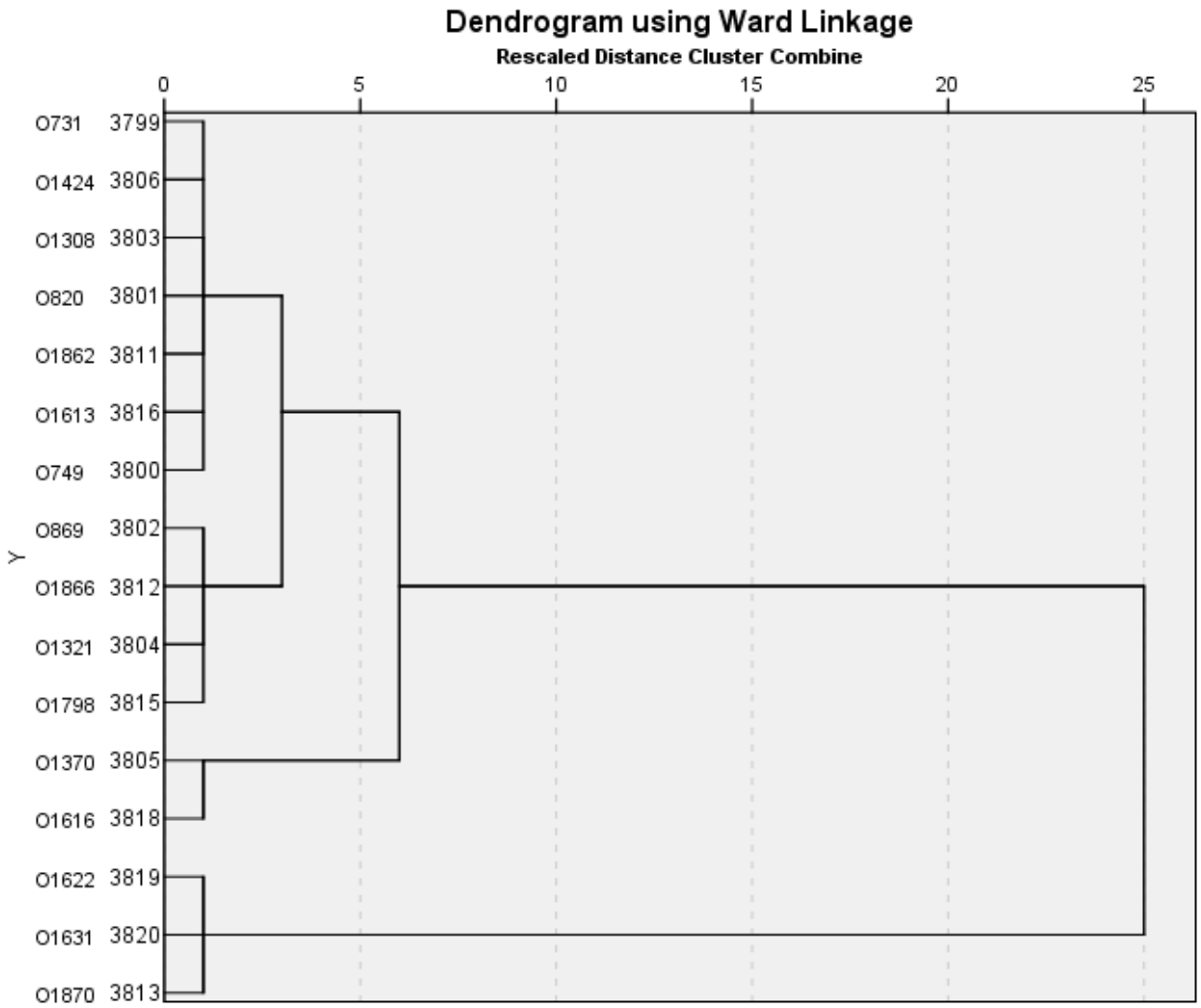

Figure 29 - Dendrogram output from hierarchical cluster analysis for the right mandibular canine for the male sample at Oakington.

Oakington, female comparisons only

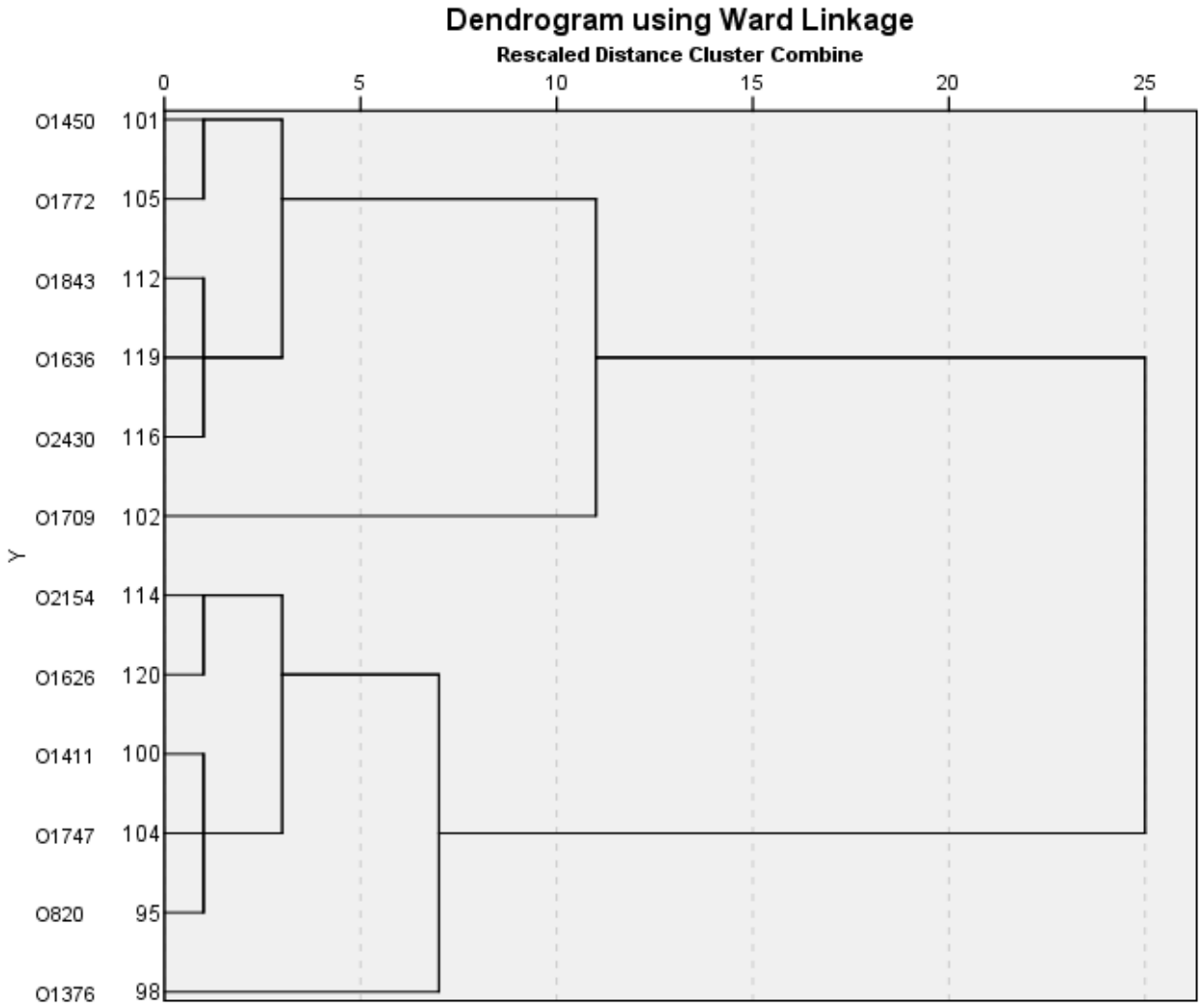

Figure 30 - Dendrogram output from hierarchical cluster analysis for the right maxillary third molar for the female sample at Oakington.

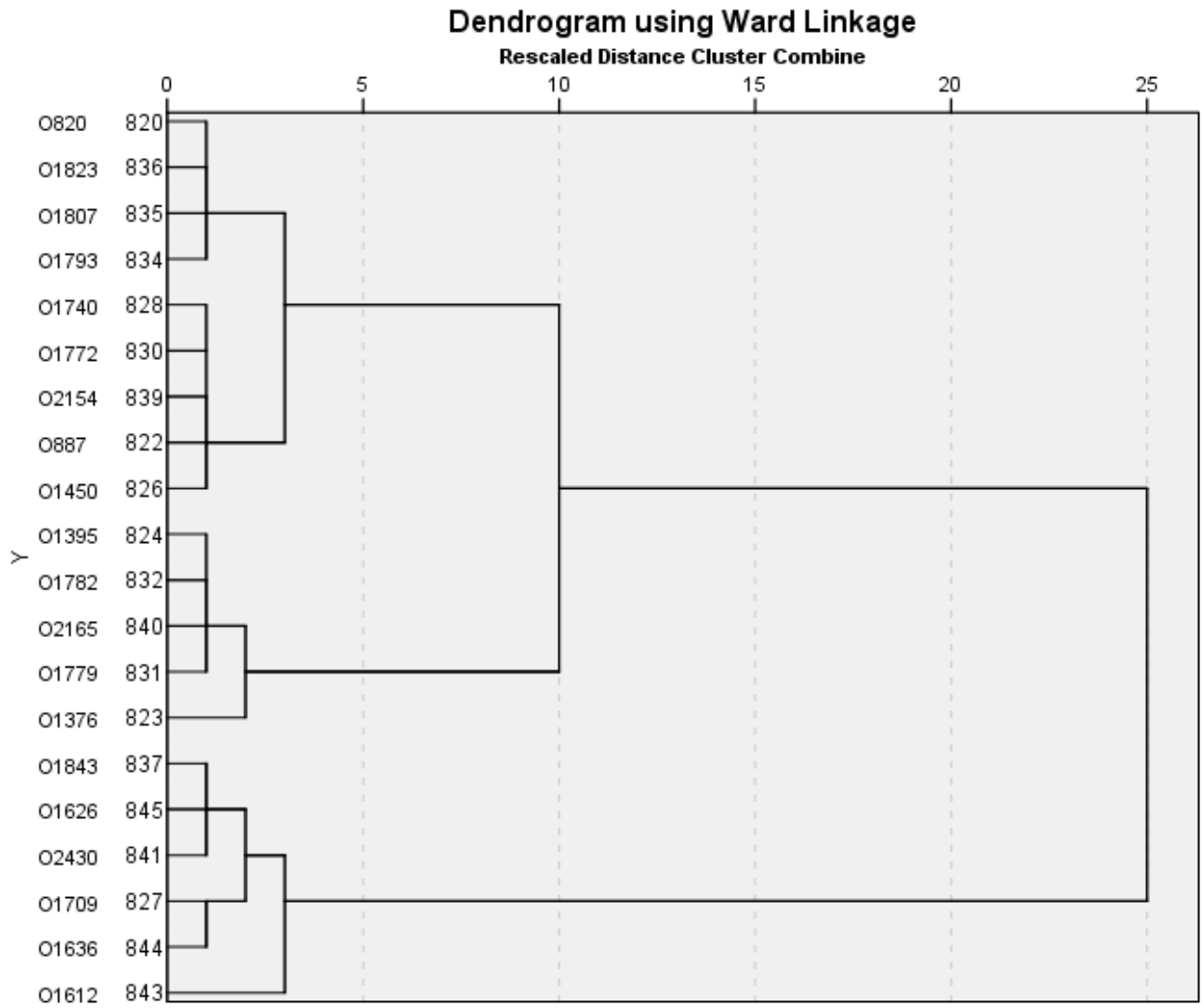

Figure 31 - Dendrogram output from hierarchical cluster analysis for the right maxillary canine for the female sample at Oakington.

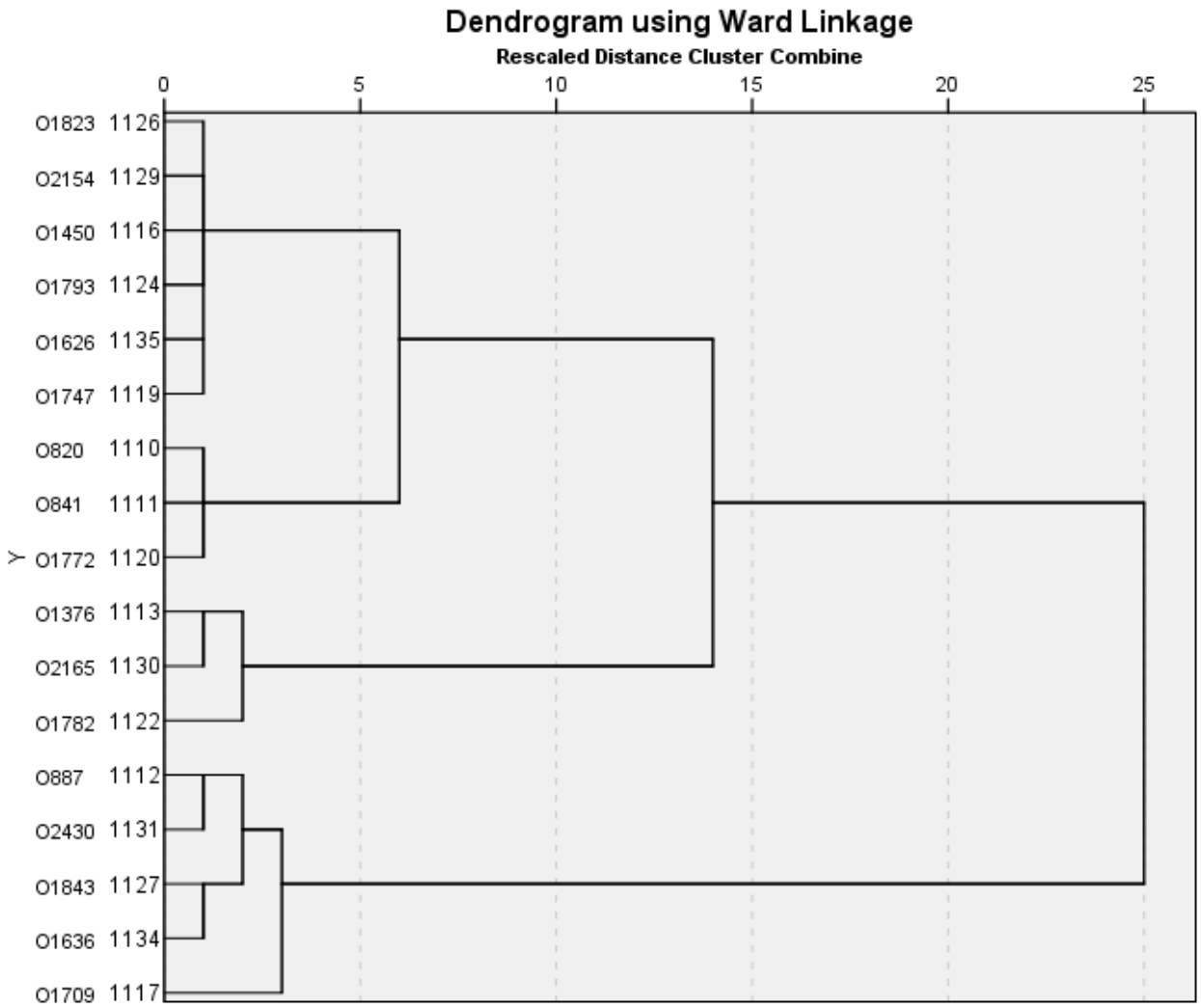

Figure 32 - Dendrogram output from hierarchical cluster analysis for the right maxillary central incisor for the female sample at Oakington.

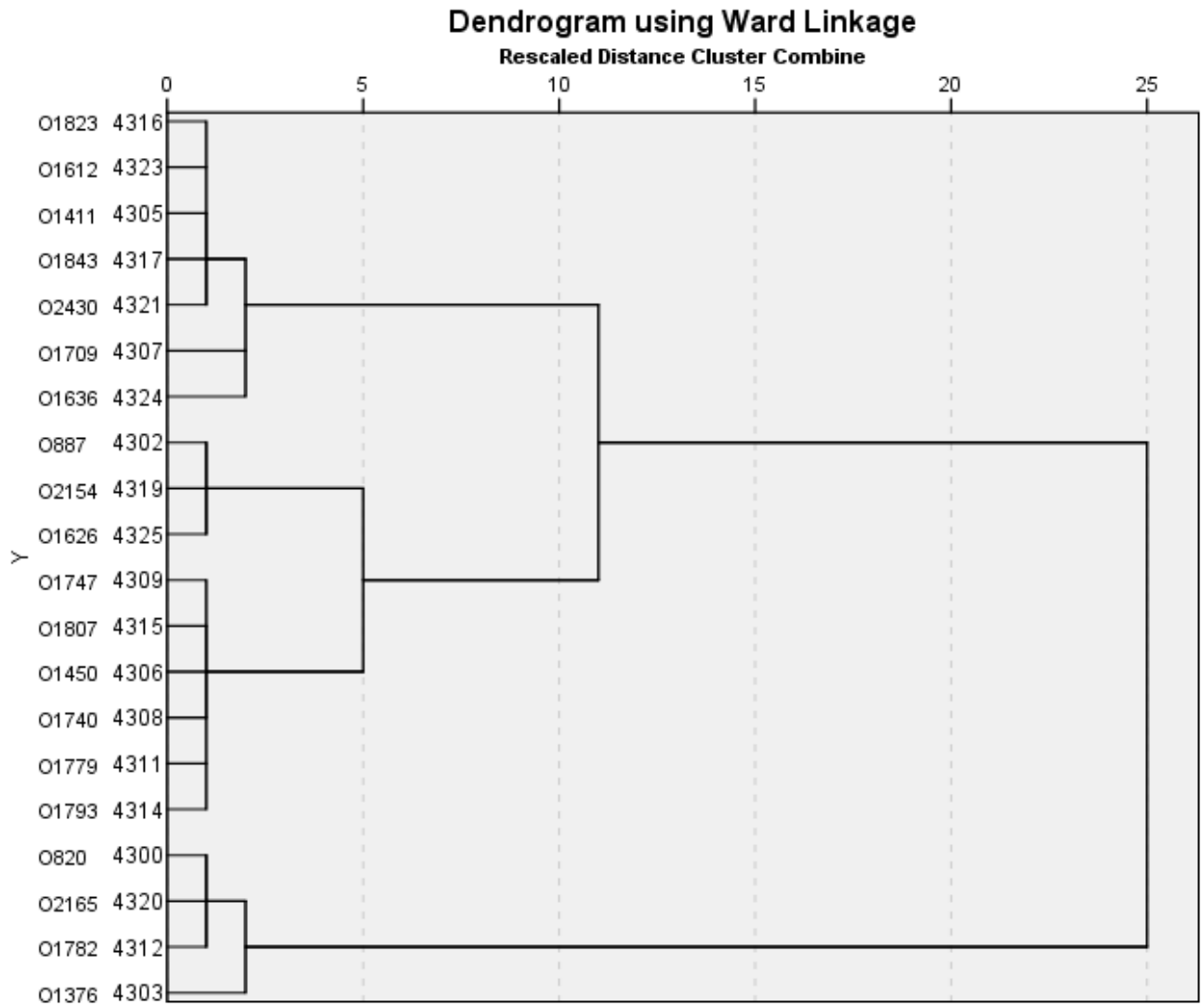

Figure 33 - Dendrogram output from hierarchical cluster analysis for the right mandibular first molar for the female sample at Oakington.

Polhill, pooled sex comparisons

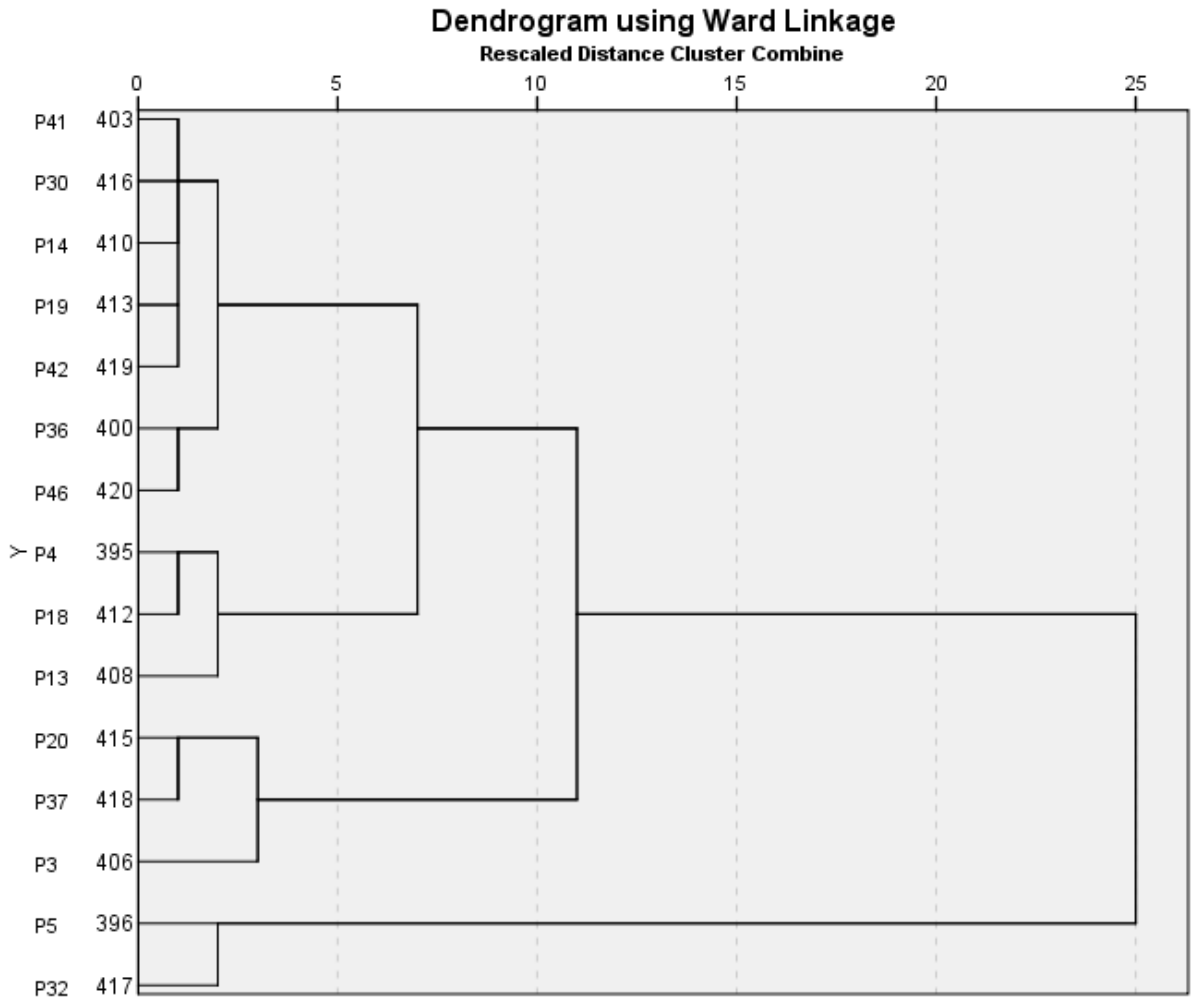

Figure 34 - Dendrogram output from hierarchical cluster analysis for the right maxillary first molar for the pooled sex sample at Polhill.

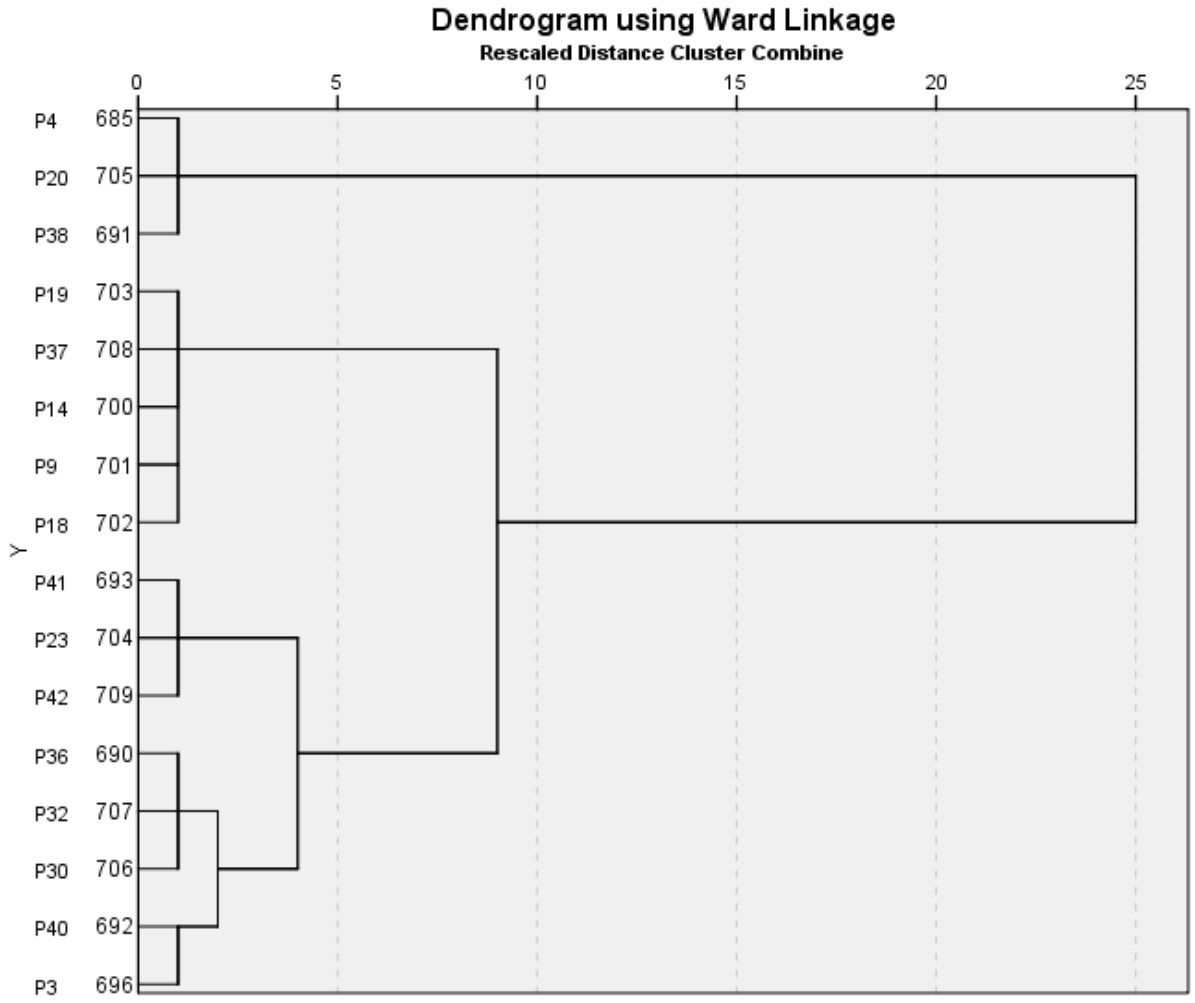

Figure 35 - Dendrogram output from hierarchical cluster analysis for the right maxillary first premolar for the pooled sex sample at Polhill.

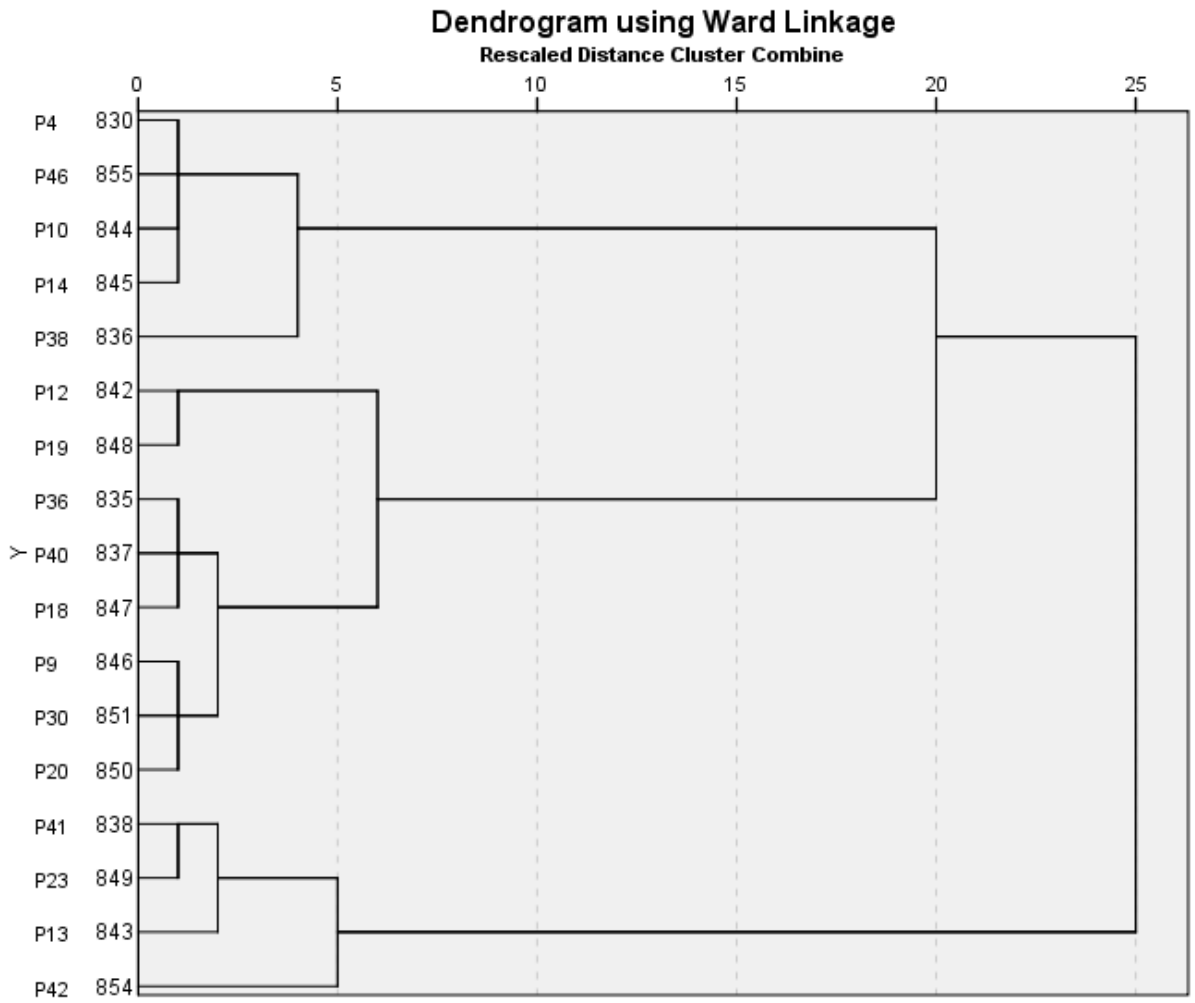

Figure 36 - Dendrogram output from hierarchical cluster analysis for the right maxillary canine for the pooled sex sample at Polhill.

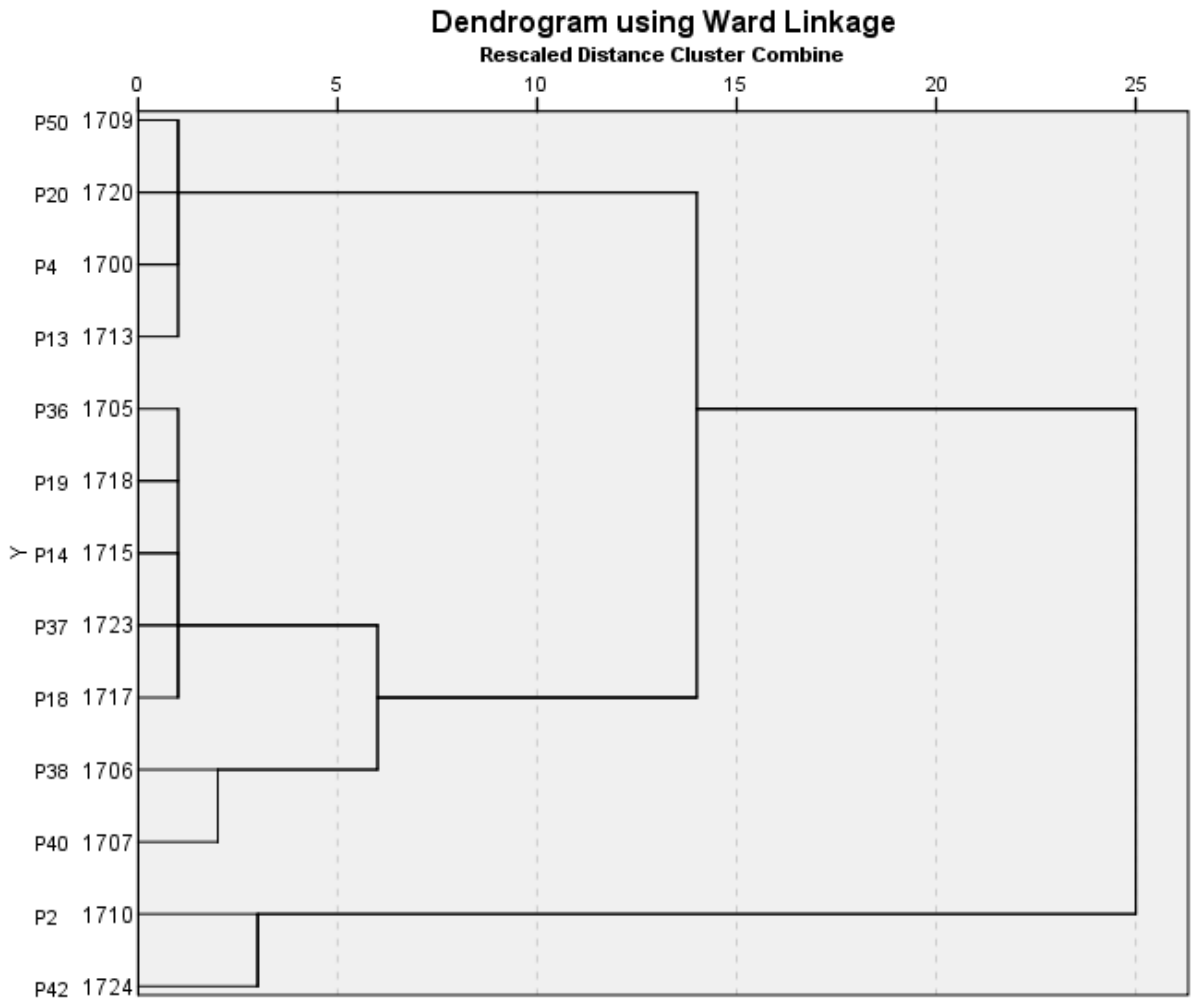

Figure 37 - Dendrogram output from hierarchical cluster analysis for the left maxillary first premolar for the pooled sex sample at Polhill.

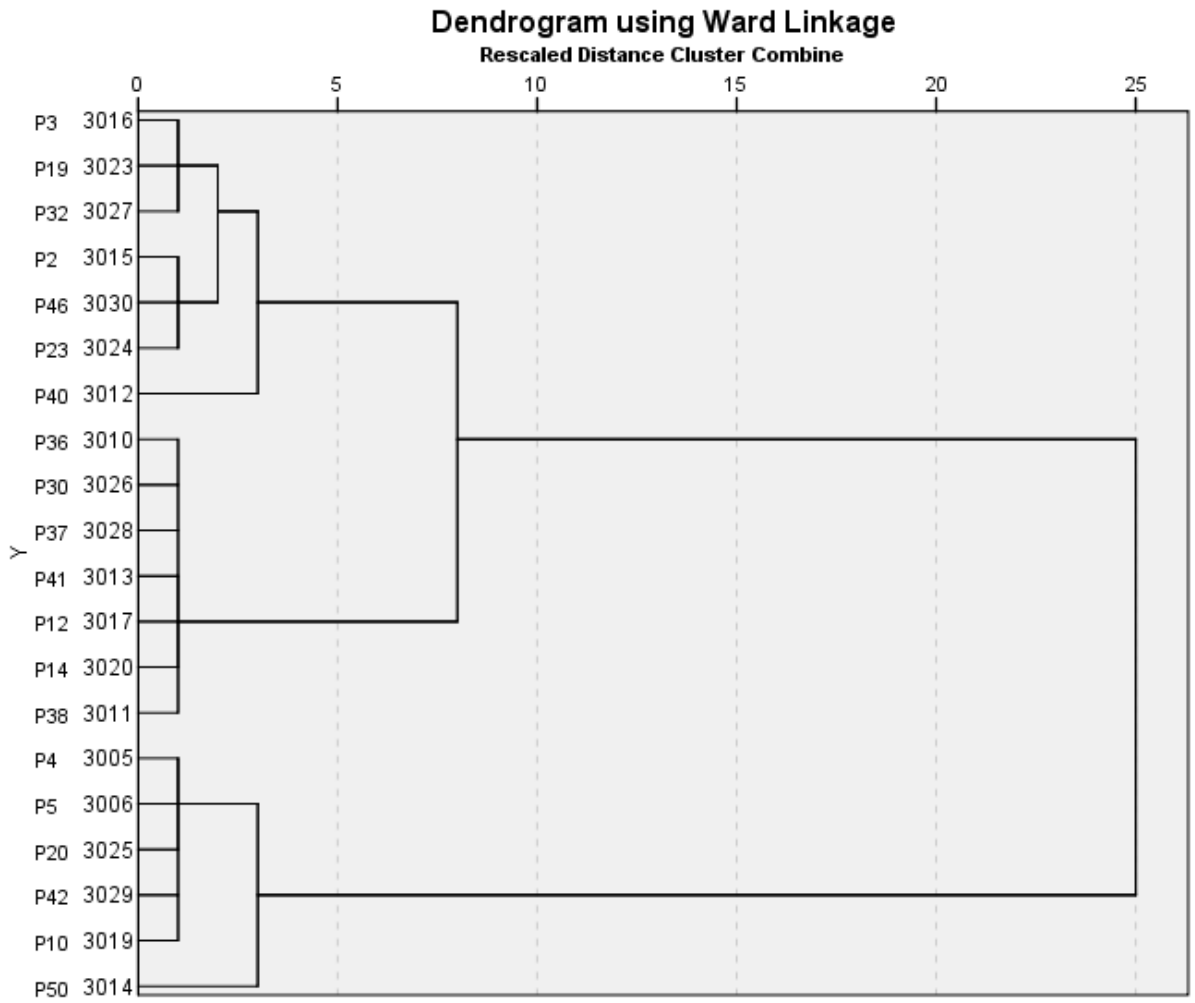

Figure 38 - Dendrogram output from hierarchical cluster analysis for the left mandibular first premolar for the pooled sex sample at Polhill.

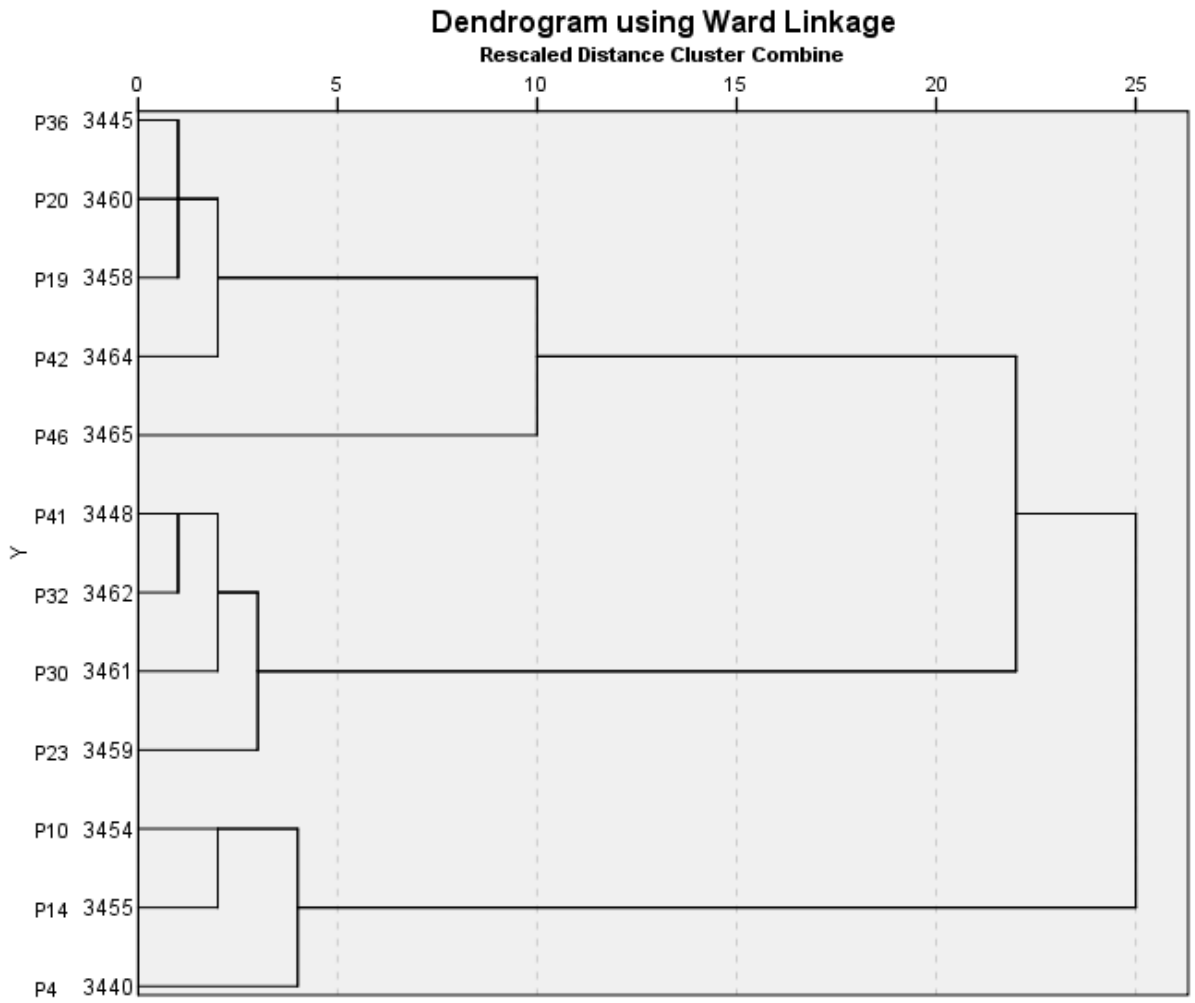

Figure 39 - Dendrogram output from hierarchical cluster analysis for the left mandibular central incisor for the pooled sex sample at Polhill.

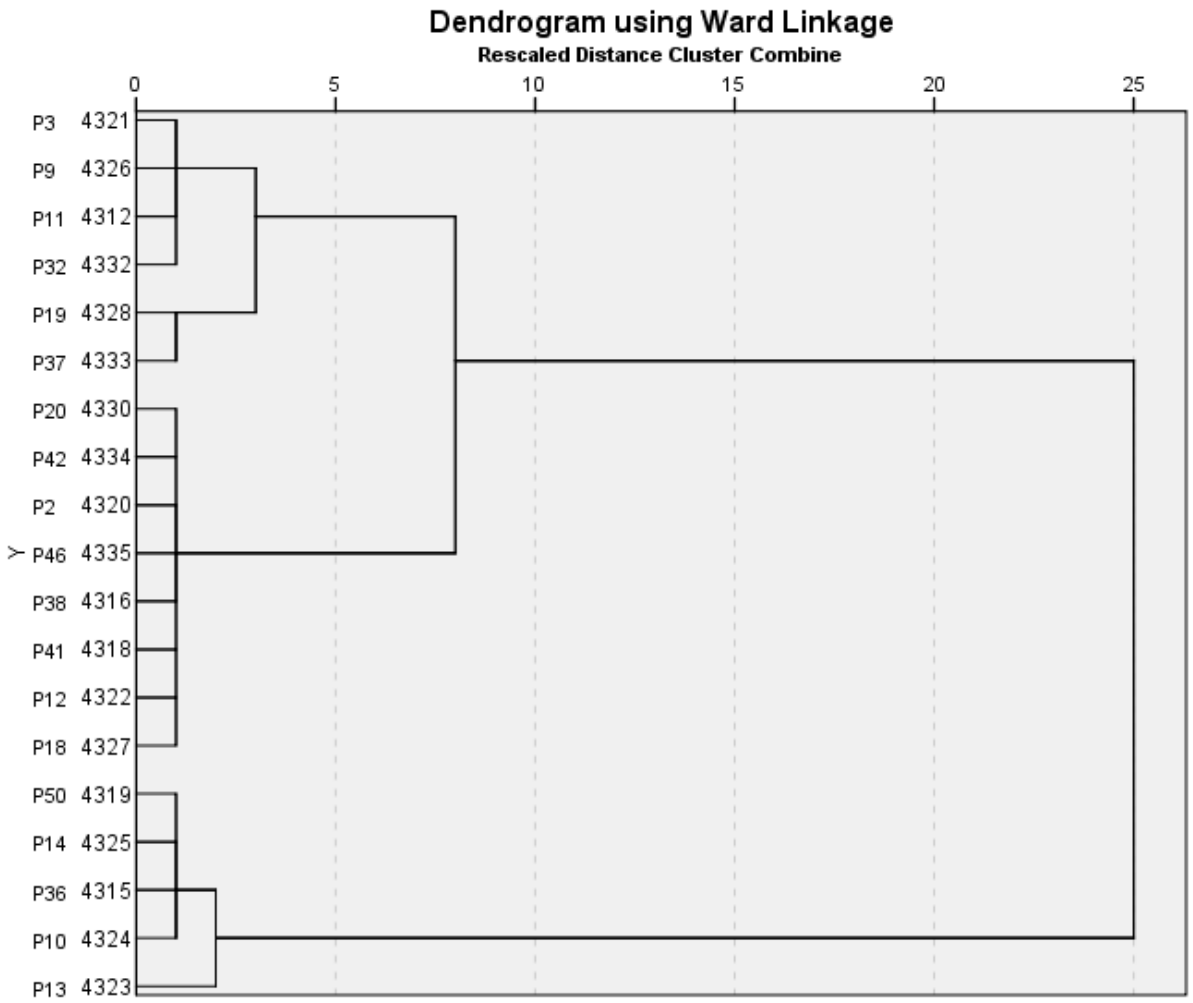

Figure 40 - Dendrogram output from hierarchical cluster analysis for the right mandibular first molar for the pooled sex sample at Polhill.

Polhill, male comparisons only

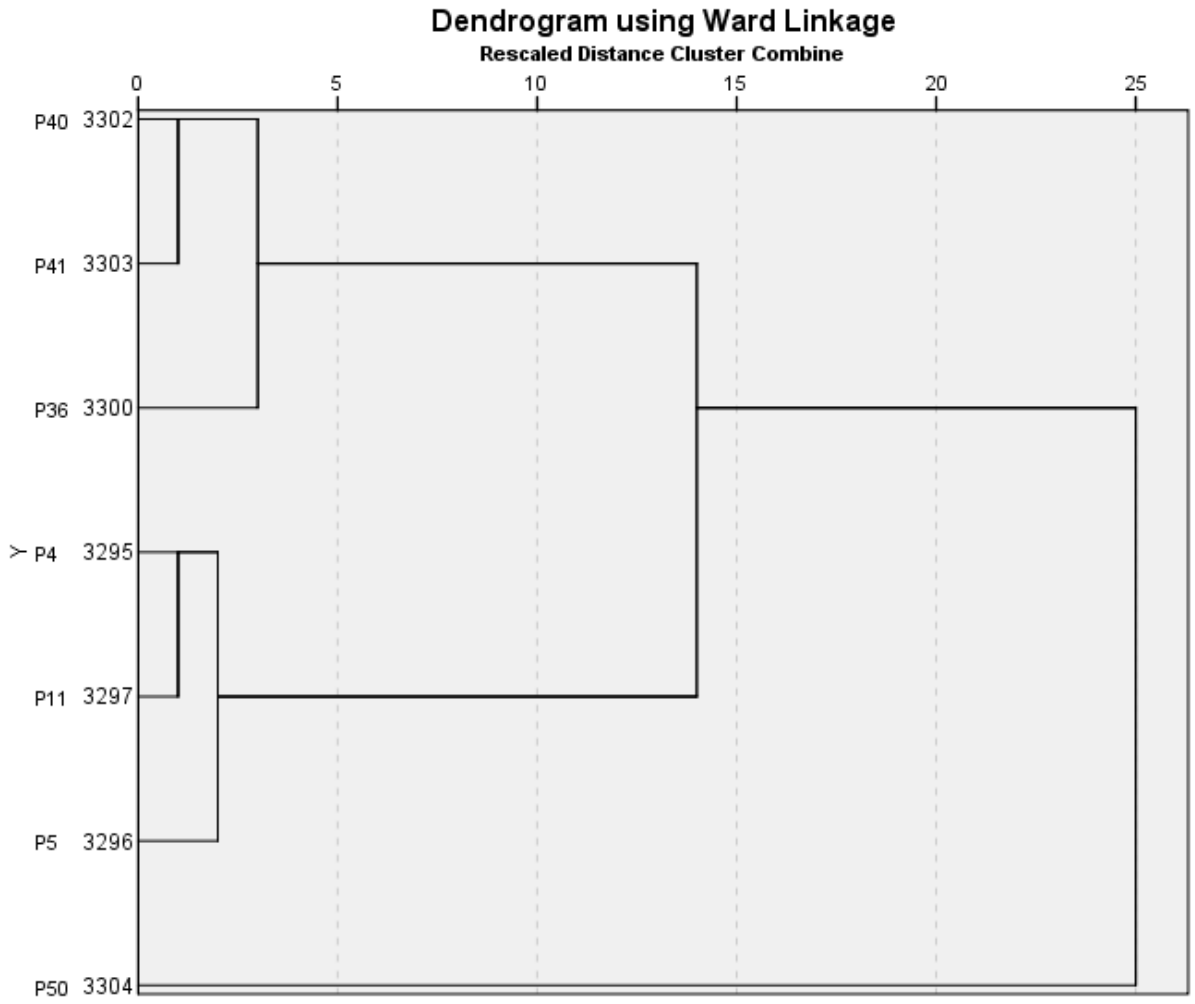

Figure 41 - Dendrogram output from hierarchical cluster analysis for the left mandibular lateral incisor for the male sample at Polhill.

Polhill, female comparisons only

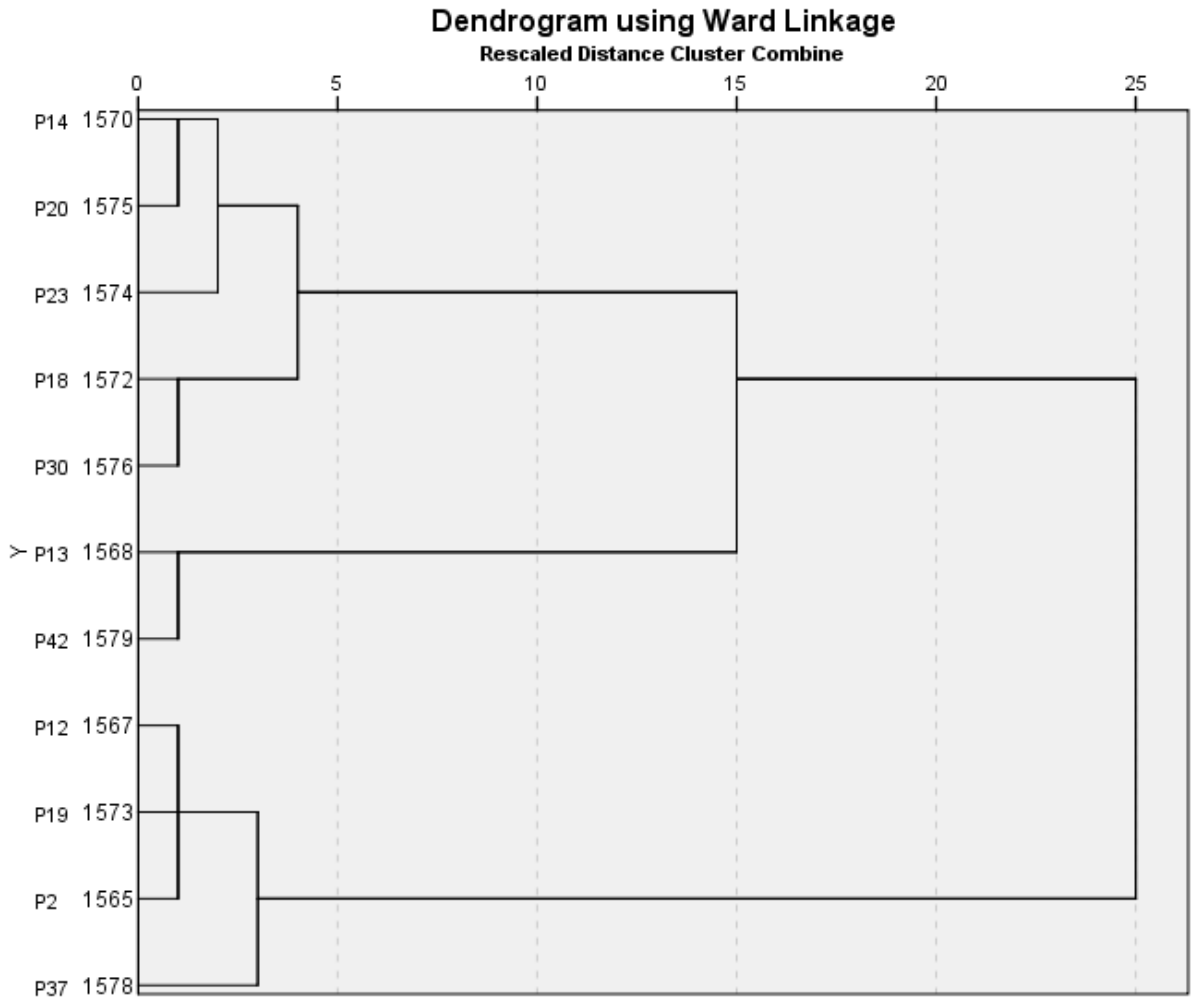

Figure 42 - Dendrogram output from hierarchical cluster analysis for the left maxillary canine for the female sample at Polhill.

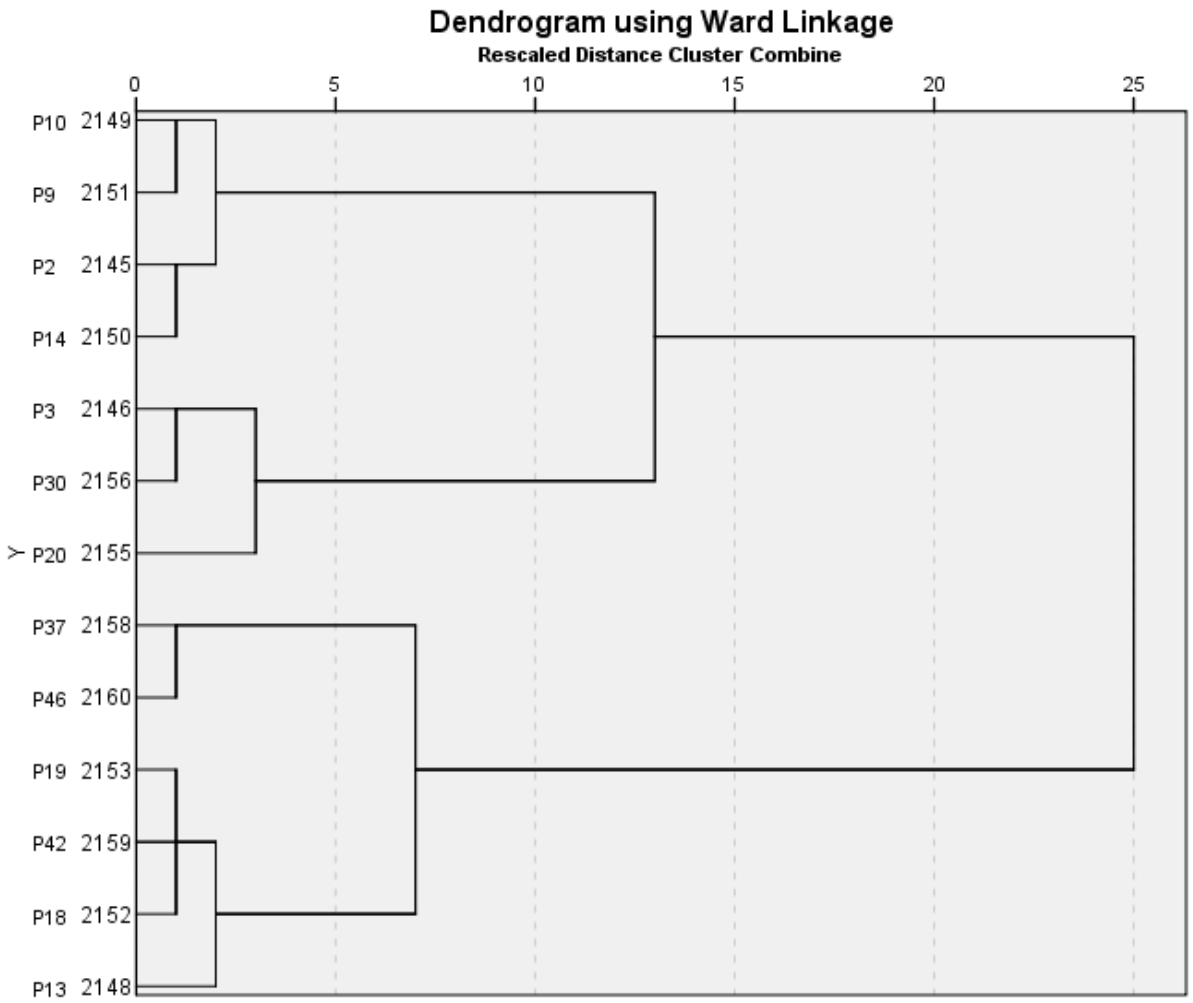

Figure 43 - Dendrogram output from hierarchical cluster analysis for the left maxillary second molar for the female sample at Polhill.

Eastry, pooled sex comparisons

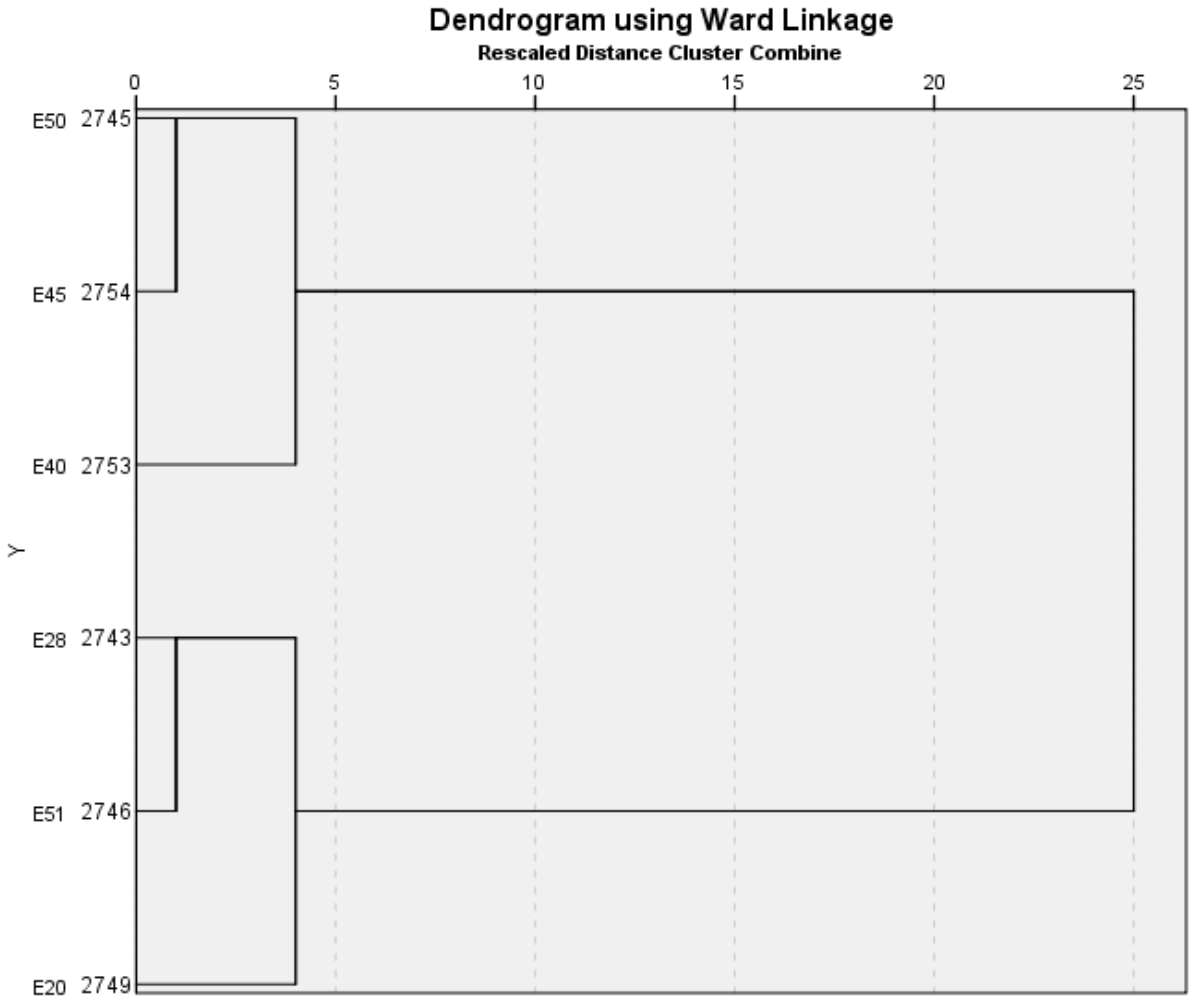

Figure 44 - Dendrogram output from hierarchical cluster analysis for the left mandibular first molar for the pooled sex sample at Eastry.

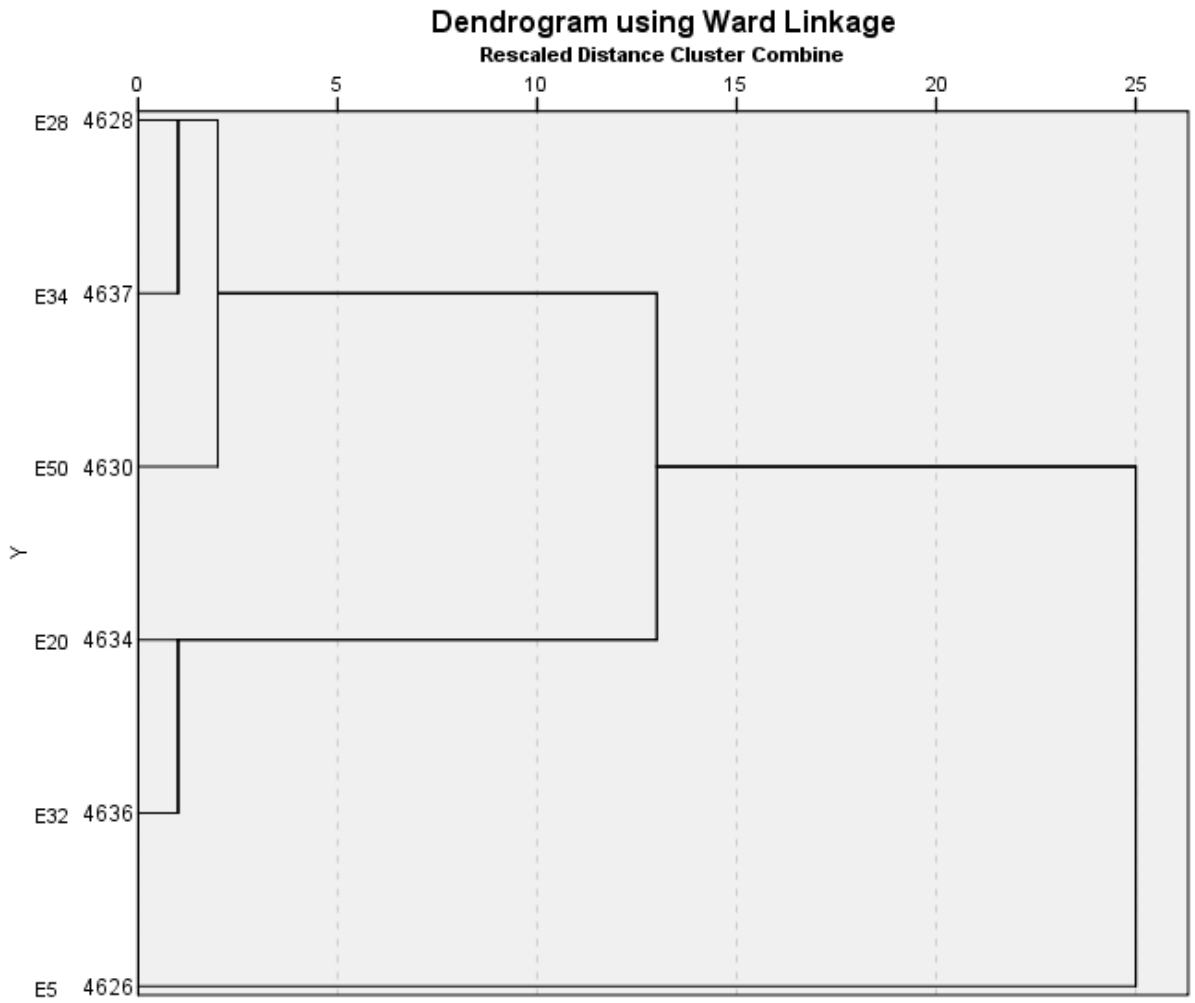

Figure 45 - Dendrogram output from hierarchical cluster analysis for the right mandibular third molar for the pooled sex sample at Eastry.

Eastry, male comparisons only

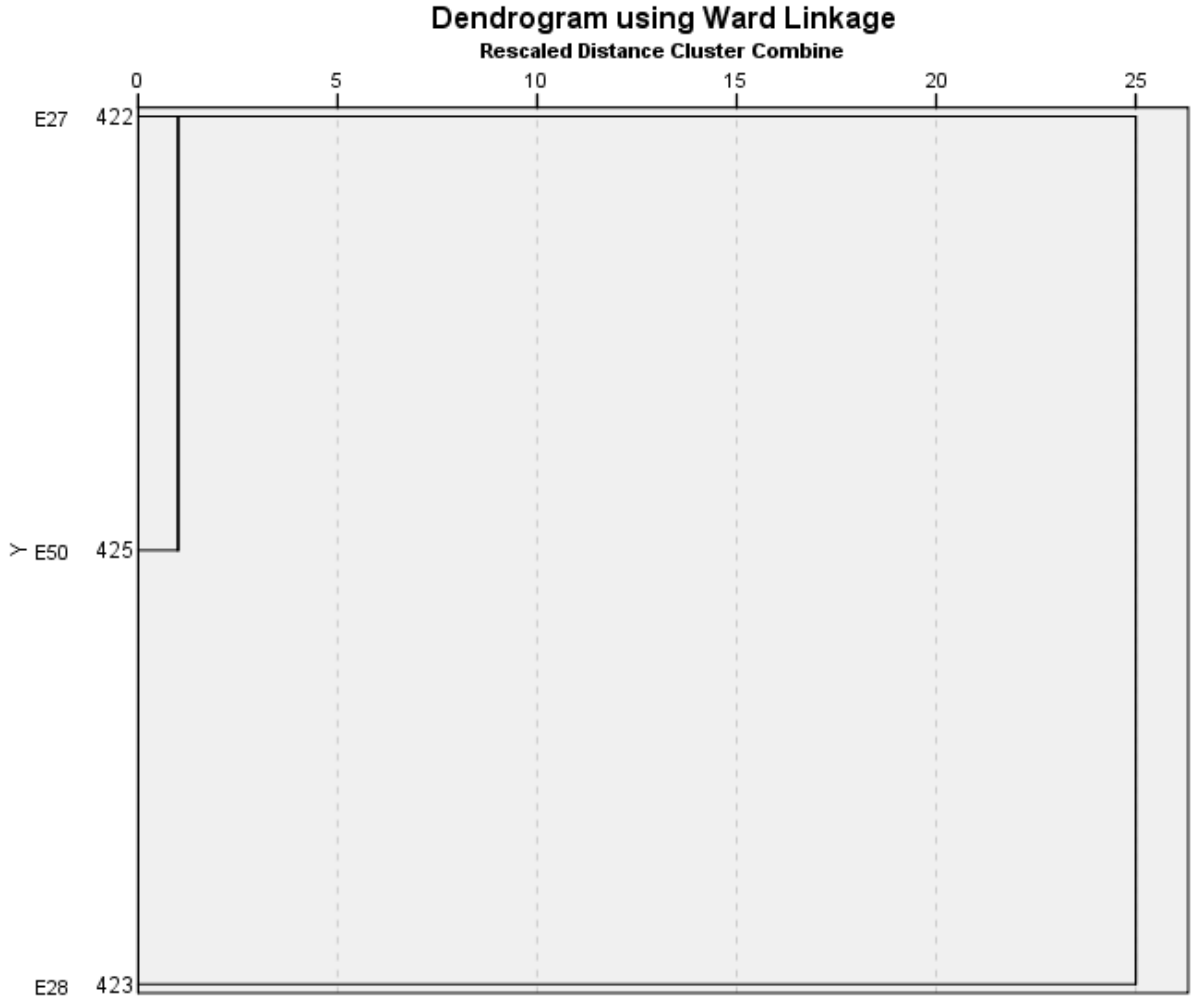

Figure 46 - Dendrogram output from hierarchical cluster analysis for the right maxillary first molar for the male sample at Eastry.

Eastry, female comparisons only

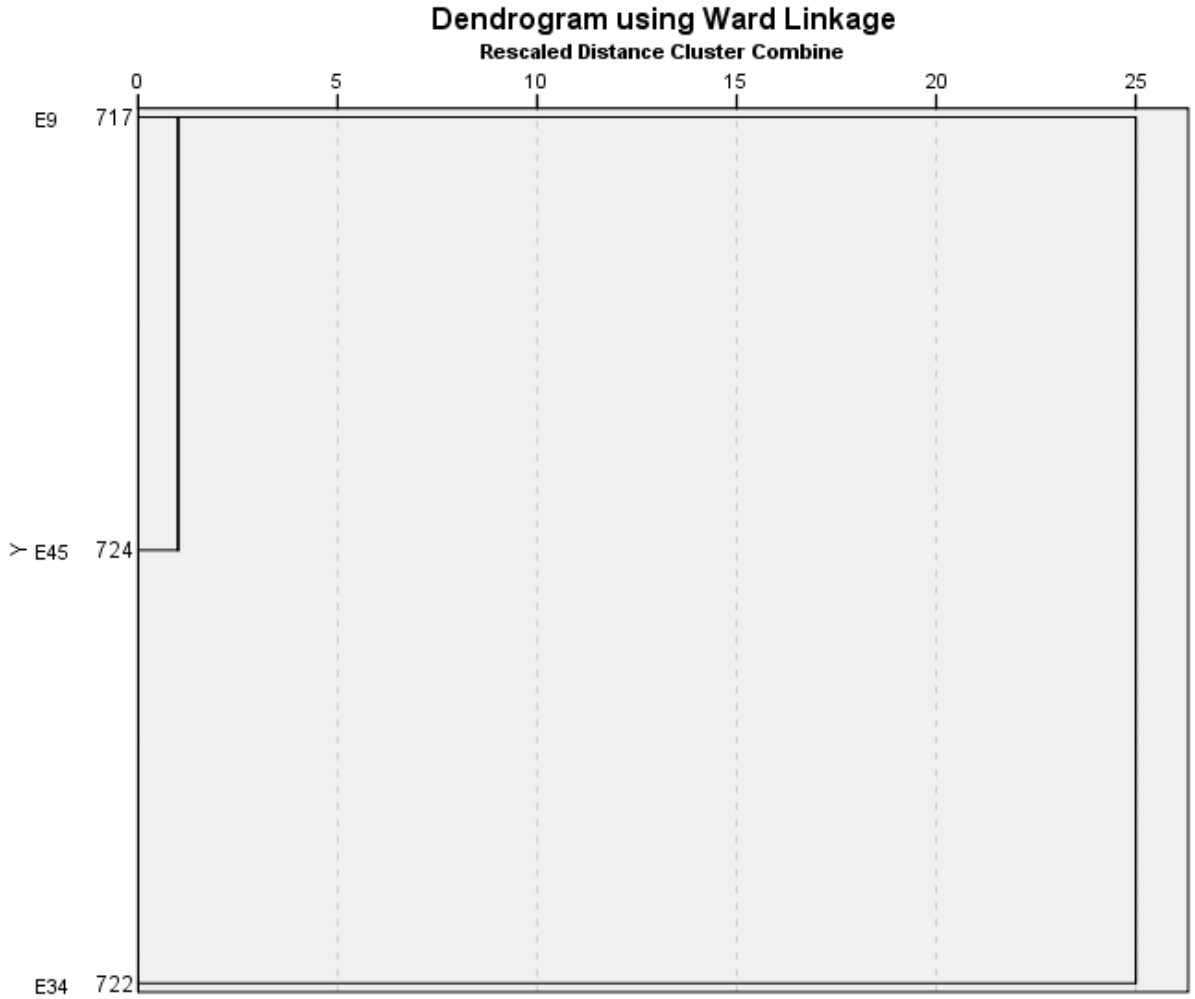

Figure 47 - Dendrogram output from hierarchical cluster analysis for the right maxillary first premolar for the female sample at Eastry.

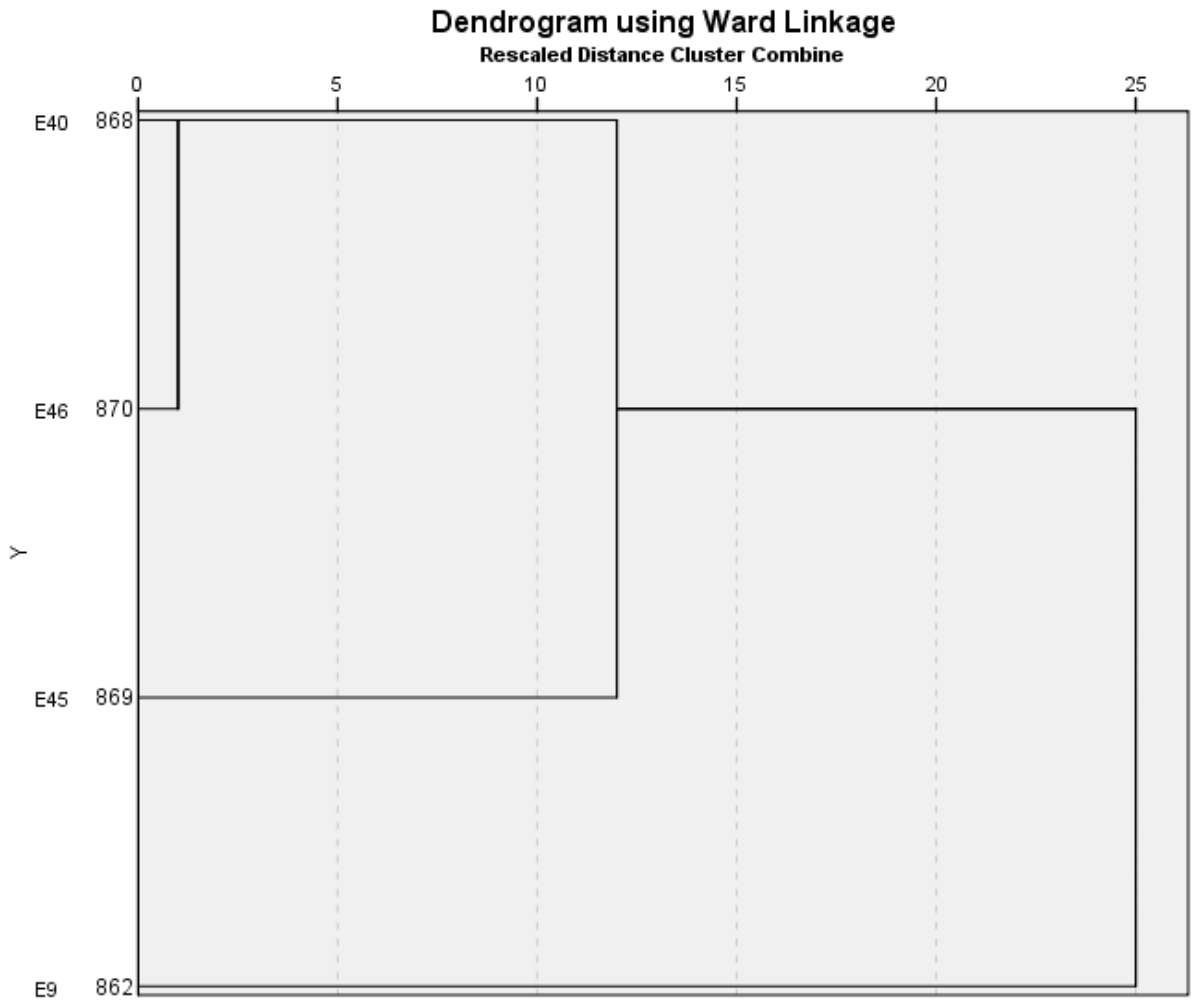

Figure 48 - Dendrogram output from hierarchical cluster analysis for the right maxillary canine for the female sample at Eastry.

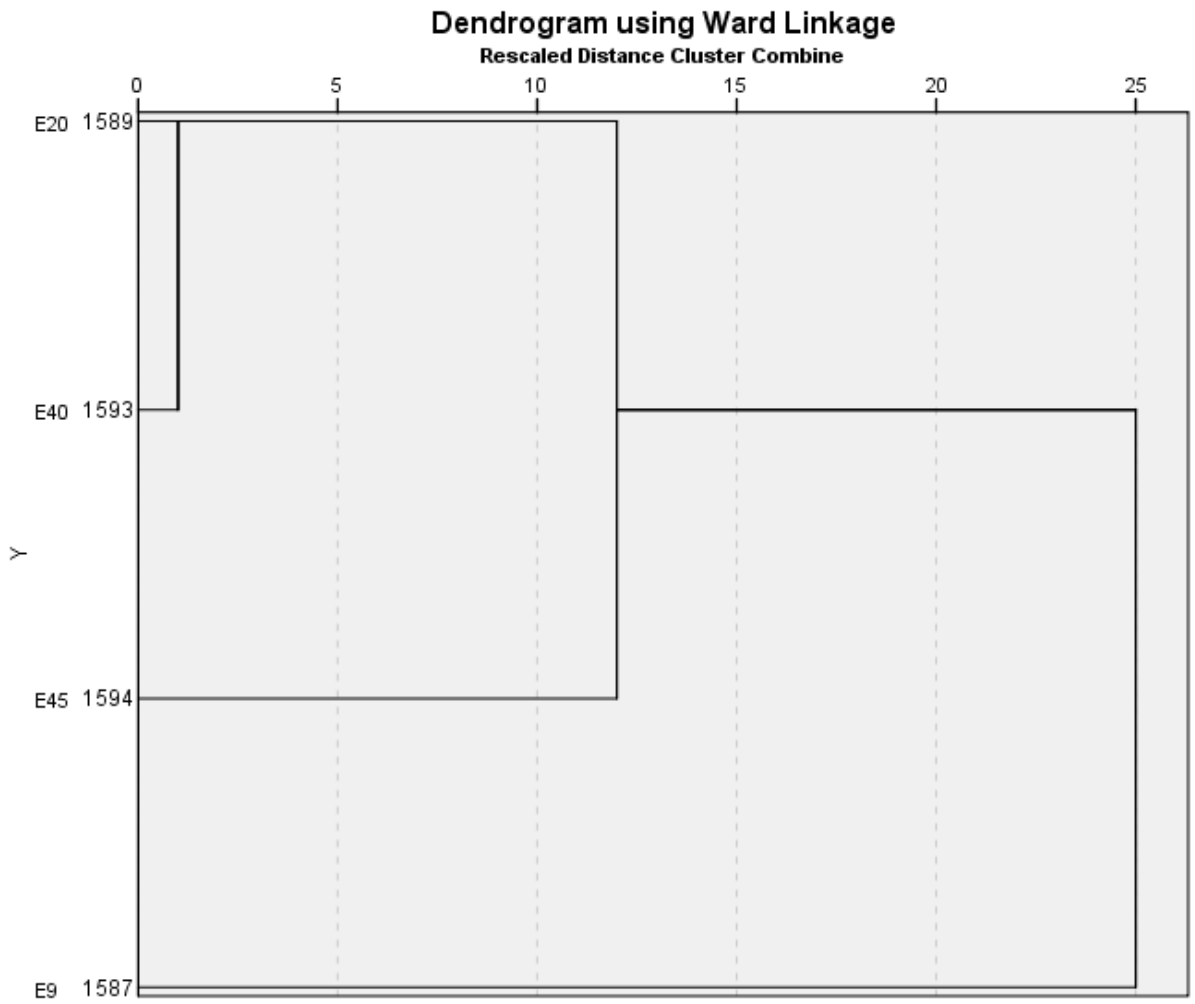

Figure 49 - Dendrogram output from hierarchical cluster analysis for the left maxillary canine for the female sample at Eastry.

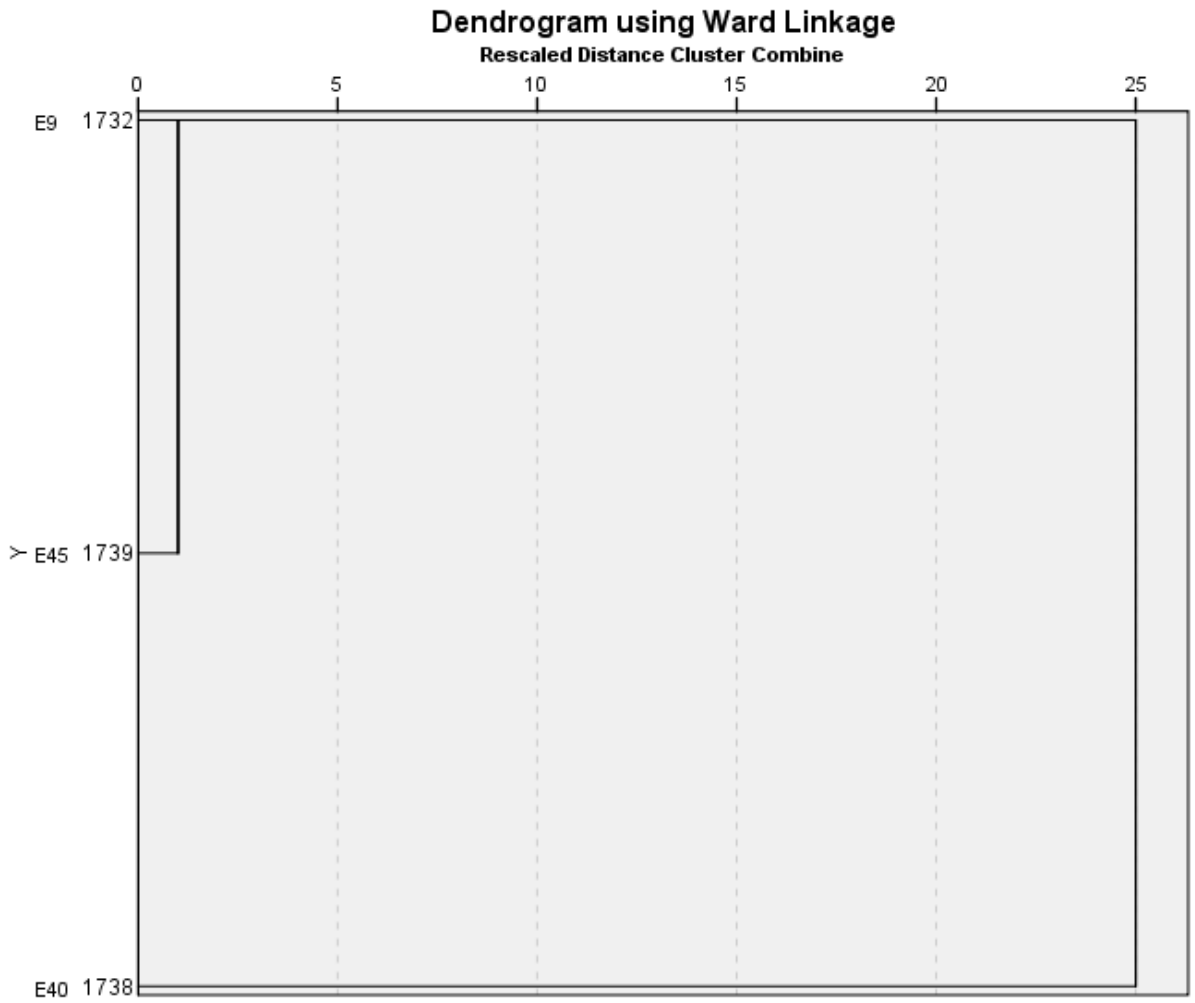

Figure 50 - Dendrogram output from hierarchical cluster analysis for the left maxillary first premolar for the female sample at Eastry.

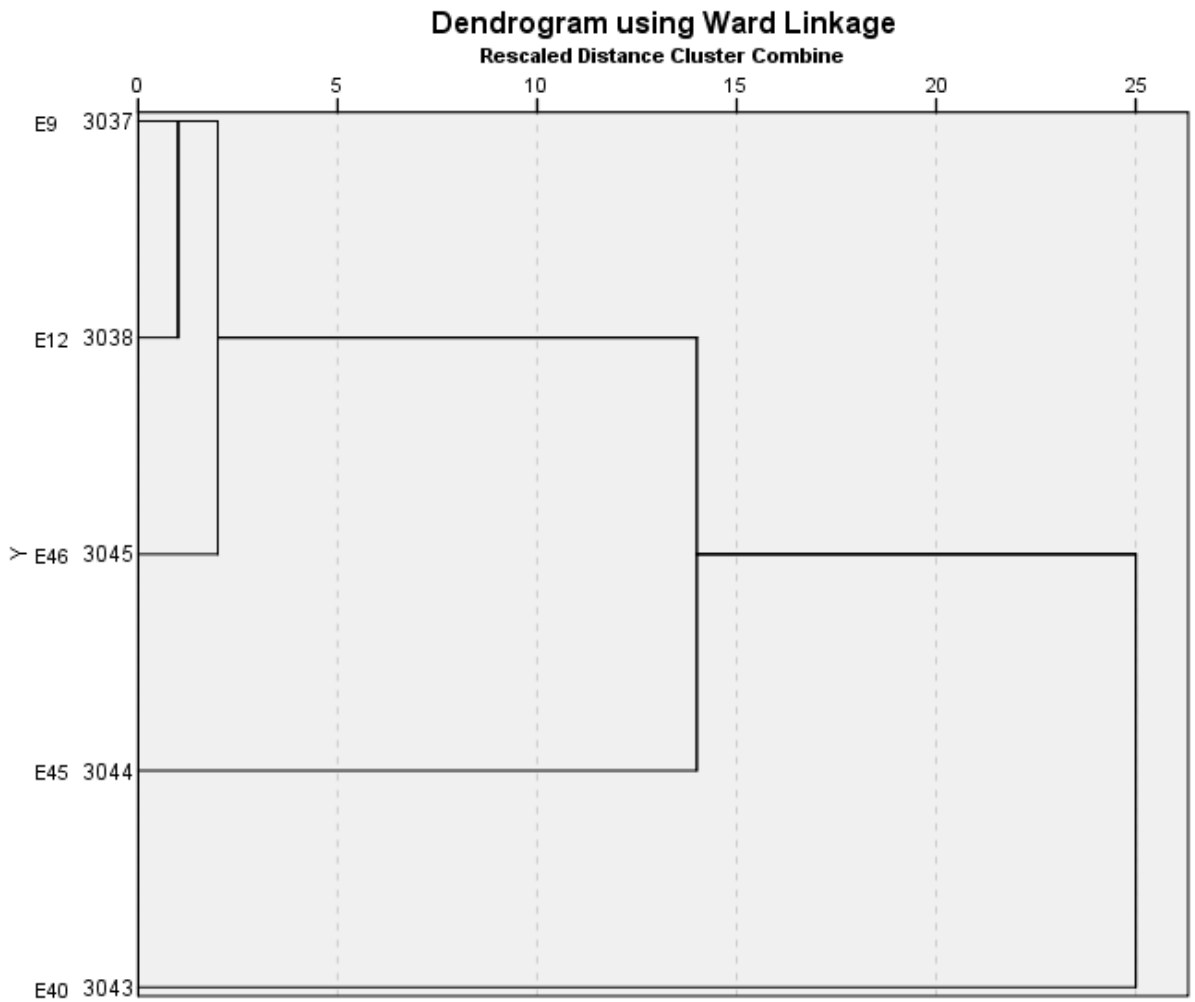

Figure 51 - Dendrogram output from hierarchical cluster analysis for the left mandibular first premolar for the female sample at Eastry.

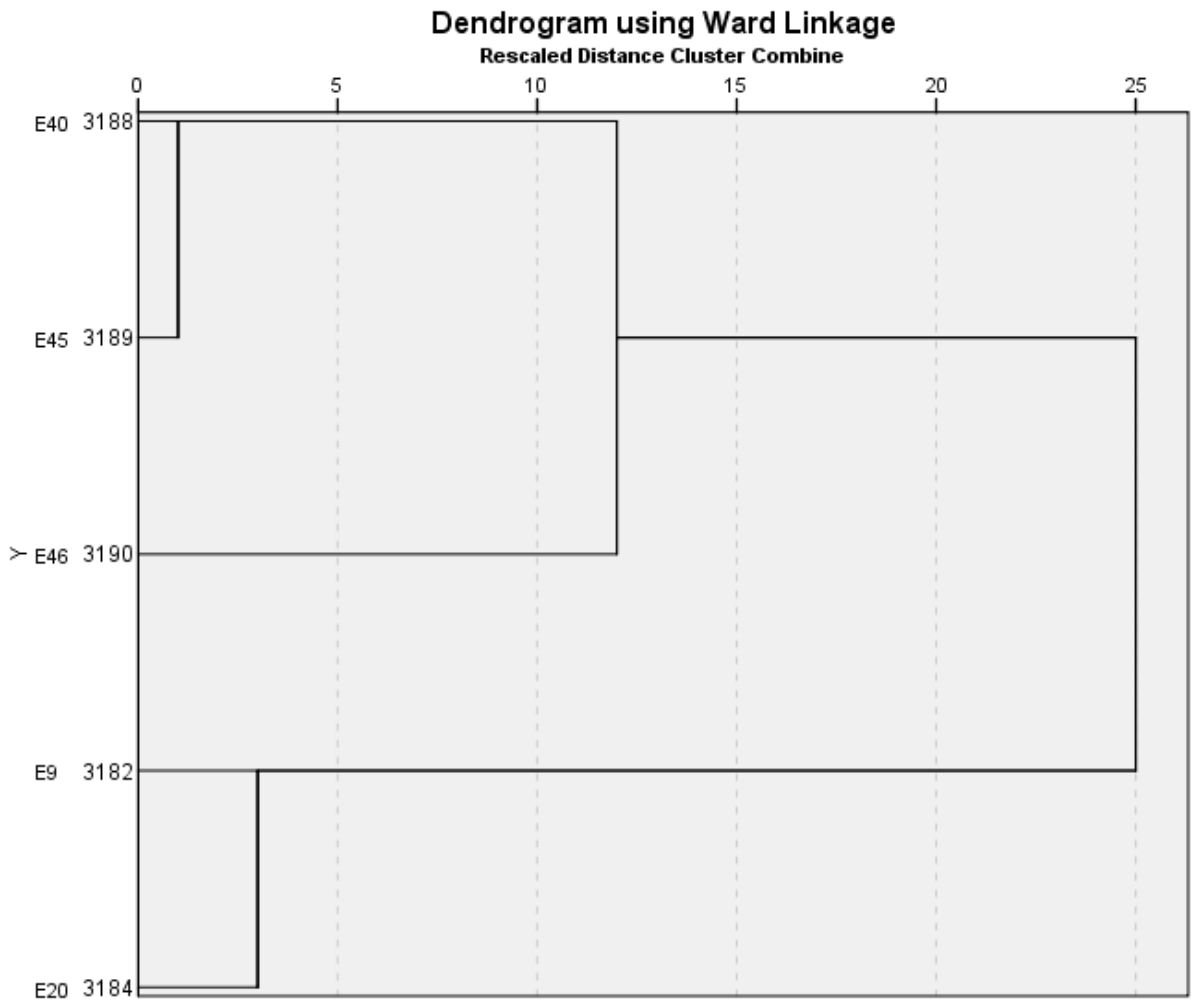

Figure 52 - Dendrogram output from hierarchical cluster analysis for the left mandibular canine for the female sample at Eastry.

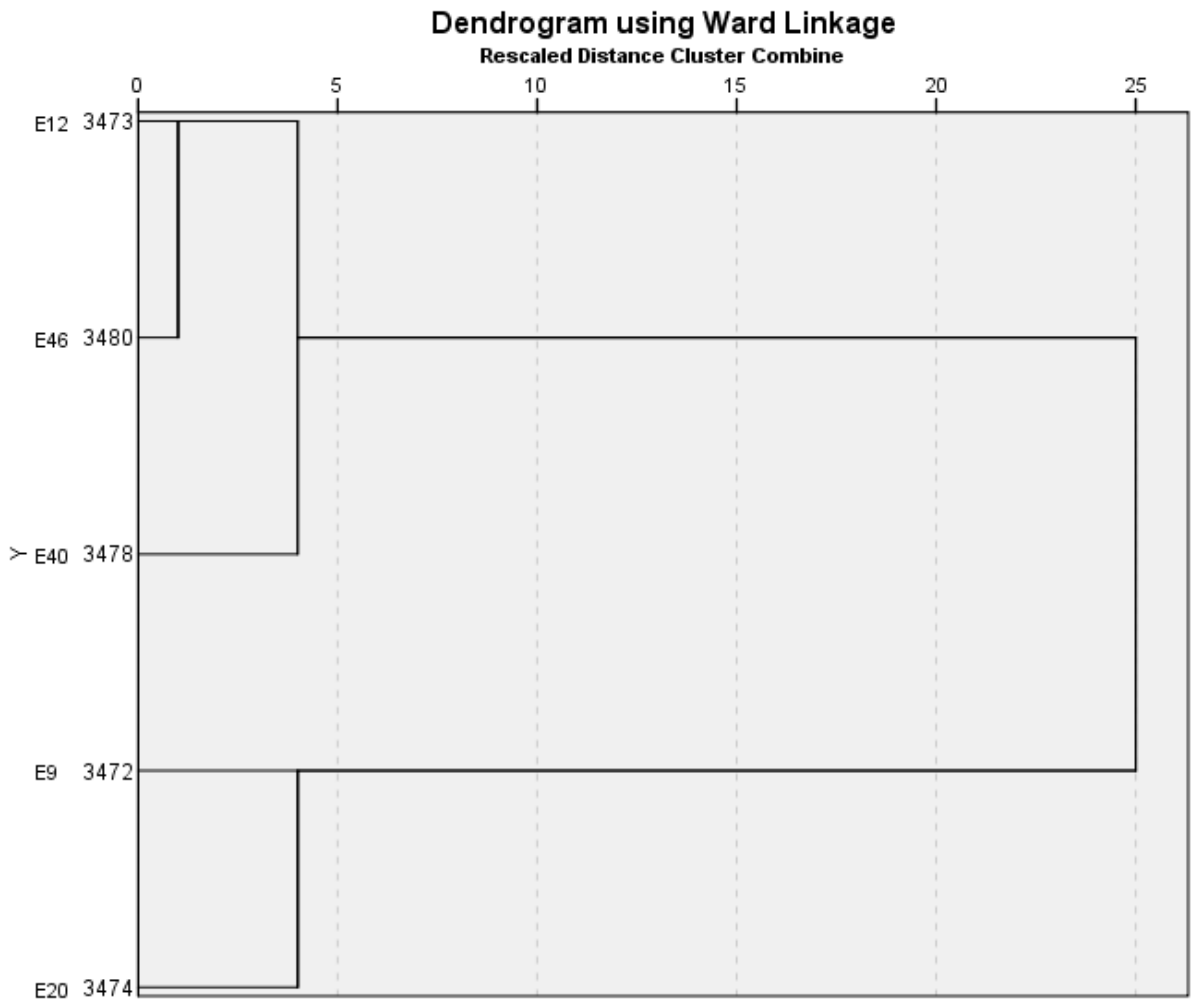

Figure 53 - Dendrogram output from hierarchical cluster analysis for the left mandibular central incisor for the female sample at Eastry.

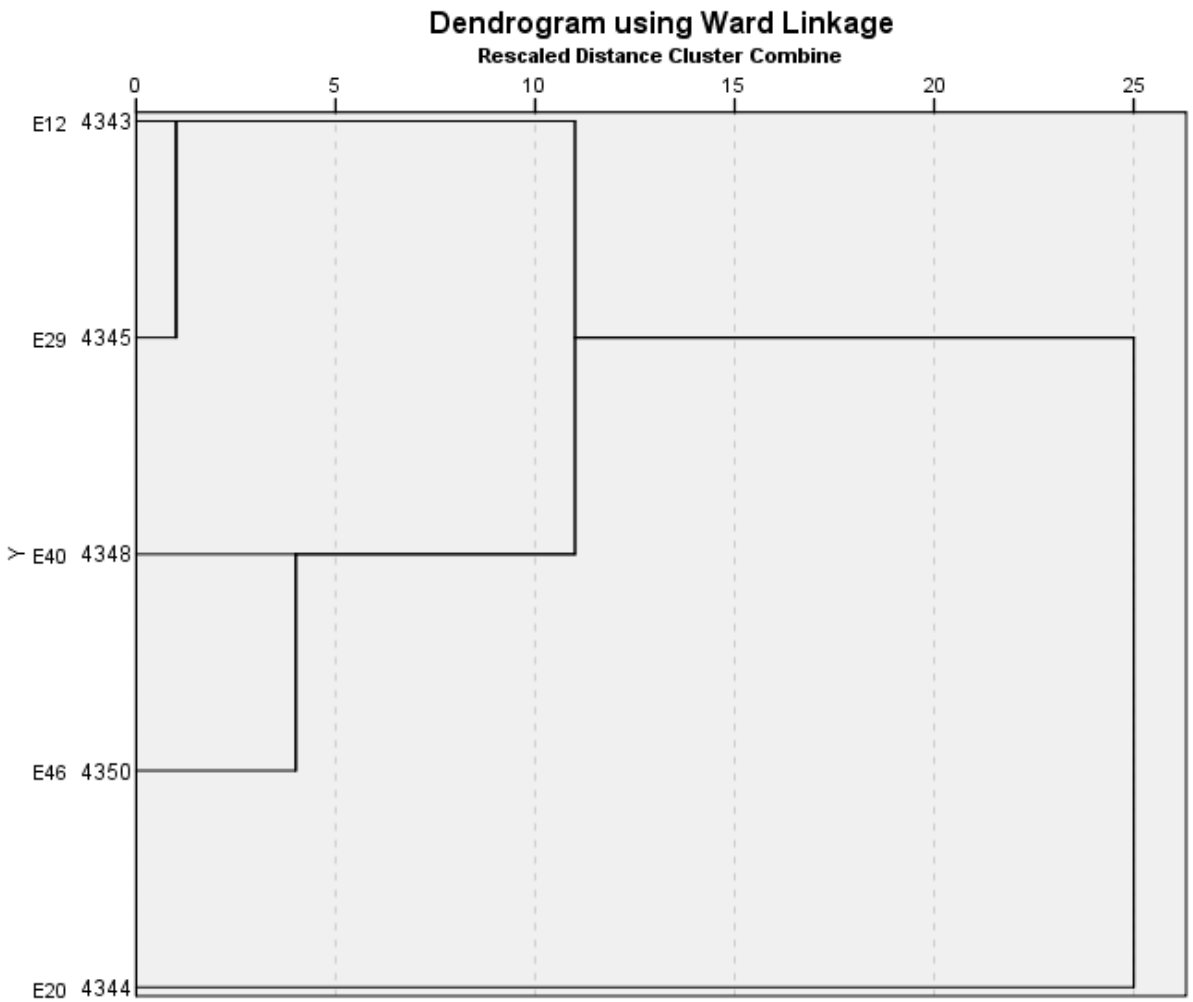

Figure 54 - Dendrogram output from hierarchical cluster analysis for the right mandibular first molar for the female sample at Eastry.

Appendix 8: Ethical Approval

4 August 2015

Duncan Sayer / Allison Card
School of Forensic and Allied Sciences
University of Central Lancashire

Dear Duncan / Allison

Re: BAHSS Ethics Committee Application
Unique Reference Number: BAHSS 242

The BAHSS ethics committee has granted approval of your proposal application '**The Use of Teeth for Estimating Biological Similarity in Early Medieval Skeletal Assemblages**'. Approval is granted up to the end of project date* or for 5 years from the date of this letter, whichever is the longer. It is your responsibility to ensure that

- the project is carried out in line with the information provided in the forms you have submitted
- you regularly re-consider the ethical issues that may be raised in generating and analysing your data
- any proposed amendments/changes to the project are raised with, and approved, by Committee
- you notify roffice@uclan.ac.uk if the end date changes or the project does not start
- serious adverse events that occur from the project are reported to Committee
- a closure report is submitted to complete the ethics governance procedures (Existing paperwork can be used for this purposes e.g. funder's end of grant report; abstract for student award or NRES final report. If none of these are available use e-Ethics Closure Report Proforma).

Additionally, BAHSS ethics committee has listed the following recommendation(s) which it would prefer to be addressed. Please note, however, that the above decision will not be affected should you decide not to address any of these recommendation(s).

Should you decide to make any of these recommended amendments, please forward the amended documentation to roffice@uclan.ac.uk for its records and indicate, by completing the attached grid, which recommendations you have adopted. Please do not resubmit any documentation which you have **not** amended.

Yours sincerely

Colin Murrell
Deputy Vice Chair
BAHSS Ethics Committee

* for research degree students this will be the final lapse date

NB - Ethical approval is contingent on any health and safety checklists having been completed, and necessary approvals as a result of gained.