UNIVERSITY OF SOUTHAMPTON

FACULTY OF HUMANITIES

Department of Archaeology

The Acquisition of Domestic Equids in Roman Britain

- the identification of domestic equids and case study with isotopic analyses

by

Richard Chuang

Thesis for the degree of Doctor of Philosophy

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ABSTRACT

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Domestic equids, namely, horses (*Equus caballus*), donkeys (*Equus asinus*), and their hybrid offspring, mules (*Equus caballus* x *Equus asinus*), played an essential role in the Roman world. As pack animals, they served in both public and private sectors in the Roman daily life. According to written sources, mules in particular were used predominantly as pack animals by the military and enabled the transport of troops, the transport of supplies, and large weaponry to every corner of the empire. The production of mules requires the presence of both male donkey and female horse, and thus mule breeding in northern Europe would necessitate the importation of donkeys to regions outside of their natural distribution and/or the import of mules from elsewhere. The importation and export of domestic equids has indeed been described in historical sources but not recognised in the zooarchaeological record.

As a result, the significant predominance of horses over donkeys and mules in Roman Britain is not currently well understood. This is mainly due to the issue of species identification. The thesis aims to refine the existing methods and develop new techniques to more accurately distinguish between different domestic equid species in an attempt to obtain, not only the representative frequency of different domestic equid species in selected Romano-British sites, but also to observe different isotopic values (oxygen, carbon, and strontium) of selected specimens in order to discuss their localness. The results suggest that, while both donkeys and mules do exist in Roman Britain, the scarce presence of donkeys and the foreign isotopic signature of possible mules imply that these two species were not systematically introduced into Roman Britain.

This study shows the potential of the use of species frequency and isotopic analyses for examining the procurement strategies of domestic equids in Roman Britain.

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DECLARATION OF AUTHORSHIP

I, RICHAD CHUANG, declare that this thesis and the work presented in it are my own and has been generated by me as the result of my own original research.

The Acquisition of Domestic Equids in Roman Britain

- the identification of domestic equids and case study with isotopic analyses

I confirm that:

1. This work was done wholly or mainly while in candidature for a research degree at this University;
2. Where any part of this thesis has previously been submitted for a degree or any other qualification at this University or any other institution, this has been clearly stated;
3. Where I have consulted the published work of others, this is always clearly attributed;
4. Where I have quoted from the work of others, the source is always given. With the exception of such quotations, this thesis is entirely my own work;
5. I have acknowledged all main sources of help;
6. Where the thesis is based on work done by myself jointly with others, I have made clear exactly what was done by others and what I have contributed myself;

Signed: .....

Date: .....28/09/2016.....

Acknowledgements

Looking back to the years in this PhD project, many aspects of the research had changed due to several unexpected issues while the ultimate aim remains the same. The present thesis has shifted from using aDNA to validate qualitative morphological traits to refining and developing several different identification techniques for the challenge regarding distinguish the subtle differences between domestic equids. The ultimate goal, however, is to re-think the introduction of domestic species from one region to another as part of a "cultural package" of the invaders. But unlike species as food or companions, species utilised as labour animals by the local populations seem much more difficult to "replace" by the invader.

As a little kid, I was still able to see farmers riding carts pulled by water buffalo (*Bubalus bubalis*) in the country side of Taiwan. Water buffalo was not native to Taiwan and was not introduced probably until early 17th century. The main users of water buffalos were the *Han* farmers from the southeast coast of China, and the Dutch systematically introduced a large quantity of water buffalo to improve local agricultural production (possibly established local breeding) for their own profit. Gradually, the local "native" population lived on the plains gradually merged with Han migrants, but there were those who continued their way of life. Horses came to Taiwan much later in time and were to be used only by selected few (mostly government officials), thus they were never considered as farm animals in Taiwan. In other words, even though horses (and other domestic equids) were introduced, they were regarded as social symbols and never replaced water buffalo as the main source of transportation among the local populations. All these make me wonder more about the role and the introduction of labour animals in the past.

Countless helps and supports from friends and colleagues that get me through the process of this PhD project. First, I would like to thank both of my supervisors, Dr. Jacobo Weinstock and Dr. Alistair Pike, for all the supports and constructive advice to keep me focus on the research topic.

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Finally, I would like to thank the understanding and support of my family throughout writing this thesis and my life in general.

Chapter 1 - Introduction

1.1 – Introduction and Research Aims

The importance of draught and pack animals has decreased dramatically since the middle of the last century due to the advanced development of new technologies in different fields, which has allowed motorised vehicles and machines to be mass produced and to become more affordable. This has radically altered the relationship between humans and the domestic animals that traditionally served as plough and pack animals. Unlike other domesticates, which are usually utilised as food and are now commonly presented to us as packed meat products, the connection with large working animals, namely, the domestic equids, has been lost in most urbanised societies (although they still play an active role in leisure and sport). While these plough and pack animals have been replaced gradually over recent generations in many areas, they are still essential in regions of the world where motorised vehicles are not suitable or affordable; in these regions, they still perform the services that they did in the past.

With changes in the demands made on draught animals, their procurement strategy will also change to accommodate the decreasing market. It is difficult to create a new market or increase an existing demand for draught animals, as their motorised competitors have established a permanent place and, therefore, the suppliers of such animals would have to change their breeding scheme in order to minimise the basic costs and avoid any surplus that would add to their costs. Since such a market, in principle, will constantly adjust itself to remain at equilibrium, and the demand will change from time to time, the breeding scheme of draught animals will have to alter to reflect the socio-economic development as well as particular events in history. For example, regarding typical Roman pack animals, the use of both donkeys and mules as labour animals is well recorded in Greek and Roman

historic documents. However, both species were foreign to many newly conquered regions/provinces of the Roman Empire, particularly in the north-west. The spread of these two species into Western Europe is undeniably associated with the westward expansion of the Roman Empire. Nonetheless, questions of their adaption by local populations and about the supply to or production of these foreign species in these areas during Roman time are rarely raised by archaeologists. For example, how was the introduction of these donkeys and mules carried out? Did the Romans make efforts to establish local breeding or were these animals supplied continuously from the heartland of the Empire? Does the presence of donkeys and mules imply a Romanised way of life, as indicated by the change in diet and husbandry (e.g. Kings, 1999; Albarella *et al.*, 2008)? Did the initial introduction of donkeys and mules make a permanent impact that altered the traditions of the local culture and farming practices, or did the use of these animals disappear with the collapse of the Roman Empire? These are questions that are essential to understand past human-animal relationship, but have not been properly investigated due to the difficulties in distinguishing different domestic equids species.

The presence of donkeys and mules has always been scarce in British archaeological records. Although their introductions have usually been credited to the Romans (Johnstone, 2008), historical records have opposed their local precence in a later time period (Holinshed, 1587); furthermore, other scholars have also questioned such early introduction (Baxter, 1998; Dent, 1972). While archaeological evidences indicate the presence of both species as early as Roman or even pre-Roman (Johnstone, 2004), it is necessary to further clarify the definition of "the introduction of a foreign species". Unfortuantly, such issue has never been explicitly discussed regarding donkeys and mules. For the current thesis, an introduction of a foreign species requires more than the presence of their skeletal remains. A sustained population which allows local breeding to be maintained as well as impact on either local ecology or cultural practise is considered

essential for the introduction of a species. That is, once donkeys and mules are introduced to the British Isles, it is expected that there would be enough of them to maintain localized breeding as well as associated artefacts such as mule-shoes or donkey mills. However, the latter may be problematic as small artefacts can be traded and "donkey mill" can be pulled by other animals. As a result, to determine their "localness" will be the key to understand the introduction of these foreign species in Roman time. This can be achieved by using stable isotopic analysis. The current thesis aims to:

1. Filling the gap by reviewing existing methods for the determination of domestic equid species and to suggest new identification criteria/techniques for specific determination. This includes the use of biometric analyses as well as geometric morphometric ananlyses. These new methods will allow the determination of the relative representation of the different equids to be established.
2. Establishing species ratios based on new identification methods, in conjunction with isotopic analyses, to ultimatedly examine possible equid procurement strategies. In other words, to understand if different equid species are used by different site/population and whether the domestic equids were supplied locally or imported from elsewhere.

According to the definition of "introduction of species" described ealier, the current thesis hypothised that if donkeys and mules were introduced by the Romans, the number of donkeys should be more abundant to maintain the local breeding of both donkeys and mules. Futhermore, based on the consideration of procurement cost, most of these donkeys and mules should show local isotopic signatures. This is because to import these animals, particularly donkeys, is more likely to make them more expensive than procuring local horses.

The characteristic of procurement strategies will be reflected in both the species representation and the localness of the domestic equids found from context. Previous speculations of the provisioning models are only based on limited biometric evidence on the frequency of different species and historical written sources for the origin and localness of breeds. However, in order to correctly interpret and examine different procurement strategies, it is necessary to first establish reliable methods that can distinguish the archaeological remains of different domestic equid species. Several studies in the past have suggested various methods for separating mule bones from those of horses (Armitage and Chapman 1979; Eisenmann 1986; Eisenmann and Beckouche 1986; Uerpmann and Uerpmann 1994; Peters 1998; Johnstone 2004, summarised in Johnstone, 2004). However, there is a general lack of mule comparative material to allow these methods to be further tested for accuracy. As a result, the present thesis first addresses the issue of existing identification methods. Following that, different methods involving both conventional and novel application of biometric and morphometric data are developed and utilised to identify species of archaeological equines. The localness of selected archaeological equines is then examined by the combination of different isotopic analyses. With species determination supported by established methods, comparison can then be made between the localness of different domestic equids from Roman Britain, allowing the second aspect of procurement strategy to be investigated.

1.2 – Domestic Equids in Archaeological Research

Among all the domestic equids, horses have attracted the most attention in archaeological research in the past few decades. The ongoing dispute regarding the origin of horse domestication and horse riding alone has stimulated numerous research projects involving different disciplines for more than 30 years (Levine, 1990; Anthony *et al.* 1991; Grigson,

1993; Brown and Anthony, 1998; Levine, 1999; Anthony and Brown, 2000; Bartosiewicz and Bartosiewicz, 2002; Jansen *et al.* 2002; Bendrey, 2012, to list but a few). In recent years, some attention has been focused on another domestic equid, namely, donkeys, whose domestication status is more difficult to determine (Rossel *et al.* 2008; Shackelford *et al.* 2013; Kimura *et al.* 2013). In contrast to the attention on horses and donkeys, mules, perhaps due to them being a hybrid species, have tended to be overlooked and have often gone unnoticed. Despite being relatively elusive, mules' renowned superiority as pack animals thanks to their hybrid vigor (Clutton-Brock, 1992) still grants them a place in history, and they were considered valuable beasts of burden in numerous historical records and were depicted in a variety of artworks.

However, mules in archaeological records have been less appreciated and well studied. The morphological differences between the remains of mules, as a hybrid species, and horses are very subtle; whether or not they can be identified unambiguously and consistently has been questioned (Johnstone, 2004). A discrepancy in the relative abundance of mules exists between historical sources of various types (written, painted, or even manufactured) and archaeological materials such as faunal remains and functional objects (e.g. mule-shoes). This is not to say that archaeological material should always match historical sources exactly, and several issues need to be considered. For example, historical texts cannot always be taken at face value and pre- and post- depositional factors may also affect bone preservation. Nevertheless, on a purely theoretical basis, it could be expected that the ratio of horses to mules – as portrayed in written records – should more or less be reflected with a certain degree of similarity in zooarchaeological finds. However, this does not seem to be the case. Only very few cases of mules have been identified and reported from Roman sites, both in the empire's heartland and the provinces (Johnstone, 2004). Some scholars have argued that the subtle morphological differences between horses and mules

cause most researchers to overlook the possible presence of mules (Johnstone, 2004; Levine, 2004; Maltby, 2010) or to use a broader category, such as "equid" for general identification, much as in the case of sheep and goats.

Since 1979, when Armitage and Chapman (1979) reported and published the case of a Roman mule found in London (see Chapter 2), the possibility of being able to identify mules has been clearly stated. Indeed, further developments of morphological criteria (both cranial and post-cranial) as well as biometric analyses have argued that it was possible to distinguish mules from horses (Eisenmann, 1986; Eisenmann and Beckouche, 1986; Peters, 1998; and summarised in Chapter 4 of Johnstone, 2004). Unfortunately, as will be described in more detail in the next chapter, there is a dearth of modern known mule material that can be used in more thorough comparative anatomical analyses. Furthermore, not only is the number of comparative mule specimens insufficient to test the validity of the putative morphological criteria, but also the intra-specific variability of these domestic equids is commonly disregarded because the possible presence of equids other than horses is not always fully recognised. These identification methods remain merely as basic guidelines for distinguishing mules from horses. In other words, it is still uncertain whether all mules will bear particular morphological traits, or whether these few known mule specimens can only represent "typical" mules, but not all. The intra-specific variation of horses is exceedingly wide; many local breeds have adapted to particular environments so that they are markedly different from each other (e.g. various pony breeds on small island settings) or special breeds have been bred for particular purposes (e.g. heavy draught horses and modern police/military horses). Whether these minor differences that researchers have identified from the skeletal remains, (morphologically or biometrically), represent intra-specific or inter-specific variation is unclear without further validation based on larger datasets amount of material. Nevertheless, there is now sufficient evidence

to alert researchers to the need to be fully aware that mules may be represented among archaeological equine remains and that they may be identified using some existing methods.

That said, the number of donkeys and mules being clearly identified based on the available published and unpublished faunal reports still appears to be extremely low, particularly in the north-western Roman provinces (e.g. Roman Britain, see section 1.6 and table1.2). This suggests that the dispersal of donkeys and mules may not have been homogeneous throughout the Roman Empire, and thus that the importance or use of these two species may have been highly localised or restricted (e.g. used by Roman officials, but not by broader local populations). As a result, it is possible that the number of these two species (particularly mules) estimated in some of the written records reflects only certain regions of the Roman Empire and so should not be assumed typical for all Roman provinces. In other words, one should not expect that the number of donkeys or mules, as well as the social role they played, would have been the same in the north-west provinces as in the Middle East simply because both regions were under Roman jurisdiction. Availablitly of these exotic beasts of burden aside, the usefulness of these pack animals may have differed under different ecological and economic considerations. In other words, would the donkey still have been an ideal labour animal when taking into account the expenses of keeping it alive in an unsuitable environment? Due to the time and budgetary constraints of a PhD research project, it was not feasible to examine evidence throughout the Roman Empire; therefore, the current thesis will use Roman Britain as a case study in order to explore the different strategies of domestic equids procurement on this remote and far-flung island of the empire.

1.3 – Domestic Equids in the Roman World

Before discussing the domestic equids in Roman Britain, some related terms should be defined to avoid confusion stemming from commonly used over-generalised names. In the current thesis, the term "mule" (*Equus asinus x Equus caballus*) is used specifically to refer to the hybrid speciation of a male donkey/ass (*Equus asinus*) and a female horse (*Equus caballus*). The hybrid from the opposite cross, which is the offspring of a male horse (*Equus caballus*) and a female donkey/ass (*Equus asinus*), is distinctively referred to as a hinny (*Equus caballus x Equus asinus*). In addition, the term "domestic equid" should be explained. This term is used loosely in the current thesis to refer to the three major equine species commonly served as labour animals: horses, donkeys, and mules. However, it is necessary to iterate that there may have also existed unmanaged horse populations in Britain; according to Harcourt (1979), some horses roamed free in the wild and were only rounded-up for the capture and training of yearlings during the Iron Age. In the present thesis, "domestic equids" may, therefore, include both horses bred in a stud farm under human management and horses living in wild-living herds before being captured and training as labour animals. In contrast, the term "donkey" in the current thesis refers only to those animals that have been tamed or domesticated, whilst "ass" is used explicitly to refer to the wild or feral animals of the same species. The reason for using different terms to describe "*Equus asinus*" is that both types could be involved in mule breeding, and thus it is necessary to separate further the local wild/feral population from the domestic one. Finally, although both hybrid species, namely mule and hinny, are partially "caballine", in the current thesis, all non-horse domestic equids will be referred to as "non-caballine" for case of distinction.

1.3.1 – The Mule: Its Infertility and Hybrid Vigour

Mules (*E. asinus X E. caballus*) are a different equid than either of the parents, i.e., male donkey (*E. asinus*) and female horse (*E. caballus*). Although this notion is generally understood, and mules are highly valued as beast of burden (Tegetmeier and Sutherland, 1895; Dent, 1972; Hyland, 1990; Clutton-Brock, 1992, Roth, 1999), the difficulties as well as the particular set of knowledge and skills required to bring these two species together successfully and produce the ideal offspring often go unrecognised. Therefore, it is necessary to pay special attention to the production of this hybrid species and establish some key concepts and terminology before discussing this species any further.

A mule is not a "natural" species in the sense that mules cannot reproduce themselves through male mules mating with female ones, although they can be bred in an all-natural setting inhabited by both horses and asses/donkeys. This type of "cross breeding" is termed "hybrid speciation". Hybrid speciation is quite common in plants, but less common in animals, and relatively rare in mammals (Mallet, 2005). Some of these hybrids are fertile (mostly homoploid hybrid speciation), while others may be sterile. The cause of infertility in hybrid offspring is still unclear as many factors are involved (Yang *et al.*, 2004; Gross and Rieseberg, 2005; Lee *et al.*, 2008; Steiner and Ryder, 2013). There are a few records of female mules and hinnies being impregnated either by a stallion or a jack and successfully giving birth to foals, but these are extremely rare, hence the Roman phase of "*cum mula peperit*" (meaning when a female mule gives birth) for describing an unlikely situation. In theory, male mules cannot produce spermatozoa; however, it is not certain if all mule stallions are completely sterile since most, if not all, are neutered. The logic of castrating an infertile mule stallion (known as a 'john', while a female mule is known as a 'molly') is that even though such stallions cannot produce spermatozoa, they still produce testosterone, which makes them act rather aggressively, similar to regular stallions (Smith, 2008). Thus, in order to keep them under control, castrating male mules is recommended. The aetiology

of mules' infertility is thought to be the uneven number of chromosomes in horses and donkeys (see Table 1.1, Trujillo *et al.*, 1962; Clutton-Brock, 1992). Nevertheless, recent advances in molecular biology suggest that the cause of hybrid sterility is far more complicated (Gross and Rieseberg, 2005). Some scholars have argued that the infertility in hybrid progeny is due to the incompatibility between the genes from different parent species rather than simply uneven chromosome pairs (Lee *et al.*, 2008; Steiner and Ryder, 2013). The best example is that the hybrid offspring of Przewalski's horse and the domestic horse are fertile even though they also have an uneven number of chromosome pairs (2n=65, see Table 1.1). In addition, other scholars have also argued that it is the complexity in the "rearrangement" of chromosomes during the process of speciation that causes the meiotic breakdown, which ultimately leads to sterility in hybrid offspring (Yang *et al.*, 2004). As for fertile molly mules, if they are bred with horses, then the offspring will be horses, and if they are bred with donkeys, theoretically, the offspring should be mules again, but this seems not always to be the case (Rong *et al.*, 1988; Yang *et al.*, 2004). Although it is possible to continue using fertile molly mules to breed with jacks to produce mules, the fact remains that fertile molly mules are very rare and that only very few foals will survive. This renders such a breeding method impractical. Since the precise cause of infertility in mules is still unclear and because of the scant number of fertile molly mules, the only approach to mule breeding remains the old fashioned crossbreeding between two species.

	Horse (2n=64)	Przewalski's horse (2n=66)	Donkey (2n=62)
Horse (2n=64)	Horse (2n = 64)	(2n=65)	Hinny (2n= 63)
Przewalski's horse (2n=66)	(2n=65)	(2n=66)	(2n=64)*
Donkey (2n=62)	Mule (2n=63)	(2n=64)*	Donkey (2n= 62)

Table 1.1 – Number of chromosomes of different equids
* - Although Przewalski's horses and donkey offspring will theoretically have an even number of chromosomes, there is no known case of such offspring and, therefore, the fertility of this hybrid is unknown.

"Hybrid vigour" or "heterosis" means the enhancement of biological functions in crossbred offspring; from a human perspective, it is sometimes advantageous to cross breed different animals. In the case of mules, they are usually not only larger in size than both parents, but are also much stronger and show more endurance (Clutton-Brock, 1992). Crossbreed progeny from a horse stallion and a female donkey (known as a jenny) is also possible, but the progeny is referred to as a "hinny" or a "jennet" (particularly in Ireland, but some have also used the same term to describe a female donkey). While hinnies are also sterile and present "hybrid vigour", their physical appearance is quite different from that of mules, and they should not be considered as the same species. However, frequently, both types of donkey-horse hybrids are generally categorised as "mule". Such a simplification can be problematic especially when trying to interpret its representation in the past. Fortunately, the presence of "hinnies" is unusual since they are not considered "ideal" labour animals compared to mules. This is mainly because, comparing to mules, hinnies are much smaller in size and are much less endurant (Tegetmeier and Sutherland, 1895).

The existence of mules, as a hybrid species, implies the existence of a jack (male donkey), and a mare (female horse), and further indicates that the other sex of these two species

must also exist in order to produce offspring to secure future breeding. Mules and horses can be similar in size, but can clearly be distinguished by their exterior physical features – the most obvious one being that mules have longer ears, much like their donkey fathers. In addition, some less obvious traits, such as smaller hooves and coarser manes and tails, can also be used to distinguish between these two animals (Smith, 2008). All these differences can be found in Roman artwork (Toynbee, 2013), indicating that most Romans, if not all, were aware of the difference between mules and horses.

1.4 – The Supply of Domestic Equids in the Roman world

At present, an examination of the domestic equid supply in the Roman world can rely only on very limited material, mostly written records; and none of these records directly addresses the question of provisioning, such as the ratio of different domestic equids or their acquisition and source. This section will review the current understandings and hypotheses of the domestic equid supply in the Roman world.

1.4.1 – The Supply of Horses

Most known Roman records focused on horses for the military, but some clues regarding horses used in other aspects of Roman life are "hidden" in contemporary writings. The subject of horse supplying has been discussed by previous scholars (e.g. Hyland, 1990; Dixon and Southern, 1997); they suggest that horses for the military were acquired through a number of different means:

1) Bulk military purchase or supply from Imperial estates,

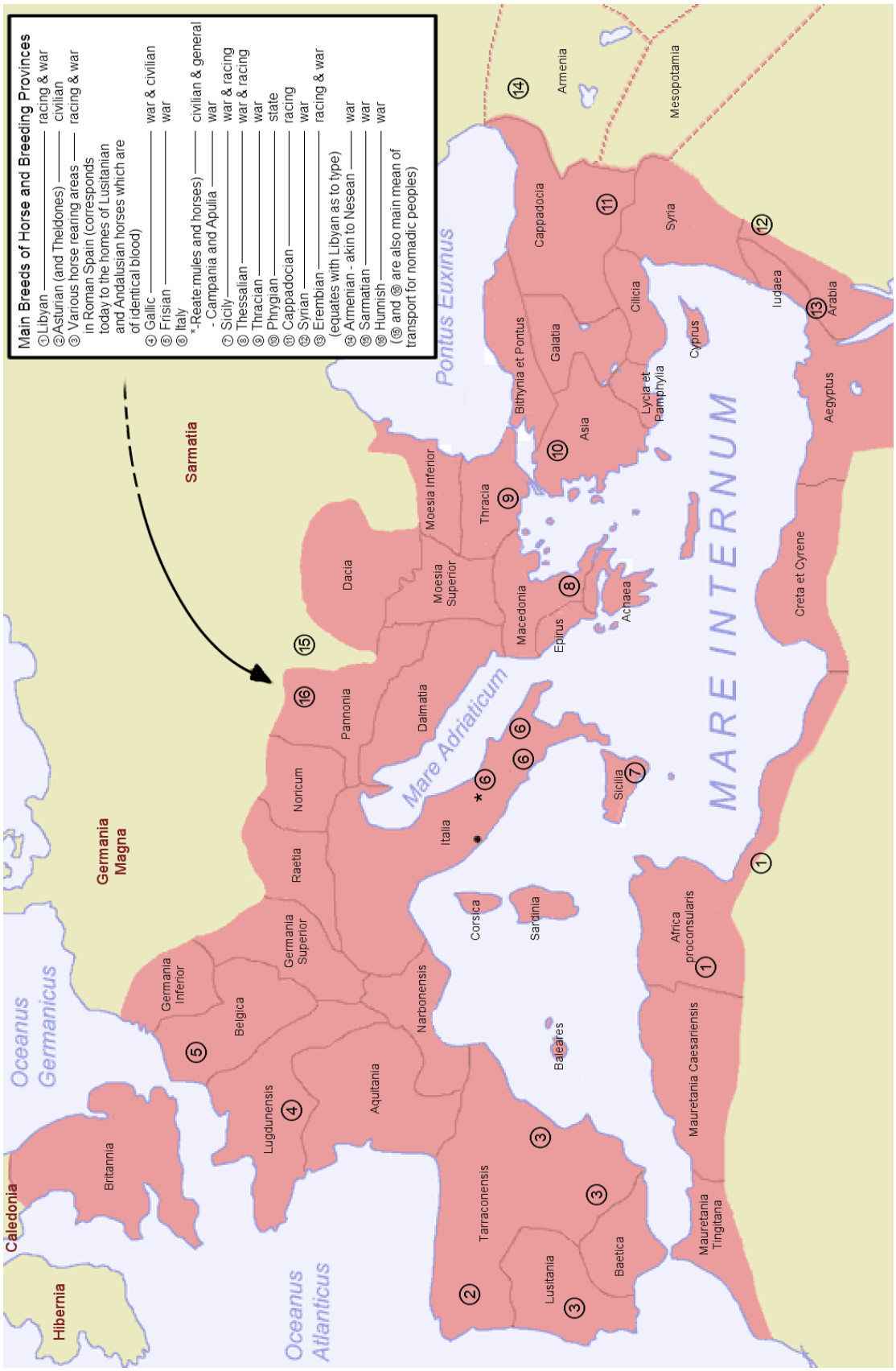
2) Tributes from allies or horses captured in battle, and

3) Local individual purchases or recruitment.

Of the three domestic equids in question, horses are the least problematic because they were abundant throughout most of Europe, including Britain. In other words, they could be easily obtained locally almost everywhere in the Roman Empire. Therefore, it can be assumed, under normal circumstances, that horses were mainly acquired locally, except when bulk purchases from specific suppliers to the military were made. Nonetheless, horses may occasionally have been imported or exported, causing them to end up in "foreign" locations. Other than being killed in action, military horses may also have been transferred between regions with the military force. For example, it is argued that 5,500 Sarmatian cavalry were sent to Bremetennacum (modern Ribchester, U.K.) around AD 175 presumably with their mounts (Hyland, 1990, p.185; Dixon and Southern, 1997, p.158). However, excavation works from Ribchester did not unearth any related archaeological evidence supporting claims regarding the importation of such a large number of horses. In fact, archaeological records indicate, the fort was abandoned not long after this date (Buxton and Howard-Davis, 2000).

In addition to horses used by the military, animals used for sport and entertainment, such as racing, may also have been transported around the empire. According to Hyland (1990), specific breeds of horses from North Africa and Spain were favoured as racehorses, and the trading and exporting of these horses was not uncommon. Map 1.1, based on the work by Hyland (1990), shows all known horse breeds mentioned in ancient Latin and Greek texts. It should be noted that whilst some regions were known to produce horse breeds that were normally used for "civilian" or "general" purposes, there is no evidence that these regions were exporting horses to other parts of the Roman Empire merely for such

purposes since horses were native to most regions in Europe and, therefore, were rather common compared to donkeys and mules.



Map 1.1 – Horse breeds mentioned in Roman and Greek sources and their main use (After Hyland, 1990)

1.4.2 – The Supply of Mules and Donkeys

In contrast to horses, little is known about mule and donkey supply. Arcadia in Greece and Reate in Italy, as mentioned in the works of Varro and Columella, are the only locations associated with Roman donkey breeding (see section 1.5.2). As for mules, Hyland (1990, p.72) states that mules for the military were likely to have been supplied by the owners of large estates or directly from imperial stud farms; she further suggests that for regions where donkeys and mules were unavailable or were unsuitable for the local climatic conditions, ponies may have been used as substitutes for mules as pack animals in the military. Johnstone (2004) further agrees with the idea that mules were bred in only a small number of centrally-managed locations. She supports this argument using the difference in size and build of horses and mules (based on her own identifications). She argues that individuals identified as mules from Roman sites were more homogenous in size/build than those she identified as horses. However, the uniformity in mule size may also be explained by the fact that these infertile hybrid creatures can never experience "selective breeding" to alter their size as intensively as could their parents. Therefore, if only certain type of mares were used to produce Roman mules, as suggested by Varro and Columella, then it is logical that the offspring would have been extremely uniform in appearance. As a result, biometric analysis will not be able to provide sufficient evidence of the possible existence of a few controlled mule production regions.

The literary sources and previous research seem to suggest that whilst horses could be obtained locally, the majority of mules – particularly those used by the military – were more likely to have been bred in a small number of locations. These were either under imperial control or managed by large estate owners. It is interesting to investigate how donkeys and mules were supplied or produced in the newly conquered regions/provinces of

the Roman Empire. Discussions on such topics are made possible with the application of isotopic analyses for detecting the mobility of individual animals. Thus, in addition to establishing species representation frequency, the second part of the present thesis is a pilot study that aims to determine the "localness" of different domestic equid species in order to further examine their procurement strategies.

1.5 – Indication of donkeys and mules in Roman Britain

The Romans are widely credited with the introduction of donkeys and mules into the British Isles (e.g. Johnstone, 2010; Baker and Worley, 2014, but see also Dent, 1972, pp.53-55 and Baxter, 2002 for alternative views). Nonetheless, some issues regarding donkey keeping and mule-breeding are often neglected when discussing domestic equids in Roman Britain or making claims about their introduction. Donkeys are not a species native to the British Isles. Thus, logically, to sustain a local population of mules, there must be a sufficient number of donkeys not only to produce mules, but also to ensure more jacks for future mule production. Irrespective of whether mules are produced as the primary aim or as a by-product of having donkeys, it is important to stress that there cannot be a local mule population without donkeys. Furthermore, unlike the introduction of species such species as fallow deer (*Dama dama*), the introduction of taxa normally found in different climatic environments (i.e. donkey) or requiring human involvement for its reproduction (i.e. mule), necessitates a particular set of skills in and knowledge about livestock management that must also be introduced with them. In this section, the skills and knowledge for donkey keeping and mule breeding will be reviewed to illustrate further the implications of the presence of these two foreign domestic equid species in Britain.

1.5.1 – Donkey-keeping in Britain

Donkeys, or their wild ancestors, are not an equine species that has adapted to the cold and damp British weather. Unlike the introduction of donkeys into America or Australia where they could find suitable habitats similar to those in their original area of geographical distribution, donkeys in Britain never felt "in their element" and thus they have never established feral populations and have never survived completely on their own. This fact indicates that this species, unaided, is probably unable to endure the differences between the British climate and their natural habitat. Livestock management is needed to ensure the welfare or even the survivorship of donkeys in Britain, for example, by the provision of rain-shelters, as donkeys possesses no adequate "weatherproof" coat (Dent, 1972, p.145). The hooves of donkeys in Britain must be cared for to avoid malformed growth caused by continuously walking on soft and soggy ground and other foot diseases such as laminitis, due to nutritional-excess problems since they are naturally adapted to a poor grazing environment (Thiemann and Rickards, 2013). In addition to foot disease, the nutrient-rich local vegetation in the UK can also lead to other health issues, such as obesity and dental problems caused by grazing on grass, which is much softer in texture than the vegetation in their home environment. This is not to say that donkeys cannot inhabit Britain, but they do require constant human care for their welfare or even their survival in this foreign environment.

1.5.2 – The "Making" of Mules in the Roman World

Today, advanced veterinary techniques used in livestock-breeding no longer require the male to be present during the process of insemination. For example, pig breeding through artificial insemination has been practised for over half a century in most countries. There

are numerous benefits in using this breeding procedure (Reed, 1982), and they can be summarised as follows:

(1) It can allow one boar to mate with more sows in a shorter time and thus reduce the number of boars kept; furthermore, it can produce piglets in a similar size range to ensure the quality of the pork.

(2) It can overcome the problems caused by age or size differences that make natural mating difficult.

(3) Collected semen can be examined, and flawed semen can be eliminated at this stage, leading to a higher breeding rate and clearer record-keeping.

The observation from pigs may not be the best analogy for equids since they are bred for completely different purposes. Some of the advantages of artificial insemination may be used to improve the breeding of mules, such as the fewer number of jacks required and the need to overcome size differences between female horses and male donkeys. Artificial insemination, or assisted reproductive technology, is gaining popularity and has forced more and more horse associations to add “natural breeding” as a qualification to register for competition (Mills and McDonnell, 2005). The benefits of dealing separately with two individuals and being able to “pre-select” healthy spermatozoa is appealing to breeding centres, but most domestic horses seem to “prefer” to reproduce without human intervention (Mills and McDonnell, 2005).

Artificial insemination was not an option to the Romans and, therefore, all mares had to be covered by jacks in order to produce mules. While the horses were usually smaller than their modern counterparts – as will be discussed later in the chapter – the variability in the size of Roman donkeys is still unknown. If they had a similar size range, like their wild

relatives, then the size-difference between Roman donkeys and the usually small-sized horses may not have been a major concern. However, there is historical evidence that size difference between two animals presented, at least occasionally, a problem. In this case, the solution was to provide some sort of facility for jacks to overcome the difference in height. Columella gives a full description of such facility as follows:

> *"A special place is constructed for these purposes — the countryfolk call it a "machine" — it consists of two lateral walls built into gently-rising ground, having a narrow space between them, so that the mare cannot struggle or turn away from the donkey when he tries to mount her. There is an entrance at each end, that on the lower level being provided with cross-bars, to which the mare is fastened with a halter and stands with her forefeet at the bottom of the slope, so that, leaning forward she may the better receive the insemination of the donkey and make it easier for a quadruped smaller than herself to mount upon her back from the higher ground."*
>
> <Columella, *de Re Rustica* VI.37, trans. H. B. Ash>

There is no mention of such a facility in Varro's work (*de Re Rustica*) and, therefore, this facility may have been developed after Varro's time (116 BC – 27 BC). Varro, nevertheless, points out the importance of grooms and the danger inherent in the process of equine mating. He refers to an incident that occurred during the mating of two horses (Varro, *de Re Rustica II.7*, as described in Hyland, 1990). In this case the stallion was unwilling to cover the mare, and to resolve this issue, the groom covered the stallion's head and forced him to coition. When the cover was removed from the stallion's head, he crushed and bit the groom to death (some other translated editions have interpreted the tragedy as being caused by incestuous breeding). Fortunately, donkeys are less aggressive when refusing a task, but the challenge of letting both species accept each other is much

greater than forcing an unwilling horse stallion. Donkeys and horses are accustomed to living in their own herds and are not naturally interested in each other even during the mating season. Jacks will refuse to cover mares, and mares will not allow jacks to come near them.

Several solutions and "tricks" regarding mule breeding are suggested in the works of Columella and Varro as well as in several other, more recent sources (Konrad, 1980). The first recommendation is that the mule-breeding jack, or specifically, mare-covering jack, should not have had previous experiences with jennies. This simple solution is not ideal when the number of jacks is limited because if jacks are used only to breed mules, there will not be enough of them to maintain the donkey population required for future mule breeding. If the jack is raised as a horse, then the success rate for covering will largely increase. As described in detail in Columella's work (*de Re Rustica VI. 37.* 7-9), the jack should be removed from his jenny mother and secretly smuggled to another foaling mare. The jack will then be fed on the mare's milk and be raised as a horse. This psychological imprint will ensure the jack will not refuse to cover mares when he is sexually mature, and mares will be less likely to refuse him, as he will smell like a horse; whether he will have a problem covering jennies afterwards is not mentioned in the text.

The rejection from a mare is much more dangerous since she will kick the donkey trying to mount her as well as the groom who is leading the donkey. The solution suggested by Columella for this situation is that different jacks should be brought to the mare to give her the illusion that she is given a choice (*de Re Rustica VI. 37. 9-11*). When the mare is willing to be covered by whatever jack she has selected, 'he' will be replaced by the mule-breeding jack. The actual practice of bringing two different species to reproduce a hybrid is

not a simple task and requires experience. Therefore the introduction of such system into a new area will need more than just the introduction of the concepts or the animals.

Even when expertise on how to bring these two species together is available, Columella adds that one must be aware of the difficulty in finding the perfect parents for the breeding of mules. He categorises horses into three different types: namely, racehorses, the mule-breeding mares, and common horses (*de Re Rustica VI. 27. 1-4*). The fact that mule-breeding mares are single out as a horse type indicates the importance of finding mares that are willing to mate with donkeys. According to Columella, suitable mule-breeding mares should be between three to ten years of age, in addition to having other physical characteristics (*de Re Rustica VI. 34. 2*). Pliny the Elder *(Naturalis Historia, Book VIII, LXIX*), writing somewhat later than Columella, suggested that the breeding mares should not be less than four years of age. This is a relatively short period, since the gestation period for a mule is about thirteen months (compared to c. 11 months for horses and c. 12 months for donkeys). Assuming a mare is no longer suitable for mule-breeding after the age of ten and that she is able to gestate every year and that she produces no twins, then a maximum of seven mules can be bred in one mare's lifetime. However, after foaling, the mare will probably need to wait until the foal weans for her next gestation and, furthermore – as Aristotle noted in his work – "a mare giving birth to two mules is regarded as unnatural and portentous" (*Hist. An*, Book VI). Judging from the above, it would be rare for a mare to have more than four mules throughout her lifetime.

In addition to the requirement for mares, Columella also points out that a good quality jacks are even more difficult to find. There are two sources for superior donkeys that were known to be the best at that time mentioned in Varro's work: the Arcadian donkeys from

Greece and the Reatine donkeys from central Italy (*Rerum rusticarum, VIII*). Interestingly, there is no mention of any other breed of donkey from the western part of the Roman Empire, such as the Iberian Peninsula or France from whence high quality modern breeds of donkeys originated. In addition, recent research has shown that donkeys were present in the former region as early as Chalcolithic times (Cardoso *et al.*, 2013). Arcadian donkeys were traditionally deemed as the ideal breed for mule breeding, but by the time of Varro, Reatine donkeys were equally valued (*Varro, Rerum rusticarum, VI*). The criteria for selecting suitable jacks are also described in detail in the works of Varro, Columella, and Pliny the Elder, but only Columella further notes that sometimes the external appearance of jacks can be deceiving; that is to say, handsome jacks do not always produce good mules (*de Re Rustica VI. 37. 4-7)*. The best jacks were believed to be the first generation offspring between a tamed wild ass of Phrygia or Lycaonia and a domesticated jenny. This account was first mentioned by Varro (*Rerum rusticarum, VI*), and probably quoted later by Columella (*de Re Rustica VI. 37. 4-7)* and Pliny the Elder (*Historia Naturalis, VIII, 81*).

These contemporary agricultural manuals and related records would seem to suggest that mule breeding was more likely to be restricted to certain regions due to the availability of "ideal" donkey breeds, especially if the first generation progeny from the tamed wild ass was involved. Given that most accounts of mule-breeding are first mentioned in the work of Varro – who also quotes Aristotle on several topics – some of these statements were outdated by the time of Pliny the Elder. As a result, very little is known about any improvements in mule-breeding traditions during the later Roman period.

Bringing together two species that naturally refuse to mate with each other is just one of the obstacles to be overcome in the production of mules. As mentioned previously, while

certain ‘tricks’ and techniques could help to overcome the problem of inter-specific rejection, and lead to the successful mounting, there were still no guarantees of a successful birth of a mule. A higher percentage of perinatal mortality has been noted for mules in comparison to horses or donkeys due to the risks of hybridization, such as neonatal isorythrolysis (Smith, 2008, see below). While obviously unknown to the Romans, the reasons for the higher rate of perinatal mortality in hybrids is now understood due to advances in modern veterinary science. In the case of mule breeding, the first risk is a greater chance (c. 10%) of neonatal isorythrolysis in mule foals, but this condition is rarely found in horse or donkey foals (Smith, 2008). Neonatal isorythrolysis is a condition where the mother’s blood type is different from the foal’s and can be relatively common in hybrid speciation. If the foal has an incompatible blood type, the mare’s body will react as if it is an invading bacterium and will develop an antibody against it (McClure, 1997). The antibody will then enter the foal through the placenta or the colostrum (also known as the first milk, which contains antibodies from the mother to prevent disease in the newborn); it will then attack the foal’s erythrocytes and start haemolytic reactions. This will lead to further complications, such as anaemia, which if not treated, will cause the death of the mule foal. The standard treatment nowadays is to prevent the foal from taking the mare’s colostrum and instead seek alternative sources of nutrition; the foal can be returned to the mare after 36 hours once the colostrum is clear (Smith, 2008). However, there is no mention of such a practice in any major Roman agricultural manual, which suggests that this neonatal condition was not understood or treated by Roman breeders, probably leading to a higher rate of neonatal mortality among mules. Mules are also more susceptible than horses to several parasitic infestations, such as ascarids and habronemiasis (Smith, 2008). Although most cases of these infestations are not necessarily fatal in equines, the high pain threshold mules inherit from their donkey fathers will make it difficult to notice the infestation before it becomes serious (Smith, 2008:54).

In summary, keeping donkeys in Britain, regardless of the time frame, will necessarily involve a high degree of human labour whether this foreign species is introduced either as a labour animal or for mule-breeding. Furthermore, mule-breeding – especially in Roman times – is a complicated process that requires specific knowledge of both horses and donkeys as well as the availability of suitable parents from both species, particularly jacks. Even with the "know-how" and the availability of suitable parents, there is still a very high death rate among neonatal mules. It is highly unlikely that the successful spread of mule breeding could have been easily achieved by the introduction of the concept or the suitable parent species alone. In other words, even if the idea of the crossbreeding of male donkeys (or asses) with female horses to produce mules were introduced to a new region, the probability of the local population successfully breeding mules would be low. In addition, even for colonists or immigrants from continental Europe with the necessary knowledge and skills, it would have been nearly impossible to gain access to the "ideal" donkey breeds, either the first generation of tamed jack ass and domestic mare or those used in *Reate* or *Arcadia*. Thus, one question should be asked: Would it have been necessary for the Romans to localise mule-breeding in a region where only one species of the parents was available, or would it have been more cost-efficient to seek out and adapt to the local alternatives?

1.6 – Zooarchaeological Evidence for Domestic Equids in Roman Britain

The frequency of domestic equid remains in Romano-British assemblages has never been high. For most Roman sites in Britain, the percentage of domestic equids is typically between 3-5%, and the ratio is somewhat higher in suburban and rural settlements (Maltby, 2010). One possible reason for such a sparse presence of domestic equids as a whole is that, unlike other livestock, they were not slaughtered in large amounts for meat consumption (King, 1978). Faunal reports from the "early days" tended to emphasise cut/butchery marks on domestic equids in Roman times in order to make a comparison with the known horsemeat consumption of the local Iron Age groups (Coy and Maltby, 1984). A general consensus that horses, and all other domestic equids, were not normally exploited as a meat resource in Roman Britain has been reached in later studies (Maltby, 2010) based on the meagre presence of butchery marks and the overall completeness of their skeletal remains in comparison to cattle. Nevertheless, despite they usually are rather small in quantity, domestic equids (although mainly identified as horses) are still a common taxon in Roman sites (e.g. tables in Maltby, 2010, and Table 1.2).

Site	Period	Cattle n (%)	Horse n (%)	Pig n (%)	Sheep/Goat n (%)	Total
Winchester northern and southern suburb	Roman	474 (51.13%)	75 (8.09%)	42 (4.53%)	336 (36.25%)	927
Borough High St, Southwark	Roman	27 (42.86%)	2 (3.17%)	25 (39.68%)	9 (14.29%)	63
Owslebusy	LIA - Roman	1059 (61.71%)	0 (0.00%)	0 (0.00%)	657 (38.29%)	1716
Alington Avenue, Dorchester	LIA - Early Medieval	10 (15.63%)	9 (14.06%)	3 (4.69%)	42 (65.63%)	64
Avonmouth	Late Roman	2 (13.33%)	1 (6.67%)	0 (0.00%)	12 (80.00%)	15
Balksbury, Andover	Roman	21 (37.50%)	19 (33.93%)	1 (1.79%)	15 (26.79%)	56
Bancroft Villa, Wolverton	Roman	185 (59.87%)	33 (10.68%)	23 (7.44%)	68 (22.01%)	309
Banjo site, Micheldever Wood	LIA - Early Roman	5 (27.28%)	0 (0.00%)	4 (22.22%)	9 (50.00%)	18
Beckford	Early Roman	11 (35.48%)	6 (19.35%)	0 (0.00%)	14 (45.16%)	31
Beddington Sewage Farm	Roman	47 (39.83%)	26 (22.03%)	27 (22.88%)	18 (15.25%)	118
Old County Hospital, Dorchester	Roman	51 (39.53%)	10 (7.75%)	16 (12.40%)	52 (40.31%)	129
Birdlip, Cowley	LIA - Early Roman	31 (75.61%)	10 (24.39%)	0 (0.00%)	0 (0.00%)	41
Chaucer House	Roman	7 (24.14%)	9 (31.03%)	4 (13.79%)	9 (31.03%)	29
Hooper Street, London	Roman	38 (67.86%)	13 (23.21%)	3 (5.36%)	2 (3.57%)	56
Land at Queen Street, Stotfold	Roman	9 (60.00%)	4 (26.67%)	0 (0.00%)	2 (13.33%)	15
London Wall	Roman	12 (54.55%)	5 (22.73%)	1 (4.55%)	4 (18.18%)	22
Maiden Castle Rd, Dorchester	Roman	5 (20.00%)	4 (16.00%)	0 (0.00%)	16 (64.00%)	25
Margate to Weatherlees Hill	LIA - Roman	76 (51.01%)	17 (11.41%)	14 (9.40%)	42 (28.19%)	149
Popley, Basingstoke	LIA - Roman	18 (47.37%)	6 (15.79%)	2 (5.26%)	12 (31.58%)	38
Rock Roman Villa, Isle of Wight	Late Roman	8 (22.22%)	2 (5.56)	0 (0.00%)	26 (73.22%)	36
Rope Lake Hole, Purebeck, Dorset	LIA - Roman	67 (34.01%)	14 (7.11%)	9 (4.57%)	107 (54.31%)	197
Sites B, C & K, Brighton Hill South	LIA - Early Roman	60 (63.83%)	12 (12.77%)	5 (5.32%)	17 (18.09%)	94
Westhampnett	Late Roman	4 (28.57%)	3 (21.43%)	0 (0.00%)	7 (50.00%)	14
Total		2227 (53.51%)	280 (6.73%)	179 (4.30%)	1476 (35.46%)	4162

Table 1.2 - Frequency of four main domestic mammals from Roman sites in ABMAP (Animal Bone Metrical Archive Project). Note the reason that a higher frequency in horses and a lower frequency in pigs than expected average (e.g. King, 1978; Maltby, 2010) is due to the fact that these numbers are based on more complete bones that can be measured. As a result, the less fragmented "horse/equid" bones appear to have higher frequency than average.

Among the species of domestic equids, horses are doubtless the most frequently identified; indeed, only a small number of non-caballine domestic equids are recorded in faunal reports. However, it could be argued that this is because mules and donkeys are usually overlooked in the process of identification due to the subtle morphological differences between these species and horses. Using the Roman invasion of Britain in AD 43 as an example, Peddie's (1997) estimation of the number of mules and horses used as well as other transportation and logistical needs based on historical records suggests that the total number of mules used would have been around 7,900 (Peddie, 1997, p.36, with 5,150 mules for carrying tentages and equipment for the *contubernia* and 2,750 for carrying rations to the troops), while he estimated that only 5,500 cavalry horses were used.

Peddie probably underestimated the number of horses because other possible uses of this species – e.g. bell-mare in a mule train, cart-pulling animals, or even as interim substitutes for mules – were not considered. However, based on legionary requirements, one mule was assigned to each *contubernium* (consisting of eight soldiers) to carry their tent, rations, and weapons (Roth, 1999) and, therefore, the number of mules in the Roman military would have been close to, if not higher than, the number of horses, which were used only as riding animals in cavalry units. However, whether such regulations were implemented to the full or whether compromises had to take place in real life (such as the use of oxen to replace mules) is unknown from official records. The Roman military was doubtless the largest user of mules since it relied on their superb performance and low maintenance as described in modern military manuals (e.g. Special Forces Use of Pack Animals, FM 3-05.213(FM 31-27), 2004). Mules may have been too costly or not suitable for commoners to purchase as draught animals, especially since mules cannot reproduce themselves.

Furthermore, depicting mules may also represent only the artist's own perception of an actual event. If the artist's impression of a typical pack animal was a mule, especially if depicting scenes from the "core" Roman region, then the scene would be more likely to present this notion using "typical pack animals" (i.e. mules) instead of depicting the actual scene in which a variety of labour animals (from horse to oxen) could have been used. Most viewers would have understood the concept of the scene rather than taking it at face value.

Since there had been Roman legions permanently stationed in Britain since its invasion, it could be assumed that there should have been mules present in Britain to match the known Roman military regulation described above. Following this assumption, it could be argued that it would have been advantageous for the Roman military administration to localise mule production in order to supply sufficient number of mules for local military needs. Consequently, the presence of donkeys could also be expected, as they are necessary for the breeding of mules. However, as mentioned above, the reported number of donkeys and mules in faunal reports is extremely small. The rarity of donkey and mule remains in Roman Britain has attracted the interest of several scholars in the past (e.g. Albarella, 1999; Bendrey, 1999; Baxter, 2002; Johnstone, 2004). Based on previous research, as well as by conducting a basic survey of the available resources (published and unpublished reports), the identification of both donkeys and mules are recorded at only a very small number of Romano-Britain sites (Table 1.2). For the present thesis, in order to include all cases of finds identified as donkeys or mules in Roman Britain, published reports were consulted (including those considered 'grey literature'). Additionally, an enquiry was made to the "Zooarch mailing list" (ZOOARCH@JISCMAIL.AC.UK) to which many researchers in related disciplines subscribe, including several experts and scholars who are familiar with

the faunal assemblages from this geographical region. Sadly, only a handful of responses were received and they added merely one more case to those previously gathered.

A total number of 19 cases of donkey identification and 11 mules have been recorded in either faunal reports or doctoral theses from British archaeological assemblages dating from the Iron Age to the end of Roman period (prior to 5th Century). Six donkey identifications and nine mules are either derived directly from Johnstone's results (2004, albeit not all are included in her discussion) or determined using the range of shape indices in her thesis. In other words, identification through a biometrical approach has largely increased the number of donkey and especially mule identifications. Table 1.2 summarises these cases and the method of identification employed as well as a list of sites either have large quantity of equids or with high potential for the presence of non-caballine equids. Several of the listed past identifications are considered dubious due to the lack of description on the element itself, or regarding the morphological criteria used, or to limitations in the methods applied. The latter will be discussed in detail in the next chapter after a review of the existing identification methods. Even without questioning the accuracy of previous works and considering the number of domestic equid remains recovered from excavated sites, the number of donkeys and mules remains extremely low. In addition to the lack of awareness of the possible presence of these species or the failure to distinguish different species due to the subtle differences between them, it can also be argued that non-caballine equids may have simply been rare in Roman Britain.

	Site	Element	Method	Reference
1	Danebury	Metacarpal	DFA (Johnstone, 2004)	Grant, 1984
2	Newstead Fort	Skull	Morphology	Ewart, 1911
3	Fairford, Thornhill Farm	Teeth	Morphology	Levine, 2004
4	Tripontium	N.A.	N.A.	Coy and Maltby, 1987
5	Frocester Court Roman Villa	First Phalanx	Morphology	Noddle, 1979; Price, 2000
6	Barnsley Park, Gloucestershire	Third Phalange	Morphology	Noddle, 1985
7	Hunt's House, Southwark	Articulated Forelimb	Morphology, Log Ratio on MC3	Bendrey, 1999
8	Rothwell Haigh, Rothwell, Leeds	Metatarsal	SD-GL Index	Ayton, 2011
9	St. John's School, Leatherhead, Surrey	Metacarpal	SD-GL Index	Ayton, 2012
10	Stonea	Metatarsal	DFA (Johnstone, 2004)	Johnstone, 2004
11	Thorpe Thewles	Femur	DFA (Johnstone, 2004)	Johnstone, 2004
12	Brading Roman Villa	Metatarsal	SD-GL Index, Morphology	Worley, 2013
13	Kilverstone, Thetford, Norfolk	Metacarpal	Log ratio	Higbee, 2006
14	Wainscott, Kent	Mandibular teeth	Morphology	Bendrey, 2009
15	Berinsfield, Oxfordshire	Radius	N.A.	Wilson and Allison, 2010
16	Magna Carta, Herefordshire	?	Size	Noddle, 1985
17	Croydon, Lower Coombe Street, Greater London	?	Size	Yeomans, 2011
18	Staines, Elmsleigh House, Surrey	?	Slenderness	Chapman and Shanks, 1976
19	Wilcote, Oxfordshire	loose tooth	Morphology	Hamshaw-Thomas and Bermingham 1993
	Site	Element	Method	Reference
1	Billingsgate Buildings, London	Near complete mandible	Morphology, biometric	Armitage and Chapman, 1979
2	Healam Bridge, Yorkshire	Partial Skeletons	Morphology	Jaques, forthcoming
3	Beddington Sewage Farm	Metacarpal	DFA	Johnstone, 2004
4	Longthorpe	Metacarpal	DFA	Johnstone, 2004
5	Orton Farm	Metacarpal Metatarsal	DFA	Johnstone, 2004
6	Thorpe Thewles	Metatarsal	DFA	Johnstone, 2004
7	Skeleton Green	Metatarsal	DFA	Johnstone, 2004

8	Scole-Dickleburgh	Metatarsal	DFA	Johnstone, 2004
9	Castleford	Metatarsal	DFA	Johnstone, 2004
10	East London Cemetery	Femur	DFA	Johnstone, 2004
11	Hayton Fort	Femur	DFA	Johnstone, 2004
Sites with high potential for the presence of non-caballine equids				
	Site	n (%)*	Note	Ref
1	Alcester**	65 (0.63%)	possible mule	Chuang, unpublished data
2	Elms Farm	169 (2.12%)	abundant equids	Johnstone and Albarella, 2002
3	Healam Bridge**		possible mule	D. Jaques, pers. Comm.
4	Ribchester Fort**		military site	Stallibrass and Nicholson, 2000
5	Thornhill Farm, Fairford**	365 (12.75%)	possible donkey and mule	Levine, 2004
6	Tort Hill West	69 (24.24%)	high equids ratio	Albarella, 1997a
7	Winchester**	75 (8.09%)	high equids ratio	Maltby, 2010
8	Wroxeter Military Site	(0.51%)	military site	Noddle, n.d.
9	Dodder Hill	(0.88%)	military site	Davis, 1988
10	the former County Hospital Site, Dorchester	(1.86%)	abundant equids	Grimm, 2008
11	Swanscombe, Kent	(6.94%)	near complete skeleton	Reilly, 2010
12	Old Shifford Farm	88 (20.23%)	high equids ratio	Lange, 1995
13	Margate-Weatherlees Hill Pipeline	92 (4.74%)		Grimm, 2009
14	Colchester	341 (0.84%)	abundant equids	Luff, 1993
15	Piercebridge Roman Fort	150 (2.05%)	military site	Rackham and Gidney, 1984
16	Alington Avenue, Dorchester	72 (7.35%)	high equids ratio	Maltby, 1988
17	Bancroft Villa	560 (11.94%)	high equids ratio	Levitan, 1990

Table 1.3 – Known cases of donkey and mule identifications.
Note: DFA stands for Discriminant Function Analysis. It is a method used by Johnstone in her thesis and will be further explained in later chapters.
* - the percentage is calculated based on the sum of cattle, sheep, pigs, and horses.
** - these sites are used in the current thesis. The number of equids bones from Winchester is based on measured records from ABMAP

1.7 – Chapter Summary

Whilst the essential role played by domestic equids in the Roman world has generally been recognised, the emphasis in past studies has always been on horses. Possible reasons for the scarcity of non-caballine equids in the zooarchaeological record are the difficulties of identifying them and/or unawareness of their possible presence, particularly in the case of mules. Horses, donkeys, and mules are different species of domestic equids with different social status and values to their owners. Of the three, only horses are native to most of Europe whereas donkeys were foreign species to most of northwest Europe, before Roman expansion. However, fairly little is known about the process of their introduction into these regions. The presence of different domestic equids in the past can contribute important information on the socio-economic and cultural aspects of societies and, therefore, it should be further examined. In this chapter, in addition to discussing the implications of the presence of non-caballine equids in Roman Britain, the difficulties of donkey keeping and mule breeding mentioned in Roman written accounts and modern veterinary perspectives are explored in the context of the introduction of donkeys to Britain by the Romans, and their breeding of mules. And finally, the current understanding of provisioning models of Roman equids and known records of non-caballine equids in Roman assemblages are reviewed.

While the ultimate goal of the current project is to examine the different procurement strategies of domestic equids in Roman Britain, this cannot be achieved without correctly determining the species of archaeological domestic equids. As a result, the first part of the current thesis aims to advance the identification methods for separating the three major domestic equids, and by using domestic equids in Roman Britain as an example to investigate the species representation ratio based on suggested identification methods. The

second part of the thesis will be a first attempt at determining the "localness" of the Roman domestic equids through isotopic analyses.

This thesis, therefore, comprises eight chapters. Chapter 1, gives a general background addressing the importance of the issue under study. As the first part of the thesis, Chapter 2 critically evaluates existing identification methods commonly used to separate different domestic equids. Chapters 3 and 4 present suggested modifications and improvements to the existing methods as well as the newly proposed techniques respectively. Results of species determinations are then summarised in Chapter 5, which provides an estimation of frequencies of domestic equid species (horse/mule/donkey) as well as supporting evidence for the species identification of the teeth used for further isotopic analyses. Chapter 6 proposes the use of ancient DNA as an alternative approach for the most precise identification method in future research. The second part of the thesis begins with Chapter 7, which presents and discusses all the results from the different isotopic analyses. Chapter 8 summarises all outcomes from both approaches and discuss the implication of current outcomes on different domestic equine procurement strategies in Roman Britain.

Chapter 2 - Equid Identification: Existing Methods

2.1 – Introduction

This chapter critically evaluates some of the identification methods that have been used by other scholars, and reviews the identification of specimens assigned to donkeys and mules in publications/reports listed in Table 1.2.

A thorough critical evaluation of most existing techniques used in identifying equids to species-level has been carried out by Johnstone (2004). In her evaluation, she discusses the advantages and disadvantages of the methods used for this purpose, and she introduces her use of Discriminant Functions Analysis (DFA) on measurements of different post-cranial long bones to distinguish between different species of domestic equids. A decade has passed since her thesis, but very little has changed on the subject of species identification except that more people considering Johnstone's slenderness index as an indirect method for separating domestic equids (e.g. Ayton, 2011 and 2012). To avoid repetition, this chapter will focus only on the main methods: morphological criteria and three different techniques of biometric analysis. Whilst these methods seemingly provide the solution to the challenge of equid identification, little has been done to test their validity and consistency. As a result, this chapter will also begin exploring the possibility of newly developed methods. Some of these methods will form the backbone of species identification in the present thesis and so will be discussed in more depth in the following chapters. However, the main aim of this chapter is to outline the main methods adapted by faunal specialists and to examine their practical efficiency and accuracy.

2.2 – Qualitative methods: species determination through morphological traits

The most direct approach for zooarchaeologists to identify various animal remains to taxon level is by using anatomical differences in analogous skeletal elements (i.e. metacarpals in cattle and horses) that are a result of evolutionary adaptation and/or history. The differences between taxa are usually apparent and can be distinguished with basic training, although some might be harder to identify than others and require the examination of more specific criteria (e.g. sheep and goats). Identification of animal remains to species level in closely related taxa, on the other hand, can be very problematic due to the subtle nature of the differences and, in the case of horses at least, large intraspecific variability. Thus, in such cases, the availability of large, adequate comparative collections that encompass the variability within taxa is critical. However, it is evident from previous studies on domestic equids (e.g. Johnstone 2004) that comparable modern mule samples are extremely rare in archaeology departments and museums. This has led to a limited understanding of the physical distinction between horses and mules, thus making the identification of domestic equids to species level extremely difficult. In addition, there seems to be a lack of understanding of the differences between these two equid species in terms of their cultural or economic impact. Both factors have resulted in the identification of most equids in Roman faunal assemblages as “horses” with little or no mention of the possible presence of mules.

Since comparable reference collections are limited, the next best option would be the use of detailed illustrations of the minor differences from published works (e.g. Armitage and Chapman, 1979; Peters, 1998). However, one must remember that these illustrations are made specifically to manifest the differences and thus the differences may have been embellished to signify the characteristics and may be subjective. Several studies have

provided detailed illustrations demonstrating the differences between horses and mules (Armitage and Chapman, 1979, Eisenmann and Beckouche, 1986, Eisenmann, 1986, Peters, 1998, Uerpmann and Uerpmann, 1994, summarised in Johnstone, 2004). All of these criteria require a certain level of completeness and reasonable preservation of the remains to allow an accurate determination from observation. All these subtle differences in physical traits are summarised and described in full in Johnstone's work (2004) and will be only briefly discussed here. However, it is necessary to point out that none of these traits have been adequately validated, mainly due to the lack of mule samples; no cross-validation has been carried out to test the consistency between the morphological traits and other existing methods. The major concern regarding these morphological traits is that the representativeness of the mules used to establish these traits is unknown. In other words, it is still uncertain if horse-traits are present only in horses, and mule-traits can only be found in mules, or if there will be horses that "look like mules" and vice versa. Most researchers suggest that mules inherit several traits from their donkey fathers, thus making them distinguishable from horses (Johnstone, 2004). The assumption that mules inherit characteristics from their father (donkey) is probably based on easily observable external characteristics such as the longer ears of mules which are always more similar to donkeys', in addition to the slenderness of limb bones in modern specimens. But this may not be valid for skeletal elements, including teeth. In fact, very little is known about hybrid heredity in skeletal elements to be certain that it is impossible for a mule to inherit some of these claimed distinguishable traits from the mother (horse) instead from the father (donkey). In other words, these morphological traits may represent mules that have inherited donkey characteristics, but they cannot represent mules that have inherited horse characteristics, and there is no evidence showing such mules do not exist. As a result, using these morphological traits, validated or not, we may be able to identify some mules that

have inherited donkey characteristics, but mules that have inherited horse characteristics will still be wrongly identified.

While observing morphological differences provides a simple and direct approach to species identification, the similarity between these two taxa has made distinguishing between them extremely challenging, and the accuracy of the outcome is currently unknown. It seems that subjectivity may also bias the determination in favour of the more common species (i.e. horses). Furthermore, the completeness of the bones will affect the feasibility of the method. For example, skulls have been suggested as having a number of clear traits that allow mules and horses to be separated easily. Bennet (2008a) argues that mules tend to inherit their heavy heads from the father and, therefore, the angle between the occiput and forehead can be used to distinguish mules from horses. This method can be used only in the rare occasion when skulls are found well preserved. In the great majority of cases, however, complete equid skulls are rare in the archaeological record. The following section will briefly describe the morphological criteria that have been used to distinguish between domestic equids and will discuss their practicality with modern or archaeological samples.

2.2.1 – Dental Morphology

The morphology of the occlusal surface in both the upper (maxillary) and lower (mandibular) cheek teeth of equids is often regarded as showing the most reliable morphological criteria for the distinction between domestic equine species (Armitage and Chapman, 1979; Davis, 1980; Eisenmann, 1986; Uerpmann and Uerpmann, 1994). However, the lower dentition has been used more commonly than has the upper for this purpose (e.g. Armitage and Chapamn, 1979; Uerpmann and Uerpmann, 1994, Levine, 2004, Bendrey, 2009) and, therefore, more emphasis will be given to the former in this

study. The first and second molars are believed by some scholars to provide more reliable identifications (Davis, 1980), and thus these are commonly used as evidence to attest to the species of equids in zooarchaeological assemblages (e.g. Armitage and Chapman, 1979; Levine, 2004). Nevertheless some researchers argue that all lower cheek teeth can, and should be used for identification (Payne, 1991; Uerpmann and Uerpmann, 1994). The earliest archaeological application utilising the lower dental morphology can be traced back to Armitage and Chapman (1979), who argued that a distinctive 'V'-shaped pattern can be observed on the linguafelxid (hereafter "lingual fold") of the first and second lower molars of mules, while a 'U'-shaped pattern is observed on those of the horses (Figure 2.1). This piece of evidence is supported by the biometric analysis of mandible measurements within the same article (Armitage and Chapman, 1979, pp.340-1). However, they also noted that this trait is known to be "variable and cannot always be used to identify species" (Groves and Mazák, 1967, as explained in Armitage and Chapman, 1979, p.343).

Uerpmann and Uerpmann (1994) used the same criterion to distinguish between mules and horses, but in addition, they supported their identification using morphological criteria in maxillary teeth. It has been suggested that the same characteristics in the occlusal morphology can be used to distinguish between horses, asses, and half-asses (Eisenmann, 1986). Eisenmann argues that a U-shaped lingual fold pattern is commonly found in *E. caballus* (horses) whilst the V-shape is characteristic of *E. asinus* (asses and donkeys, see Figure 2.2); she notes, however, that this trait is not always present in half-asses (Eisenmann, 1986, pp.75-6). In addition to the lingual fold, Eisenmann further argues that the length of the ectoflexid (hereafter "buccal fold") can also be used as a criterion to distinguish between equids; *E. caballus* is often associated with a deep/long buccal fold whereas *E. asinus* shows a shallow/short one (Eisenmann, 1986, and Figure 2.3 below). In contrast to their parent species, mules' mandibular teeth are regarded as possessing an even

deeper/longer buccal fold than that of horses which nearly connects with the lingual fold (Table 4.1 in Johnstone, 2004, p.165).

The variations in dental morphology based on qualitative traits, however, are challenged by Payne (1991), who uses quantitative data to test this criterion. He concludes that the intraspecific variability of the lower dentition overlaps between two very different equid species from two different sites. According to Davis (1980), molars are more reliable than premolars for specific determination, but he also warns that dental morphology may not be consistent even within the tooth row of a single individual and, therefore the identification of isolated teeth is unreliable. Nevertheless, Payne (1991) suggests that species identification is still feasible if all cheek teeth are present.

Unfortunately, the detailed process of how species determination is carried out when contrasting characteristics are observed in different teeth from the same mandible is not explained. As an example, the mandible of a modern Shetland pony from the reference collection at the University of Southampton (604) shows an inconsistent morphology in its mandibular teeth (Figure. 2.4). The lingual fold of the third premolar and second molar forms a more pointed end than the fourth premolar and the first molar. Even if the premolar is excluded, the dental morphology of the second molar still resembles more closely the traits regarded as being characteristic of mules; in this, it is dissimilar to the first molar. As a result, without detailed quantitative analyses, the inconsistency in the morphology of enamel patterns in molars may lead to dubious determinations. In addition to the difficulties mentioned above, the situation is further complicated by age and/or pathology-related changes (Johnstone, 2004, p.163; Figures 2.5a and 2.5b)

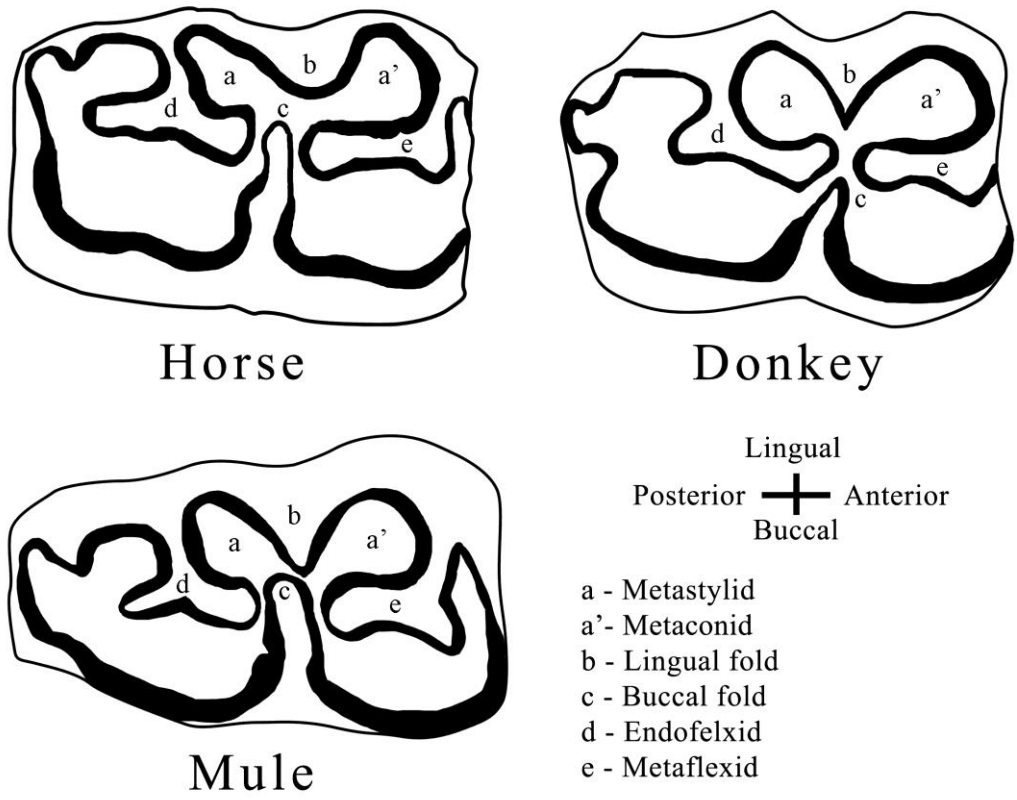


Figure 2.1 – Dental pattern in three major domestic equids

Horse: The metastylid (a) and metaconid (a') in horses are not symmetrical. The metastylid is often more elongated than metaconid. The "U"-shaped lingual valley (b) is considered to be a typical caballine trait. The buccal fold (c) shows a partial penetration in horses and, therefore, the bucco-lingual distance in horses is shorter than donkey, but larger than mule.

Donkey: The metastylid (a) and metaconid (a') in donkeys are symmetrical. Both metastylid and metaconid are much more round comparing to horses. The "V"-shaped lingual valley (b) is considered to be a typical asinine trait. The buccal fold (c) shows no partial penetration in donkey and, therefore, the bucco-lingual distance is largest in donkeys.

Mule: The dental morphology of mules is argued to be more donkey-like. That is the symmetrical and round metastylid (a) and metaconid (a'), as well as the "V"-shaped lingual fold (b). The only main difference is the extremely short bucco-lnigual distance (c) deep penetration of buccal fold).

Figure 2.2 – Lingual fold pattern in caballine and asinine
Left (A): Caballine U-shape - Observed mostly in horses.
Right (B): Asinine V-shape - Observed mostly in donkeys. (images from Hite, 2008)

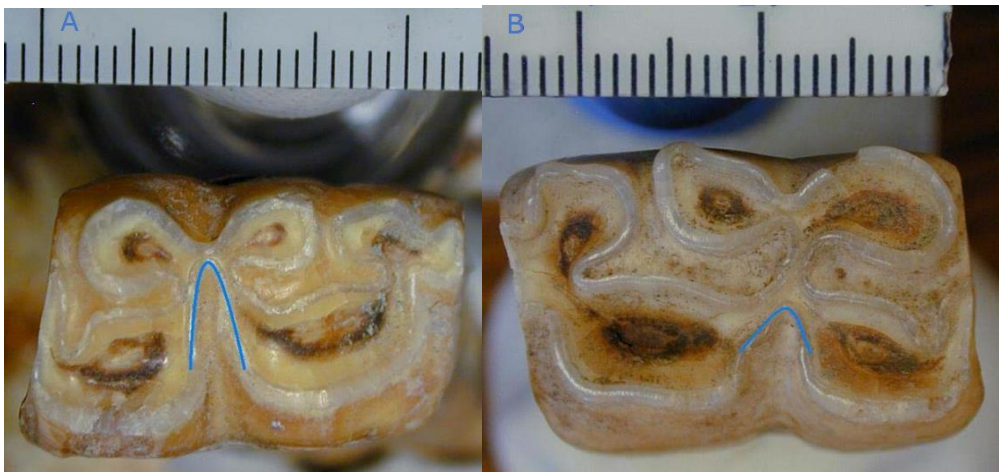


Figure 2.3 – Buccal fold penetration in caballine and asinine
Left (A): Caballine mandibular teeth with deeper/longer buccal fold.
Right (B): Asinine mandibular teeth with shallower/short buccal fold. (Images from Hite, 2008)

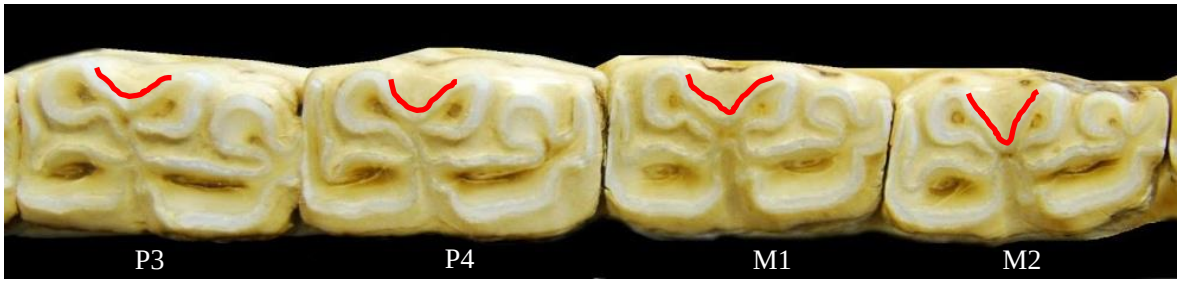


Figure 2.4 – Left mandible of a modern Shetland Pony. (604, Department collection, University of Southampton)
From left to right: third premolar (P3), fourth premolar (P4), first molar (M1), and second molar (M2). Note that the premolars are more of U-shaped than V-shape, whereas M2 are V-shaped.

Figure 2.5a – Different stage of wear
Left: Extremely worn molars, no lingual fold or buccal fold pattern can be observed. (from Winchester, NR75-557) Right: Teeth (probably M2) not in wear, also no pattern can be observed. (from Winchester, VR74-434).

Figure 2.5b – pathological or non-metrical variation (from Winchester, HA74-401)

The description of the morphological criteria for the discrimination of the maxillary teeth in equids is based on Uerpmann and Uerpmann's work (1994), and is summarised by

Johnstone (2004, pp.164-5, Table 4.1 and Figure 4.3, shown in Figure 2.6 below). Uerpmann and Uerpmann (1994) point to the presence of the *pli(ca) caballina* and the symmetry of the protocone as being characteristic of horses (Figure. 2.6). However, the differences between horses and other equid species in these traits are very subtle, thus making taxonomic determination rather challenging. There has been little use of these criteria in zooarchaeological studies and thus their reliability is uncertain. However, both criteria appear to be inconsistent in the skulls of modern horses and donkeys in the reference collections of the University of Southampton (137, 604, DC209, and 132).

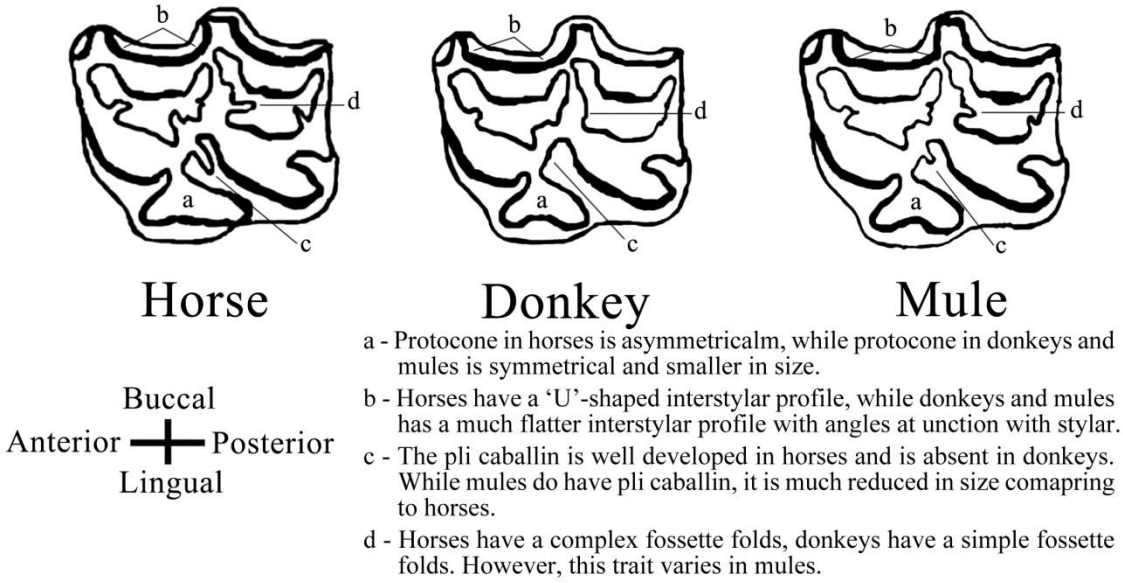


Figure 2.6 – Dental morphology of maxillary teeth in different domestic equids. (after Johnstone, 2004)

2.2.2 – Post-Cranial Morphological Traits

Although postcranial bones attract less attention than cranial elements in the taxonomic determination of equids, morphological criteria to separate equid species have also been suggested for this purpose. Peters (1998) carried out a detailed comparison of postcranial elements of horses and mules; however, these have not been widely applied to separate mules from horses. Very few bone reports in Britain are known to follow his criteria,

certainly at least partially due to the original work being published in German; only in 2004 were they summarised in English by Johnstone (2004). Furthermore, these morphological traits may be evident in modern, well-preserved samples, but they are unlikely to be observable in most archaeological materials. Figure 2.7 to 2.11 summarise all post-cranial morphological traits proposed by Peters (1998, images from Johnstone, 2004) to distinguish mules from horses. It must be mentioned that Johnstone's work (2004) only summarises the criteria within her literature review (her actual identification is done through biometric analysis which will be discussed later in this chapter). It is surprising that, while Johnstone was aware of these criteria and had measured several mule skeletons in her data-collecting process, there is no mention of whether these criteria were also observed in her modern samples. Recently, through Johnstone's work (2004), more researchers have become aware of Peters' morphological criteria. Nevertheless, the only case of mule identification using Peters' (1998) criteria reported for a Roman site in Britain is from Healam Bridge (D. Jaques, forthcoming, see section 3.3.2).

In addition to unfamiliarity with Peters' work, the difficulty in practically applying these criteria is probably a further reason why they are not commonly used. While the illustrations depict clear differences between horses and mules, most of the time, the actual elements present an intermediate morphology. For example, the horse tibiae from the comparative collection at the University of Southampton (Specimens 123, 137, 604, and 132) vary, ranging between two extremes when compared with Peters' illustration (1998) (Figure 2.12). Like most guides for comparative anatomy used in archaeology, although the descriptions are as objective as possible, it is still up to the observers to decide whether the examining elements meet the criteria or not.

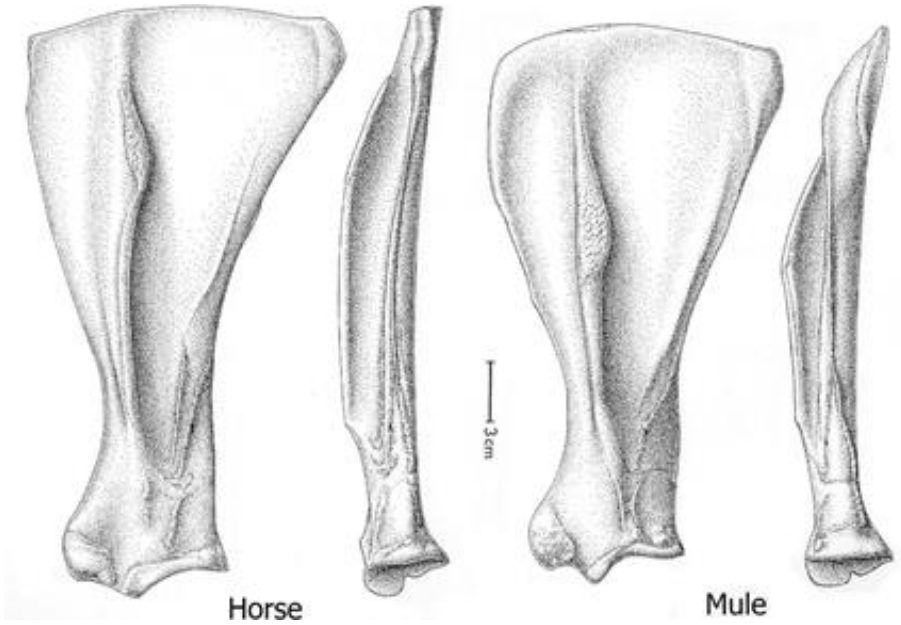


Figure 2.7 – Scapula of horse (left) and mule (right). (From Peters, 1998)

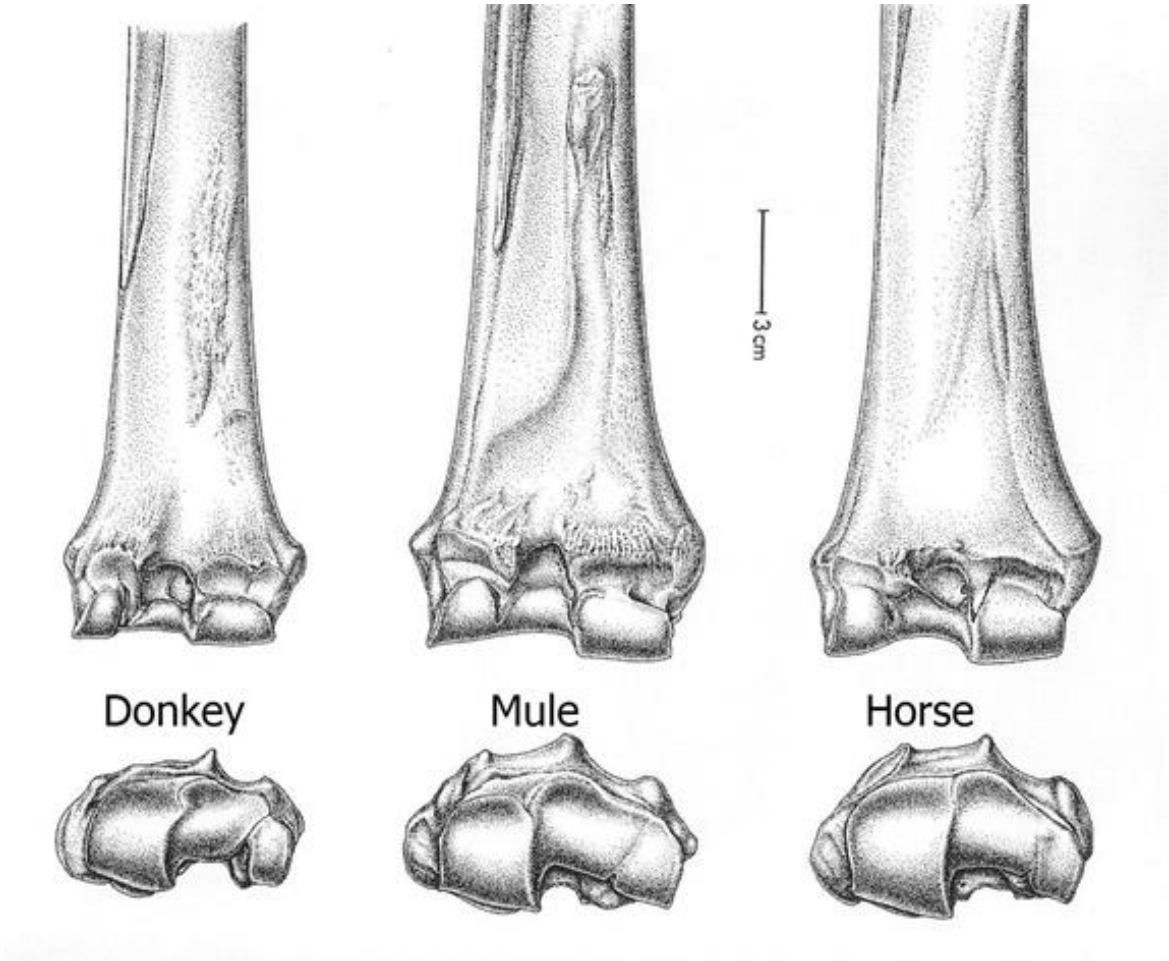


Figure 2.8 – Distal radius of donkey (left), mule (middle), and horse (right). (From Peters, 1998)

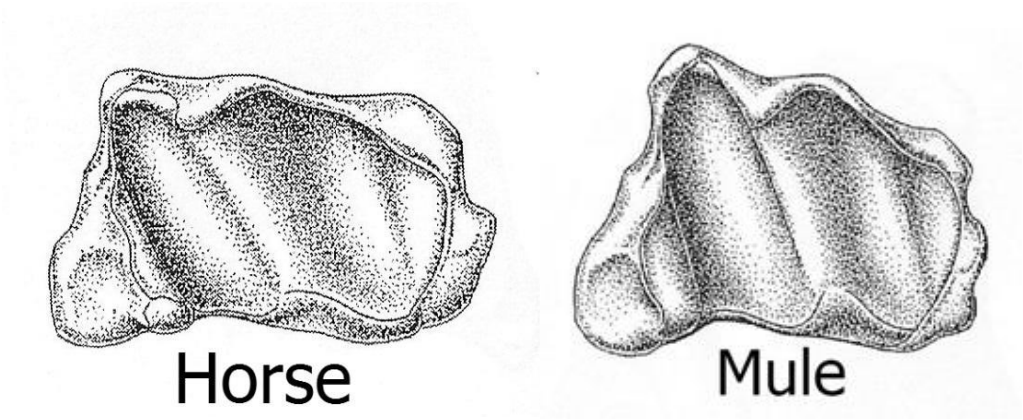


Figure 2.9 – Distal articulation of a horse tibia (left) and a mule tibia (right). (From Peters, 1998)

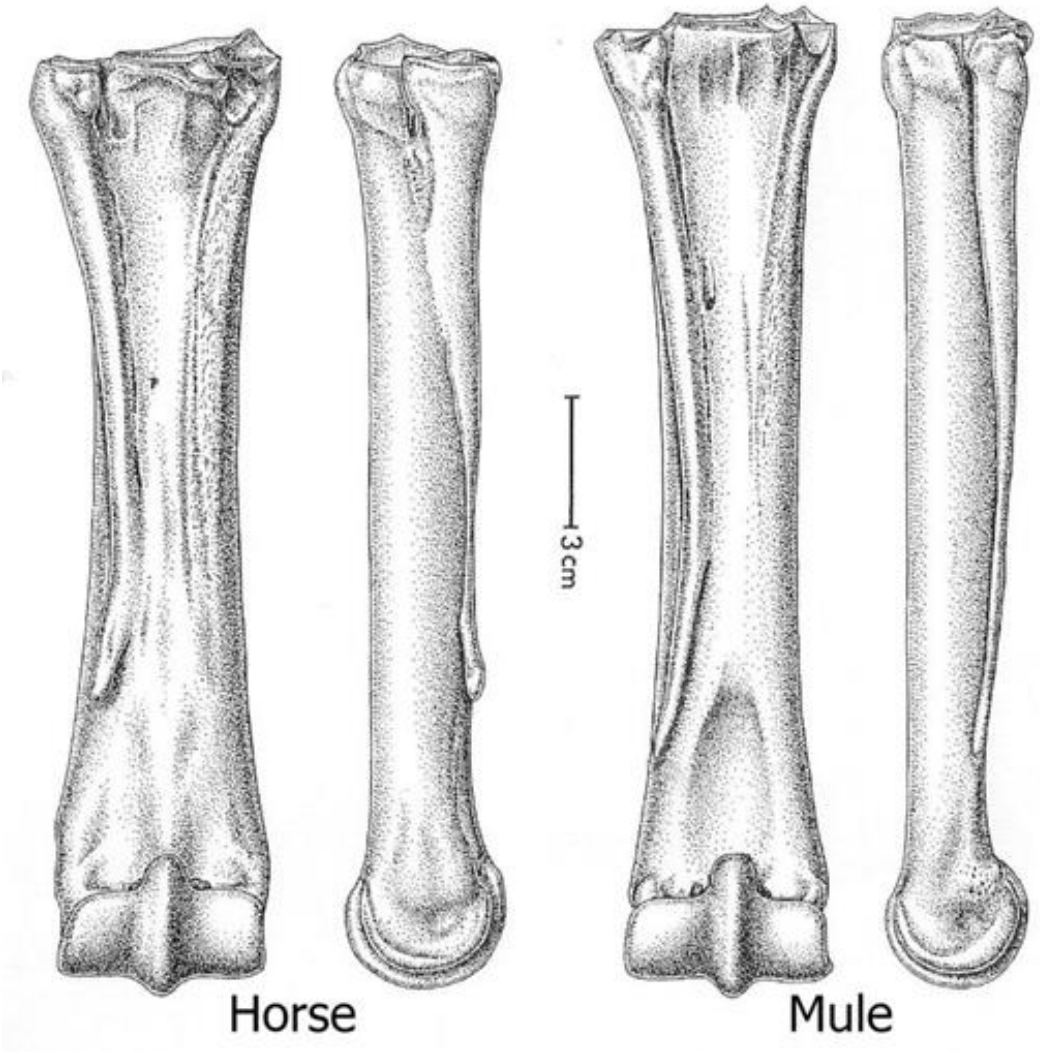


Figure 2.10 – Third metacarpal (MC3) of horse (left) and mule (right). (From Peters, 1998)

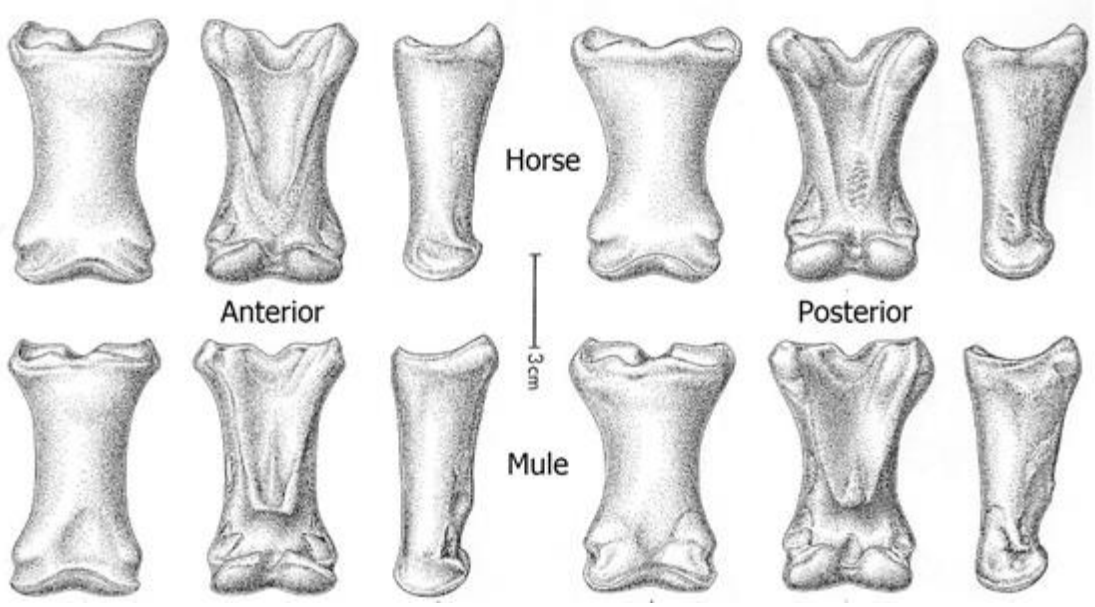


Figure 2.11 – Anterior (left) and posterior (right) first phalanx (PH1) of horse (above) and mule (below). (From Peters, 1998)

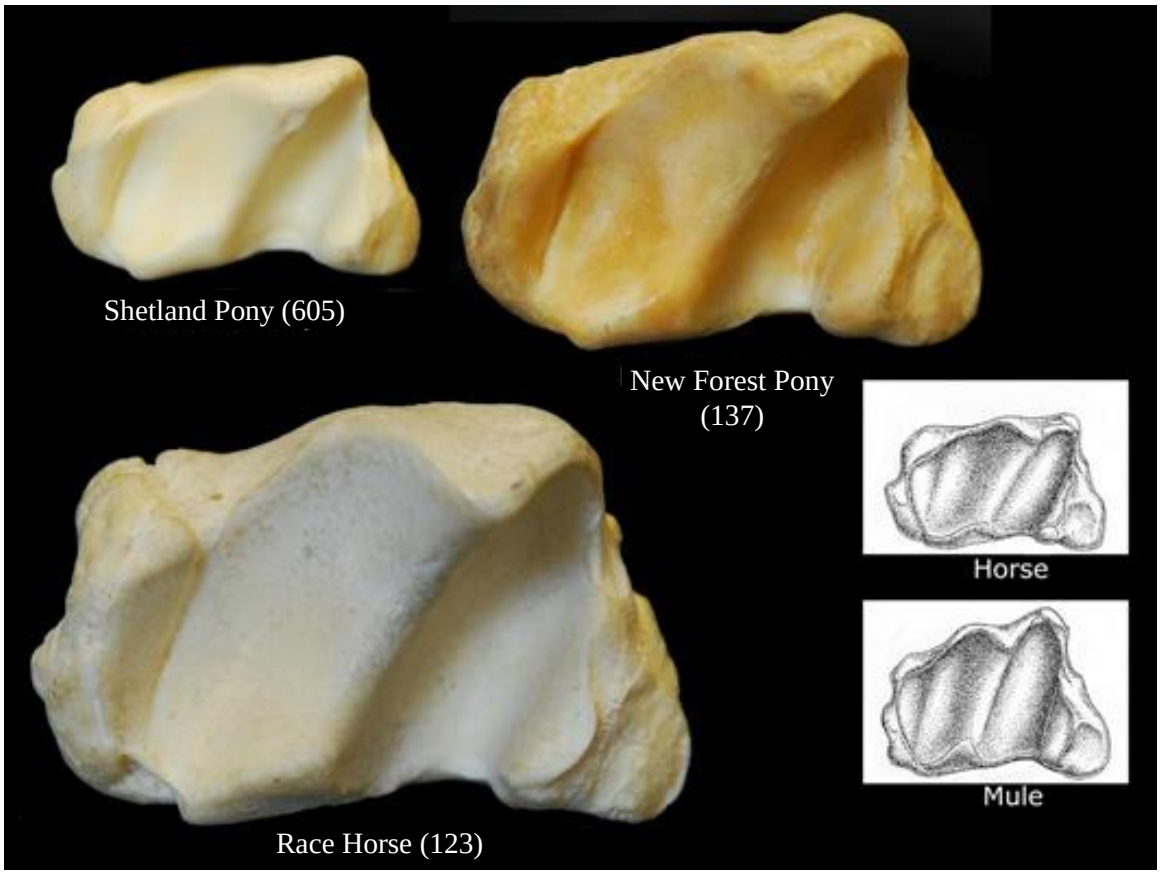


Figure 2.12 – Shape of distal tibia articulation.
Only modern race horse appears to match Peters' (1998) illustration.

2.3 – Quantitative methods: species determination through biometric analysis

It could be argued that the use of quantitative, biometric analysis would provide a more "objective" alternative to the use of rather subjective and vague terms such as "slender" or "more gracile". Through the careful measurement of the multiple dimensions of a skeletal element and the analysis of these measurements, it could be possible to identify minor differences in thickness, robusticity, and/or general proportions between species. Nevertheless, determining what the cut-off point is between two species will inevitably be subjective, given that overlaps commonly occur. The basic principle of biometric analysis resides in the assumption that bones not only differ in taxonomy which, is largely determined by evolutionary process related to the surrounding environment, but also show adaptations to a particular, individual's life-style. For example, Shackleford *et al.* (2013) suggest that domestic donkeys used as labour animals have a limited and repeated pattern of locomotion in comparison to wild asses and, therefore, it is possible to distinguish domestic donkeys (or tamed asses) from wild asses. However, it will require an immense number of specimens to build up a representative standard. The benefit of building a large database is that the outcomes can be tested statistically, and all future studies can benefit from it.

A substantial amount of research has been dedicated to the separation of different species of *Equus* using biometrical analyses (e.g. Davis, 1982; Eisenmann and Beckouche, 1986; Eisenmann, 1986; Payne, 1991; Bendrey, 1999; Baxter, 2002; Johnstone, 2004; Barrón-ortiz *et al.*; 2008; Davis, 2008) and yet, reliable taxonomic separation of mules and horses using these methods cannot be achieved. There are two main obstacles to the application of biometrical techniques in the discrimination of horses, donkeys, and mules:

i) the limited availability of modern comparative mule skeletons

ii) the large morphological variability in horses and donkey breeds

Before being largely replaced by automobiles and other machinery, domestic equids were the major mechanisms for land transportation as well as an essential power source in agricultural activities. During the course of history, intense selective breeding of horses and donkeys was exercised to "improve" the build and obtain desirable characteristics for the fulfilment of different tasks. As a result, the biometric profile of modern domestic equine samples may be quite different from those in the past. While the ideal Roman conformation for domestic equids may have remained similar to the modern ideal, particularly for horses (Hyland, 1990), the morphology of certain elements may have changed without altering the overall build of domestic equids (commonly referred to as "conformation"). For example, the change in the weight-bearing capacity may reflect the alteration of the geometrical profile of a limb bone without affecting its length. This change will not be noticed when considering the conformation, but will be amplified only during analysis of the biometrics of a particular element. As a result, the inclusion of multiple breeds, where each has been bred for specified tasks – such as large draught horses, or large mule-breeding donkeys – may bias the biometric analysis.

Despite being more "objective" than the qualitative observation of physical traits in taxonomic determination, the outcomes of biometric analyses should not be accepted uncritically. After all, biometric analysis reflects only a statistically sound determination for which a margin of error must be allowed. The reliability of the results will depend chiefly on the representativeness of the sample (dataset) used. The paradox here is that large datasets that include different breeds of horse and donkey will result in a larger overlap between different species; in contrast, a smaller dataset, restricted to one or few breeds, will result in less overlap between species, but will also be less representative.

Thus, the selection of modern samples to be included in the analysis becomes crucial when attempting the taxonomic identification of archaeological equid specimens. This will be discussed further in the next chapter.

A number of different biometric analyses have been used to distinguish equid species in the past, such as log-ratio (Eisenmann and Beckouche, 1986), trivariate morphometric analysis (Davis, 1982), multivariate analyses (Dive and Eisenmann, 1991), discriminant function analysis (Johnstone, 2004), and bivariate plotting (Davis, 2008). However, there are also a few potentially useful techniques that have never been tested by previous scholars, for example, Principle Component Analysis (PCA). Most biometric analyses have been carried out with the aim of separating wild from domestic equids. Only Discriminant Function Analysis (hereafter DFA) has been used specifically for distinguishing between donkeys, mules, and horses. In this section, two more recently developed biometric analyses will be reviewed and evaluated: DFA and bivariate plots. The section will end with an exploration of the potential use of PCA as well as introducing the concept of a geometric morphometric approach (GMM). This section will examine the practical efficiency of these formally used biometric methods and outline the concept for shape analysis as a potential identification method.

2.3.1 – Discriminant Function Analysis

DFA is a multivariate analysis technique suitable for identifying a predefined group to which a sample is more likely to belong (Hair *et al.*, 2010). It has been commonly applied in studies that aim to group different samples that can be described by different sets of quantitative data. The utilisation of DFA as a method to identify horses, donkeys, and mules is proposed by Johnstone (2004, 2005, 2008, 2010), as a potentially better method

than those based on qualitative morphological criteria. However, similar to other methods based on biometric analysis, there are limitations to DFA. This section will focus on the principle of DFA for distinguishing between horses, donkeys, and mules by describing the principles and limitations of DFA. The next chapter will further evaluate this method as one of the mainstream biometric analyses for the identification of domestic equids in archaeology. However some slight modifications are made in order to not only refine, but also to revise this method by adding a new dataset and using updated software.

As an analytical method, DFA has been gaining awareness and popularity in recent archaeological studies (DeGusta and Vrba, 2003; Barrón -ortiz, 2008; Germonpré *et al.*, 2009; Phillips *et al.*, 2009; Kovarovic *et al.*, 2011; DiMichele and Spradley, 2012, etc.) and, therefore, is inevitably being criticised for exaggerated manipulation of the data and for overstating interpretation (Kovarovic *et al.*, 2011). It is important first to understand some of the basic principles of how this analytical method works.

DFA can only be used when the dependent variable is nonmetric/nominal based (e.g. species) and the independent variables are metrical data (e.g. measurements). When the discriminant functions are calculated based on predefined groups, and then the group to which an unknown individual with the same set of variables should belong can be predicted. Thus, it is appropriate to use DFA for distinguishing between different domestic equines, and predicting the identification of unknown archaeological remains.

However, a discriminant function is, by definition, “a variate of the independent variables selected for their discriminatory power used in the prediction of group membership” (Hair

et al., 2010, p.233). Therefore, the variable selected to form the variate must be "discriminatory". In other words, the general shape of the same element from different domestic equids must be different and can be represented through their measurements. This is an essential point to remember when using DFA. If the variables, in this case, metrical data, are not significantly different between groups, then DFA will still perform to a certain degree by having overlaps between groups, but this will not represent much of an improvement over the use of qualitative morphological traits in the specific assignation of a specimen.

Simply stated, DFA will emphasise the best variate from all data (variables) entered that can best categorise all members to their predefined groups. That is to say, if the samples are best separated by length, then length will be weighted more in functions; if they are mostly different in width, then the width measurement will be accentuated. It is also important to note that DFA can only treat data as they were entered and will not be able to recognise characteristics such as robustness or slenderness as in the log index approach.

The primary purpose and main requirements for using DFA to distinguish between domestic equids seems to fit the current aim of species identification perfectly, but there are more specifications of this method that need to be fulfilled in order to allow it to operate properly. The first issue is still the problem with the availability of samples. Ideally, there should be enough of them to be separated into two groups: one to calculate the functions, and one to test it (Hair *et al.*, 2010). However, such an ideal is much less likely to be applicable in practice, especially in archaeological research. Nevertheless, it is recommended that for each group, there should be at least 20 observations or, as a minimum, for each group, the number of observations (n) should be at least one more than

the number of variables (v) (n=v+1); otherwise, the outcomes will become unstable as the number of observations decreases (Hair *et al.*, 2010, p248). The scarcity of available modern mule specimens has been mentioned several times before, but here it will significantly affect the stability of this method from the outset.

The second possible problem is the representativeness of the variables. Similar to most other biometric analyses, it is assumed that the general shape is different between domestic equids and that their measurements can reflect these differences. This is based on the assumption that the directional growth of the same element has different growth rates in different species. This is known as "allometry", i.e. the changes in shape relating to the change in size. This is in contrasted to "isometry", i.e. the changes in size without any change in shape (Klingenberg, 1998). In equids, allometric differences are usually shown in the slenderness/robustness of the limb bone. However, unlike the log-ratio index technique, which calculates the proportion of different measurements in an attempt to detect trends reflecting the slenderness or robustness of the limb bone (Eisenmann and Beckouche, 1986), DFA takes all the measurements at face value and amplifies the differences by giving more weight to those that seem more discriminatory and less weight to those that seem less so. Using the current equine limb bone as an example, a racehorse metacarpal is significantly longer than that of a Mediterranean donkey of the common breed and, therefore, using the greatest length of the metacarpal makes it possible to distinguish successfully between these two species. According to the definition of allometry, if the greatest length (GL) increased at a different rate to the smallest shaft width (SD), this difference will be represented by the change in the robustness of the shaft. Thus if GL and SD of the third metacarpal (MC3) from horses and donkeys are included in a scatter plot (Figure 2.13), it is quite clear that a linear correlation exists between the two measurements in both species (r^2 coefficient = 0.94233) and, therefore, it suggests that the

morphometric relationship between the two taxa is isometric rather than allometric. In other words, "size" in all dimensions may be viewed as most "discriminatory" when calculating discriminant functions. Therefore, if such a high linear correlation (coefficient > 0.90) exists between most dimensions, instead of separating mules from horses and donkeys, DFA will only separate large equids from medium and small ones. In addition, a high linear correlation between multiple variables is known as multicollinearity in statistic and will significantly compromise the accuracy of the prediction in DFA. The software can still perform DFA with inadequate sample size and multicollinearity, but both specifications are so critical that the result and prediction will be unstable and inaccurate if they are not fulfilled. The use of additional variable such as z-scores (Shenan, 2014) can significantly improve the accuracy of classification in DFA, but the z-score cannot be calculated for archaeological specimens of unknown species. Since more than two measurements are taken to describe the overall shape of an element and, therefore, DFA may still be applicable for evaluating the overall allometric relationship between every measurement taken if due care is paid to their linear correlations.

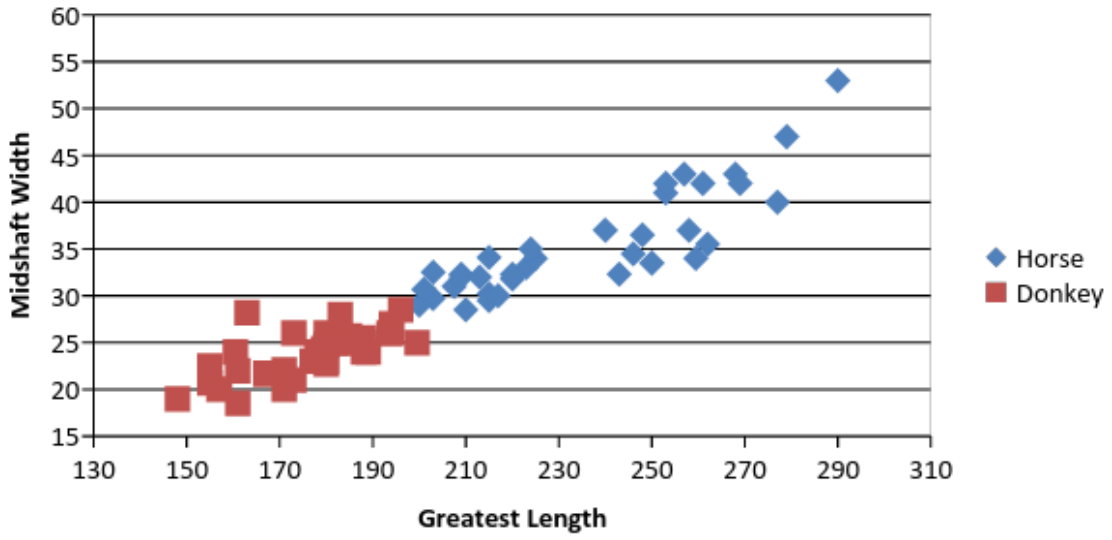


Figure 2.13 – Linear correlation between greatest length (GL) and midshaft width (B) of horses MC3 (GL>200) and donkey MC3 (GL<200) from Eisenmann's dataset.
The diagram shows the linear correlation between both dimensions in the both species; individuals with 'overlapping' sizes (e.g. ponies and Poitou donkeys) are excluded for clarity.

Although Johnstone (2004) develops a relatively detailed description of the DFA technique in her thesis, the original dataset was not available until recently. As a result, even though this method has gained much attention among researchers facing the same challenge, there have, to my knowledge, no publications by other scholars in which DFA has been used to separate equid remains. As mentioned in Chapter 1, to compensate for the absence of the original dataset, faunal specialists have turned to use the index ranges derived from DFA predictions as an indirect method for species identification (e.g. Ayton, 2011, 2012). Further comments will be made on using ranges of shape indices as a means to distinguish between domestic equid species and evaluate their impact on interpreting domestic equids in Roman Britain (see section 2.5)

2.3.2 – The "*Davis Method*": First Phalanges (PH1) Slenderness Index

An Index calculated from a number of measurements to represent approximately the general shape of an element have often been used when analysing subtle differences between groups of individuals to investigate issues such as sexual dimorphism and taxonomic assignation (Davis, 2000). Since this technique can roughly distinguish between groups according to the different shapes of elements, this concept has been used by Simon Davis as a method to distinguish *Equus asinus* from *Equus caballus* (Davis *et al.*, 2008), and thus it will be referred simply as the "Davis method". As mentioned above, the post-cranial elements of donkeys are generally assumed to be more slender and gracile than those of horses. Based on this assumption, Davis *et al.* (2008) calculated the slenderness of PH1 using the greatest length (GL) and smallest shaft width (SD) and plotted it against the distal articular facet breadth (BFd) to separate donkeys from horses. In addition to requiring only three measurements, which are usually routinely taken, this method circumvents the issue of differences between the anterior and the posterior PH1. As mentioned earlier, in most reports, it is rare that a distinction is made between these two

elements due to the subtle differences between them, and this has often resulted in the exclusion of all proximal phalanges from further biometric analysis. Nevertheless, this method has never been used to distinguish mules from other domestic equids and its validity for species determination is still unclear. In addition, it has very little statistical power to support the outcomes; that is the significance was never calculated in previous studies. However, the simplicity of the method and its success on separating donkeys from horses in previous research, makes testing its suitability to separate mules and horses with the available data worthwhile (see Chapter 3).

2.4 – Potential Biometric Methods for Equid Identification

Various multivariate analyses have recently been introduced to the field of archaeology, but only a few are applicable and appropriate for the species determination. In this section, two "mainstream" analytical approaches are introduced to explore their potential as feasible methods for identifying domestic equids.

2.4.1 – Principal Component Analysis

Principal component analysis (PCA) is a statistical method of dealing with multiple variables, which has recently attracted more attention in archaeological studies (Arsuaga and Carretero, 1994; Pizarro *et al.*, 2012). PCA is usually not used as an interpretive analytical method directly, but more often as a translating tool for explaining the relationship between data sets and, therefore, it is more commonly associated with the use of metadata, e.g. in "shape analysis" (see section 2.4.2). PCA and DFA operate in a somewhat similar fashion. Both take the original data and generate a new matrix to relocate the data. Instead of calculating function(s) based on the discriminating power of

each variable, PCA generates several principal components (PC) that give the original data different loadings, and produces a bivariate plot using the desired PC as output. PCs are generated by orienting the axis multiple times to remove all linear correlations. One of the differences between DFA and PCA is that while the former determines the likelihoods based on Mahalanobis distances to decrease the effect of linear correlation, PCA uses the Euclidean distance, since linear correlations have already been removed.

The removal of the linear correlation between data is ideal for testing the morphological profiles of equid limb bones since, as was shown above in the example of the third metacarpal (GL and SD) of horses and donkeys, some dimensions are highly correlated and they may impact DFA. However, PCA is not as ideal as DFA for species identification in the sense that PCA can only reduce the number of correlated variables but does not maximise differences between them. As a result, PCA is not efficient for predicting the likelihood of an unknown specimen. Nevertheless, PCA can still provide assistance as a useful tool to evaluate the efficiency of DFA-based predictions.

2.4.2 – Geometric Morphometric Method

The geometric morphometric method (GMM) is an analytical method commonly used in zoological and botanical research for identifying shape differences between species and breeds. It can be referred to as “shape analysis” in general; indeed, broadly speaking, it can refer to methods as simple as biometric analysis based on a few measurements or as sophisticated as comparing 3D shapes involving multiple sets of coordinates. Regardless what approach is used, the ultimate aim is to analyse the shape the data (i.e. Cartesian coordinates of defined points) are describing. Shape analysis is becoming increasingly common in archaeology, especially in zooarchaeology (Bignon *et al.*, 2005; Owen *et al.*,

2014; Seetah *et al.*, 2014; Evin *et al.*, 2015), with a number of methods and software packages being developed and adapted. However, it should be remembered that the basic concept of shape analysis is to distinguish differences between shapes using statistical approaches. There are numerous methods to compare shapes, from the simple use of distances between landmark points to the comparison of entire outlines of specimens. The important thing to remember is that *it is not the complexity of the method that determines the efficiency of the outcomes*, as we shall see in Chapter 4 and 5. Shape analysis has a long history, and it has been further adapted for similar uses in different disciplines. Thus, it is difficult to provide a comprehensive review of this method due to its complexity and the rapid advances that have been made in recent years. This section will provide a general overview of the concept of GMM.

The term, "geometric morphometric" is first used by Corti (1993) to generalise the method for different approaches of shape analyses developed by various researchers such as Bookstein (1991). The basic concept, as briefly mentioned above, is to analyse the similarity and differences in shape using coordinates of defined points. In order to compare these coordinates, it is necessary to alter some of the attributes that are irrelevant to shape; these attributes include size, orientation, and position. A shape will remain the same even if all three of these attributes are changed (Figure 2.14). Therefore, it is possible to describe an object as a shape using predefined points or general outlines and then to rescale and reorient these shapes to overlay (reposition) them on top of each other to allow comparisons to be made. This process is termed "Procrustes fitting", which repositions and orients all shapes based on the group centroid point generated by each set of coordinates. After this process, the coordinates can be further analysed under the same scale and orientation using the distance or angle of points to determine whether they are significantly different from each other.

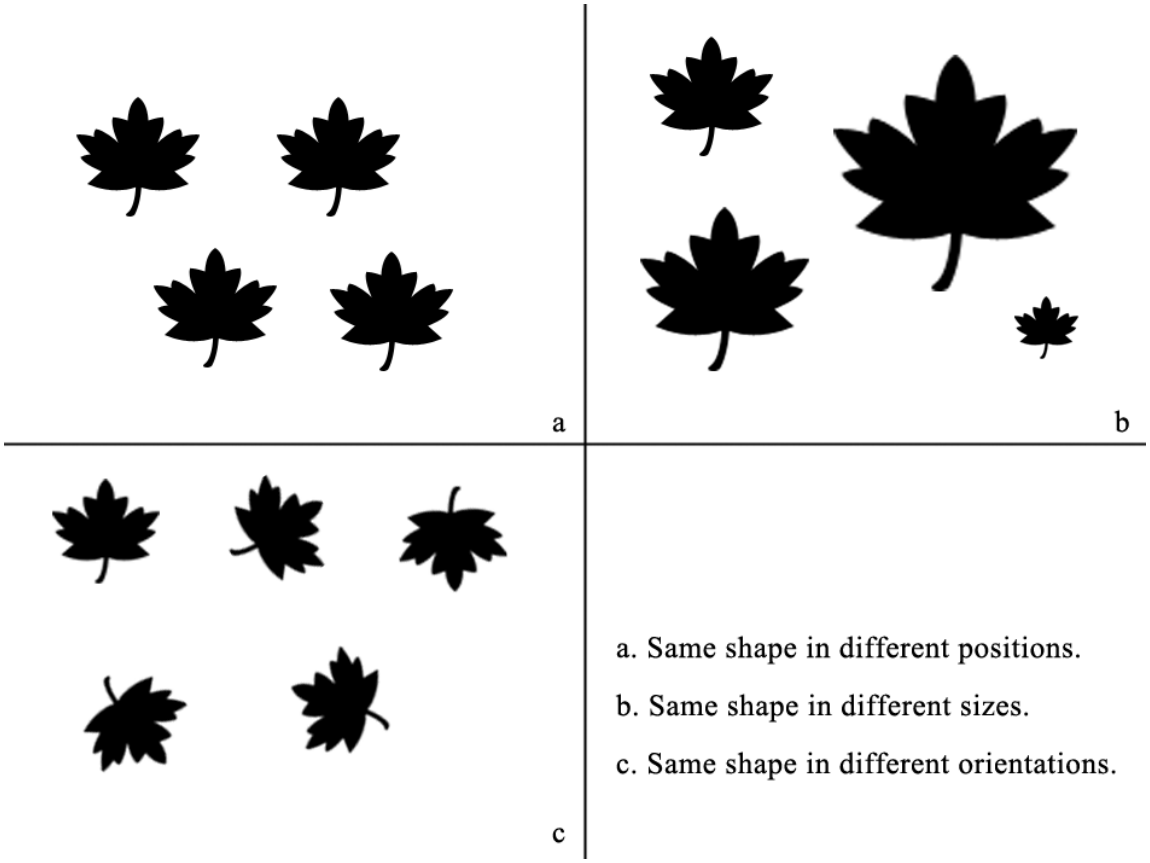


Figure 2.14 – The size, position, and orientation do not change a shape.

Strictly speaking, there are two main approaches in GMM: landmark-based and outline-based; the selection of an approach is determined by the nature of the testing subjects. For the landmark-based approach, it is necessary that there are sufficient numbers of landmarks on the testing subject to allow the shape to be correctly described. A landmark in GMM is a point that can define the shape of the testing subject and that has a corresponding (homologous) point on all specimens. Using the human face as an example, the eyes and nose can be used as landmarks because they are defining a shape and are generally present on all humans. In contrast, a chin dimple is not an ideal landmark because it does not appear on all human faces. The landmark-based approach is, however, not suitable for subjects that lack shape-defining landmarks that have a one-to-one correspondence, e.g. ovals or round subjects. In these cases, the general outline of the subject can be used instead of landmarks. It should be noted, however, that an outline is still made up by a

number of points that do not need to correspond to another set in other outlines. An outline can be open (e.g. a line) or closed (e.g. a shape) and, therefore, has an advantage in comparing not only featureless objects, but also in focusing on the part of object that is of interest.

The application of GMM has been used in the study of equids remains. Seetah *et al.* (2014) uses modern domesticated horses to investigate the dental morphological differences between breeds. Seetah *et al.* (2014) use the upper second premolars and the third molar from Icelandic and Thoroughbred horses and concludes that there is a significant difference between the two breeds. If small differences between breeds of a single species can be successfully detected using GMM, then this method may be promising for separating the arguably stronger observable differences between the three domestic equids under study. For the specific determination of domestic equids, all skeletal elements with morphological traits are potentially candidates for GMM. For example, Bignon *et al*. (2005) used the distal end of metapodials to examine if there were long distance migration of wild horse populations in the Late Glacial Europe. However, as a first attempt at using GMM for domestic equid species determination, the current thesis will use only the dental morphology of lower molars; further details will be provided later (see Chapter 4).

2.5 – Identification issues with purported non-caballine archaeological specimens

Cases of non-caballine domestic equids (i.e. mules and donkeys) recorded in archaeological literature were listed at the end of the last chapter (section 1.6). Some of these claims regarding donkey or mule identification are, however, problematic due to the lack of description and the ambiguity of the methods used in the original reports. From the

list (Table 1.2), it is clear that most of the mule identifications were from Johnstone's thesis, and that nearly half of the donkey identifications were determined either using Johnstone's DFA method directly or by referring to the SD-GL indices derived from her DFA results as supporting evidence (i.e. Ayton, 2011, 2012; Worley, 2013). An SD-GL index is calculated as follows: GL/SD x 100; it is an index that reflects the general slenderness of a limb bone. Some of the outcomes derived from Johnstone's method are not referred to individually in her thesis, since only selected elements are considered to produce more "reliable" predictions. Nonetheless, they are still used for the calculation of shape indices of different species and, therefore, will be considered as having been identified. The present thesis utilises a revised version of Johnstone's DFA method, and claims of donkey and mule identifications will be discussed in detail in Chapter 5. More attention should be paid to the three donkey identifications based on the SD-GL indices. In all three cases, species determination was based on the series of tables and histograms presented by Johnston (2004, Chapter 6). However, it should be emphasised here that Johnstone (2004) did not claim or suggest that her shape-indices could be used as an alternative to other methods to identify domestic equids.

Indeed, these shape indices were originally discussed by Johnstone (2004) in detail – divided into geological regions and chronological period, and in conjunction to DFA outcomes (Johnstone, 2004, pp.292-304) for the specific purpose of discussing the differences between domestic equids in time and space. However, perhaps due to the absence of her original data for further DFA application, researchers search for biometric criteria in domestic equids have utilised these indices as a method of species determination. The potential risk in using these shape indices directly is that they are merely a by-product derived from DFA and, therefore, the reliability has never been cross validated by the use of a dataset of known species. In other words, if the shape indices were accurate, then there would be no need to develop or use a more complicated method such as DFA in the first

place. Johnstone's aim in calculating these indices was to discuss the changes in either the size or build of domestic equids in the Roman world through time and space. She did not use these indices – or suggest that they should be used – as an identification method. This is in all probability because the degree of overlap between species would render the method inadequate as an identification technique.

For example, using the broadest ranges of SD-GL index, which consider only the metacarpals (MC3) of the "identified" individuals from the Roman period in Johnstone's thesis (2004), the ranges of the three major domestic equids are as follows: horse 12.13 - 16.89 (mean=15.01), mule 13.05 - 15.84 (mean=14.52), and donkey 12.53- 14.96 (mean=13.55). While their means suggest differences in the slenderness in the metacarpals of these three species, the range for horses clearly overlaps both mules and donkeys. A similar situation is found with the metatarsals (MT3) (Johnstone, 2004, pp.317-341). The ranges for Roman metatarsals are as follows: horse 10.10 - 14.40 (mean=11.83), mule 9.40 - 12.37 (mean=11.14), and donkey 9.53 to 11.43 (mean=10.65). Again, the level of overlap between the three species makes identification based on the SD-GL index rather questionable. Not all measurements are given for the three cases identified as donkeys based on their SD-GL indices, and some ranges are obviously misquoted (i.e. Ayton, 2011, 2012). As a result, the identifications of these specimens as donkeys should be reconsidered albeit one of the metatarsals from Brading Roman Villa (Worley, 2013) is unusually short (GL=216mm) compared to other archaeological equid metatarsals.

Some of the remaining donkey identifications are also dubious because of the lack of details on the specimen themselves and the criteria used to distinguish them. For example, according to the site report, the earliest Roman donkey identification from Newstead Fort

was based on a complete skull (Ewart, 1911). However, there is no mention of whether the identification was based on the morphology of teeth or on the overall shape of the skull. Furthermore, no photographic or illustration is given for this skull. Similarly, very little information is provided by Noddle (1979) to support her identification of the donkeys from Frocester Court and Barnsley Park, both in Gloucestershire. For the Roman villa at Frocester Court, inconsistent information is given for the identification of a number of equid specimens. Noddle (1979) argues for the presence of donkeys on the basis of the unusually short greatest length (GL) of a metapodial (there is an inconsistency between the text and the table regarding whether this is a metacarpal or a metatarsal). However, the final site report (Price, 2000) states that three donkey bones, all first phalanges, were identified; no mention is made of the metapodial. The GL measurements listed for equid first phalanges from the same report are also extremely unusual, with 10 GL measurements out of 23 first phalanges under 50mm. Using Eisenmann's factors for small ponies (2009), first phalanges with a GL this short will give a maximum estimated withers height of 80 cm. Given that such a withers height is much too short compared to the size of the modern small Mediterranean donkeys (roughly between 90 to 120 cm), it is very likely that these records contain some errors. However, unless the assemblage is re-examined, the identification of specimens as donkeys may never be confirmed. For Barnsley Park, the only information provided for the identification of a third phalanx as that of a donkey is as follows: "A 3rd phalanx, which undoubtedly came from a donkey, was found dating from the pre-villa phases. This must be one of the earliest occurrences recorded in Britain" (Noddle, 1985, p94). Although there are differences between the small and narrow hooves of donkeys and the larger and wider ones of horses, it is difficult to accept such a description as objective evidence for the presence of donkeys without additional information such as a photograph showing the specimen comparing the hooves of known donkeys and horses. This is rather important especially when there are no claims in the

relevant literature that the 3rd phalanx has distinguishable characteristics. It could be argued that the small-sized local horses known to have existed in Iron Age Britain may lead to misidentifications as pointed out by Harcourt (1979, p.153). While it is understandable that due to publication costs, faunal reports are often limited in the number of pages, photographs and figures, and tables (including measurements), that may be included, the implications of the identification of these specimens for understanding the presence and provisioning of donkeys (and mules) in Britain, which will provide further insight into past human-animal relationships, would certainly have merited a more detailed description.

Regarding the metacarpal from Hunt's House (Bendrey, 1999), it was found in articulation with a radius and a partial humerus. In addition to the morphological traits in the radius, Bendrey (1999) utilised the data from Eisenmann and Beckouche (1986) to create a log-ratio diagram to compare and determined that this individual was more likely to be a donkey. However, the measurements from this metacarpal are also used in Johnstone's DFA (as well as in the DFA in the present thesis – see Chapter 5), and both fail to characterise this individual as a donkey. Further comments will be made regarding this specimen (section 5.3.1.2), but it seems that the evidence supporting its identification is rather slim.

Judging from the above, most identifications of mule and donkey either lack objective evidence (illustration or proper description of the criteria used) or show a mis-application of the biometric criteria. As a result, very few cases of donkey and mule identification are unambiguous, and most of these are based on dental morphological traits, e.g. Armitage and Chapman (1979) and Levine (2004), although the photograph of the latter is not

included in the publication (Levine, pers. comm.). The present thesis include the Roman Britain samples from Johnstone's dataset (2004, including the Hunt's House metacarpal), as well as the material from both Fairford (Levine, 2004) and Healam Bridge (D. Jaques, forthcoming) for further analysis, and the outcomes will be discussed in Chapter 5. Unfortunately, no reply was obtained for an application for access and sampling of the mandible from the Billingsgate site housed at the Natural History Museum, London.

2.6 – Further comments on species determination

According to the review of donkey and mule identification (see above), several "basic criteria" or assumptions have been made – either explicitly or implicitly – when determining the species of an unknown (domestic) equid. Size and slenderness are the two criteria that have most frequently affected species determination, perhaps subconsciously, and thus undermine one's ability to inspect the specimen more objectively. This section will further explore their possible effects in the identification of domestic equids.

2.6.1 – Size

Size is usually the first thing noted in the process of identification, and it may have influenced species determination. Most faunal specialists are aware that horses in the past – including Roman times – were notably smaller in Britain than their modern counterparts, before serious efforts to improve the size of horses were made during Henry VIII's reign (Thirsk, 1984). However, the visual impression may still induce some bias. For example, when making a direct comparison of an archaeological specimen against a much larger modern horse (particularly the improved breeds), the difference may lead to the rejection of an identification as "horse". Such bias may not exist if the archaeological specimen is

first compared with an unimproved breed of horse, such as a pony. In addition, preconceptions on the size of these animals may also influence species determination. Although farmyard animals are less regularly in contact with modern urban-dwellers (which, presumably, most of us are likely to be), images of horses and donkeys still constantly appear in either films or books, and whenever these images are used, regardless of the time frame of the content, the horse is typically shown as being a significantly larger animal than a donkey. Ultimately, this has created a stereotype of their relative sizes, which may have led to the assumption that these domestic equids can be discriminated objectively through biometric analysis. There is no doubt that the use of quantitative data in species determination can eliminate some of the effect of "stereotyping". However, even if we are able to objectively distinguish modern domestic equids based on their biometric differences, how well these modern samples represent the domestic species that have been greatly improved and continuously modified in the past few hundred years?

Despite the fact that a wide range of withers heights for Roman horses has been estimated based on archaeological speciemens (assuming species identification is correct), the consensus on the average withers height range of Roman horses seems to be between 12 and 14 hands (121.92 to 142.24 cm, e.g. Rackham, 1995, p.170, Figs. 128). This completely overlaps with that of wild asses (*E. africanus*) and what is considered as the standard withers height for a modern common donkey (Orhan *et al.*, 2012; Kugler *et al.*, 2008). Very little is known about the morphological or size changes that occurred to donkeys after their domestication, and unless they were significantly smaller than their wild relatives (*E. africanus*) in Roman times, then they would have had a withers height range similar to that of some horses. Furthermore, according to Aristotle (*Hist. An*. Book VI-36), the onager (*Equus hemionus*) was referred to as a "mule" (half-ass, *hēmi-ónos*) in ancient Syria because they resembled this domestic species. He further explained that they

were different species because, unlike mules, onagers were fertile, confirming that he was not referring to other equine species. If size were one of the physical similarities shared by these two equine species in addition to the long ears, then the withers height of mules would be about 10.75 to 12.5 hands (109 to 127 cm), which would actually be similar to both modern donkeys and small Roman horses. It must be mentioned that the onagers that Aristotle depicted are probably the extinct Syrian onagers, the smallest sub-species. In addition, it is important to understand that while "size" is considered as a virtue for mules in modern times, given that they are bred mainly as large labour animals for heavy ploughing, such use did not exist in Roman times due to the lack of a proper equine harness (Langdon, 1986). For pack animals, size really did not matter because the carry capacity of domestic equids seems to be related to species/breeds rather than size (e.g. Hyland uses the carry weight to size ratio between pony and riding horse, 1990, p.72). In contrast, in addition to the increased amount of food required for larger mules, they would also be more difficult to load (the taller they are, the higher up people need to lift the load). All the above suggests that the size between these three domestic species may not have differed as significantly as represented by modern perceptions. As a result, size cannot be relied upon as a morphological feature for species determination and extreme precaution needs to be taken when interpreting the biometric data.

2.6.2 – Slenderness and robustness

A further issue in distinguishing different domestic equine species is the assumption of the different robustness/ slenderness among species. As mentioned above, shape indices presented in Johnstone (2004) were used in order to discuss the variability of domestic equids, both chronologically and geographically. One of the reasons that the shape indices seem to be separating species neatly in Johnstone's thesis is that the specimens used to calculate the indices were determined by another method (namely DFA), which had

already grouped them based on similar considerations (see Chapter 3). However, since they were used to examine further the changes of determined species in time and space, their accuracy was not an issue for her discussion. Among these shape indices, the SD-GL index – representing the general robustness/slenderness of a long bone – is most commonly used as a criterion for species determination. The risk of using this index directly is that there is not enough evidence supporting its accuracy as a method for distinguishing between different species of domestic equids. In particular, the robustness of horse limb bones varies considerably depending on "breed" (e.g. Arabs versus most pony breeds) and possibly castration of stallions in their early years.

As discussed in Johnstone (2004, p.111-5), it is difficult to assess the effect of castration in Roman equids. It is suggested that since horses were castrated after four years of age (when most epiphysis of limb bone are fused), they are more likely to have much more robust limb bone than those of jacks, which were castrated much ealier in life (about two years of age). However, very little is known about the castration of mules. Modern breeders recommend the castration of john because they can be as aggressive as stallion even if they are infertile (Smith, 2008). Therefore it is assumed that mules were also castrated in their early years since they were not used for breeding and were mainly used as packed animals. As a result, while it is possible that some mules (i.e. castrated johns) might have more slender bones as the result of early castration, those of uncastrated mules may not be differientiated from those of horses. On the other hand, since stallions were castrated much later in life in Roman time, it is less likely to have a casreated stallion with slender limb bones to be misidentified as mule.

In addition, present available knowledge of bone robustness in hybrid species such as mules is too scarce to warrant its use as a criterion to separate it from the other domestic equids. While it is true that available metric data gained from modern samples of known species may suggest that one species has a more robust or more slender long bone than others, at best, this can only be used to increase the plausibility of analyses. It should not be forgotten that a degree of overlap exists between species. One way to strengthen the claims of an identification is through the use of other measurement or indices, in addition to robustness/slenderness (e.g. Davis method, see Chapter 3). Additional factors will allow different aspects of long bone geometry to be taken into consideration and will avoid the determination being monopolised by a single index.

Given the high degree of similarity between these domestic equids, the subtle differences between their skeletal morphology require a more comprehensive examination. One difference detected in one method or element may not be significant in another. As a result, the current thesis aims to use different methods in an attempt to test their accuracy, but also to use the outcomes to cross-validate morphological traits that have been claimed to characterise different equid species.

2.7 – Chapter Summary

Most faunal specialists are probably aware of the main methods used to distinguish between different domestic equids and may have used them either directly or indirectly. Nevertheless, very little attention and effort is being made to validate or cross-check these methods. As a result, their reliability and consistency is still questionable. The use of qualitative morphological traits is no doubt the most direct and cost-effective method of

determination. However, one must be aware of the risks involved when there is no comparative collection physically available (i.e. mule), and the identification can be made only through illustrations and text descriptions. This is especially true when these illustrations and descriptions may have been created using only a very small number of modern samples. Not to mention that there is no consideration of the impact of recent selective breeding (particularly on the infertile species, which can represent only their immediate parents) and contemporary standards for the ideal beast-of-burden. Even though biometric analyses may be more objective in nature than qualitative criteria, it is crucial to understand the limitation of the statistical methods employed and to be cautious when selecting representative samples.

Perhaps due to their more recent history, both the DFA and Davis methods have not been widely utilised. For DFA, this may also have been due to the complexity of the method – namely, the involvement of statistical concepts and software – or to the absence of the original dataset to carry out the analysis. However, several publications directly or indirectly derived from Johnstone's DFA indicate that this method has made an impact on the species identification of domestic equids. In contrast, the Davis method seems to receive very little attention, although it is relatively easier to comprehend than DFA. Perhaps the fact that this method can deal only with first phalanges has limited its practicality. In the next chapter, some modifications proposed to both methods which are then applied to the archaeological material in order to investigate the frequency of the three major domestic equids at selected Romano-British sites (see Chapter 5).

In addition to the conventional methods, the potential application of GMM is also explored as an alternative method for determining domestic equids to species level (Chapter 4). It is

unfortunate that as no research has focused on applying GMM to a broad range of skeletal elements of equids in order to cross-validate the claimed morphological criteria. Nevertheless, the feasibility of this method for future practise is demonstrated. In contrast to conventional biometric analyses, GMM considerations more aspects and dimensions of a skeletal element, and better discriminate between the subtle differences that are deemed unmeasurable by conventional approaches that rely on callipers and a measuring board.

This chapter has also questioned the reliability of some previous identifications of archaeological specimens as donkeys or mules. Thus, the frequency of these species in Romano-British sites may have been even lower than previously believed. Issues with past determinations have been discussed, and the risk of using shape indices derived from Johnstone's DFA outcomes should be iterated

Since the ultimate aim is to examine the procurement strategies of different domestic equids in Roman Britain, it is vital to be able to identify them to species. A determination of domestic equids to species level is not only crucial for establishing the representation frequency of these animals between various types of sites, but is also essential for comparing the localness of different species. In order to attain an accurate species frequency, it is essential to employ multiple identification approaches to verify the reliability of and consistency between different methods (or different elements of the same individual). The verification through cross validation is indispensable because in real practice (and more often than not) not all methods can be utilised for the identification of a faunal remains. In the next chapters, practicable methods of performing the quantitative analysis discussed above will be reviewed in greater depth and will then be applied to

available modern specimens – not only to test their accuracy, but also to establish a standard for determining the identification status of archaeological specimens.

Chapter 3 - Biometric Analysis: DFA and the Davis Method

3.1 – Introduction

Biometric analyses using measurements taken directly from skeletal elements provide, theoretically, a more objective approach for taxon/species identification. This chapter aims to demonstrate the application of the two biometric techniques that were briefly reviewed in the previous chapter: Discriminant Function Analysis (DFA) and the Davis Method. Both biometric approaches will be explained, and their limitations and risks i will be evaluated. The first part of this chapter will focus on the DFA, and this will be followed by a discussion of the Davis method. The chapter will conclude with a comprehensive discussion of the prevalent issues for biometric analyses based on the measurement of post-cranial elements.

3.2 – Rethinking Discriminant Function Analysis

In Johnstone's pioneering attempt at using DFA to distinguish between horses, donkeys, and mules (2004), she demonstrated that it is possible to separate different species using modern samples of known species with relative success. Despite the fact that there are some issues regarding her dataset (see below), her attempt is still very valuable in suggesting a reasonable solution to settle the current predicament on equid determination. The aim of using the DFA method in the present study is to utilise a biometric approach that can objectively predict the species of archaeological material included in this thesis. However, as the original dataset became available to other researchers through the national thesis archive, the high of accuracy claimed for Johnstone's (2004) DFA study looks more uncertain. This chapter will first explain the reasons for modification of Johnston's DFA technique and then provide a more detailed step-by-step instruction of how DFA is applied

in SPSS with explanations of some specific functions. Then, the rectified DFA method is applied to an updated and expanded dataset.

3.2.1 – Some Comments on Johnstone's DFA Approach

As the present author was making an initial trial of the DFA method with a smaller dataset at an early stage of this research (i.e. previous to the date in which Johnstone's original dataset became available), the accuracy of its outcomes was noticeably dissimilar to those in Johnstone's (2004) work. It was first assumed that the reason for such a divergence was the small sample size. However, when the original datasets became available, efforts were made to recreate her original DFA technique step by step; the results, however, still did not match those described in her original work. After a number of further attempts, it became apparent that the discrepancy may be due to differences in the version of SPSS used and/or on whether certain settings were used in Johnstone's study. For example, in SPSS 21 used by the present study, there is an option whether or not the mean value should be used as the substitute for missing data. That is, if a measurement in a sample is missing, the software will automatically calculate the mean of that measurement from the same designated group and use it as the missing measurement. This will allow more samples to be included in the analysis even if not all measurements were taken (or available due to other conditions). However, since the measurement is estimated, the accuracy of the grouping may be affected. Unfortunately, the older version used by Johnstone (SPSS 10) was not available for the present author, and it was deemed impractical to test all possible combination of multiple options in order to recreate her steps.

Another possible contributing factor for the different results between Johnstone's (2004) study and the present one is some errors found in Johnstone's original dataset. Most of the

errors are probably simple typographical mistakes. For example, the smallest shaft width measurement of a humerus is given as 337.3 mm (Johnstone, 2004, p.512 and in the .DB file), when the normal range would be between 30 to 40 mm. There are also some data that may have been misplaced; for example, measurements for the femur are all in reverse order (i.e. GLC and GL, SD and DC, Bp and Bd, p.516 and in .DB file) when compared to other datasets. The same problem is also found for the Bp, SD and Bd measurement for tibiae (p. 517 and in the .DB file). Similarly, there are also several independent entries with possible reverse order (e.g. one Przewalski's horse may have its radius SD and BFd measurement reversed; p.513 and in the .DB file). It is unclear whether these errors occurred only in the printed version of the thesis, or whether they also took place in the DFA. Nonetheless, this adds to the difficulty of fully recreating Johnstone's DFA technique since the errors cannot be corrected without accessing the original material and only on the few occasions where they have been picked up by DFA as outliers in scatter plots. Since it is not possible to recreate Johnstone's analyses, no further comment will be made regarding the accuracy of the original method fully. The species determination in the present study will rely on the revised version of DFA analyses initially proposed by Johnstone.

3.2.2 – Revising Johnstone's DFA approach: Materials and Method

This section outlines some of the main differences between the original method and the revised one. The main advantage of the revised method is that a larger and more refined dataset is used. Selecting a representative samples is vital for DFA in order to be able to make a more accurate prediction of species assignation. This consideration was briefly mentioned by Johnstone (2004, p206), but it requires further filtering following the same train of thought (see below). The second part of this section will then provide a detailed step-by-step description of how to operate DFA in SPSS along with a more in-depth

explanation of the concept. As a statistical method for predicting the membership of an unknown entry, several assumptions need to be made before the method calculates the functions used for assigning membership. Representative samples and suitable DFA approaches are two main factors that were not fully explained and described in Johnstone (2004), but that are essential for the application of DFA. The present study aims to improve on previous applications of this method by refining the standard dataset chosen and choosing a different approach for the application of DFA. These changes will lead to more realistic results that would permit more reliable predictions of archaeological equid taxa.

3.2.2.1 Materials: Representative Samples

The representativeness of standard samples is crucial for the DFA method to make classifications and predictions. Not only should specimens be representative of their population (or taxon), but it is also important that the measurements used as variables represent differences that separate one group from another. Of these two considerations, the former is by far the more challenging. In this thesis, datasets of modern domestic equids from the following sources were used: the original dataset in Johnstone's thesis (2004), an extensive dataset from Vera Eisenmann's website (http://www.vera-eisenmann.com/, accessed 2013), and additional specimens from the collection at the University of Southampton and Historic England at Fort Cumberland (Table 3.1, all data are listed in Appendix I). The limited number of mule skeletons available has already been mentioned, but the wide variety of horse and donkey breeds is equally disconcerting. Many of these horses and donkeys are the creations of modern selective breeding techniques – in some instances bred for very specific purposes – and, therefore, will not be adequate as a comparative standard for archaeological material.

This same concern was also recognised by Johnstone as she excluded Shetland ponies, Thoroughbreds and Shire horses from the dataset because "*they were considered to be smaller or larger than anything likely to be present in the archaeological samples*" (2004, p206). While the size of horses was obviously restricted to minimize the effect of selective breeding in modern horses, the same consideration did not apply to donkeys in her work. Two Poitou donkeys are included in her dataset. The Poitou donkey (a.k.a *Le Baudet de Poitou*) is a special breed of large-sized donkey that has been intentionally bred for the specific purpose of mule breeding. Surprisingly little is known about its origin except that this breed begins to be known in France during the Middle Ages (Delannoy, 2007). Since the time frame that the current thesis is considering predates the known origin of Poitou donkeys, it is only reasonable to exclude this massive modern donkey breed from the dataset as well. In contrast to the large-sized equids that have resulted from modern artificial selective breeding, the exclusion of small-sized horses, such as Shetland ponies, from the dataset should be reconsidered. Even though it is true that, compared to most common horse breeds, Shetland ponies are extremely small and may be miniaturised in more recent history, an archaeological equids of similar size to modern Shetland pony were found in the Bronze Age level from Jarlsh site, Shetland (Platt, 1956; Trow-Smith, 2013). Thus, their possible presence in Roman assemblage endorses the inclusion of this breed in current dataset. However, the assumption of Shedland pony existed locally since the Bronze Age is based on the esmitation of wither's height. Moreover, it is not certain whether the Shedland ponies in current dataset are further miniaturised as a result of modern selective breeding. Thus, it is recommended for future research, more attentions should be paid to the inclusion or exclusion of this breed.

Source	Species	Humeri	Radii	MC	Femora	Tibiae	MT	PH1A	PH1P
Johnstone (2004)	Horse	34	34	36	37	37	29	33	33
	Donkey	13	12	14	12	14	13	12	13
	Mule	9	9	9	9	11	9	10	9
Eisenmann Website	Horse	0	28	50	28	24	52	36	37
	Donkey	0	17	42	17	18	37	20	20
	Mule	0	7	12	10	8	12	5	6
Southampton University	Horse	3	3	5	3	4	4	3	4
	Donkey	2	2	2	2	2	2	1	1
	Mule	0	0	0	0	0	0	0	0
Historic England (Fort Cumberland)	Horse	0	2	3	3	3	2	3	2
	Donkey	0	2	2	2	2	2	2	2
	Mule	0	0	0	0	0	0	0	0
Total		61	116	175	123	123	162	125	127

Table 3.1 – Number of modern equids used as standard dataset in the present thesis.

Deciding which breed can be included and which breed should be excluded is crucial for setting up a method that can be applied to archaeological material. This is because the level of selective breeding is so intensive that modern perceptions of horses may be considerably different from those of the Roman times. To state an obvious example, separating ponies from horses is a relatively new cultural concept, as well as being a regional one. While there still seems to exist some debate from the equestrian perspective on whether ponies are a sub-species of horses (Hyland, 1990, p.67) instead of a breed with noticeably different conformations (Sidnell, 2006, p.2), the general consensus is that they are biologically the same species, which can artificially be divided by the height of the withers. The dividing point between horses and ponies is set at 148 cm (about 14.2 hands) as defined by the International Federation for Equestrian Sports. According to this definition, most of the Romano-British horses will be on the pony side of the scale. It is not clear when the cultural concept of separating ponies from horses began, but there must have been a time when ponies and horses could not have been separated from one another based on the current standard because the size of horses did not dramatically increase in Britain before Henry VIII established the famous Horses Act 1540 which set strict limit for the

size of horses (Thirsk, 1984). As a result, removing the known modern larger breeds in an attempt to minimise the impact of breeding due to intense artificial selection may be just the tip of the iceberg of the problem regarding using modern samples; not only do we not know which breed is "new" or "function-specific" for every single specimen, but also, there is little background information regarding the breeds of either of the parents that procreated the mules. Since mules are sterile and do not reproduce, every generation of mules represents only their immediate parents. This means that mules bred from modern breeds of horses and donkeys may be comprehensively different from those bred from Roman horses and donkeys, which may both be significantly smaller than their modern counterparts. This is by far the most serious potential risk of performing biometric analysis for identifying infertile hybrid species using modern specimens, and it should be kept in mind when interpreting the outcomes.

Although it was not feasible or necessary to exclude all the "modern" horse/donkey breeds, it was still important to remove those with extreme sizes and builds that are known to be the outcome of recent selective breeding. As a result, all known Poitou donkeys in both Johnstone's and Eisenmann's dataset were excluded as well as an unusually large donkey individual from the comparative collection of Historic England, Fort Cumberland. In addition, two massive draught horses and one donkey from Eisenmann's dataset were removed because they seem to suffer from a pathological condition that translates into unusual measurements. Furthermore, as mentioned in an earlier section, some errors can be found in Johnstone's dataset; among which all the typographical mistakes or errors that cannot be confidently corrected (e.g. it cannot be established if the value of 337.3 mentioned above is actually 33.73 or 37.3) were also removed from the dataset. It should be kept in mind that there are still numerous individuals in the dataset for which there is no background information regarding their breed and, therefore, it is possible that the dataset

still includes some unsuitable specimens. However, comparing the outcomes before the exclusion, there is evident improvement in the accuracy of the taxonomic classification.

In addition to the possible differences between comtemprory breeds and past ones, it should also be noted that information regarding sex and castration are lacking in the current dataset. While it has been argued that there is little sexual dimorphism in horses (Johnstone, 2004), it is not clear that if any of these modern equids were castrated. However, as mentioned earlier (section 2.6.2), horse castrations in Roman time take place at four years of age. At this stage, equids limb bones have stop growing and thus would not affect the proportion of limb bone in castrated male as observed in modern sheeps (Johnstone, 2004). Therefore it is assumed that the chance of castrated horses being misidentified as mule will be slim for Roman material.

3.2.2.2 Methods: DFA in SPSS 21

As for choosing the appropriate variables (i.e. measurements) for DFA, it is necessary to reiterate the aim of DFA for the current research. DFA is a statistical method that is mainly used for group classification, but can also be used to predict the group to which a catagory of data with unknown membership is likely to belong. The later usage makes it more advantageous than other statistical methods since the present study requires a method to determine the species of archaeological specimens. There are two different approaches in DFA: the *simultaneous* approach and the *stepwise estimation* approach (Hair *et al.*, 2010). The simultaneous approach will treat all variables as determining factors, although they are assigned different loadings to each variable depending on their discriminant power. In contrast, the stepwise estimation approach considers only those variables that have more discriminant power and neglects those that play only minor roles in the discrimination. This is achieved by removing one variable at a time, hence the name “stepwise estimation

approach". In other words, the stepwise estimation approach considers only the variables that have greater differences, and completely discards those that have little impact on separating the groups.

For separating domestic equid species using various dimensions describing the general profile of particular skeletal element, it is necessary to maintain the control of the variables used for group classification. Although in the present analysis, DFA will continue using "simultaneous estimation" as used by Johnstone, her step of eliminating multiple measurements to achieve a better classification rate will not be carried out here. As explained above, the removal of variables with less discriminating power to increase the classification rate will be considered equal to using the "stepwise estimation" approach, which the present author believes to be unsuitable for the present aims. This is particularly important since the size differences between the three species in question can be clearly established by visual observation based on their typical representation: donkeys are usually the smallest and, on average, mules are the largest whilst horses have a wide range of different sizes. Therefore, it is rather the assumption that *allometric* differences existed between these species that we should examine using DFA. As metioned earlier (section 2.3.1), although the use of Z-score can largely improve the classification accuracy, this approach cannot be applied onto archaeological specimens of unknown species and, therefore, will not be used in the current study. As a result, all the dimensions should be used together regardless of their discriminating power. It should be noted that there is one apparent disadvantage: when a specimen lacks a measurement (due to incompleteness, erosion, or pathological condition); such specimen cannot be used in the analysis (that is, unless the missing value is replaced with the group mean, which would decrease the accuracy and, therefore, is not practised here). The steps of performing DFA using SPSS 21 are shown in the following figures.

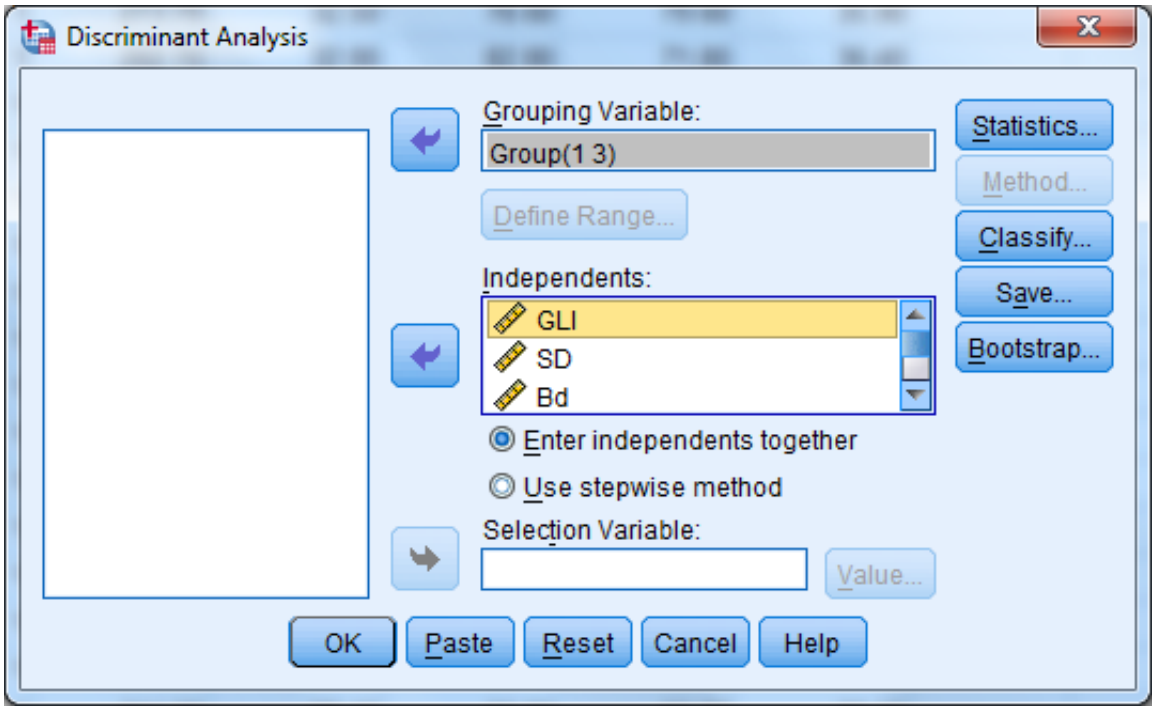


Figure 3.1 – DFA Step 1.
To perform DFA using simultaneous estimation, the option of "Enter independents together" should be ticked (default setting in SPSS 21). Ideally, bootstrap is also highly recommended as reinforcement for any datasets with small sample sizes. However it is not used in current thesis due to hardware limitations.

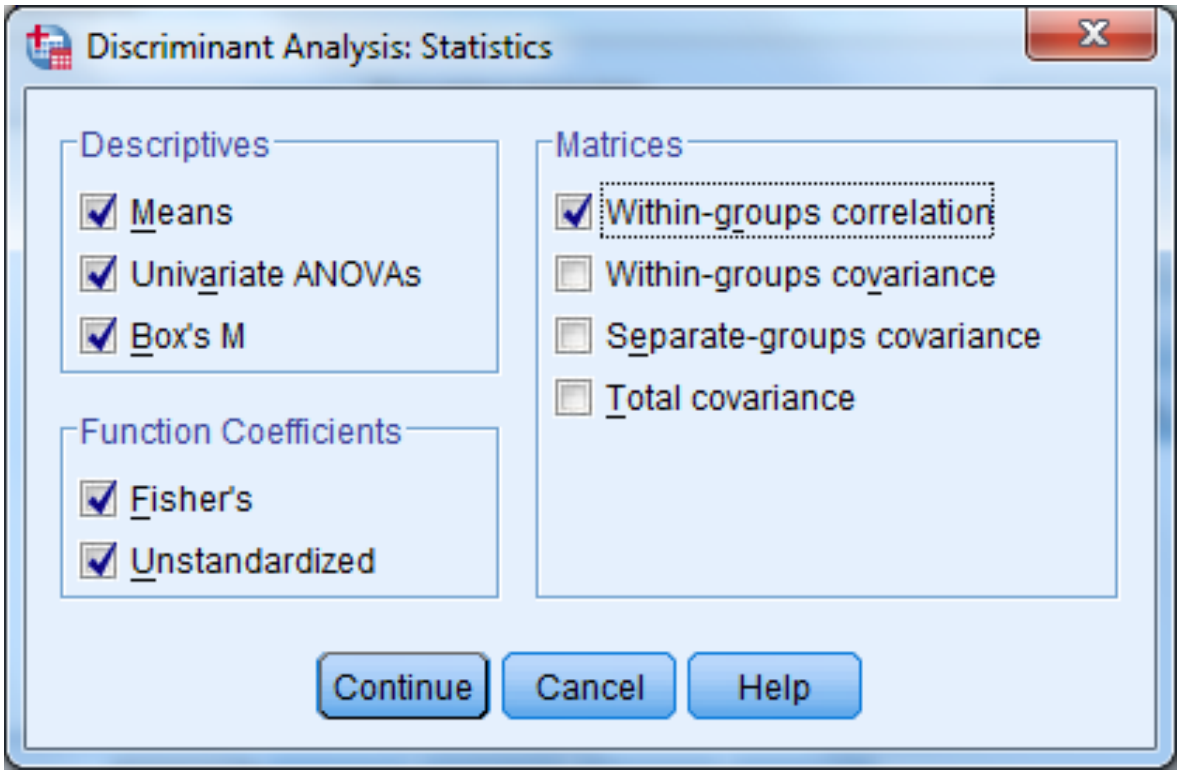


Figure 3.2 – DFA step 2.
In the "Statistics" setting, all descriptive methods are chosen, as well as both methods for function coefficients. This will allow the user to examine the significance of each variable in the output.

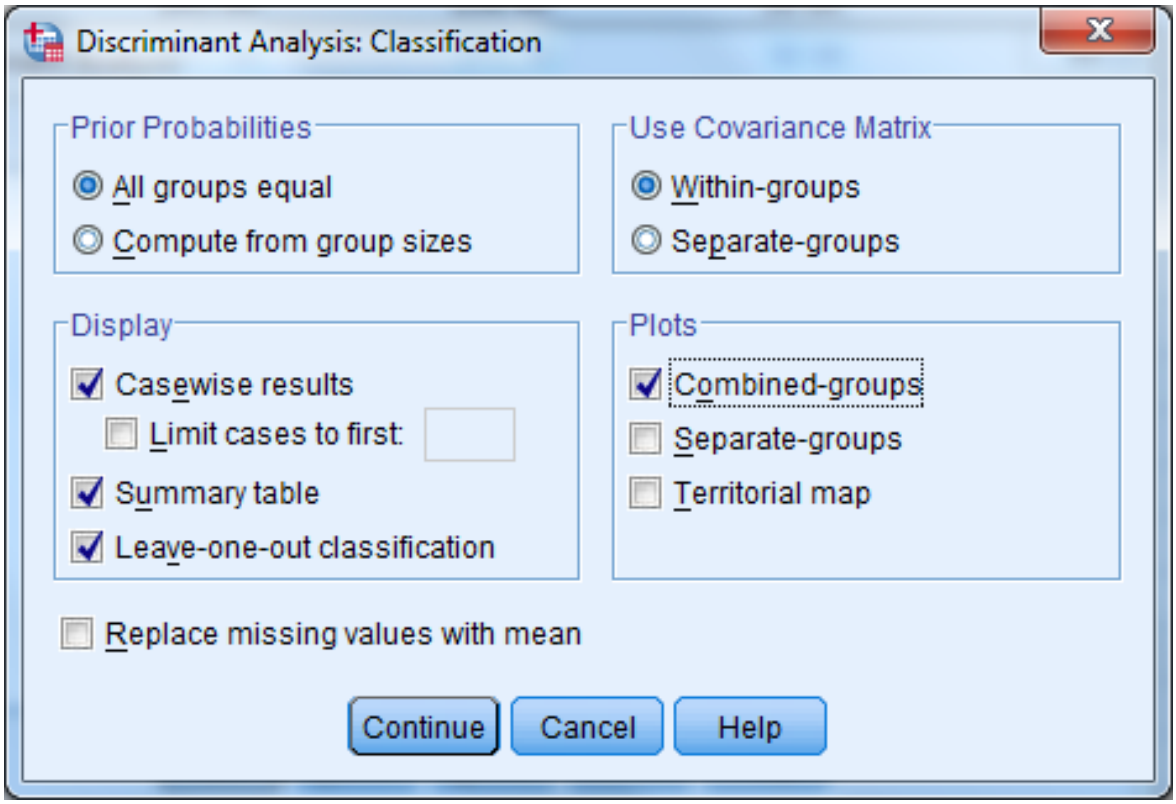


Figure 3.3 – DFA step 3.
In the "Classification/(Classify…)" settings, it is essential to choose "Leave-one-out classification" for the software to perform cross-validation by taking one sample out at a time. Since the current dataset is still considerably small, it is important to allow the software to reclassify the dataset. This method is also known as "jack-knifed classification". Also, since known mule specimens are significantly lesser than the other two groups, thus all groups are considered as equal.

3.2.3 – Modified DFA method: Results

The results are described by element, and the measurements considered for each element are shown in Table 3.2. It should be pointed out that there is a difference in the selection of measurements between Johnstone's original method and the present one: the lateral length (Ll) is not considered in the present analysis. Although Johnstone excluded this measurement for some elements since her method is closer to the "stepwise estimation" approach that allows measurements to be removed to increase accuracy, the consideration here is somewhat different. As a secondary length measurement to the greatest length (GL), Ll does not provide any essential information that can contribute to the description of bone shape, and it is often not recorded in most faunal reports albeit it is used as a factor for withers height estimation by Kiesewalter (1888).

Element	Measurements Considered
Humerus	GLl, SD, Bd, BT, HTc
Radius	GL, Bp, BFp, SD, Bd, BFd, DFd
Metacarpal	GL, Bp, Dp, SD, BFd, Dd
Femur	GL, DC, Bp, SD, Bd
Tibia	GL, SD, Bp, Bd, Dd
Metatarsal	GL, Bp, Dp, SD, BFd, Dd
PH1	GL, Bp, Dp, SD, Bd, Dd

Table 3.2 – Measurements used for each element.
GLl – greatest lateral length, **SD** – smallest shaft breadth, **Bd** – greatest distal breadth, **BT** – greatest trochlea breadth, **HTc** – height of the trochlea constriction, **GL** – greatest length, **Bp** – greatest proximal breadth, **BFp** – greatest breadth of proximal articular facet, **BFd** – greatest breadth of distal articular facet, **DFd** – greatest depth of distal articular facet, **Dp** – greatest proximal depth. **DC** – greatest diameter of caput femoris.

3.2.3.1 Humerus

Only 61 available specimens have all of the required measurements. All of Eisenmann's dataset were excluded due to the lack of the greatest distal breadth (Bd). This is because according to Eisenmann's measuring scheme, the greatest distal trochlea breadth (BT) is the same as Bd while in von den Driesch's measuring scheme they are separate measurements. Based on von Driesch, Bd is very difficult to measure in equids and ruminants because "the most lateral and the most medial prominent points fo not lie in the same plane" (1976, p.77). It is also worth noting that the measurements for humerii used by Johnstone in her pioneering work included greatest proximal breadth (Bp, 2004, p.194) as a variable for DFA. However, this measurement is not listed in her dataset and, therefore, is not used in the present analysis in order to maximise the dataset. The classification rate is calculated based on the number of specimens being correctly grouped into its known taxon. The overall classification rate is 78.7%, the lowest being of horses (73.3%) and the highest being of mules (88.9%). There are more cases of misclassified specimens in all species in the cross validations.

Of the four horses misclassified as donkeys, all are known to be ponies. Three of the six horses misclassified as mules are Arab horses of considerably large statures (estimated wither's height at about 14½ hands, about 147 cm) while only one slightly shorter Arab horse is correctly classified. These cases suggest that the classification seems to be based mostly on length measurements.

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	27 (73.3%)	4 (10.8%)	6 (16.2%)	37 (100%)
	Donkey	2 (13.3%)	13 (86.7%)	0 (0%)	15 (100%)
	Mule	1 (11.1%)	0 (0%)	8 (88.9%)	9 (100%)
Cross-validated[b]	Horse	25 (67.6%)	6 (16.2%)	6 (16.2%)	37 (100%)
	Donkey	3 (20.0%)	12 (80.0%)	0 (0%)	15 (100%)
	Mule	2 (22.2%)	0 (0%)	7 (77.8%)	9 (100%)

Table 3.3 – Classification rate of humerii.
a. 78.7% of original grouped cases correctly classified
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.
c. 72.1% of cross-validated grouped cases correctly classified

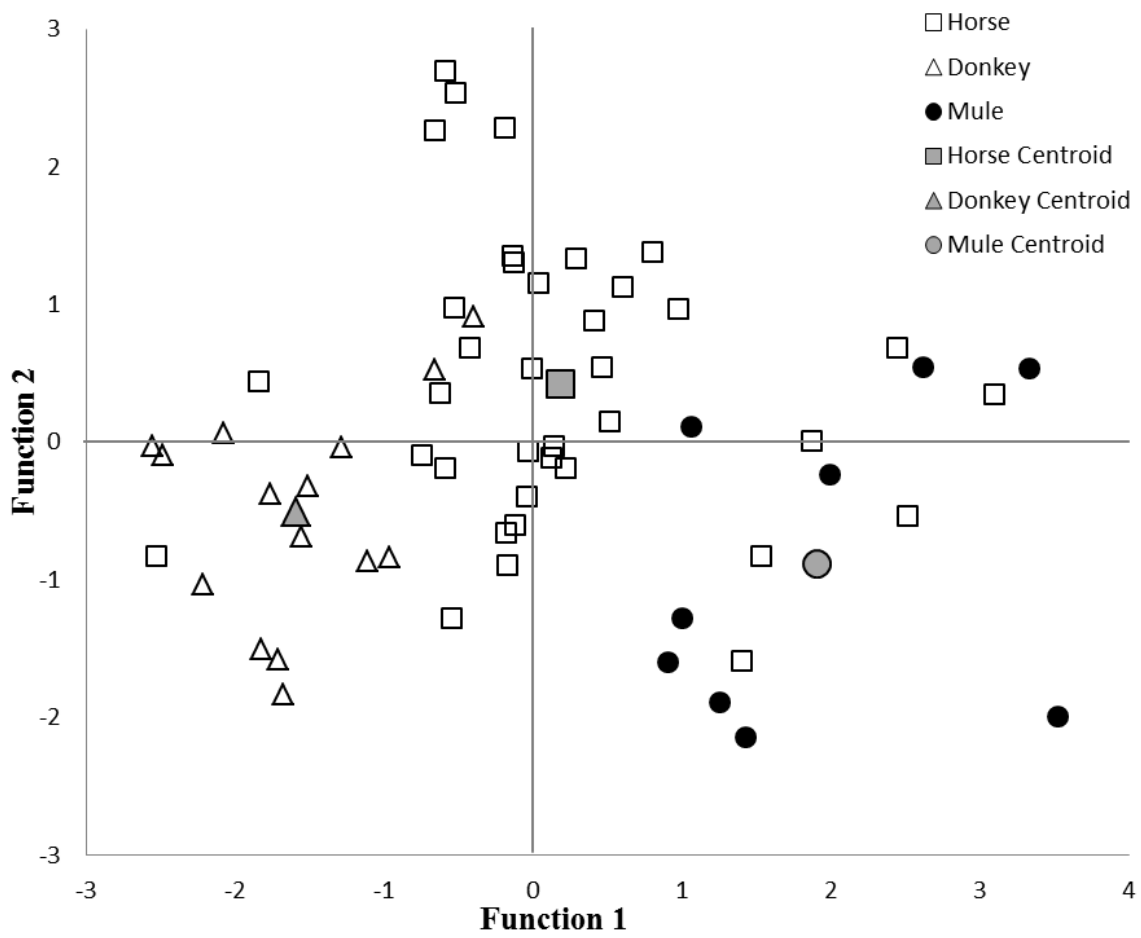


Figure 3.4 – DFA scatter diagram for humerii

3.2.3.2 Radius

A total of 116 specimens were used in the analysis. The overall classification rate is 73.3% with the lowest being of horses (62.7%) and the highest being of donkeys (93.9%). The cross-validation rate of donkeys remains the same as for the original grouping from first classification, but it drops by 12.5% in mules due to the increasing number of specimens wrongly assigned to horses. The overall cross-validation rate does not differ much from the original classification, indicating that the analysis is more reliable and stable than humerus. Over half of the horses misclassified as donkeys are known to be ponies, but not as many Arabs were misclassified as mules (see Appendix I-II).

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	42 (62.7%)	10 (14.9%)	15 (22.4%)	67 (100%)
	Donkey	2 (6.1%)	31 (93.9%)	0 (0%)	33 (100%)
	Mule	4 (25.0%)	0 (0%)	12 (75.0%)	16 (100%)
Cross-validated[b]	Horse	41 (64.2%)	10 (14.9%)	16 (23.9%)	67 (100%)
	Donkey	2 (6.1%)	31 (93.9%)	0 (0%)	33 (100%)
	Mule	6 (37.5%)	0 (0%)	10 (62.5%)	16 (100%)

Table 3.4 – Classification rate of radii.
a. 73.3% of original grouped cases correctly classified.
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.
c. 70.7% of cross-validated grouped cases correctly classified.

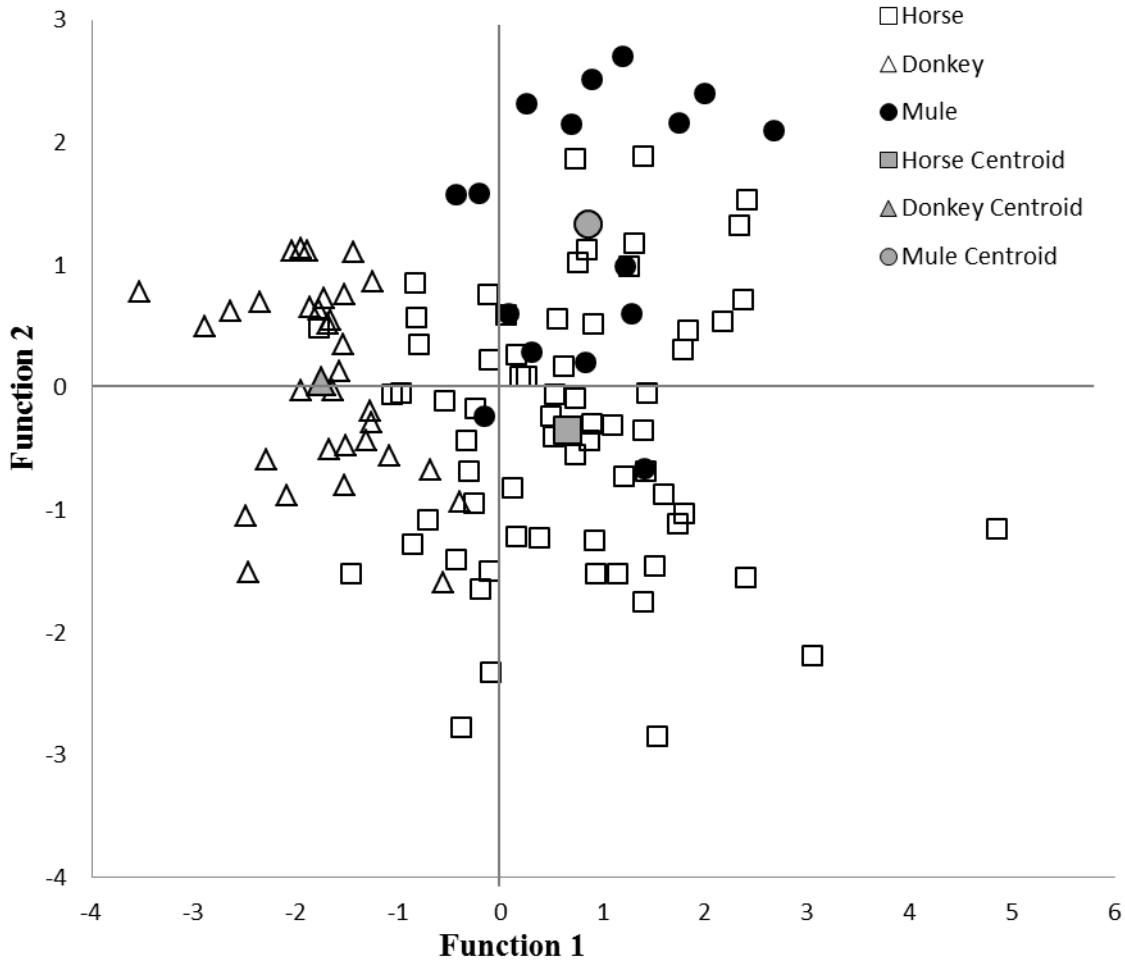


Figure 3.5 – DFA scatter diagram for radii

3.2.3.3 Metacarpal

A total of 175 specimens were used in the analysis. The overall successful classification rate is 87.4%, and all species have a classification rate of over 80%. The lowest accurate classification rate is of horses at 80.9% and the highest is of donkeys at 96.7%. The cross-validation rate is only slightly lower, with no changes in either donkeys or horses. The ratio of Przewalski's horse being misclassified as mules is relatively high, but no other apparent pattern is noticed.

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	76 (80.9%)	4 (4.3%)	14 (14.9%)	94 (100%)
	Donkey	1 (1.7%)	58 (96.7%)	1 (1.7%)	60 (100%)
	Mule	2 (9.5%)	0 (0%)	19 (90.5%)	21 (100%)
Cross-validated[b]	Horse	76 (80.9%)	4 (4.3%)	14 (14.9%)	94 (100%)
	Donkey	1 (1.7%)	58 (96.7%)	1 (1.7%)	60 (100%)
	Mule	3 (14.3%)	1 (4.8%)	17 (81.0%)	21 (100%)

Table 3.5 – Classification rate of metacarpals.
a. 87.4% of original grouped cases correctly classified.
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case
c. 86.3% of cross-validated grouped cases correctly classified.

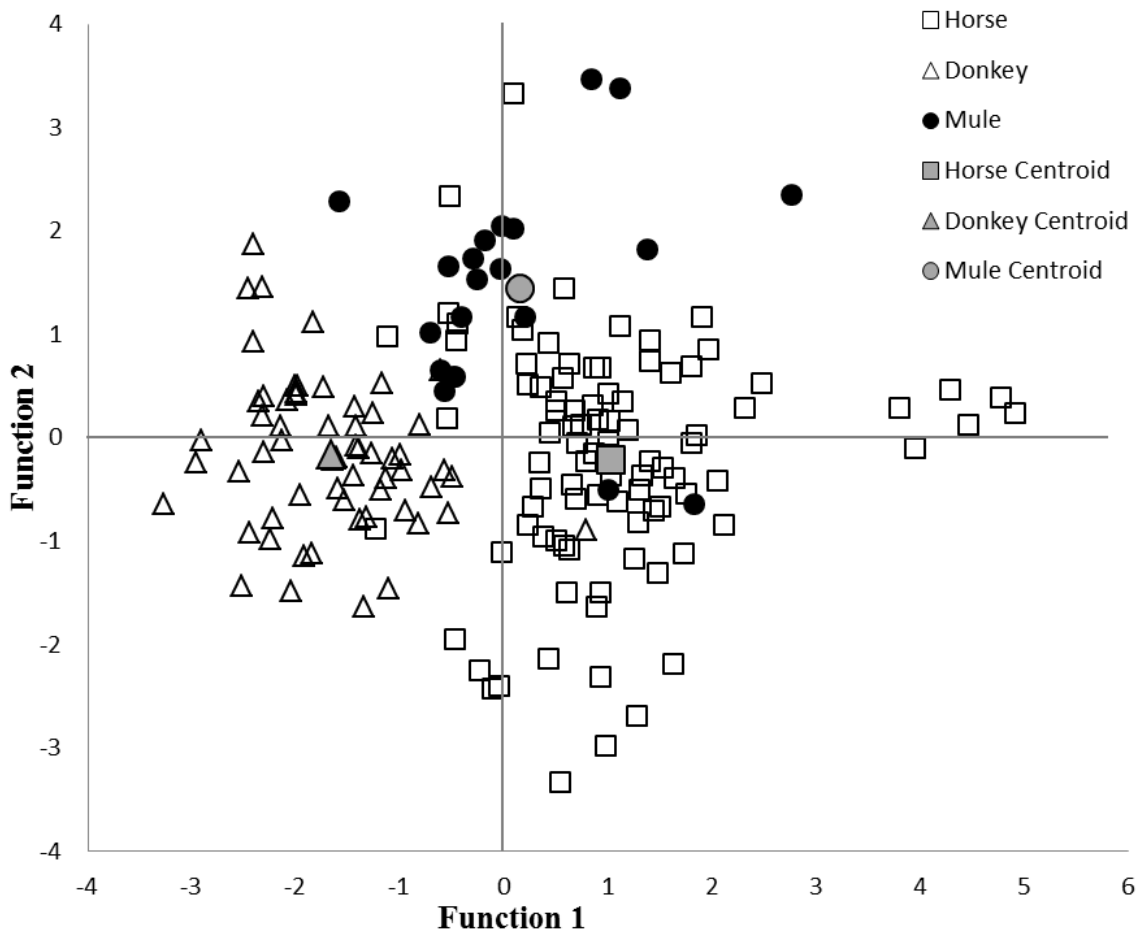


Figure 3.6 – DFA scatter diagram for metacarpals

3.2.3.4 Femur

A total of 123 specimens were used in the analysis. The overall successful classification of specimens is low at 62.6%, making this element extremely inaccurate for species determination. The lowest classification is that of horses at 46.5%, meaning that more than half of the horses were misclassified. However, the classification rate of donkeys is 97.0%, with only one individual being misclassified. The misclassification pattern is similar to that in the humerus. The majority of horses mistakenly classified as donkeys are known to be ponies (13 out of 14 cases), and all the Arab horses are misclassified as mules (n=7).

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	33 (46.5%)	15 (21.1%)	23 (32.4%)	71 (100%)
	Donkey	1 (3.0%)	32 (97.0%)	0 (0%)	33 (100%)
	Mule	6 (31.6%)	1 (5.3%)	12 (63.2%)	19 (100%)
Cross-validated[b]	Horse	31 (43.7%)	16 (22.5%)	24 (33.8%)	71 (100%)
	Donkey	0 (0%)	32 (97.0%)	1 (3.0%)	33 (100%)
	Mule	7 (36.8%)	1 (5.3%)	11 (57.9%)	19 (100%)

Table 3.6 – Classification rate of femora
a. 62.6% of original grouped cases correctly classified.
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.
c. 60.2% of cross-validated grouped cases correctly classified.

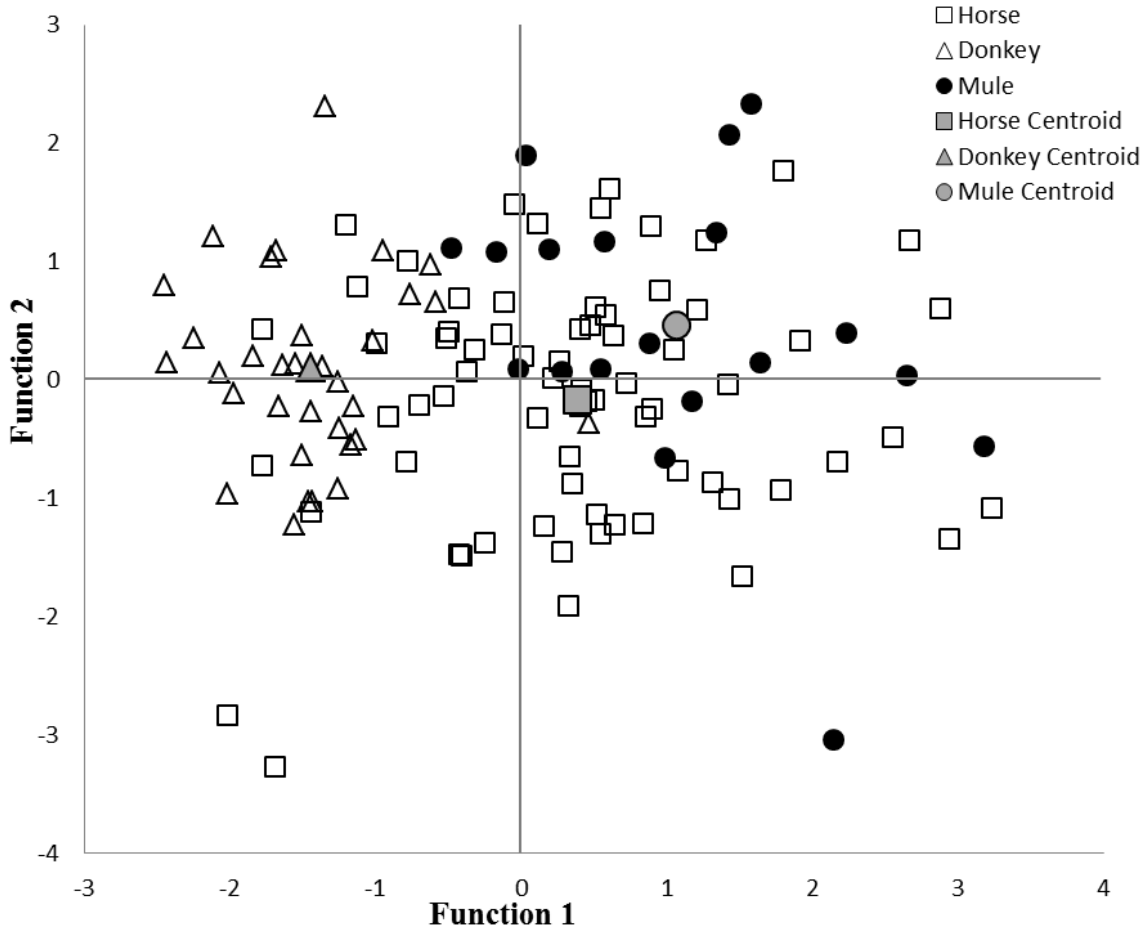


Figure 3.7 – DFA scatter diagram for femora

3.2.3.5 Tibia

A total of 123 specimens were used in the analysis. The overall successful classification rate of 89.4% seems high, but there is a large gap between the lowest classification rate of 73.7% of mules and the highest rate of 100% of donkey. The cross-validation rate implies that the mule classification is not stable since it drops by 21.1% after cross-validation was performed. The relatively low accuracy and stability in both horses and mules makes this element less ideal for identification than MC. In addition, the ratio of misclassified Arab horses is also considerably high with 3 out of 7 Arab horses misclassified as mules.

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	60 (88.2%)	0 (0%)	8 (11.8%)	68 (100%)
	Donkey	0 (0%)	36 (100%)	0 (0%)	36 (100%)
	Mule	3 (15.8)	2 (10.5%)	14 (73.7%)	19 (100%)
Cross-validated[b]	Horse	56 (82.4%)	1 (1.5%)	11 (16.2%)	68 (100%)
	Donkey	0 (0%)	36 (100%)	0 (0%)	36 (100%)
	Mule	5 (26.3%)	4 (21.1%)	10 (52.6%)	19 (100%)

Table 3.7 – Classification rate of tibiae
a. 89.4% of original grouped cases correctly classified.
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.
c. 82.9% of cross-validated grouped cases correctly classified.

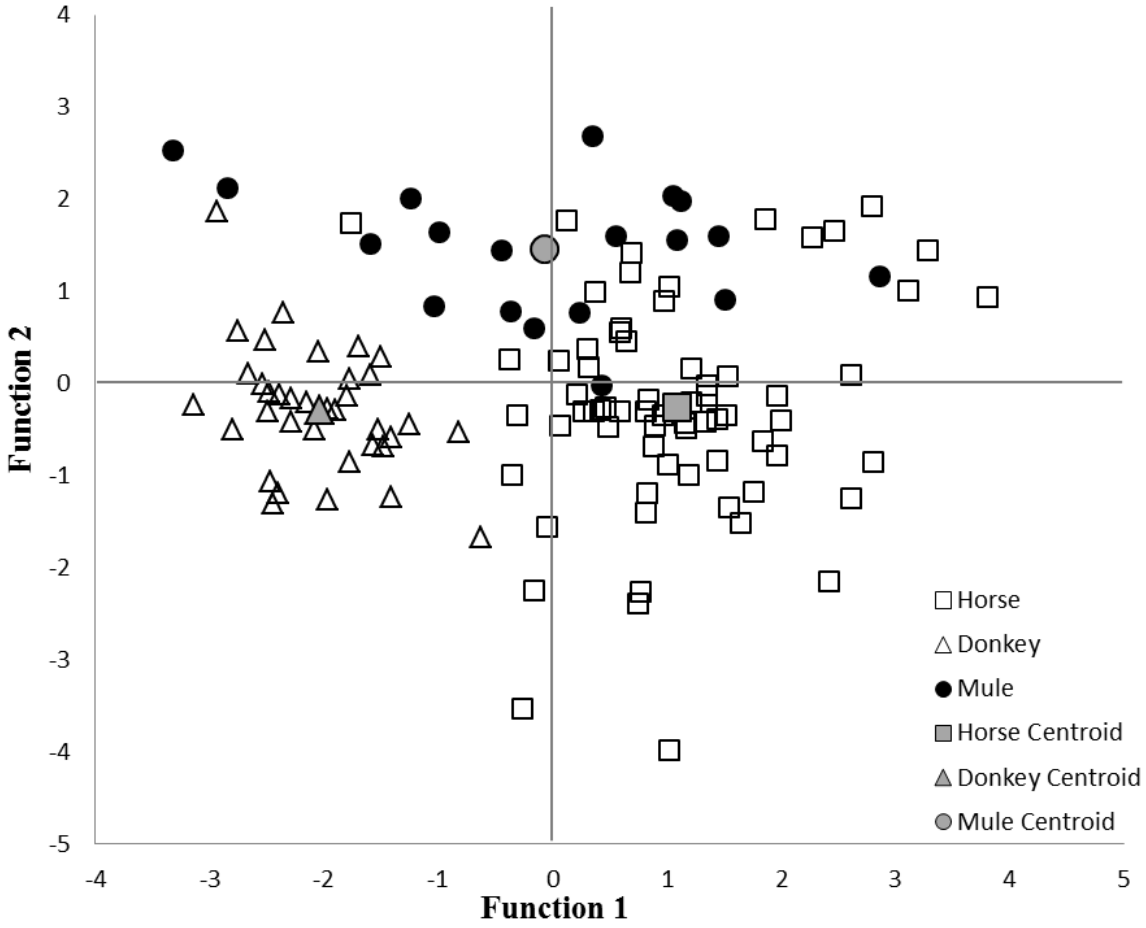


Figure 3.8 – DFA scatter diagram for tibiae

3.2.3.6 Metatarsal

A total of 162 specimens were used in the analysis. The overall successful classification rate is 81.5%, which is not as high as in metacarpals. However, the minor differences between the original classification and the cross-validation rate of both elements suggest that the stability of both elements is similar. The lowest classification rate is 74.7% for horses and the highest is 92.6% for donkeys. Similarly to the metacarpals, the ratio of Przewalski's horses being misclassified as mules is significantly high. This may be taken as evidence that using DFA slenderness may play an essential role in species determination in both metacarpals and metatarsals. Nevertheless, there is still an overlap between horses and mules, meaning that more than slenderness is required to make accurate distinction between the two. Compared to metacarpals, with a classification rate of over 80% for all species, the potential risk of identifying more horses than mules is higher in metatarsals.

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	65 (74.7%)	1 (1.1%)	21 (24.1%)	87 (100%)
	Donkey	2 (3.7%)	50 (92.6%)	2 (3.7%)	54 (100%)
	Mule	2 (9.5%)	2 (9.5%)	17 (81.0%)	21 (100%)
Cross-validated[b]	Horse	64 (73.6%)	1 (1.1%)	22 (25.3%)	87 (100%)
	Donkey	2 (3.7%)	50 (92.6%)	2 (3.7%)	54 (100%)
	Mule	3 (14.3%)	2 (9.5%)	16 (76.2%)	21 (100%)

Table 3.8 – Classification rate of metatarsals.
a. 81.5% of original grouped cases correctly classified.
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.
c. 80.2% of cross-validated grouped cases correctly classified.

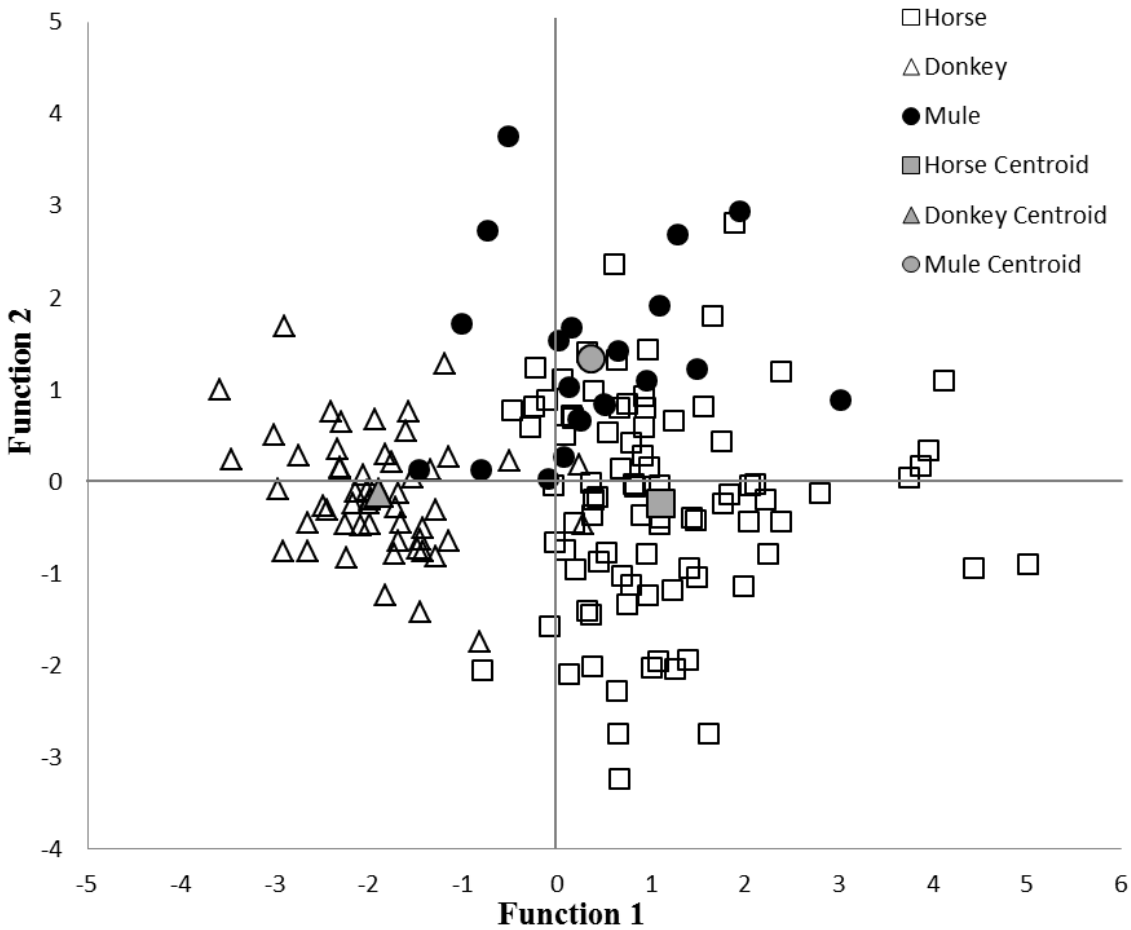


Figure 3.9 – DFA scatter diagram for metatarsals

3.2.3.7 First Phalanges

The approach for dealing with the first phalanges will require closer consideration. This is because, while it has been suggested that anterior and posterior elements first can be distinguished based on their morphological features (Dive and Eisenmann, 1991), this is not routinely carried out by faunal specialists. It would be ideal if first phalanges could be used in DFA regardless of their anatomical position (anterior or posterior); however, the evident size differences between the two – anterior being longer than the posterior ones – may affect the accuracy of species classification. Thus, separate DFA were initially carried out for anterior and posterior first phalanges before attempting a subsequent joint analysis (i.e. anterior and posterior combined).

3.2.3.7a - Anterior First Phalanx (PH1A)

A total of 125 specimens were used in the analysis. The overall successful classification rate is 85.6%, but there is a large gap between the lowest classification rate (66.7% of mules) and the highest (97.1% of donkeys). In addition, a significant drop is noticed in the cross-validation rate for all species, thus indicating that the classifications are not stable. Although the fact that there is no misclassification between horses and donkeys suggests that the determination did not rely heavily on size, there is no clear relationship between the measurements for the classification to be consistent. No meaningful patterns were detected from the misclassified cases.

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	63 (84.0%)	0 (0%)	12 (16.0%)	75 (100%)
	Donkey	0 (0%)	34 (97.1%)	1 (2.9%)	35 (100%)
	Mule	3 (20.0%)	2 (13.3%)	10 (66.7%)	15 (100%)
Cross-validated[b]	Horse	58 (77.3%)	0 (0%)	17 (22.7%)	75 (100%)
	Donkey	2 (5.7%)	31 (88.6%)	2 (5.7%)	35 (100%)
	Mule	4 (26.7%)	2 (13.3%)	9 (60.0%)	15 (100%)

Table 3.9 – Classification rate of anterior first phalanges
a. 85.6% of original grouped cases correctly classified.
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.
c. 78.4% of cross-validated grouped cases correctly classified.

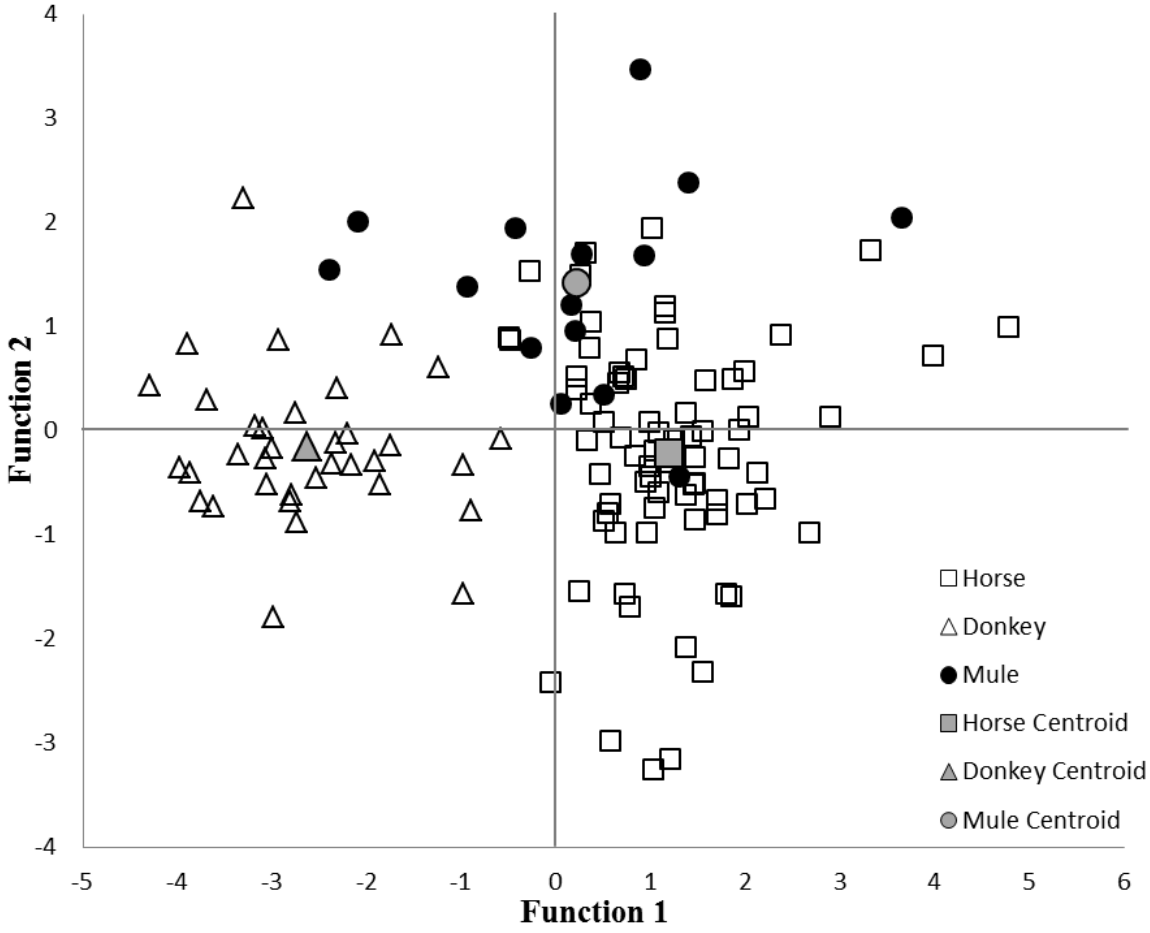


Figure 3.10 – DFA scatter diagram for anterior first phalanges

3.2.3.7b -Posterior First Phalanx (PH1P)

A total of 127 specimens were used in the analysis. The overall successful classification rate is 83.5%, somewhat lower than for the anterior counterparts. The lowest rate of successful classification is in horses (77.6%), whereas donkeys show the highest rate (94.4%). The differences between the original classification and the cross-validation are similar to that in PH1A analysis, which again shows the species classification does not have a very stable matrix. All except one Arab horse are misclassified as mules, but other cases of misclassification appear to be random.

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	59 (77.6%)	0 (0%)	17 (22.4%)	76 (100%)
	Donkey	0 (0%)	34 (94.4%)	2 (5.6%)	36 (100%)
	Mule	1 (6.7%)	1 (6.7%)	13 (86.7%)	15 (100%)
Cross-validated[b]	Horse	56 (73.7%)	0 (0%)	20 (26.3%)	76 (100%)
	Donkey	1 (2.8%)	33 (91.7%)	2 (5.6%)	36 (100%)
	Mule	5 (33.3%)	1 (6.7%)	9 (60.0%)	15 (100%)

Table 3.10 – Classification rate of posterior first phalanges
a. 83.5% of original grouped cases correctly classified.
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.
c. 77.2% of cross-validated grouped cases correctly classified.

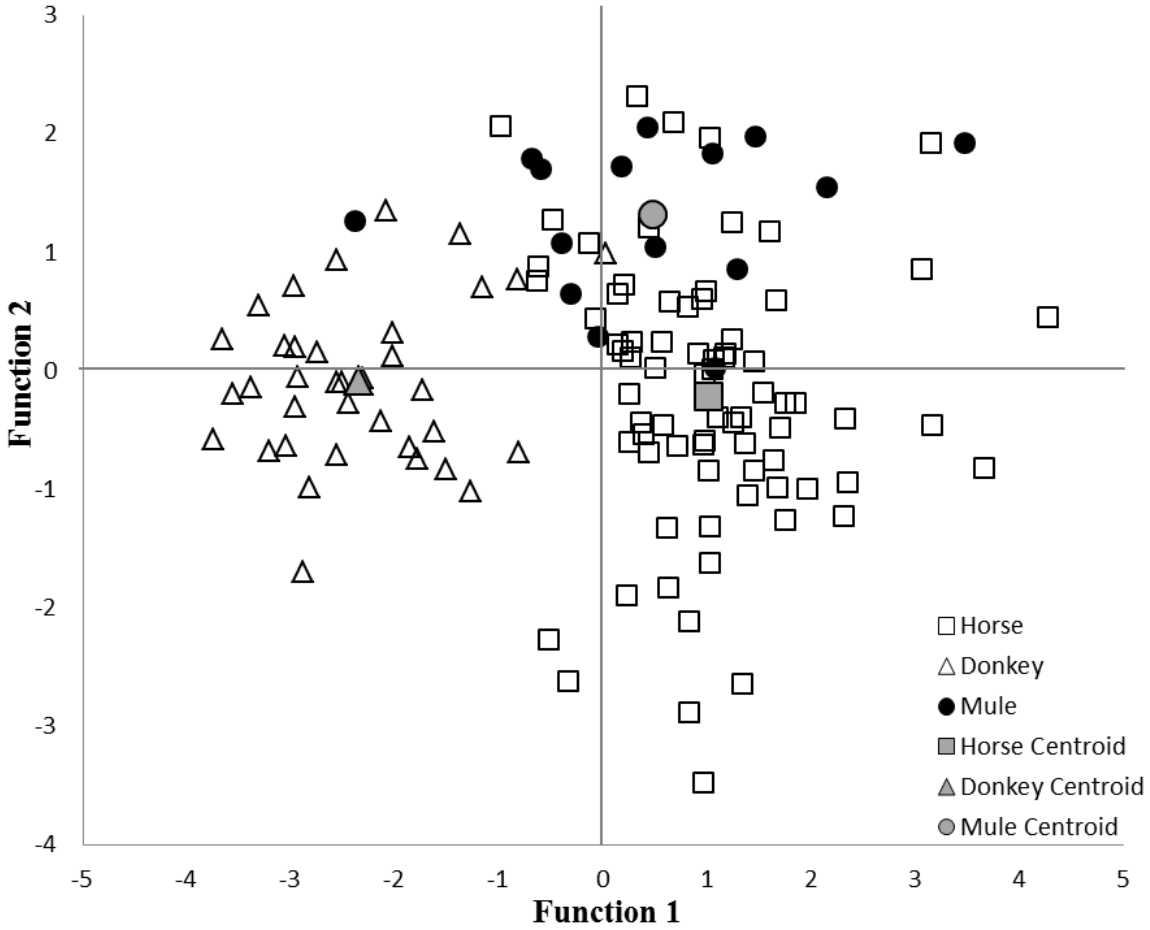


Figure 3.11 – DFA scatter diagram for posterior PH1

3.2.3.7c - First Phalanx Data Combined

Combining the data of both first phalanges results in nearly the doubling of the available specimens (n=252); it should be borne in mind, however, that the specimens derive from 134 individuals. The aim of combining the datasets for both first phalanges is to test whether this element can be used regardless of its anatomical position (anterior vs. posterior) without affecting species determination. This is carried out here by comparing the classification of the same individual in both the independent and the joint analyses.

The overall successful classification rate is 82.9%, i.e. lower than in both analyses conducted with separated datasets. The highest accurate classification rate still belongs to donkeys (95.8%), whereas the successful classification rates for both mules and horses are relatively low and have a smaller difference than in the previous two analyses (76.7% and 78.1% respectively). However, the cross-validation rate for the combined first phalanges dataset actually increases to 80.6%, the highest of all three analyses, and that largely reduces the difference between the rate of the original classification and that of the cross-validation. In other words, *although the combined dataset is less accurate, it provides a more stable matrix for prediction*. Nevertheless, it is not clear whether such an outcome is the result of the significant increase in the number of specimens, or whether one specific element (either anterior or posterior first phalanx) suffers more from loss of accuracy than the other. To clarify this, it is necessary to compare the outcomes of the different analyses.

The total number of misclassified cases in the combined dataset is 43, and the sum of misclassified cases in PH1A and PH1P analyses is 39. Thus, there are three more cases of misclassifications in PH1A and only one more in PH1P. The difference of four more misclassified cases does not provide much information regarding the impact of combining datasets on the same element from different anatomical positions. We need to examine the consistency of misclassification and its occurrence in different anatomical positions. Among the 134 individuals used in the combined analysis, there are 15 cases of inconsistency between the independent and the combined analyses from different individuals. Eight of these cases occurred in PH1A, six cases in PH1P, and one in both. This suggests that analysing this element without reference to its anatomical position affects PH1A more than PH1P. This supports the increase in the number of misclassification. Moreover, when the cases of inconsistent classification are examined, it appears that in PH1A, more horses are misclassified (n=6) while the inconsistencies in the

other two species are the result of misclassified cases being correctly classified in the joint analysis. In PH1P, the opposite is true: all except one inconsistency are misclassified horses being correctly classified in the joint analysis. In short, the impact of combining datasets is more evident in PH1A and it has a positive impact for non-caballine species in PH1A, but a negative impact on non-caballine species in PH1P. On the whole, however, the inclusion of both anterior and posterior first phalanges in a single DFA analysis does not seem to alter to any significant extent the accuracy of the results.

Classification Results[a,c]

	ID	Predicted Group Membership			Total
		Horse	Donkey	Mule	
Original	Horse	118 (78.1%)	0 (0%)	33 (21.9%)	151 (100%)
	Donkey	1 (1.4%)	68 (95.8%)	2 (2.8%)	71 (100%)
	Mule	5 (16.7%)	2 (6.7%)	23 (76.7%)	30 (100%)
Cross-validated[b]	Horse	114 (75.5%)	0 (0%)	37 (24.5%)	151 (100%)
	Donkey	1 (1.4%)	68 (95.8%)	2 (2.8%)	71 (100%)
	Mule	6 (20.0%)	3 (10.0%)	21 (70.0%)	30 (100%)

Table 3.11 – Classification rate of first phalanges
a. 82.9% of original grouped cases correctly classified.
b. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.
c. 80.6% of cross-validated grouped cases correctly classified.

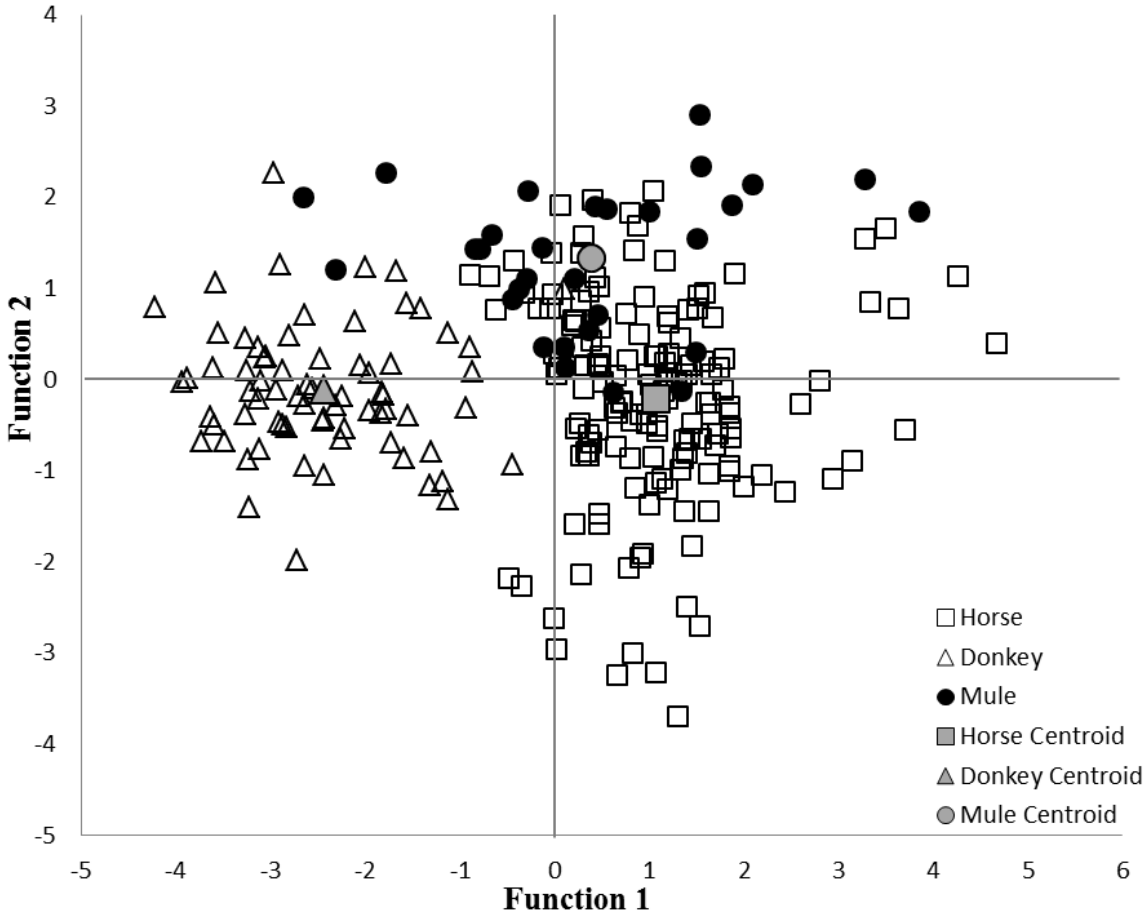


Figure 3.12 – DFA scatter diagram for first phalanges

3.2.3.8 Discussion

The analysis of eight skeletal elements using the modified DFA technique suggests that, while DFA may be a useful method for separating donkeys from the other two equid species, it may not be sufficiently conclusive to accurately distinguish between mules and horses (Table 3.12). The modified DFA suggests a different reliability ranking of element from Johnstone's (2004). Contrary to Johnstone's decision of excluding metacarpals due to their poor identification rate, the present study indicates that metacarpals provide the best overall accurate classification (above 80% in all three species) despite the fact that tibia has the highest successful classification rate on average. However, the latter are due to the high rates in the accurate discrimination of donkeys (100%), but it performed much less satisfactory in the discrimination of mules (73.7%). By contrast, metacarpals performed

rather well with classification rate above 80% for all three species. While metatarsals did not produce a very high classification rate for horses, the rate for correct classifications of mules is still higher than for other elements (e.g. radius, anterior first phalanx, femur). The use of femur in species determination should be avoided; this element failed to correctly identify more than half of the horses and only performed slightly better for mules.

Element (n, H:D:M)	Horse	Donkey	Mule	Mean	Overall*	Johnstone (2004, p194, Table 4.9)
Humerus (n=61, 37:15:9)	73.3%	86.7%	88.9%	82.97%	78.7%	85.7%
Radius (n=116, 67:33:16)	62.7%	93.9%	75.0%	77.20%	73.3%	86.0%
MC (n=175, 94:60:21)	80.9%	96.7%	90.5%	89.37%	87.4%	81.4%
Femur (n=123, 71:33:19)	46.5%	97.0%	63.2%	68.90%	62.6%	82.8%
Tibia (n=123, 68:36:19)	88.2%	100.0%	73.7%	87.30%	89.4%	91.9%
MT (n=162, 87:54:21)	74.7%	92.6%	81.0%	82.77%	81.5%	86.5%
PH1A (n=125, 75:35:15)	84.0%	97.1%	66.7%	82.60%	85.6%	N.A.
PH1P (N=127, 76:36:15)	77.6%	94.4%	86.7%	86.23%	83.5%	N.A.
PH1 Combined (n=252, 151:71:30)	78.1%	95.8%	76.7%	83.53%	82.9%	83.0%
Mean	74.00%	94.91%	78.04%	82.32%	80.54%	85.33%
Highest Overall	88.2%	100.0%	90.5%	89.37%	89.4%	91.9%

Table 3.12 – Summary of highest classification rate by element
* - The overall classification rate is calculated using the total of correctly classified specimens over the total of available specimens, and not as the mean of the classification rates of different species.

The second important observation derived from the modified DFA is that several individuals are repeatedly misclassified as other species. The dataset contains 190 individuals, from which 41 are represented by all 8 elements. 7 out of these 41 individuals have more than half of the 8 elements misclassified. 6 out of these 7 cases are horses misclassified as mules. Other than these seven individuals, several others (n=11) that have fewer available elements have more than half of the available elements misclassified. Some trends are apparent. Firstly, there is a high tendency for Arabian horses to be misclassified as mules. Four out of seven Arab horses have more than half of their elements misclassified as mules. It is worth mentioning that two of these individuals – with all skeletal elements available for study – have only two elements correctly classified (radius and metacarpal, radius and PH1A). Two of the mules are constantly misclassified as horses (M005 and M013). One individual is from a mounted skeleton (M005, "Eml mlt 1" in Johnstone, 2004) with wither's height of 123 cm, is perhaps the smallest mule in the dataset. It is not certain whether the misclassification is because of the size of these individuals or due to other factors.

As for the differences in robustness and slenderness of limb bone, based on the calculation of SD-GL shape index (i.e. SD / GL x 100) in the current dataset (Appendix IV), it is found that the degree of overlap indicates the use of slenderness is not a reliable trait for distinguish different equid species. This is because the intra-specific variation in horses appears to be greater than the interspecific differences with donkeys and mules. Moreover, when comparing the DFA classifications with the actual species, it is found that the current DFA does not rely on SD-GL shape index for the species classification.

3.2.4 – DFA Method Summary

This chapter evaluates the results of the modified DFA analysis in terms of the consistency of its predictions based on different elements of the same known individuals. From a critical perspective, DFA appears not be ideal as an accurate biometric method for domestic equid identification. The main reason is that the parameters being used are not adequate enough to discriminate the subtle differences that exist between these species. Thus rather than rejecting DFA outright as a valid method, an attempt could be made to design different parameters that can better capture the minor differences between the skeletal elements of these taxa. Alternatively, one can use these measurements differently to avoid the analysis being dominated by only a few variables – for example by using logarithms to reduce the differences between measurements, or replacing direct measurements by calculating various shape indices (e.g. SD/GL) as variables. Alternatively, since including z-scores as variables can improve the accuracy for classifying modern specimens, it could be further developed to apply onto the archaeological specimens.

An important issue in the DFA analysis of domestic equids remains the central influence that length measurements play. This in turn and in all probability, is caused by the inadequate availability of reference specimens. As discussed previously, donkeys show the highest correct classification rate of the three species, and the chances of horses and mules being misclassified as donkeys are low. Thus, it seems that DFA may be able to provide strong support for the identification of archaeological faunal specimens to this taxon. However, it should be borne in mind that the reason why donkeys can be so successfully identified is that there is a significant size difference between horses/mules and donkeys in modern comparative specimens of known taxonomic status. Donkeys can be sufficiently

separated from the other two species because the size of horses has increased notably since the medieval period (Rackham, 1995). This rapid modification in non-asinine equids (or the lack of modification in donkeys) is mainly determined by the functions that these animals were designated to provide, which resulted from the complicated human ideology and cultural prejudices towards the species. Therefore, even though some donkey breeds, such as *Baudet du Poitou* or the American Mammoth donkey, can be as large as the largest horses, they will never replace the latter because they were created for a specific purpose: mule breeding. Since current zooarchaeological evidence suggests that most Roman horses were much smaller than modern ones on average (Rackham, 1995), when carrying out biometric analyses the question arises: if modern samples can truly represent the species of the past disregarding the size differences? Despite the efforts made by eliminating inadequate specimens from the dataset – e.g. the Poitou donkeys or very small ponies – to minimize the impact of modern selective breeding practices, there is still very scant background information about the changes in hybrid species. With the recent "creation" of giant donkey breeds, such as Poitou and American Mammoth donkeys specifically for mule-breeding, it is clear modern mule specimens may create a size-bias, rendering modern mule specimens less than ideal as a starting point in the identification of archaeological specimens of this species.

As for the classification rate by skeletal element, it is difficult to establish which element gives the best results, as this varies according to species. The metacarpal seems to be more accurate than other elements, with the highest average classification rate (and no lowest classification rate for all three species) (Table 3.12). In contrast, the femur is probably the least accurate element for species identification – more than half of the horses were misclassified when using this element – as well as there being a low classification rate for mules (68.4%, Table 3.12). Due to the restriction of the "simultaneous estimation"

approach, which requires all measurements to be used, this analysis may not be very practical in zooarchaeological applications. The reason is that several measurements are not described by von den Driesch and, therefore, are usually not taken by faunal specialists – including the height of the trochlea constriction (HTc) in humerii, the greatest depth of distal articular facet (DFd) in radii, and the greatest distal depth (Dd) in the first phalanx. Furthermore, some measurements are defined differently in other measurement schemes, such as the greatest distal width (Bd) and the greatest trochlea width (BT) of humerii in Eisenmann's measuring scheme mentioned earlier. Values for archaeological specimens that lack these measurements cannot be determined using modified DFA.

A critical evaluation of a previous study using the DFA method and an attempt to refine it have been carried out in this section. It aims also to remind the reader to consider the impact of intensive selective breeding in domestic species when comparing modern samples with archaeological ones. It should be reiterated that this section does not attempt to devalue the previous attempts at using the DFA technique by pointing out errors in the original dataset. In fact, it is uncertain whether these errors were typographic errors or were also used in the analysis, and the inconsistency of outcomes may simply be caused largely by different settings in different versions of the same software (SPSS). Furthermore, it is important to stress that some reductions in accuracy are to be expected when additional specimens are added to the dataset: a larger number of samples will include a larger variety of breeds, and this, in turn, will result in an increase in the inter-specific variability, which may blur intra-specific differences. At present, it is difficult to comprehensively evaluate DFA as a biometric method for distinguishing between the three domestic equid taxa, given that the current dataset of modern material may not be ideal as a starting point for archaeological applications. Having said this, and with the reservations expressed above,

DFA is still used as a biometric method for distinguishing between different domestic equids in the present thesis.

3.3 – The *Davis Method*: First Phalanges (PH1) Slenderness Index

Indices calculated using a number of measurements to roughly represent the general shape of an element are often used in zooarchaeological investigations. Davis *et al.* (2008), aiming to identify Medieval equid specimens from a site in Portugal, used this approach to distinguish horses, donkeys, and wild equids (namely *Equus hydruntinus* and *Equus hemionus)*. His results show two distinct clusters, one including modern horses and the second including modern donkeys, *E. hemionus*, and Pleistoncene *E. hydrontinus* (with some overlap between the three species in the latter cluster). One advantage of this approach is that it does not show notable impact even when the differences between the anterior and the posterior first phalanges are ignored. As mentioned earlier, in most reports, these two elements are rarely distinguished because of their small differences (Dive and Eisenmann, 1991) and, therefore, this has often resulted in researchers having to exclude proximal phalanges from further biometric analysis.

3.3.1 – Method: Scatter Plot and Mahalanobis Distance

Three measurements chosen to describe the general profile of PH1 in equines are: the greatest length (GL), the smallest shaft width (SD), and the greatest width of the distal articulating surface (BFd) (Figure. 3.13). An index is then calculated as BFd/GLx100 to represent the general slenderness of the element. The calculated index is then used as the x-axis in a scatter diagram, with the SD measurement used as the Y-axis. The more slender PH1 will cluster towards the lower left side of the diagram, whilst the more robust PH1

will cluster towards the upper right. It should be noted that in this approach, the SD measurement is used "raw", i.e. without forming part of an index. While, as explained in the previous chapter, this will strongly affect DFA results, it is less critical here, and in fact can serve as a guideline for species separation. Since mules are argued to have more slender PH1s, the assumption is that they should cluster away from those of horses towards the left and assuming they are, in general, larger than donkeys, should cluster above them. Furthermore, the small-sized horses, i.e. ponies, will cluster underneath the typical horses, as hypothesised in Figure 3.14.

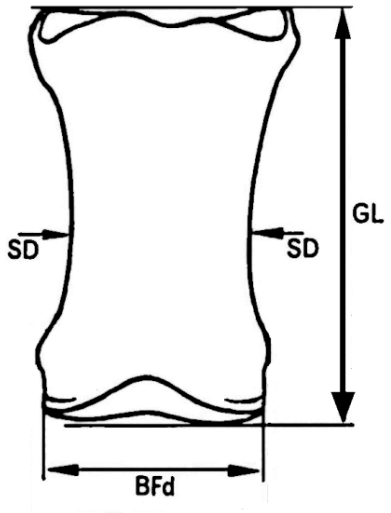


Figure 3.13 – PH1 measurements taken for the Davis method.

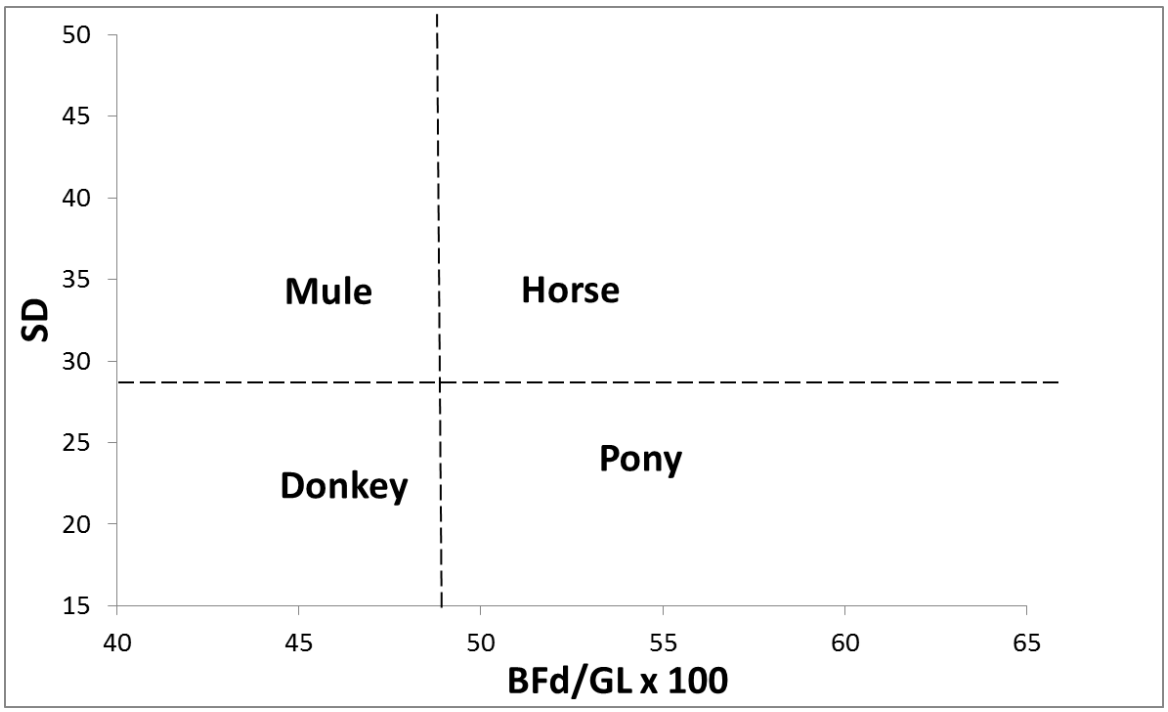


Figure 3.14 – Hypothesised clustering region for different species/breed

To demonstrate the results quantitatively, in addition to visuals provided by diagrams, the centroid of each group is calculated, as are the Mahalanobis distances between each sample and group centroid. The Mahalanobis distance (M-dist) is used in various statistical methods such as DFA and PCA, to calculate the distance between a data point and the group centroid. In contrast to the Euclidean distance, which is a measurement of the straight distance between two points, the M-dist is used only to calculate the level of distribution between data points and the centroid and, therefore, is a rather useful tool to detect outliers in a dataset (De Maesschalck *et al.*, 2000; Franklin *et al.*, 2000). The M-dist also has the advantage of removing the possible interference from linear correlation. It can be seen as a measure that expresses the relationship between two points. Various statistical software packages, such as R, SPSS, MATLAB, etc., provide their own approach for the calculation of the M-dist. It is also possible to calculate the M-dist using MS Excel. In the present study, the M-dist are calculated using R package (version 3.2.1). The M-dist between each data point and the group centroid is calculated using the following script (words in red indicating a "name" defined by the user):

```
# reading original data saved in .txt format
species/breed_a <- read.table("name_of_data_file_a.txt", header=TRUE)
# calculate the mean coordinates
ave_a <- colMeans(species/breed_a)
# generate the covariance
cov_a <- cov(species/breed_a)
# calculate the M-dist between each point and group centroid
Mdist_a <- mahalanobis(species/breed_a, ave_a, cov_a)
# export the outcome into .txt file
write.table(M-dist_a, file = "output_file_name.txt", sep="\t")
```

The M-dist between different species/breeds is calculated using the following script:

```
# reading original data, separated by species/breeds

(species/breed_a) <- read.table("name_of_data_file_a.txt", header=TRUE)

(species/breed_b) <- read.table("name_of_data_file_b.txt", header=TRUE)

# calculate the mean coordinates

ave_a <- colMeans(species/breed_a)

ave_b <- colMeans(species/breed_b)

# generate the covariance

cov_a <- cov(species/breed_a)

cov_b <- cov(species/breed_b)

# generate the inverse pooled covariance, a and b represent the total number of

# individuals of respective species/breed.

ipc_a_b <- solve(((a/(a+b-1))*cov_a)+((b/(a+b-1))*cov_b))

# calculate the differences between two sets of mean coordinates

dif_a_b <- ave_a – ave_b

# calculate the Mahalanobis distance between two species

MDist_a_b <- sqrt(tcrossprod(crossprod(dif_a_b, ipc_a_b), dif_a_b))

MDist_a_b

# Returns with the Mahalanobis distance between two species/breeds
```

3.3.2 – Material: Additional Data and Grouping

In addition to the standard dataset used for the DFA, donkeys and horses from the dataset published by Davis *et al.* (2008) are also included for this analysis in order to increase sample size. Other than attempting to distinguish the three domestic equids – horse,

donkey, and mule – attention is also paid to the variations between different breeds/types of horses, i.e. ponies and Arabs. As mentioned in a previous section, the concept of separating ponies from horses has no basis in real biological divergence, but rather reflects an artificial separation according to a modern cultural perspective. Ponies are grouped to see if they are distinctly different from other horses in conformation. Modern Arab horses are also grouped to observe if their similarity with mules, as suggested by DFA, can also be detected using this technique. The second part of the discussion considers all horses as a single group, regardless of breeds/types, and examines the overall diversity between these domestic equids.

3.3.3 – Results and Discussion

3.3.3.1 Scatter Plot

From the scatter plot (Fig 3.15), it is evident that donkeys cluster at the bottom left corner as hypothesised, confirming that their PH1 is much more slender than those of horses. Ponies, on the other hand, are considerably more robust than most horses but have a smaller absolute SD value due to their small size. However, there is still a large overlap between ponies and other horses. Nevertheless, it is still quite noticeable that numerous ponies fall in the hypothesised region. Similar to the results obtained through DFA, the Davis method also indicates that Arab horses and mules share a similar proportion as regards to their first phalanges. As shown in Figure 3.15, Arab horses are more slender than other horse breeds and overlap considerably with mules. The close clustering of the horses after the exclusion of Arab horses and ponies is worth noting. Unfortunately, the exclusion of Arab horses and ponies does not result in an improved separation between horses and mules; a large degree of overlap still remains. It seems that even though mules overall tend to have a more slender PH1 than horses, a high level of overlapping between

the horse and mule convex hulls makes distinguishing between the two species challenging..

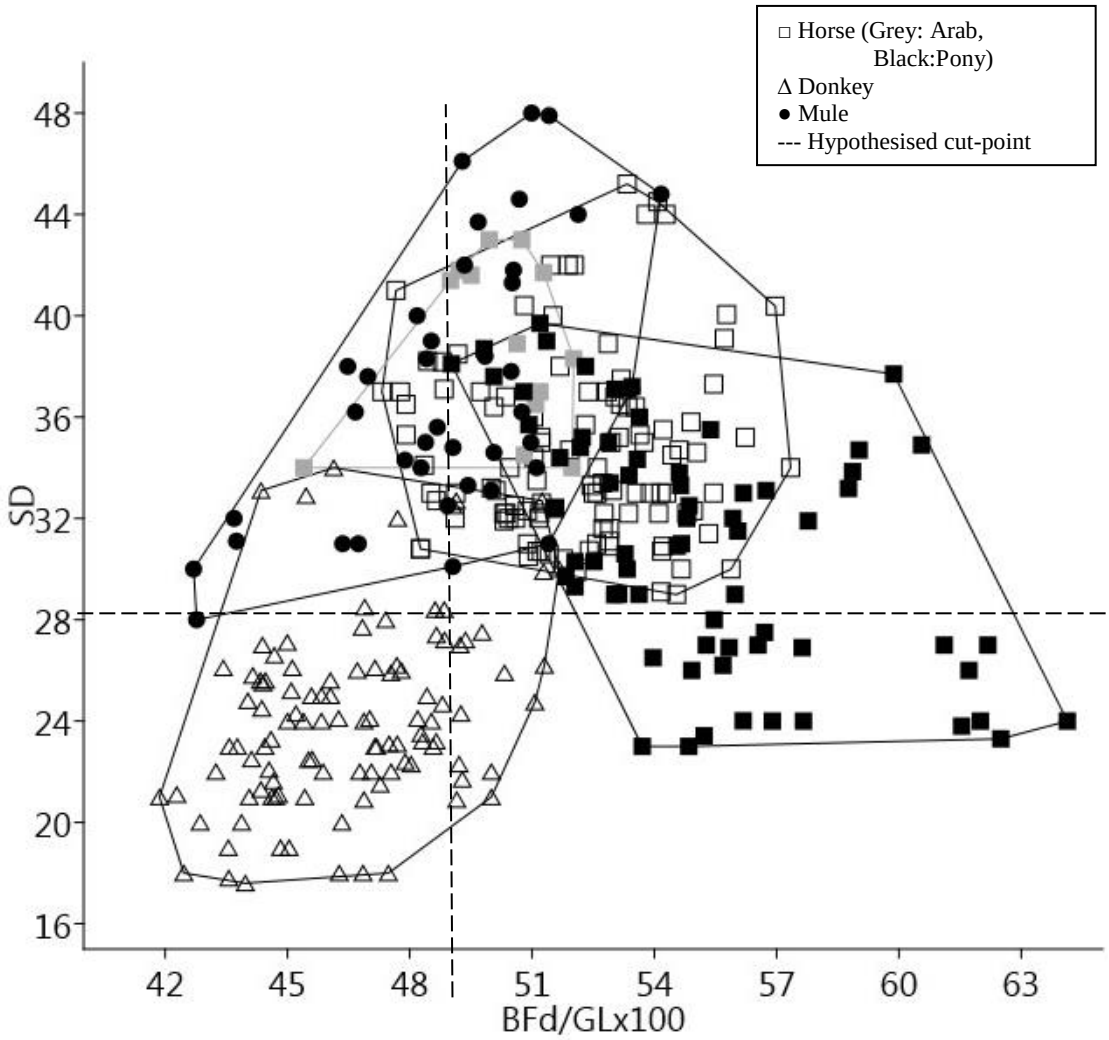


Figure 3.15 – BFd/GL index and SD scatter-gram.
The convex hull is enclosed by the outmost cases of each breed/species.

3.3.3.2 Mahalanobis Distance

Observations made in the previous section can be further supported with evidence from the Mahalanobis distances (M-dist). Table 3.13 summarises the M-dist between different breeds/species. Note that in this table, horses are subdivided into three groups to explore the differences within *E. caballus* and, therefore, the differences between species (i.e. horse vs donkey and mule) are not conclusive here. As observed in the previous section,

while numerous ponies fall into the hypothesised region, the level of overlap between ponies and other horses (excluding Arabs) is still conspicuous. The M-dist between these two groups is 1.81, which is significantly smaller than the distance between only ponies and donkeys and mules. Furthermore, the much shorter distance between Arab horses and mules (M-dist = 0.55) can explain the large overlap of these two groups in the scatter plot. In contrast, the M-dist between Arabs and other horses (excluding ponies) is much larger (M-distHA = 1.49), although a large degree of overlap between these two groups still exists. This result seems to suggest that there would be a high risk of misidentifying Arabian horses – or horses with the similar body conformation to Arabs – as mules.

	Horse	**Arab**	**Pony**	**Donkey**	**Mule**
Horse		**1.486047**	**1.809607**	**3.496504**	**1.633418**
Arab	**1.486047**		**1.91938**	**4.109556**	**0.545385**
Pony	**1.809607**	**1.91938**		**3.743742**	**2.18474**
Donkey	**3.496504**	**4.109556**	**3.743742**		**3.136808**
Mule	**1.633418**	**0.545385**	**2.18474**	**3.136808**	

Table 3.13 – The Mahalanobis distances between different breeds/species.

All horses are combined for further inter-species comparison, and the outcomes are summarised in Table 3.14. The outcomes confirm the observation based on the scatter plot. Donkeys can clearly be distinguished from the other two domestic equids, while the separation of horses and mules remains ambiguous.

The degree of potential misidentification of specimens can be tested by comparing the M-dist between the coordinates of the data points and the group centroids of other species. If

the M-dist between a datum and its group centroid is larger than the M-dist to the centroid of other species, then it can be considered to have a higher likelihood of being misidentified. Judging from the results, 15.58% of mules have a shorter M-dist to the horse centroid than to the mule centroid. On the other hand, 21.47% of horses are likely to be misidentified as mules as a result of they are having shorter M-dist to the mule centroid than to their own centroid. Furthermore, the majority of Arabian horses (8 out of 13) would be likely to be misidentified as mules; a sharp contrast to ponies, where merely five specimens would be likely to be misidentified as mules. Table 3.15 summarises the potential misidentification among the three species. It is also interesting that whilst donkey has the highest rate of correct classification using M-dist, it is also the only species that has a possible misidentification in both other two species. From a different perspective, with no case of misidentification as donkeys in the other species, it means that when the method suggests that a PH1 of an unknown species belongs to a donkey, it is much less likely that it will belong to a horse or a mule. Mules, however, have an overall reclassification rate of only 75.72%, which is similar to the outcomes suggested by DFA as shown in a previous section.

	Horse	**Donkey**	**Mule**
Horse		**3.68488**	**1.411282**
Donkey	**3.68488**		**3.136808**
Mule	**1.411282**	**3.136808**	

Table 3.14 – The Mahalanobis distances between three domestic equids species.

	Horse Centroid	Donkey Centroid	Mule Centroid	Total
Horse	**150 (78.53%)**	**0 (0.00%)**	**41 (21.47%)**	**191 (100.00%)**
Donkey	**3 (2.83%)**	**97 (91.51%)**	**6 (5.66%)**	**106 (100.00%)**
Mule	**6 (15.38%)**	**0 (0.00%)**	**33 (84.62%)**	**69 (100.00%)**
Overall Reclassification Rate	**81.17%**	**100.00%**	**75.72%**	

Table 3.15 – Number of species determined.
Determination made by using the shortest distance to each group centroid.

3.3.4 – The Davis Method Summary

Both the scatter plot and the M-dist have demonstrated that donkeys can be quite clearly distinguished from horses and particularly from ponies. In contrast, the differences between donkeys and mules are somewhat less evident, albeit the comparison between M-dist suggests that it is more likely for mules to be misidentified as donkeys, rather than the other way round. Unfortunately, it seems that using only the scatter plot may not be sufficient to separate mules and horses from each other partially because of the high degree of overlap between mules and Arab horses. Nevertheless, the use of the M-dist comparison can provide further support for the determination of unknown species using the current method.

The Davis method was designed to separate species through a visual representation of quantitative data. The advantage of such a representation is that it is self-evident and requires no further explanation. However, it cannot be used to resolve the taxonomic membership of data points that fall into the overlap zone between two species. The use of M-dist can benefit the original method in two ways: by increasing the resolution that can help distinguish inter-group differences and by providing quantitative values for the determination of an unknown archaeological specimen which may fall into an overlap zone.

3.4 – Chapter Summary

In this chapter, two different biometric approaches have been reviewed and their limitation and potential risks were evaluated. Both methods have been utilised, directly or indirectly, in a number of studies of equid remains (Johnstone, 2004, 2005, 2008, and 2010; Davis *et al.*, 2008; Ayton, 2011 and 2012, Worley; 2013). Shortcomings in the application of DFA in a previous study (Johnstone, 2004) are discussed, and modifications in the application of the technique and supplementary steps recommended for future studies of equid remains were suggested. More importantly, this chapter has also pointed out the ambiguities and uncertainty in both methods that are at least in part a production of the difficulty in finding suitable and representative samples (see below). In short, neither method is able to resolve species determination with absolute confidence. They are only tools that provide an objective and quantifiable likelihood regarding the taxonomy of archaeological equids; they provide a guide to the degree of plausibility of a taxonomic determination. Having said that, this is still an improvement on and addition to the sole reliance on purely qualitative traits, the application of which may depend in part on the experience and subjective evaluation of each researcher. It must be stressed that this should not be seen as an absolute rejection of the role of qualitative morphological features. On the contrary, it should add reliability to the qualitative morphological traits based on more objective criteria. The benefit of having biometric methods is that it allows all specimens to be determined using the same standard, so that further support is available for ambiguous morphological features.

Despite the objectivity offered by biometric analyses, their limitation must be clearly established and understood. The most important factor regarding the accuracy and reliability of biometric techniques discussed here is the suitability of modern equid

specimens as representative samples for archaeological domestic equids, especially for horses. It is argued here that the morphological variability of horses has been drastically increased through modern, intensive selective breeding practices. The result of such phenomenon is that a careful "selection" of equine breeds must take place before any biometric analysis can proceed. In addition to horses, it is necessary to reiterate here the problems of using modern mule specimens. As mentioned previously, as an "artificial" species, modern mules represent only their immediate ancestor (i.e. parents). Every generation of mules represents the creation of a new 'species'. Thus, the relationship between different generations of mules is no closer than the relationship between them and the relatives of their immediate parents. The question that we need to ask here is whether a Roman mule was, morphologically, rather more similar to its parents (i.e. Roman horse and donkey), or whether it resembled (morphologically) different generation of mules, e.g. those procreated by chronologically distant (e.g. modern) horses and donkeys? It is true that the mules never seem to fail to deliver animals with hybrid vigour, and in this sense every generation of mules are alike. However, whether this translates into a high degree of phenotypic similarity in the skeleton still needs to be determined.

The other concern for biometric approaches is that of the consistency between methods and skeletal elements. The results suggest that both methods – DFA and Davis method – are relatively consistent regarding the accuracy of classification; and both indicate that Arab horses are constantly misclassified as mules. Nevertheless, the consistency between different elements in DFA still requires further assessment, since it is related to the classification rate of different elements. While identification seem more reliable when based on elements such as metacarpals, first phalanges, and metatarsals, identifications based on femora are unreliable and should be avoided. At present, the major concern for current biometric analyses of domestic equids is not the methods themselves, but rather the

(un)availability of samples that can be used as appropriate proxies for archaeological equids. In this thesis, the methods are applied with these limitations in mind.

Chapter 4 - Geometric Morphometric Methods

4.1 – Introduction

Geometric morphometrics (GMM) is an analytical method commonly used in zoological and botanical research for comparing the shape differences between groups (Slice, 2007). In recent years, this method has been adopted in a number of archaeological studies (e.g. Bignon *et al.*, 2005; Owen *et al.*; 2014; Ros *et al.*, 2014; Seetah *et al.*, 2014; Gunz and Bulygina, 2012, etc.). The concept of this method is to compare the shape (both 2D and 3D) defined by landmark co-ordinates which have one-to-one corresponding points in all specimens or by outlines or curves that describe the profile of a specific area in an object, or the entire object. By positioning and scaling these defined shapes with the same coordinate origin, comparisons can be made by applying various statistical methods such as Principle Component Analysis (PCA), Canonical Variate Analysis (CVA), and even Discriminant Function Analysis (DFA). The advantage of this method is that it can quantify some morphological traits that do not lend themselves to be studied by other biometric techniques. As explained in the previous chapter, one of the problems with the available data in DFA is that the slenderness in mule long bones, which is often regarded as an important characteristic of this taxon, was not clearly indicated by the measurements used. Theoretically, an infinite number of points can be set on an image of a long bone along its shaft (Fig 4.1); this will allow an unlimited number of measurements to be taken for analysis. In addition to the distance measurements, the changes in the angles between points can also be used as variables for GMM. Thus, to some extent, GMM should be the ultimate solution for quantifying morphological features that could previously only be described by “subjective” qualitative criteria.

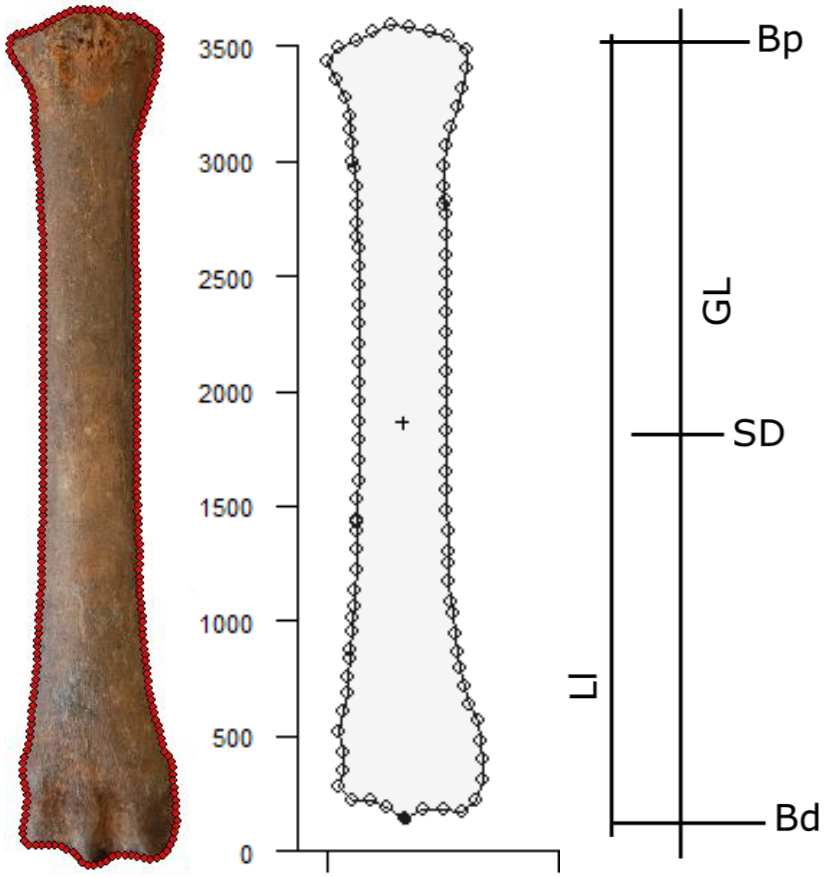


Figure 4.1 – Example of geometric morphometric method
– Using 300 points along the profile of MC (dorsal view) in MorphoJ (left image) or using Momocs package in R to automatically capture outlines of MC from the same pictures (middle image) can better describe the shape of MC than using conventional standard measurements (right image).

This chapter will explore the potential use of GMM in the identification of the three domestic equids in question, horse, donkey and mule using dental morphology in the lower molars. This will involve four different approaches representing different levels of GMM applications:

I. using direct measurements from predefined landmarks,

II. using geomorph package in R (Adams and Otárola-Castillo, 2013) to perform landmark-based GMM

III. using geomorph package in R (Adams and Otárola-Castillo, 2013) to perform outline-based GMM

IV. using Momocs package in R (Bonhomme *et al.*, 2014) to analyse the shape describing the region of interest.

This chapter will provide full illustrations of how to use these methods in the attempt to separate different domestic equid species using the morphological features of the lower molar occlusal surface from known species.

4.2 – Material

Although, in theory, every skeletal element that bears morphological features could be studied for its suitability for species identification, restrictions on equipment, technique, or available samples have limited the opportunity to fully explore the possibilities of GMM in most elements. As a result, this part of the thesis should be regarded as a pilot study, a first attempt to use GMM for the identification of domestic equids using the morphological characteristics of equid lower molars. While some qualitative morphological criteria in post-cranial elements have been suggested as being useful in the determination of domestic equid species (Peters, 1998), most species determinations of equids still rely on the dental morphology of lower molars (e.g. Armitage and Chapman, 1979; Uerpmann and Uerpmann, 1994; Levine, 2004). In addition, dental morphological differences between *E. caballus* and *E. asinus* have been validated, to some extent, by aDNA analysis (Hite, 2008, see Chapter 6). One evident advantage of choosing the lower molar morphology is that the morphological features are all arranged on a flat, two-dimensional surface, as opposed to the situation in the post-cranial elements. The benefit of dealing with a flat surface is that the shape information containing the morphological features can be sufficiently captured in a 2D image, whereas capturing the shape of post-cranial elements would be more complicated.

As reviewed in Chapter 2, the morphology of the lower molars in domestic equids has been argued to possess reliable traits to distinguish horses, donkeys, and mules – more specifically the shape of the enamel pattern formed by the metastylid and the metaconid (also known as the lingual-fold) (Figure 2.1). Previous researchers (Armitage and Chapman, 1979; Davis, 1980; Eisenmann, 1986; Uerpmann and Uerpmann, 1994) maintain that a typical caballine trait is a U-shaped lingual fold, whereas a V-shaped pattern represents an asinine trait that is also characteristic of mules. In practice, however, the determination of this trait can be quite subjective, since the shape is commonly observed as somewhere between the two extremes or has a zigzag profile (See Figure 4.2). It is, therefore, essential to have a method that allows such types of criteria to be determined more objectively.

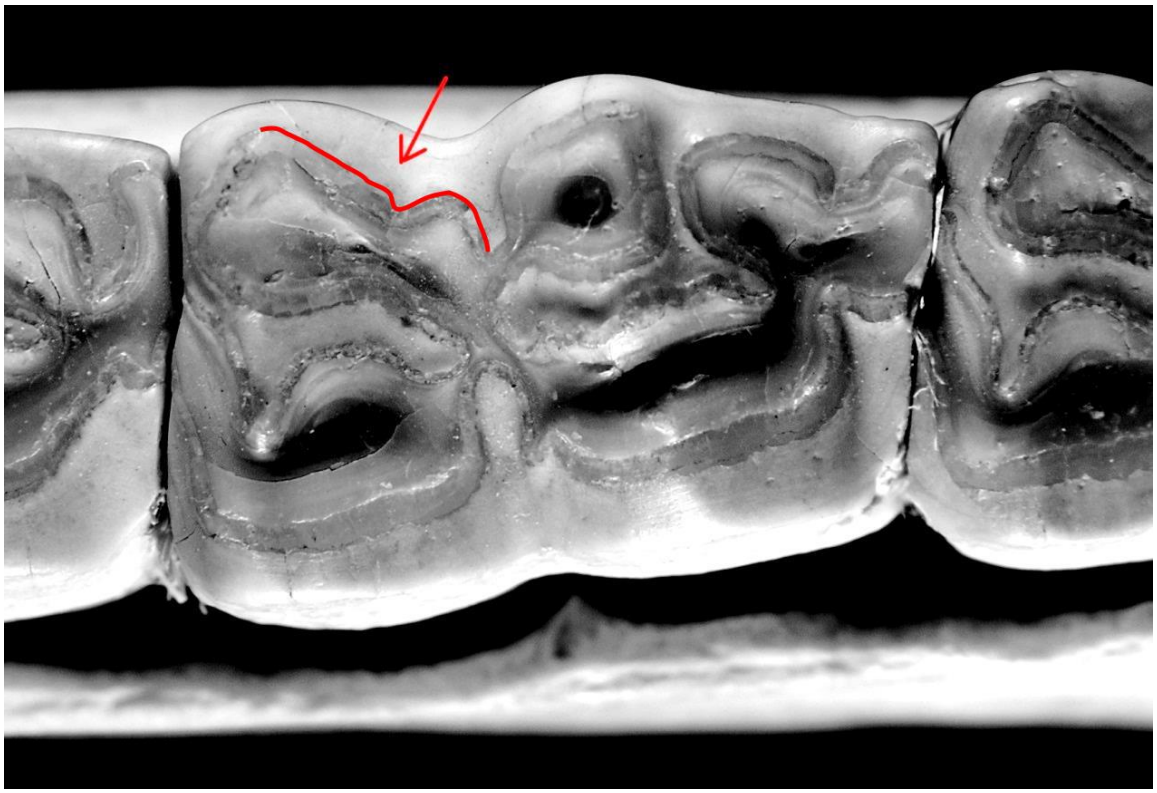


Figure 4.2 – Example of Non-metric variation in equid molars.
This trait is observed in known donkey mandibular teeth as well as several archaeological equids.

The topic of quantitative analysis of dental morphology has not been completely overlooked by previous researchers. Both Eisenmann (1986) and Payne (1991) attempted to use measurements taken from equids' lower teeth for a similar purpose. The outcomes of both attempts remain inconclusive regarding equid species determination. In addition, these quantitative methods are not widely practised for the determination of domestic equids. One principal reason for the inconclusive outcome may be that the measurements taken for quantitative analysis were not sufficient to capture the specific shape differences between the morphological characteristics of different taxa. For instance, in Payne's (1991) dental scheme, there is no measurement that can be used to distinguish the shape of the lingual valley or to determine the symmetry of the metaconid and the metastylid. The only measurement that is related to these morphological differences is the bucco-lingual length.

Images of the comparative collection available at University of Southampton are taken by the current author using the same camera setting (Nikon D80 with Sigma 17-70mm, at 17mm/F2.8). All molars are positioned with the occlusal surface levelled horizontally (perpendicular to the lens). It should be noted that such position does not always resemble the position of the molar as in the animal's mouth. This is because, based on personal observations, in most cases, the occlusal surface will be tilted towards either buccal or lingual side instead of having a perfectly levelled occlusal surface. Nevertheless, this should only have limited impact on species determination since there is no fixed viewing angle suggested for visually inspecting these qualitative morphological traits. The reason to set a fixed angle is to minimize possible distortion resulted from tilted occlusal surface as the tooth positioned in mandible.

Unfortunately, this will only yield to an extremely small number of samples (3 horses and 1 donkey). An attempt was made to increase sample size by asking colleagues for images of equids' lower molars; however, very few responded. As a result, only 36 specimens were available for the study (Table 4.1). These included 13 donkey and 23 horse molars from the following sources: illustrations published by Davis (1980), the collection from Historic England, Fort Cumberland (image taken by Dr. Fay Worley), in addition to the faunal collection in the Archaeology Department, University of Southampton. Images of equids' mandibular teeth were also available from Eisenmann (http://www.vera-eisenmann.com) and Baxter (1998), but regrettably, the resolution was too low to be used here. The risks of inter-observer error (Arnqvist and Martensson, 1998) as well as possible distortions occur in images taken from different camera settings (Mullin and Taylor, 2002) are considered. However, under limited budget and resource, it is decided to include these images in this pilot anlaysis to increase the sample size. Another obvious problem in this standard dataset is the complete lack of mule molars. The issue with the extreme scarcity of mule samples has been repeatedly raised here and by Johnstone (2004), and it is a serious challenge for all related studies.

No.	Species	Element	Source
D01	Donkey	Molar	Davis, 1980
D02	Donkey	Molar	Davis, 1980
D03	Donkey	Molar	Davis, 1980
D04	Donkey	Molar	Davis, 1980
D05	Donkey	Molar	Davis, 1980
D06	Donkey	Molar	Davis, 1980
D07	Donkey	Molar	Davis, 1980
D08	Donkey	Molar	Davis, 1980
D09	Donkey	Molar	Davis, 1980
D10	Donkey	M1	Southampton, 132
D11	Donkey	M2	Southampton, 132
D12	Donkey	M1	HE, Fort Cumberland, 546
D13	Donkey	M2	HE, Fort Cumberland, 546
H01	Horse	Molar	Davis, 1980
H02	Horse	Molar	Davis, 1980
H03	Horse	Molar	Davis, 1980
H04	Horse	Molar	Davis, 1980
H05	Horse	Molar	Davis, 1980
H06	Horse	M1	Southampton, 209
H07	Horse	M1	Southampton, 209
H08	Horse	M2	Southampton, 209
H09	Horse	M2	Southampton, 209
H10	Horse	M1	Southampton, 137
H11	Horse	M1	Southampton, 137
H12	Horse	M2	Southampton, 137
H13	Horse	M2	Southampton, 137
H14	Horse	M1	Southampton, 604
H15	Horse	M1	Southampton, 604
H16	Horse	M2	Southampton, 604
H17	Horse	M2	Southampton, 604
H18	Horse	M1	HE, Fort Cumberland, 760
H19	Horse	M2	HE, Fort Cumberland, 760
H20	Horse	M1	HE, Fort Cumberland, 3329
H21	Horse	M2	HE, Fort Cumberland, 3329
H22	Horse	M1	HE, Fort Cumberland, 3868
H23	Horse	M2	HE, Fort Cumberland, 3868

Table 4.1 – Modern specimens used in GMM.
- HE stands for Historic England

4.3 – Approach I: Angle analysis

This method aims to quantify the relationship between the differences in the shape of the lingual valley and the degree of penetration of the buccal valley. The basic assumption is that since the lingual valleys of the three domestic equids can be divided into two types, the V-shaped and the U-shaped, then by comparing the geometric differences between the U and the V shapes, it should be possible to separate the domestic equids into two groups. The discrimination between donkeys and mules, which are both said to have a V-shaped lingual valley, can be attempted by measuring the physical distance between the bottom of lingual valley and the apex of the buccal valley; this will describe the penetration level of the buccal valley. Before making the comparison, the geometric difference between the U and the V should first be established. It is apparent (Fig 4.3) that three fundamental points share the same position in both shapes, with the difference being mainly determined by the degree of curvature of the line connecting the points. Thus, the comparison between these two shapes is possible by quantifying the degree of curvature.

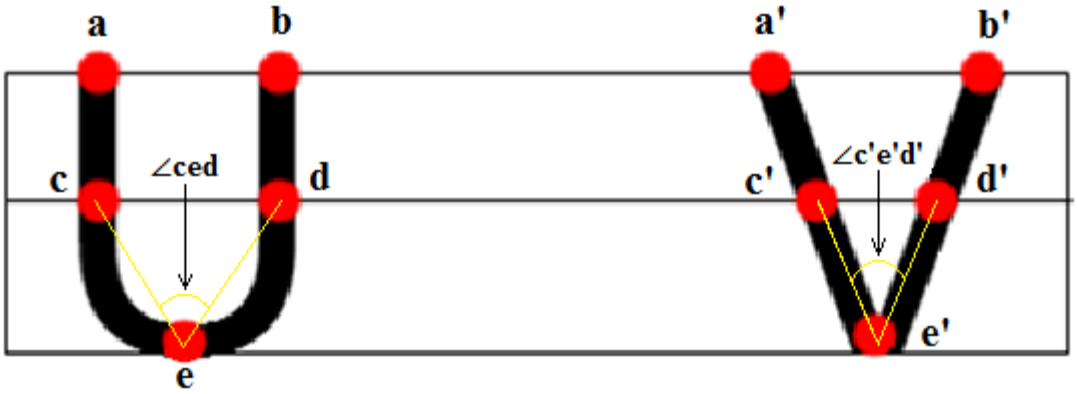


Figure 4.3 – Shape difference between U and V.

There are several possible ways to quantify the degree of curvature. One way is to measure the greatest distance of the two valley apexes ($\overline{ab}$ and $\overline{a'b'}$) and compare it to the distance taken from any other predefined line connected by two points along the valley slope, but that remain parallel to the first line. For example, in Figure 4.3, the distance $\overline{cd}$ is different

from the distance $\overline{c'd'}$ whilst the distance $\overline{ab}$ and the distance $\overline{a'b'}$ is the same. Then the differences between shapes can be determined by the decreasing rate between two distances (i.e. $\overline{cd}$ / $\overline{ab}$ v.s. $\overline{c'd'}$ / $\overline{a'b'}$). If the decreasing rate increases gradually at a constant rate, then the shape resembles a V-shape. On the other hand, if the rate does not change much throughout the valley, then this implies a U-shape.

An alternative approach is to measure the angle of a set of predefined point (e.g. ∠ced). A narrow valley is indicated by a smaller angle. For example, in Figure 4.3, ∠ced is larger than ∠c'e'd', and thus V-shape has a narrow valley than U-shape. It is crucial for either approach, however, to define a set of arbitrary points, so that the measurement can be repeated in different specimens. Since the changes are more apparent towards the bottom of the lingual valley, two additional points are set three quarters of the way down from the apex (Figure 4.4). This is done by first aligning both apices (point a and b) to a horizontal line, and then measuring the vertical distance between the line and the bottom point (e). Another horizontal line is set which divides the lingual valley in an equal half (line 1), and repeat the process for the lower half of lingual valley (line 2). The intersection of the lines that divide the lower lingual valley in half and the slope line on both sides of valley are the points that will be used as artificial measuring points (point f and g). Theoretically, the changes between U and V curves can be detected in the middle of the slope as explained above using ∠ced and ∠c'e'd'. However, a non-metrical dental variation, which causes either the metastylid or the metaconid to form a "zigzag" slope line often occurs at the middle of slope and affects both the distance and the angle of the slope (See Figure 4.2). This non-metric dental variation is found in both modern specimens of horses and donkeys, and they are also present is some of the archaeological specimens used in this study. As a

result, points (f and g) further down the slope are used to avoid the impact caused by this non-metric variation.

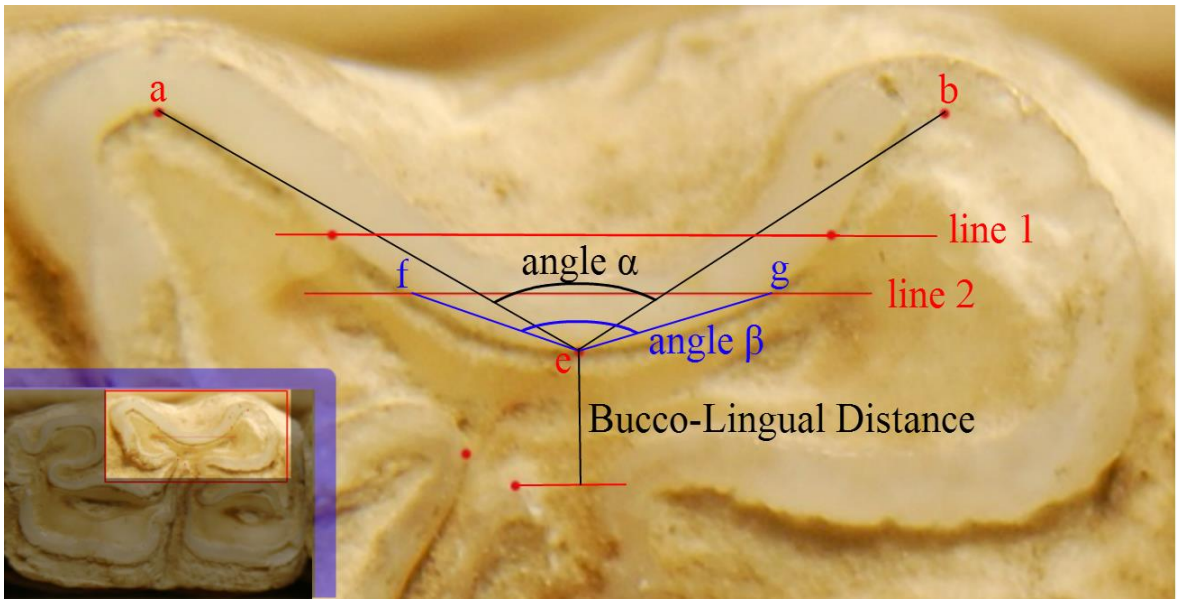


Figure 4.4 – Measurements taken for Angle Analysis.
The differences between angle α and angle β are used to determine the lingual valley shapes.

4.3.1 – Method: Angle acquisition using ImageJ

ImageJ is a free image analysis program that allows users to measure various data from images (Schneider *et al.*, 2012; Abràmofff *et al.*, 2005). It allows the measurements of an angle and a distance to be taken and is, therefore, ideal for the present study. After the measurements are taken, the data are then imported into PAST software (Hammer *et al.*, 2001) to create a scatter plot of the distribution of the different species. These can be done using any other software package available.

According to the alleged differences in the morphological features of domestic equids (Armitage and Chapman, 1979; Davis, 1980; Eisenmann, 1986; Uerpmann and Uerpmann, 1994), the location where each species is more likely to fall in a bivariate plot can be hypothesised. Angle β in U-shaped lingual fold is usually larger than angle α, and vice versa in a tooth with a V-shaped lingual fold (Figure 4.4). The U-shaped tooth is more likely to have a negative value when angle β is subtracted from angle α. Thus, horses with

a U-shaped lingual valley should cluster towards the left side of the scatter plot (Figure 4.5). In contrast, donkeys and mules are hypothesised to fall towards the right side of the plot, given that they would have a positive angle difference. According to suggested qualitative criteria (Armitage and Chapmann, 1979; Uerpmann and Uerpmann, 1994; Johnstone, 2004), the bucco-lingual distance can further distinguish the three species (see Figure 2.1 previously). With the smallest penetration level of the buccal valley indicated by a larger bucco-lingual distance, the donkeys will cluster near the top of the scatter plot while mules should fall near to the x-axis, the lower end of the graph. Horses should occupy an intermediate position between donkeys and mules. The Mahalanobis distance was also calculated in order to quantitatively describe the interval between species and to assess the method regarding its accuracy in classification.

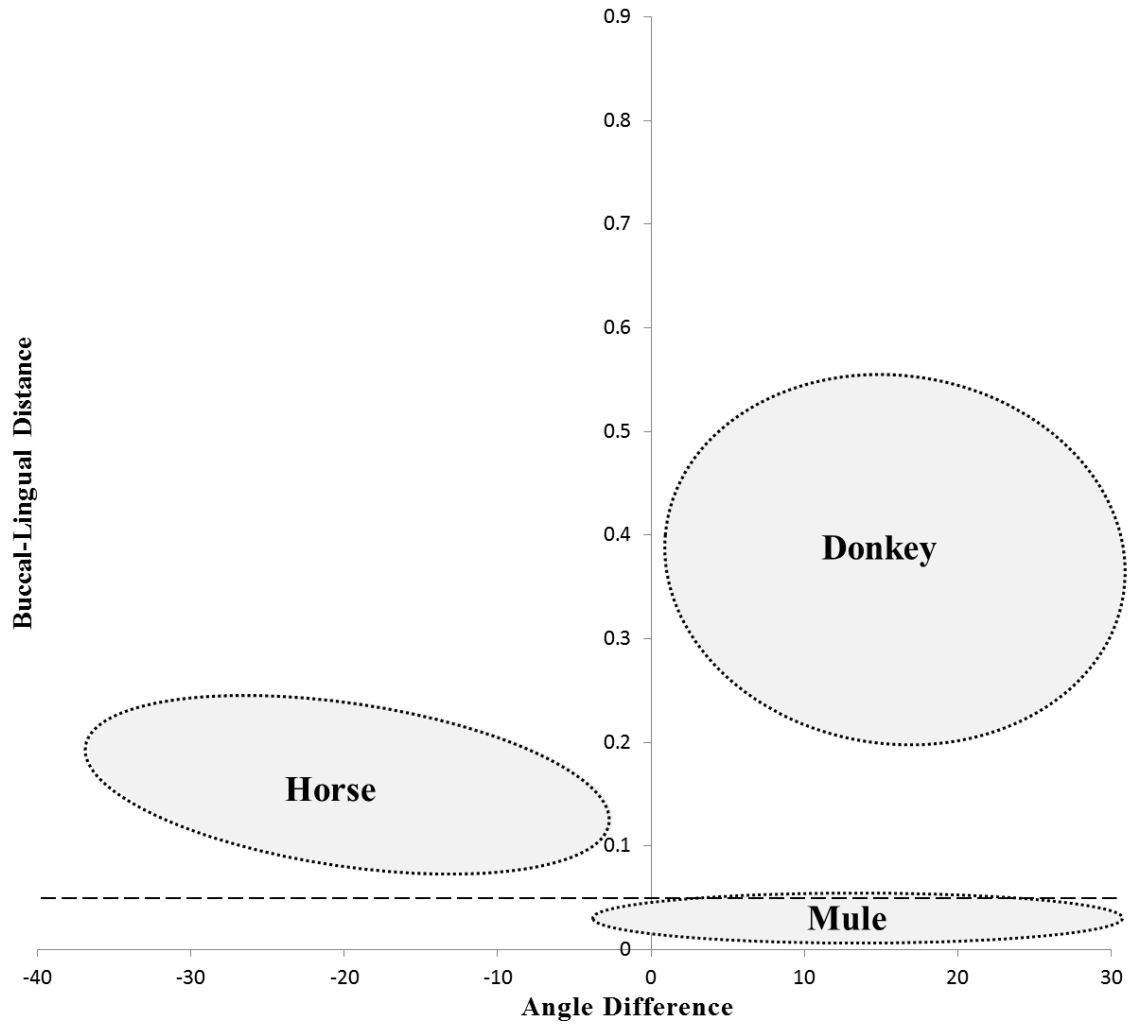


Figure 4.5 – Hypothesised regions for each equids species

4.3.2 – Results

Modern specimens of horses and donkeys are distinctly clustered as hypothesised (Figure 4.6). However, there is one donkey with an atypical lingual valley angle, which seems to resemble teeth with a U-shape lingual fold. In addition, the bucco-lingual distance of some horses in the modern sample is exceptionally short, which conflicts with the claim that horses showing only a partial penetration of the buccal valley. This has a serious implication on whether this trait is considered valid to separate mules from horses. The buccal and lingual valleys will nearly be in contact when the distance between them is less than 0.05 cm. Five horse molars from three different individuals in the standard dataset (H18, H20, H21, H22, and H23, all from images of modern specimens in Historic England collections, Fort Cumberland) have a bucco-lingual distance less than 0.05 cm. It is unclear whether the very short bucco-lingual distances in these individuals are related to breed variation or age (i.e. tooth wear stage). Exceptionally short bucco-lingual distances were observed in some deciduous teeth in comparative collections, but these were excluded from this analysis. Some molars with an exceptionally large bucco-lingual distance were observed in younger horses, but again, these were excluded from the analysis. As a result, the five molars mentioned above can at present only be considered as one end of horse variability. For the purpose of the present study, 0.05 cm was set as the putative cut-off point between horses and possible mules in later determination of archaeological specimens based on above observations. This still makes it possible to set a narrow range for mules since the shortest bucco-lingual distance in the modern donkey sample is 0.065 cm, much shorter than expected from previous claims. As a result, a certain level of overlap is expected for all three species.

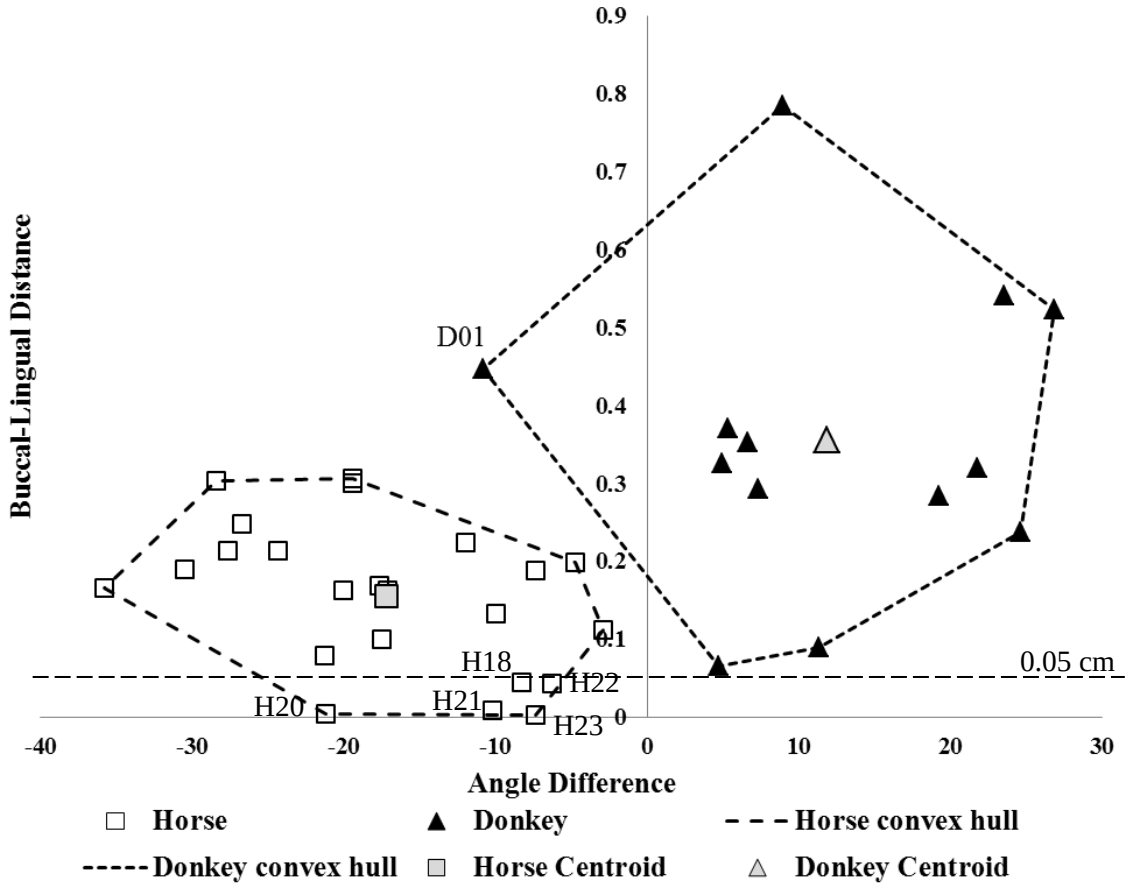


Figure 4.6 – Scatter plot using the difference between angles and bucco-lingual distance. Note the possible overlap in angle difference of one donkey and several horses with unexpected short bucco-lingual distances.

The Mahalanobis distance between horses and donkeys is 3.50 and is significantly greater than the group mean M-dist (donkey mean M-dist = 1.85, horse mean M-dist = 1.91). Comparison of the M-dist of each specimen and the group centroid of the two species shows that only one horse specimen has a higher likelihood of being misidentified as a donkey. This result runs contrary to what could be inferred from viewingt Figure 4.6, namely that the donkey specimen (D01) with a negative angle difference is closer to the horse centroid. Results also indicate that archaeological specimens are highly unlikely to be donkeys misidentified as horses (Table 4.2). In contrast, if a specimen of unknown taxonomic membership is identified as a donkey using this method, then there is a slight possibility that the specimen is, in fact, a horse. Unfortunately, due to the lack of mule

samples, the relationship between mules and the other two domestic equids remains undetermined.

	Horse Centroid	Donkey Centroid	Total
Horse	22 (95.65%)	1 (4.35%)	23 (100.00%)
Donkey	0 (0.00%)	13 (100.00%)	13 (100.00%)
Overall Reclassification rate	100.00%	95.83%	

Table 4.2 – Reclassification rate using M-dist

4.3.3 – Angle Analysis Summary

Strictly speaking, the Angle Analysis method is not a typical GMM method as general considered, because it still requires measurements to be taken "manually" albeit with the aid of image analysis software, rather than conventional tools, such as callipers or a measuring board. Most GMM no longer involves the direct measurement of any kind and analyses stem directly from the coordinates of points describing the subjects. Nevertheless, the method described in this section will still be considered as GMM in the broader sense since conventional biometric analyses, at least in zooarchaeological studies, does not involve Angle Analysis. Results indicate that Angle Analysis can separate donkeys and horses with some realistic degree of accuracy. However, since no mules were used in this method, the determination of specimens with unknown taxonomic position as mules can be made only on the postulated differences in lingual valley shape and bucco-lingual distance. In addition, it should be remembered that this approach examined only two of the three qualitative morphological criteria postulated by a number of authors. The symmetry of the metaconid and the metastylid is not considered in this approach. Thus, it is still not certain if an identification based on only two traits is consistent with the third trait.

4.4 – Approach II: Landmark-based GMM

Recent developments in GMM allow more aspects of the morphological criteria to be considered by evaluating the correlation between multiple points in the targeted subject. This makes it possible to examine the symmetry of the metaconid and the metastylid, something that is overlooked in the previous method. Similar to the shape of the lingual valley, this is a morphological trait that has been used specifically to separate horses from donkeys and mules. Thus, in principle, adding this criterion should increase the reliability of the species determination. A Landmark-based GMM is able to directly compare the coordinates of predefined landmark points by overlaying all the samples on to the same coordinate system based on the concept that a "shape" will remain the same regardless of the scale, orientation, and position (Bookstein, 1991).

To perform a landmark-based GMM analysis, several requirements need to be fulfilled. First, since the analysis is based on shape, the predefined landmarks need to be able to represent a shape (Bookstein, 1991). Although GMM can also deal with curves or open outlines, it requires a different approach based on sliding- or semi-landmarks, which will be discussed in the next section. The second criterion is that all landmarks need to have a "one-to-one" correspondence in all samples. Missing landmarks can be replaced by the group averages at the expense of accuracy and representativeness, but this is not followed in this analysis. The final requirement for landmark-based GMM is that the scale of the original image is required for calibrating the uniform scale, which is necessary to overlay all specimens. The process of overlaying landmark points using the same coordinate system is crucial for all shape analyses. Such a process is termed the "Procrustes fit" (Bookstein, 1991). The Procrustes fit takes the group centroid of a set of landmarks and calculates the correlation of each landmark and the centroid. All group centroids are then

used as the origin of the new coordinate system, and all landmark points are reconstructed from the previously calculated correlation and plotted into the new coordinate system. A new covariance matrix for these reconstructed landmark points can then be generated for further analysis. For landmark-based GMM, the most commonly used analysis is PCA, although other types of analysis, such as DFA, can be performed.

To compare the three morphological features on the lower molar occlusal surface, eight landmark points (LM) were defined from the area of interest (Figure. 4.7). The most posterior point in metastylid is defined as LM1, while the most anterior point in metaconid is LM7. The most lingual point in metastylid and metaconid is defined as LM2 and LM6 respectfully. LM5 is defined by the bottom tip of the lingual fold and LM 8 is the apex of the buccal fold. The remaining two of these eight landmarks (LM3 and LM5 in Figure 4.7) are not "actual" landmarks with corresponding features that allow them to be identified visually from the image; instead, they are "artificial" landmarks designated by calculating the equal distance between two other points. Even though these two points are not used directly, their acquisition has been discussed with regard to the previous method. LM1 to LM3 are used to describe the general shape of the metastylid. If the metastylid is relatively round, then the distance between these three points would be roughly equal. In contrast, if the metastylid is elongated, then the distance between LM1 and LM2 will decrease significantly while their distance to LM3 will not differ much. LM5 to LM7 serve the same function in the metaconid. The shape of the lingual valley is described by LM2 to LM6; the potential bias of LM3 and LM5 due to the occasional presence of a non-metric trait was discussed above (section 4.2, Figure 4.2). However, the use of midpoints is more beneficial for determining the shape of both the metastylid and the metaconid and only causes potential bias on the determination of the lingual valley shape.

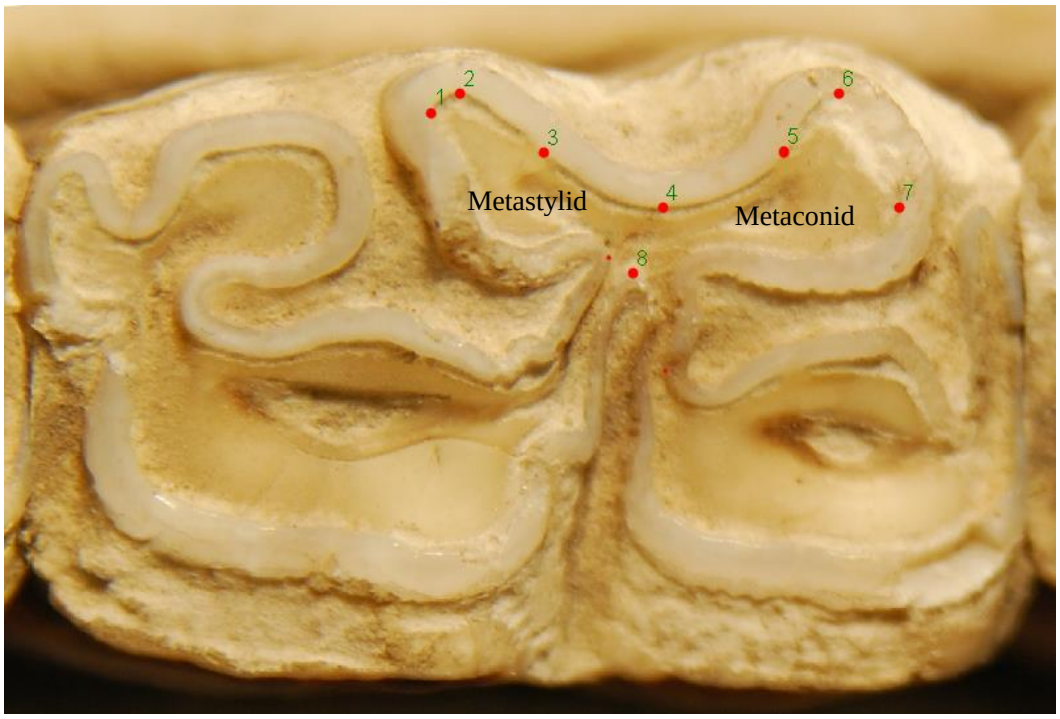


Figure 4.7 – Eight landmarks used for landmark-based GMM

4.4.1 – Method: Landmark-based analysis using the geomorph package in R

Since GMM has recently been gaining a significant amount of academic attention in a number of different disciplines, a large variety of software packages have become available for conducting landmark-based analyses. One of the very basic tools for GMM is the "tps package" developed by Rohlf (2004) for data acquisition. Other software packages, such as MorphoJ (Klingenberg, 2011) and PAST (Hammer *et al.*, 2001), can all perform landmark-based geometric morphometric analyses. However, these software packages are designed to deal with purely "landmark-based" analyses and are thus are not ideal for the outline-based GMM, as will be described in the next section. The geomorph package (Adams and Otárola-Castillo, 2013) is able to perform a wide range of geometric morphometric analyses and allows data obtained from other software packages, such as tpsDig2 (in the tps package developed by Rohlf (2004)) to be imported and analysed. For the present analysis, landmark coordinates were acquired using tpsDig2. This was done by first creating a .tps file including all the images that were be used as standard using

"tpsUtil"; then, all the images were scaled and all eight landmarks for each tooth were designated using tpsDig2 (Figure 4.7).

The .tps file was then imported into geomorph using the following script:

```
# set the working directory to the location where all data files are saved

# load geomorph package

> library(geomorph)

# import landmark coordinates saved in .tps file

> lmk <- readland.tps("landmarks.TPS", specID="ID")
[1] "Specimen names extracted from line ID="
```

Subsequently, species were assigned to each set of landmark coordinates. The known species of corresponding specimens were first saved in a .csv file with the following format:

ID	species
DON01	D
DON02	D
DON03	D
DON04	D
.	.
.	.
.	.

This .csv file can then be imported and used to assign species to each set of coordinates.

```
# import .csv file and assign the species to dataset

> classifier <- read.csv("classifier.csv", header=TRUE, row.names=1)
```

```
> sp <- factor(classifier$species)

# note the term “species” following the $ sign correspond to the header in .csv

# file for species.
```

As mentioned in the introduction to this section, Procrustes fitting is the most essential process in all GMM analyses. Only when all the coordinates are from the same datum point at the same scale, and have the same orientation and position, can they be compared and analysed. Procrustes alignment can be performed in geomorph with the following script:

```
# perform general Procrustes alignment

> gpa <- gpagen(lmk)
```

A graph can be then produced showing the mean coordinates and the location of all the landmarks in every specimen (e.g. Figure 4.8). A rapid impression of how each landmark varies in comparison to the others can be gathered from this graph. However, the differences between groups can also be tested statistically in geomorph using ANOVA (analysis of variance) or MANOVA (multivariate analysis of variance). ANOVA is a statisitical approach used to test the difference in group means between two or more groups while MANOVA can be seen as an ANOVA with multiple dependent variables (Hair *et al.*, 2010). Therefore, the next step is to test whether the designated landmarks can attest that these two species – horses and donkeys – are different by performing ANOVA. This task can be carried out in geomorph using the following script:

```
# perform ANOVA using GPA coordinates

> procD.lm(two.d.array(gpa$coords)~gpa$Csize, iter=99)
```

The outcome provides associated values including a P-value that can be used to determine the significance level of shape variations between horses and donkeys (e.g. Table 4.3). For statistical reasons, it is recommended to perform PCA even if the P-value indicates that the differences are not significant (i.e. $P < 0.05$). PCA is a standard analytical approach for most GMM analyses, because it can show the degree of separation visually through scatter plots. In addition to PCA, the geomorph package makes it possible to use other advanced analysis techniques to explore other associations between datasets. Nevertheless, PCA was deemed sufficient for the aims of the study. PCA in geomorph is combined with a graphic function that automatically plots the dataset onto a scatter plot by using the following script:

```
# perform PCA using GPA coordinates

>  plotTangentSpace(gpa$coords, groups=sp)
```

The geomorph package is a powerful analytical tool for GMM analysis with numerous functions allowing various specific questions to be investigated. However, in this thesis, it is used only as one of several tools to examine the differences between domestic equid species and, therefore, only PCA is used for species determination.

4.4.2 – Results

Based on the landmark distribution after GPA, it is clear that the coordinates of LM1 and LM2 as well as LM4 and LM8 vary to a greater extent than LM6 and LM7. In addition, the degree of variation in both LM3 and LM5 is also noticeable (Figure 4.8). This observation confirms the claim that the bucco-lingual distance (LM4-LM8 distance) and the shape of the lingual valley (LM3-LM5 distance) both play important roles in distinguishing between donkeys and horses, as established in the previous section. In addition, the graph suggests that the roundness of the metastylid indicated by LM1, LM2, and LM3 can also be used to

separate these two species. The outcomes from ANOVA suggest that there is a significant difference between the dental morphology of donkey and horse molars (P = 0.05, Table 4.3).

	df	SS	MS	Rsq	F	Z	P.value
gpaST$Csize	1	0.05162	0.051619	0.065057	2.3658	1.9035	0.05
Residuals	34	0.74183	0.021818				
Total	35	0.79344					

Table 4.3 – Outcomes of ANOVA for landmark-based GMM analysis.
Df – degree of freedom, SS – sums of squares, MS – mean squares, Rsq – R square

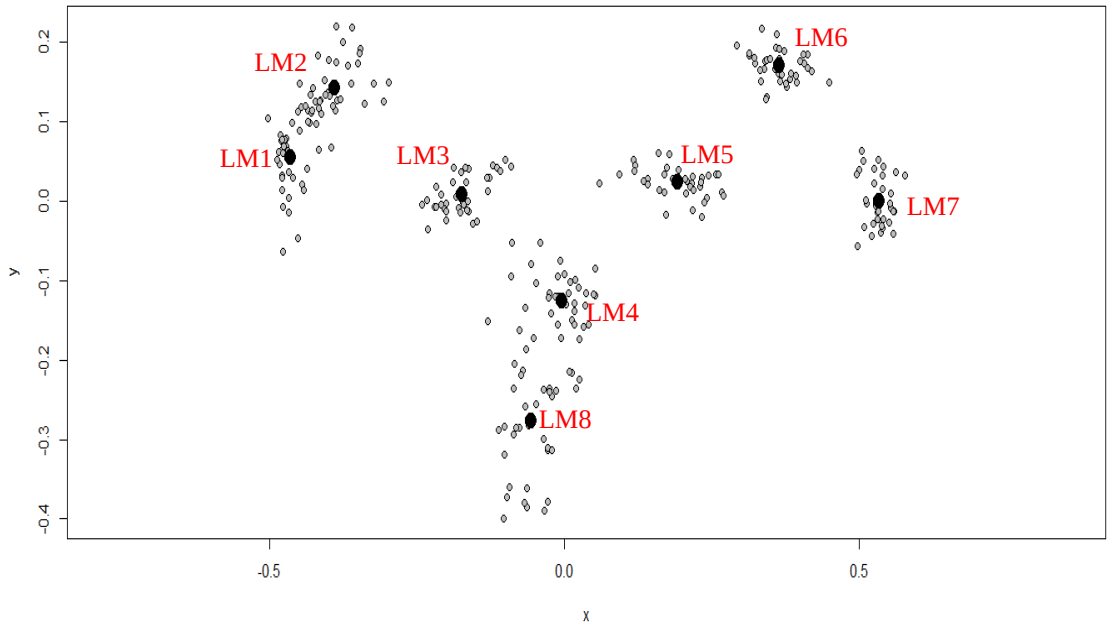


Figure 4.8 – Distribution of all landmarks from every sample after GPA.
Black dots indicate the average coordinates of the landmarks and the grey dots are the locations of the original landmarks after GPA.

As for PCA, the proportion of variance for each PC is listed in Table 4.4. Over half of the variance can be explained either by PC1 and PC2 (64.067%), PC1 and PC3 (57.254%), or PC1 and PC4 (52.39%). Therefore any three of these combinations can be used to observe the degree of separation between two species. The two species seem to cluster separately on the PCA scatter plot (Figure. 4.9). PC1 (x-axis) indicates the bucco-lingual distance as well as the shape of the lingual valley while PC2 (y-axis) describes the different shape of

the metastylid (difference between LM1 and LM2). Based on Figure 4.9, it suggested that PC1 can better separate the two species than can PC2 since both species have data located evenly throughout the y-axis.

	PC1	PC2	PC3	PC4	PC5	PC6
Standard deviation	0.1001	0.06545	0.05446	0.04317	0.03392	0.02828
Proportion of Variance	0.4417	0.18898	0.13084	0.0822	0.05076	0.03527
Cumulative Proportion	0.4417	0.63067	0.76151	0.84371	0.89446	0.92974

Table 4.4 – Proportion of each PA in PCA.
PC1 and PC2 can explain 63.07% of the variance.

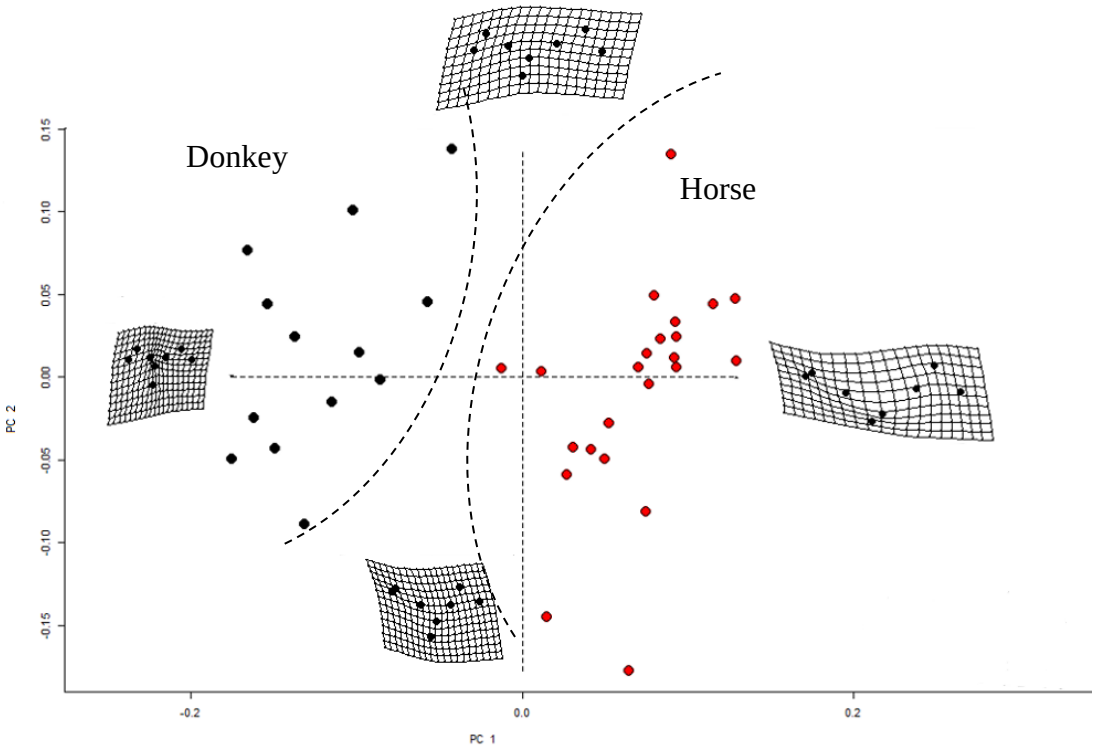


Figure 4.9 – Species separation using PC1 and PC2.
Black dots represent donkeys and red dots represent horses. The four grids at the two ends of both PC1 and PC2 represent the deformed shape of specimens (thin-plate splines) at the ends of the range of variability.

4.4.3 – Landmark-based GMM Summary

The PCA scatter plot (Figure 4.9) shows that both horse and donkey can be distinguished by this approach. However, one disadvantage of this approach is that it considers all three morphometric traits simultaneously, and attempts to maximize the differences by describing these traits at the same time. That is, each end of the axis is represented by the extreme or most typical case of donkey or horse, but it is not clear where mules – a species that is suggested to be characterised by an admixture of morphological traits of horses and donkeys – would be located in this scatter plot. The lack of available mule samples places a limit to the practical use of this method for distinguishing archaeological specimens of unknown taxonomic membership. In addition, although the roundness of the metastylid is indicated through three landmarks in this method, the outcomes seem to fail when they relate to this morphological trait along with the symmetry between the metaconid and the metastylid. Fortunately, the second disadvantage can be compensated for by using a different approach of GMM, which will be described in the next section.

4.5 – Approach III: Outline-based GMM

As explained above, a landmark-based approach relies on landmark points that have a one-to-one correspondence on all specimens to define the coordinates of the shape in any comparison. However, for shapes that lack corresponding features, it is difficult to designate landmark points that can be used in every sample. This is the case when attempting to determine most of the morphological features in equids' lower molars. With the exception of the bucco-lingual distance, the remaining morphological traits are based on "shapes", namely, the shape of the lingual valley, the shape of the metastylid, and the symmetry of the metaconid and the metastylid, all of which are relatively smooth and lack any physical features that can offer a correspondence in every specimen. As a result,

artificial landmarks will need to be assigned, as demonstrated in the previous methods. Therefore, it would be a significant advantage to have a method that allows an analysis to be made based on outlines or curves and that does not to have the requirement of every point having a one-to-one correspondence in all specimens. While outline-based GMM is built on the foundation of the landmark-based approach, it allows the use of "semi-landmarks" instead of fixed landmark points. A semi-landmark is a point that can "slide" between two landmarks and, therefore, does not need to correspond to any particular features in an object (Bookstein, 1997). The use of a series of semi-landmarks, then, can better describe an outline or a curve than setting artificial landmarks in shapes that lack corresponding features. Therefore, outline-based GMM may provide a more precise method for distinguishing the lower molars of different domestic equids than may the landmark-based approaches.

4.5.1 – Method: Outline-Based analysis using geomorph package in R

One advantage of using the geomorph package in R is that it can perform both landmark-based and outline-based GMM analyses. The procedure of an outline-based analysis is quite similar to that of a landmark-based analysis except that a set of curve (or outline) coordinates is added to each sample. It is necessary to clarify that the term "curve" refers to a line defining the edge of a shape between two specific points, while the term "outline" normally refers to a line defining the edge of a closed shape. In other words, the starting point for an "outline" is also the end point, but these two points are independent in a curve. As a result, although this approach is called "outline-based", it is the "curve" that is being analysed in the current method.

This method relies on the use of curves to analyse the morphological differences between donkeys and horses. Nevertheless, since the bucco-lingual distance cannot be described by a curve, the two landmarks used to define this distance (LM1 and LM2, Figure 4.10) were kept in the analysis, but no additional "artificial" landmarks were set. (Figure 4.10). A curve along the inner edge of both the metastylid and the metaconid was thought suitable to describe the remaining morphological traits (i.e. roundness, symmetry, and lingual valley shape). The most mesial point of the endoflexid was used to define the starting point of the curve whilst the most posterior point of the metaflexid was regarded as the end point of the curve. The coordinates of both the landmarks and the curve were obtained through tpsDig2 (Rohlf, 2004). The curve coordinates can be obtained by using the "Draw background curves" function in tpsDig2 and can be saved into the same .tps file. The number of points along the curves can be set according to the requirements of the user. These points were then used as "semi-landmarks" in this analysis; this means that, as mentioned above, they can slide along the curve and do not have one-to-one correspondence to physical features. Considering the smooth profile of the region of interest, 100 equidistant points were set along the curve.

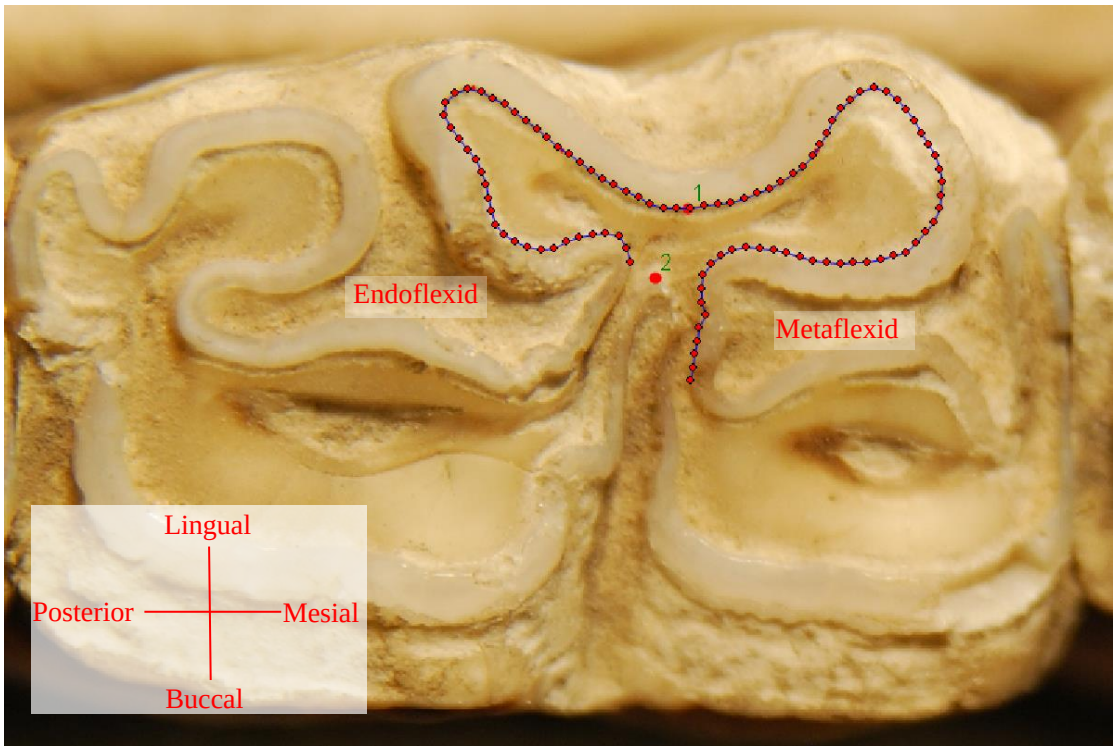


Figure 4.10 – Landmarks and curve used in outline-based GMM

After the coordinates of all four landmark points and curves were obtained, they were imported into geomorph for further analysis.

```
# set the working directory to the location where all data files are saved

# load geomorph package

> library(geomorph)

# import the coordinates saved in .tps file

> cur <- readland.tps("curve.TPS", specID="ID", readcurves=TRUE)
 [1] "Landmarks 1:2 are fixed landmarks."
[1] "Landmarks 3:102 are semilandmarks."
[1] "Specimen names extracted from line ID="
```

The same procedure as in the previous method was used to assigning specimens to species using the same .csv file.

```
# import .csv file and assign the species to dataset

> classifier <- read.csv("classifier.csv", header=TRUE, row.names=1)

> sp <- factor(classifier$species)
```

Although the software recognizes the presence of the 100 “semi-landmarks”, it is still necessary to define the starting point and end points of the line along which these semi-landmarks can slide. This can be implemented by using the “define.sliders()” function in geomorph. Alternatively, a .csv file that explains the relationship between each semi-landmark can be imported for the same purpose. For dealing with a bulk number of semi-landmarks, it is recommended to use .csv file, which should be saved in the following format:

before	slide	after
3	3	102
3	4	102
3	5	102
3	6	102
.	.	.
.	.	.
.	.	.

The first and third columns represent the first and last points respectively between which a semi-landmark can slide, whereas the second column indicates which point can slide between the first and the last points. Using the second row as an example, point 4 can slide between point 3 (the first point of the curve) and point 102 (the last point of the curve). More than one set of sliders can be assigned depending on the aim of the analysis. For the present analysis, all points on the curve were treated as semi-landmarks so that the analysis

can better describe the morphological traits. The .csv file was imported using the following script:

```
# import .csv file to explain the relationship of semi-landmarks
> semilmk <- as.matrix(read.csv("sliders.csv", header=T))
```

After defining how all the semi-landmarks can be slide along the curve, the data can then be Procrustes fitted and the significance level tested using ANOVA.

```
# perform general Procrustes alignment including curve coordinates
> gpaC <- gpagen(cur, curves=semilmk)
# perform ANOVA using GPA coordinates of landmarks and curves
> procD.lm(two.d.array(gpaC$coords)~gpaC$Csize,iter=99)
```

Again, the result of ANOVA is used only to determine the significance level of the differences between the two groups. It does not affect PCA directly, but will be important for the interpretation of PCA results. The final step for the outline-based approach is the same as in the landmark-based one: to produce a PCA scatter plot.

```
# perform PCA using GPA coordinates
>  plotTangentSpace(gpaC$coords, groups=sp)
```

4.5.2 – Results

The distribution of semi-landmark points after GPA suggests that the general shape of the metaconid is more stable than that of the metastylid, and that the penetration level of the buccal valley (indicated by LM2) seems to vary to a larger degree than the location of LM1 (Figure. 4.11). The first observation supports the argument that horses and donkeys differ in the shape of their metastylid. The second observation lends further support to the finding

of the analyses performed with other techniques – as well as claims by a number of authors (Armitage and Chapman, 1979; Davis, 1980; Eisenmann, 1986; Uerpmann and Uerpmann, 1994) – that horses and donkeys differ in the extent of the penetration of the buccal valley. Results from ANOVA analyses show that these differences are significant (p=0.04, Table 4.5). The mean shape of horses and donkeys also suggests that the two species are noticeably different (Figure. 4.12).

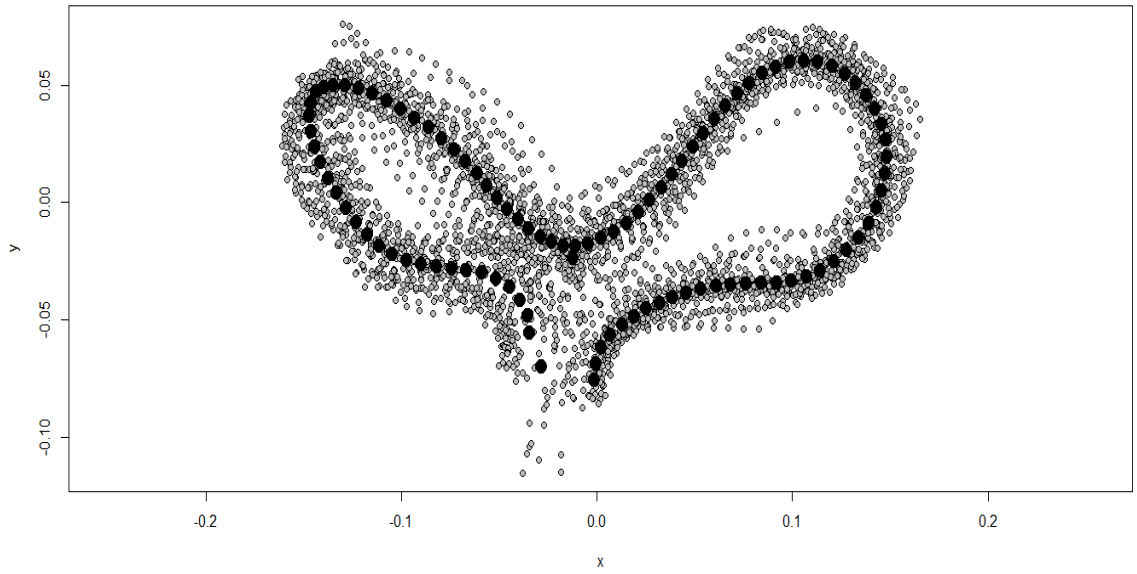


Figure 4.11 – Distribution of all points from every specimen after GPA. The black dots represent the average coordinates of all specimens and the grey points represent both landmarks and curves/semi-landmarks of all specimens.

	df	SS	MS	R^2	F	Z	P.value
gpaST$Csize	1	0.04531	0.045313	0.06696	2.44	1.944	0.04
Residuals	34	0.63141	0.018571				
Total	35	0.67672					

Table 4.5 – Outcomes of ANOVA for outline-based GMM analysis
Df – degree of freedom, SS – sum of squares, MS – mean squares, F – F ratio

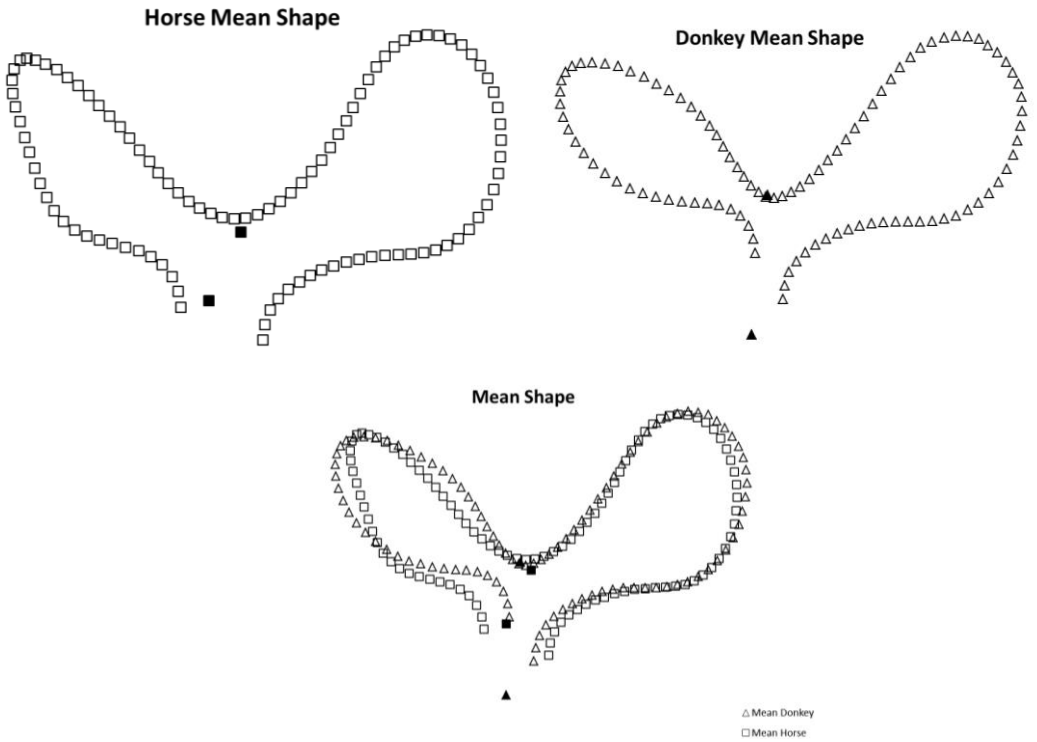


Figure 4.12 – Mean shape of the curves from two species.
The pair solid squares/triangles represent the two landmarks defined: LM1 and LM2 (see Figure 4.10).

Only 39% of the variance can be explained by PC1, but more than 60% of the variation can be explained by the first two PCs, (PC1 and PC2) (Table 4.6). PC1 and PC2 were used to examine the possible 'clustering' of horses and donkeys in Figure 4.13. Although donkeys seem to form a relatively tight group, two horse specimens fall in the midst of this cluster. Horses appear to have a larger variation in terms of PC1 (x-axis). Based on Figure 4.13, it is suggested that the main differentiation of these two species is largely on the bucco-lingual distance, which is associated with PC2.

	PC1	PC2	PC3	PC4	PC5	PC6
Standard Deviation	0.08687	0.06498	0.04344	0.0406	0.0321	0.0272
Proportion of Variance	0.39034	0.21839	0.09758	0.08525	0.05329	0.03828
Cumulative Proportion	0.39034	0.60873	0.70631	0.79156	0.84485	0.88313
	PC7	PC8	PC9	PC10	PC11	PC12
Standard Deviation	0.02339	0.02158	0.01625	0.01443	0.01334	0.01045
Proportion of Variance	0.0283	0.02409	0.01366	0.01077	0.0092	5.65E-03
Cumulative Proportion	0.91143	0.93552	0.94918	0.95995	0.96915	0.9748

Table 4.6 – Proportion of each PA in PCA.
A total of 36 PCs calculated, showing only the first 12 here.

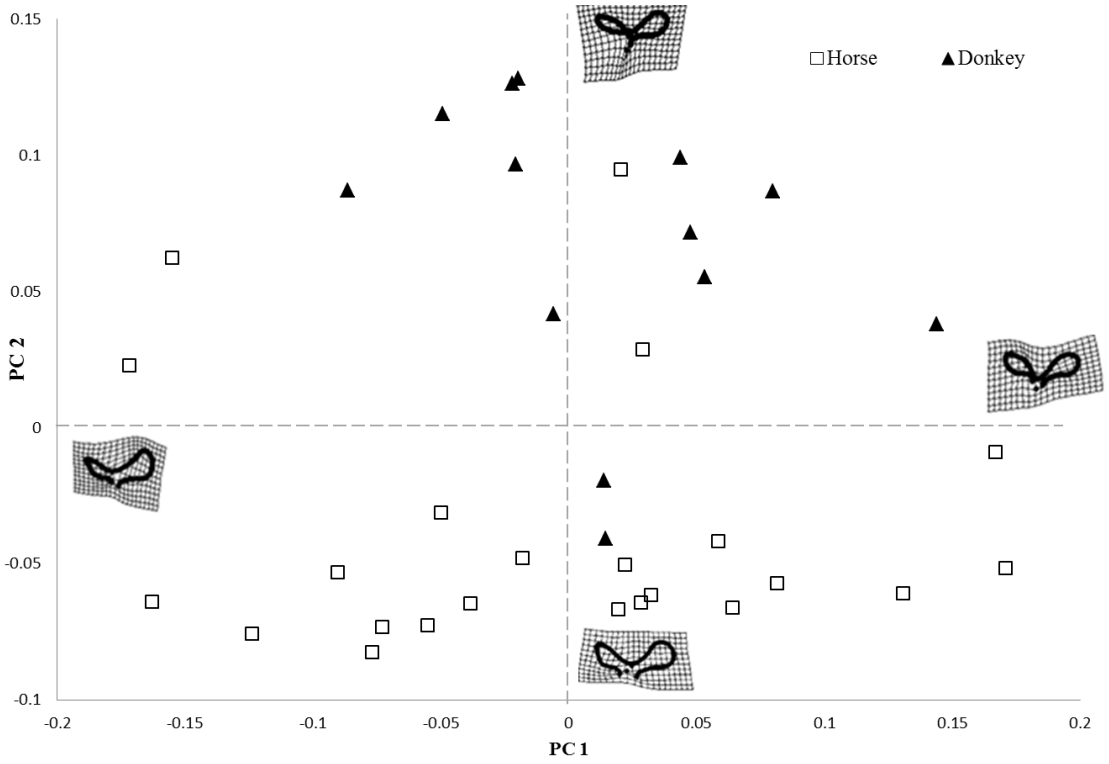


Figure 4.13 – PCA scatter plot for outline-based GMM. The four grids at the two ends of both PC1 and PC2 represent the deformed shape of specimens (thin-plate splines) at the ends of the range of variability

4.5.3 – Outline-based GMM Summary

The outcome of this method is somewhat surprising since it was argued that the use of curves would help to increase the resolution regarding some morphological traits. Instead, although ANOVA suggests significant differences between horses and donkeys exist, these cannot be clearly observed in the PCA plot (Figure 4.13). A possible cause of the overlap between the clusters may be due to the wide variation in the morphology of horses, which is accentuated by the high resolution of the curve lines. Nevertheless, one positive aspect of the outline-based approach is that morphological traits are better separated from each other than when using the landmark-based approach. Two PCs can explain most of the variation; PC1 has a stronger affiliation with the shape of the metastylid and the metaconid as well as the lingual valley, whereas PC2 is more related to the bucco-lingual distance. As a result, it is possible to predict that the mules will more probably be located on the upper-right side of the plot. While this method does not provide an absolute accuracy for the

species determination of horses and donkeys, it does highlight the wide variation in horses as one of the main issue that we need to be considered.

4.6 – Approach IV: Shape Analysis

An alternative approach to the outline-based GMM discussed above is shape analysis. While the aim of the outline-based GMM is to analyse curves or outlines, an equal number of points are required to be defined for the curve in all specimens. As a result, the emphasis is still on points, and not on the curve. Shape analysis, on the other hand, takes the data directly from the shape, and the number of coordinates required to describe each shape depends on the complexity of the shape instead of an equal number of points for all the specimens. Thus, the analysis focuses on comparing shapes instead of aligning points; this may provide an opportunity to investigate some morphological traits that had to be excluded from both angle-analysis and landmark-based GMM. This section will discuss the use of shape analysis as an alternative method for species determination based on the morphology of lower molars in domestic equids.

4.6.1 – Method: Shape analysis using Momocs in R

To begin with, it is necessary to decide what "shape" should be used for the analysis. The enamel in equid molars conveniently forms a closed outline that is ideal for shape analysis, although the enamel in contact with other teeth tends to wear out with age. However, in the present study, only the shape of the lingual valley, the penetration level of the buccal valley, and the symmetry of the metaconid and the metastylid are considered relevant to species identification. In order to ensure that the shape analysis focuses mostly on the morphological differences that have been suggested to be indicative of taxonomic membership, it is advised not to include features that have not been put forward in previous studies as being characteristic of particular species (e.g. the shape of the endoflexid and the

metaflexid). The outlined area for this analysis is defined by Figure 4.14. It is to be expected that a typical shape representing horses will be “butterfly-like”, while a typical shape for donkeys will resemble to some extent a ‘heart shape’.

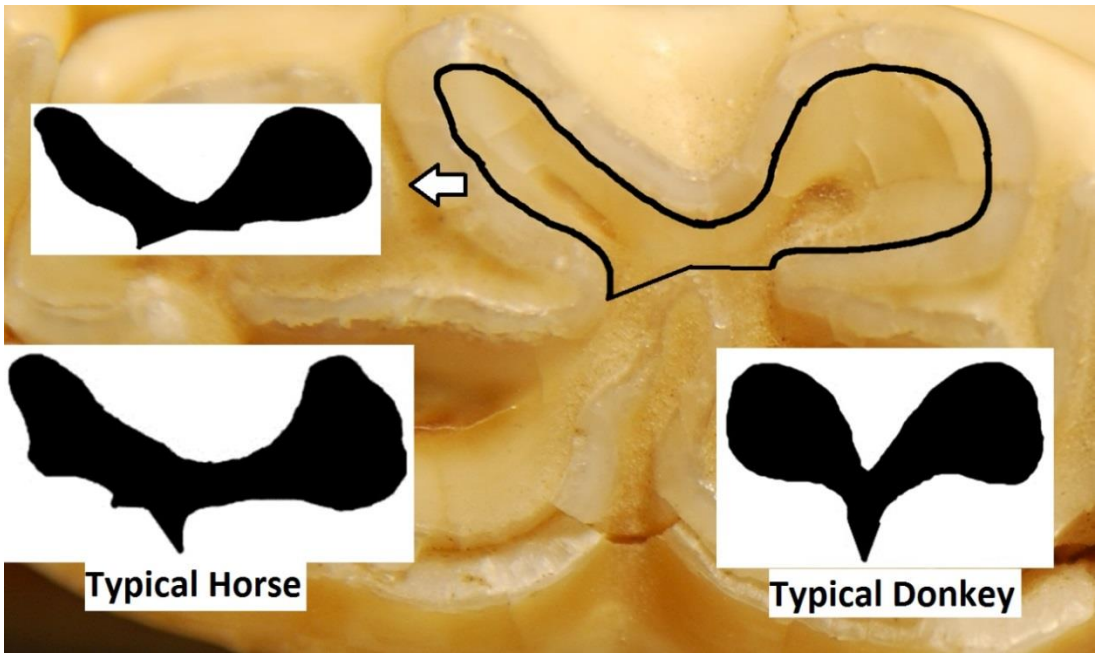


Figure 4.14 – Shape extracted for shape analysis. The selected area including both the metastylid and the metaconid (indicated by the solid black line [upper right]) is extracted as a shape (upper left) for the present study.

The Momocs package (version 0.2) in R (Bonhomme, 2012) was selected to perform the analysis of the lingual valley shape of specimens of known taxonomic affiliation (e.g. horses and donkeys). Momocs is not the only shape analysis software package available; there are other packages, such as “Efourier” (McLellan and Endler, 1998) and “Shape” (Iwata and Ukai, 2006), both of which are free software packages that are designed to perform shape analysis. However, the ability to produce graphic outputs directly from Momocs makes it an ideal analytical tool for comparing shape being both powerful yet easy to access. This package allows data to be input either directly as an image or using data coordinates obtained from other software packages, and to analyse it using methods such as general Procrustes analysis and PCA. A comprehensive graphical introduction to Momocs is available (Bonhomme *et al.*, 2014); as a result, this section will describe mainly

the steps taken in the current analysis. It should be borne in mind that the Momocs package is still being frequently updated; the version used for the present thesis is version 0.2 under R 3.2.1. Some changes have been made in more recent updates and thus the functions used here may differ from those in later versions (Bonhomme, per. comm.)

The coordinates for a shape are generated directly from images that have been converted into an 8-bit grey scale .jpeg format using free graphic software (i.e. GIMP 2). After setting the work directory to associate with the file folder, the following scripts were used to generate the coordinates.

```
# load Momocs package (package loading can also be done using the file menu
# on top)
> library(Momocs)


# import .jpg files (in 8-bit, grey scale), note names in red, such "sa" and "coo" #
can be replaced with any other names desired, but need to be consistently
# used to refer to the same subject.
> sa <- list.files()
> coo <- import.jpg(sa)


Extracting 36 .jpg outlines...
================================================
```

It is crucial that image files are named in an orderly fashion, so that the species the files represent can be recognised by the software and can be identified with a corresponding ID.

For the present method, all .jpg files were saved in the format “species”_”ID”, e.g. “H_01.jpg” refers to the first horse in the horse dataset.

```
# Define the first character of file names as group name
> Species <- substr(names(coo), 1, 1)
> Species <- data.frame(Species)
```

In order for Momocs to proceed to a further analysis, it needs to create a new class, ‘Coo object’, to handle the coordinates of the extracted outlines. A Coo object can be created by using the following:

```
# create a Coo object.
> EQ <- Coo(coo)
# requesting a summary of Coo object, EQ.
> EQ
```

After the Coo object has been created, it is necessary to add taxonomic information to the Coo object, so different species can be treated as different groups.

```
# add group attribute to dataset
> EQ@fac <- Species
```

Since the coordinates are generated directly from images, they are not properly aligned to any guidelines. As a result, landmarks are needed as reference points to allow all shapes to be properly aligned, so that Procrustes fitting can be performed. Unfortunately, Momocs does not support the .tps file at this point and, therefore, landmarks cannot be obtained

using tpsDig2. However, Momocs allows landmarks to be added within R by clicking on the outline recreated using the generated coordinates. A clear disadvantage of this is that these landmarks need to have clear physical features that can be identified from recreated shapes. Four landmarks were added to each outline: two coordinates defining the most lingual points of the metastylid (LM1) and the metaconid (LM3); one defining the lowest point of the lingual valley (LM2); and one defining the apex of the buccal valley(LM4) (Figure 4.15). The decision regarding the number of landmarks or which landmarks are used does not affect the analysis significantly since the analysis is based on the reconstructed shape. However, the inclusion of landmarks allows these reconstructed shapes to be better oriented, as Procrustes fitting are performed based on these landmarks.

```
# define landmarks to perform Procrustes alignment. Six landmarks are used.
> EQldk <- defLandmarks(EQ, 4)
```

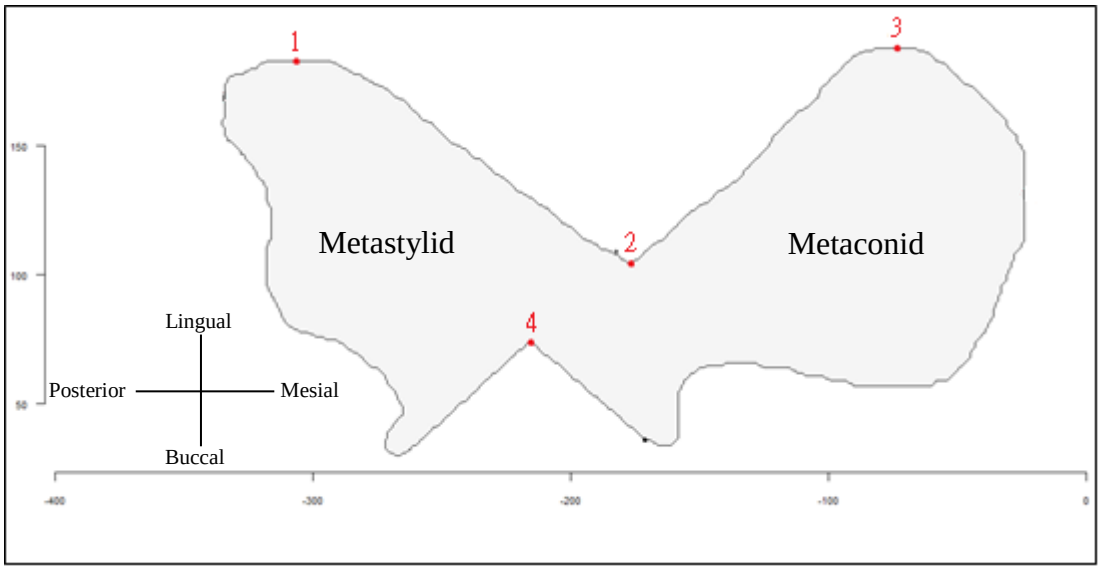


Figure 4.15 – Landmarks used in Momocs.
The number indicates the order in which these four points are taken; the order needs to remain consistent for all outlines.

```
# perform Procrustes alignment based on the landmarks
> EQgpa <- procGPAlign(EQldk)
```

A further advantage of setting up landmarks is that a pair of them can then be used as a new baseline to align all shapes (using baseline( ) function). This function was not used in the current analysis because LM1 and LM3 are already aligned during the preparation process.

The following step is to decide on the appropriate number of harmonics being used for shape analysis. The term "harmonic" refers to a function in the Fourier series with frequencies multiplied by an integer (see Bonhomme *et al*, 2014). To put it in a different way, a harmonic is associated with the degree of reconstruction of the shape based on the coordinate data. With one harmonic, the shape will be reconstructed into an oval, but the more harmonics used, more details will be depicted in the reconstructed shape. However, this does not mean that an increase in the number of harmonics will necessarily result in a more accurate reconstruction of the shape. The number of harmonics adequate for an analysis is determined by the Fourier method chosen and how the reconstructed shape represents the original shape. Therefore, it is necessary to determine an appropriate number of harmonics that can sufficiently describe the outline and maintain the shape's smooth contours. A number of different statistical approaches can be used to determine the number of harmonics that should be used. Nevertheless, the current analysis applies only the elliptic Fourier (eFourier) analysis, due to its clear superiority over other approaches in outline analysis (Bonhomme *et al*, 2014). An eFourier analysis establishs the outline as the sum of the absolute least number of ellipses needed to reconstruct the shape (Schmittbuhl *et al.*, 2007). One advantage of this Fourier method is that while it seems to suffer only when insufficient numbers of harmonics are chosen, it is not affected by the use of an exceedingly large number of harmonics. As a result, it is only necessary to determine the absolute minimum number of harmonics required. Momocs provides two different approaches to assess the minimum number of harmonics required: *qualitative estimation*

and *quantitative estimation*. In the qualitative estimation, different outlines are recreated based on a given set of harmonics, and the decision can be made by visual inspection of which outline is best represented by a particular number of harmonics (Figure 4.16). Alternatively, graphs can be produced to determine the number of harmonics by comparing the deviation in the number of pixels and the number of points sampled along the outline (Figure 4.17). Nevertheless, the most efficient approach is to calculate the cumulative harmonic power achieved by a given number of harmonics (Figure 4.18). This can be calculated using the following function:

```
# calculating the cumulated harmonic power
> hpow(EQgpa, probs=c(0.25, 0.5, 0.75), drop=FALSE, legend=TRUE,
+ title="eFourier three quartiles")
```

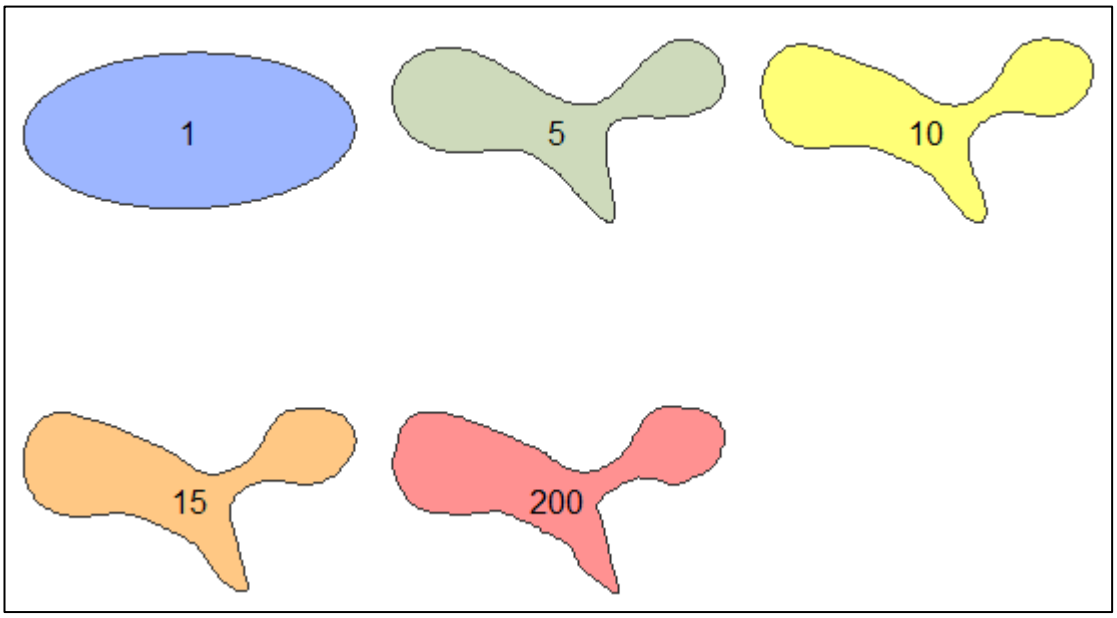


Figure 4.16 – Qualitative estimation of harmonic number.
The number indicates how many harmonics are used to reconstruct the shape. When using one harmonic, the reconstructed shape is usually represented as an oval. Note that when a high number of harmonics are used, the contour will include excessive details and create a crinkled outline.

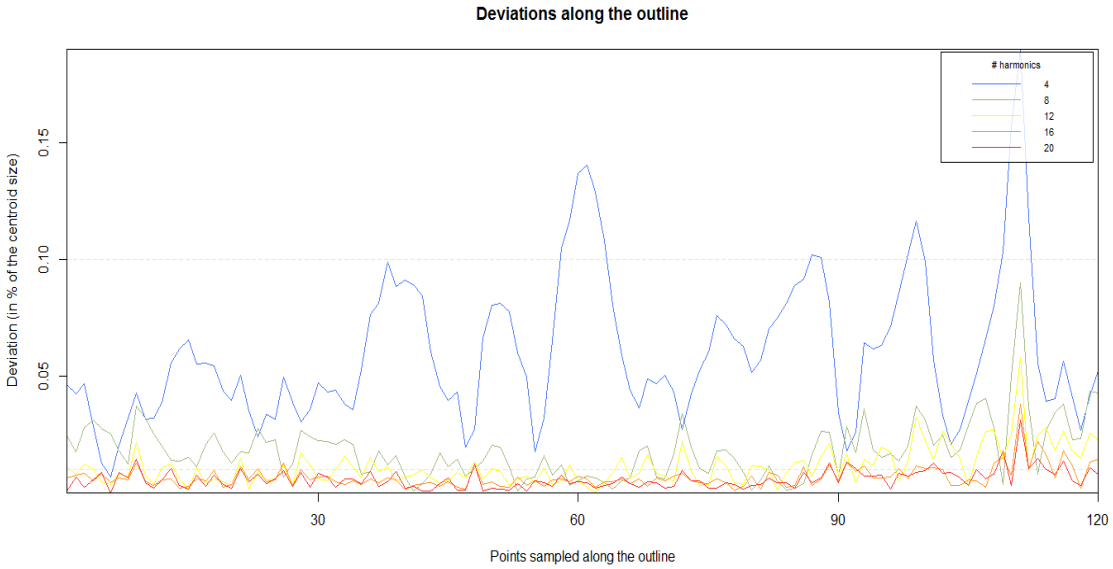


Figure 4.17 – Quantitative estimation of harmonic number.
This approach is less intuitive and, therefore, not recommended.

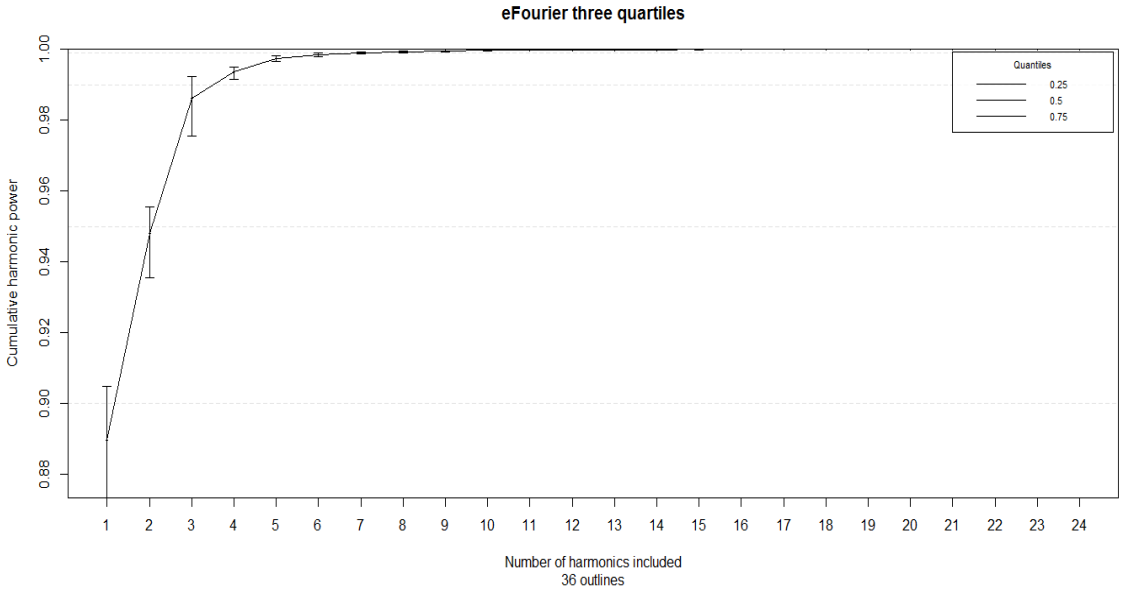


Figure 4.18 – Graph showing the cumulative percentage of harmonic power.
Harmonic power is nearly reaching 100% by using eight harmonics in the current dataset, and thus a further increase in the number of harmonics will not improve results significantly.

For the current analysis, it was decided to use 15 harmonics for the reconstruction of the shape in the present study. Although Figure 4.18 has shown that 8 harmonics is sufficient, the decision of 15 harmonics is based on the reconstruction of shape in Figure 4.16. After deciding on the number of harmonics, Momocs requires the user to create a "Coe object"

for further multivariate analysis, such as MANOVA and PCA (Bonhomme *et al.*, 2014). Similar to the function of ANOVA mentioned in previous methods, MANOVA is used to establish the significance level of the differences between groups. It should be remembered, however, that even if the p-values suggest that there is no significant difference between groups, it does not compromise the use of PCA for further observation of the clustering of taxonomic groups in the scatter plot. The above steps can be performed in Momocs using the following script:

```
# creating a “Coe object” based on decided number of harmonics
> EQf <- eFourier(EQgpa, nb.h=16)
# perform MANOVA
> manova.Coe(EQf, "Species")
# perform PCA
> pca(EQf)
```

Since PCA outcomes are used for creating a scatter plot, it is recommended to assign the result of PCA with an object name to create the graphic output. An important feature of Momocs is that it allows various types of graphs to be produced. The details of the graph-producing scripts are given in Bonhomme *et al.* (2014) and, therefore, they will not be detailed here. The script for a basic PCA scatter plot is given here as an example:

```
# assign PCA outcomes as an object in R
> EQpca <- pca(EQf)
```

4.6.2 – Results

When comparing the mean shapes generated from the images of horses and donkeys specimens, it is evident that they possess different morphological characteristics (Figure 4.19), and that they resemble the shapes hypothesised for each of these taxa. Nearly all the morphological differences between the lower molars of horses and donkeys, which have been suggested in previous studies (e.g. Armitage and Chapman, 1979; Davis, 1980; Eisenmann, 1986; Uerpmann and Uerpmann, 1994) are captured in the reproduced shapes (Figure 4.19): the penetration level of the buccal valley, the shape of the lingual valley, and the roundness of the metastylid. The only exception is that the size symmetry between the metaconid and the metastylid is less conspicuous than other morphological traits. In donkeys, while both the metastylid and the metaconid are round in shape, the metaconid is arguably larger in size. In comparison to donkey, the metaconid and the metastylid in horses are rather more similar in size, although the latter is more elongated. The MANOVA test indicates that these differences between horses and donkeys are significant (P = 0.03342, Table 4.7)

	Df	Hotelling-Lawley Trace	Approx.. F value	Df den	Df	Pr(>F)
Fac	1	122.41	11.476	32	3	0.03342
Residuals	34					

Table 4.7 – MANOVA outcomes for shape analysis using Momocs.
Df den - the number of degrees of freedom associated with the model errors. Pr(>F) - the p-value associated with the F statistic of a given source.

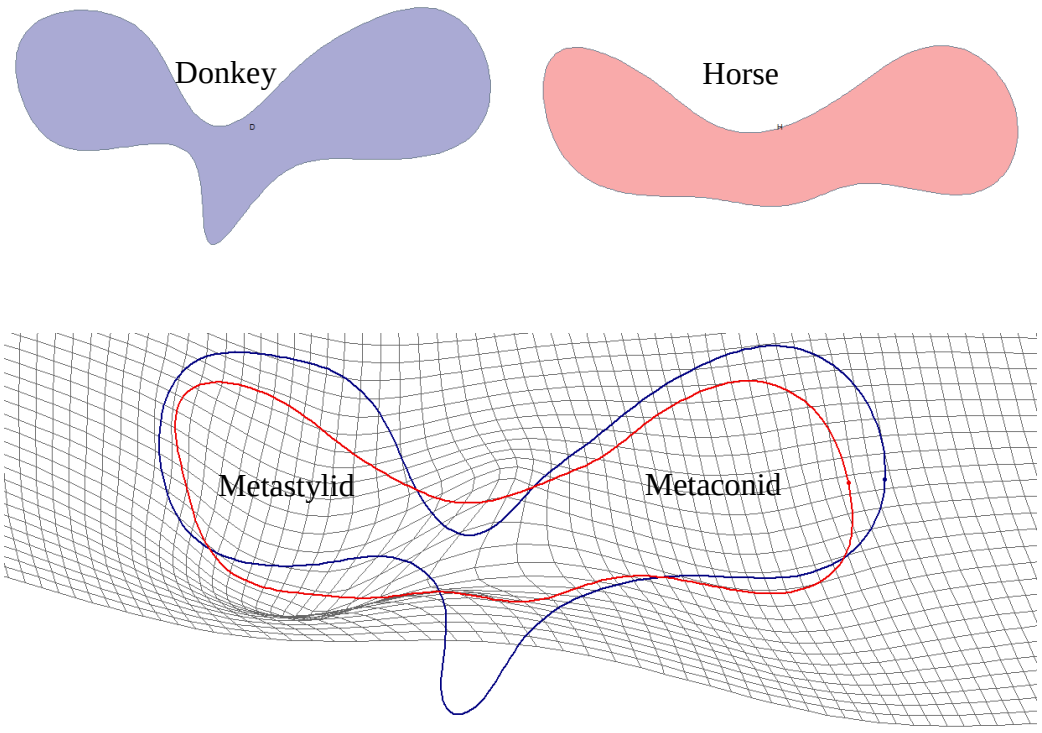


Figure 4.19 – Comparison of the mean shapes generated by image of different species. The thin-plate spline graph (bottom) clearly demonstrates that changes in the metastylid (left) are significantly greater than in the metaconid (right).

However, if the approach is to be of use in the species determination of archaeological specimens (i.e. specimens with unknown taxonomic affiliation), the differences need to be observable in a scatter plot. To observe the scattering pattern of the data, a PCA scatter plot can be created using the following script:

```
# producing a basic PCA plot

> dudi.plot(EQpca, star=FALSE, ellipses=FALSE, eigen=TRUE, "Species")
```

The dudi.plot function has several options that allow the user to decide how to present the results. Although in PCA, the variances are usually explained by the first few PCs, different combinations of PCs in the scatter plot can sometimes better demonstrate the correct grouping. For example, PC1 may explain more than half of the variances, but the groups may be better separated in the scatter plot by using PC3 and PC4. This is because each PC will build the reconstructed shapes based on different variables, and when too

many variables are changed at the same time, it may ultimately build a reconstructed shape that is less relevant to the dataset. Momocs allows the examination of shapes reconstructed using each PC, which are then compared to the mean shape. This allows the user to decide the PCs combination better suited for grouping the dataset. To compare the contribution of each PC, the following script is used:

```
# examining the PC contribution

> PC.contrib(EQpca)
```

This function produces a graph as shown in Figure 4.20. It is apparent that reconstructed shapes using only PC1 have the tendency to be “over exaggerated”, resulting in shapes that cannot physically occur in nature (i.e. overlapping of lines and upside-down images). Therefore, using PC1 in the PCA scatter plot for grouping may not be an ideal choice although it explains the majority of the variances in the coordinates. Instead, using the combination of PC2 and PC4 or PC2 and PC5 can better evaluate the morphological traits of interest in this study (PC2 for the bucco-lingual distance, PC4 for the roundness of the metastylid and the lingual valley shape, and PC5 for the lingual valley shape and symmetry of the metaconid and the metastylid).

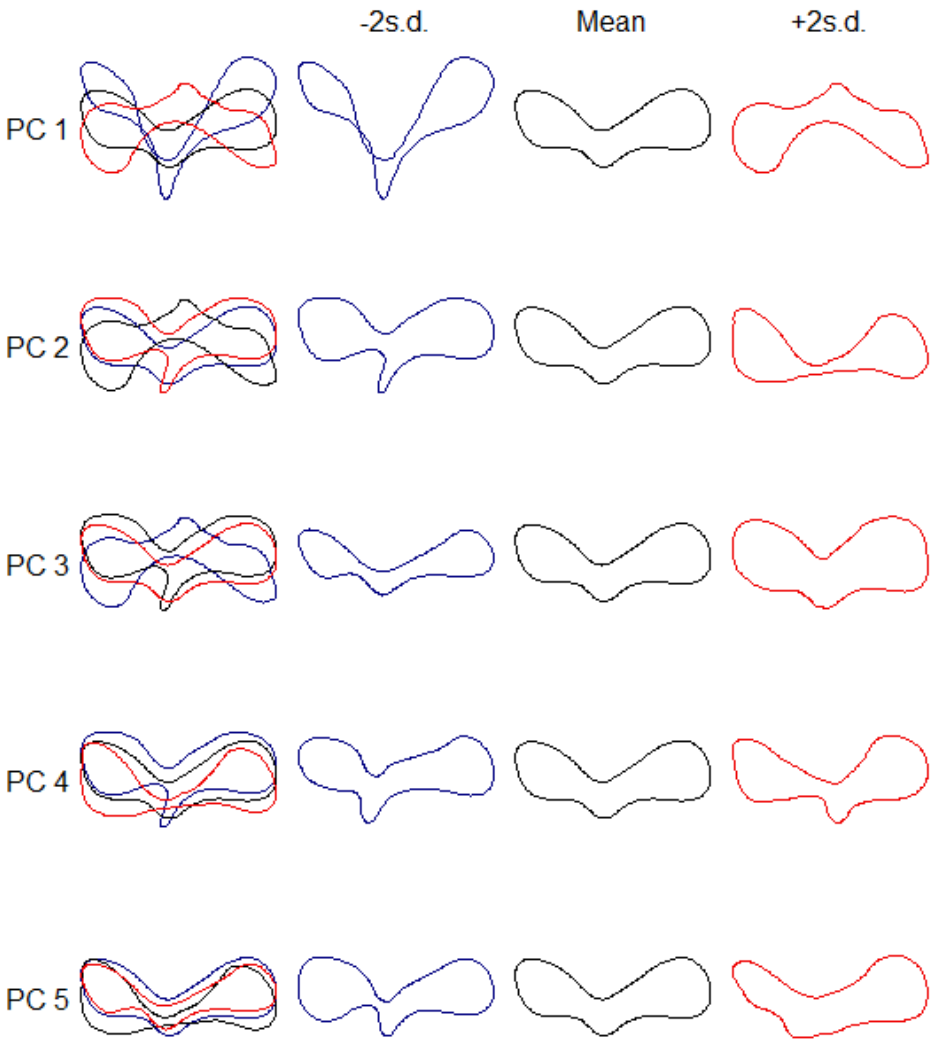


Figure 4.20 – Contribution of PC in shape reconstruction. Note the “exaggeration” in the lingual valley of the PC1 reconstructed shape.

Given that the combination of PC2 and PC5 makes it possible to examine all the morphological traits of interest, they were used to plot the data points in the current analysis. Once the decision has been taken regarding which pair of PCs are to be used in the scatter plot, the following script is used to produce the PCA scatter plot presenting the grouping of specimens of known taxonomic affiliation:

```
# producing a basic PCA plot using PC2 as x-axis and PC5 as y-axis

> dudi.plot(EQpca, xax=2, yax=5, star=FALSE, ellipses=TRUE, "Species")
```

The scatter plot (Figure 4.21) shows that donkey and horse ellipses are clearly separated from each other, but a number of specimens from both species are obviously outliers. It is evident that PC2 is the dominant factor in the grouping, as horses fall mainly on the right hand side, whilst there is more of an overlap in the y-axis (PC5). One advantage of Momocs is that it has a superb capability for producing graphs that can produce various reconstructed shapes in the PCA plot. It is not difficult to predict where the mules are more likely to fall, despite that there is no mule specimens included in the analysis.

Based on the reconstructed shapes, mules are more likely to be located in the bottom right corner where two molars (M_2) from the same Shetland pony are located. These two lower second molars do resemble the described characteristics for mules when examined visually except that the metastylid in both teeth is somewhat more elongated. However, it is no surprise that there should definitely be an overlap between horse and mules, given that horses have extremely wide variation – as suggested by all the methods reviewed here. Without actual mule specimens, however, it is impossible to predict the extent of this overlap.

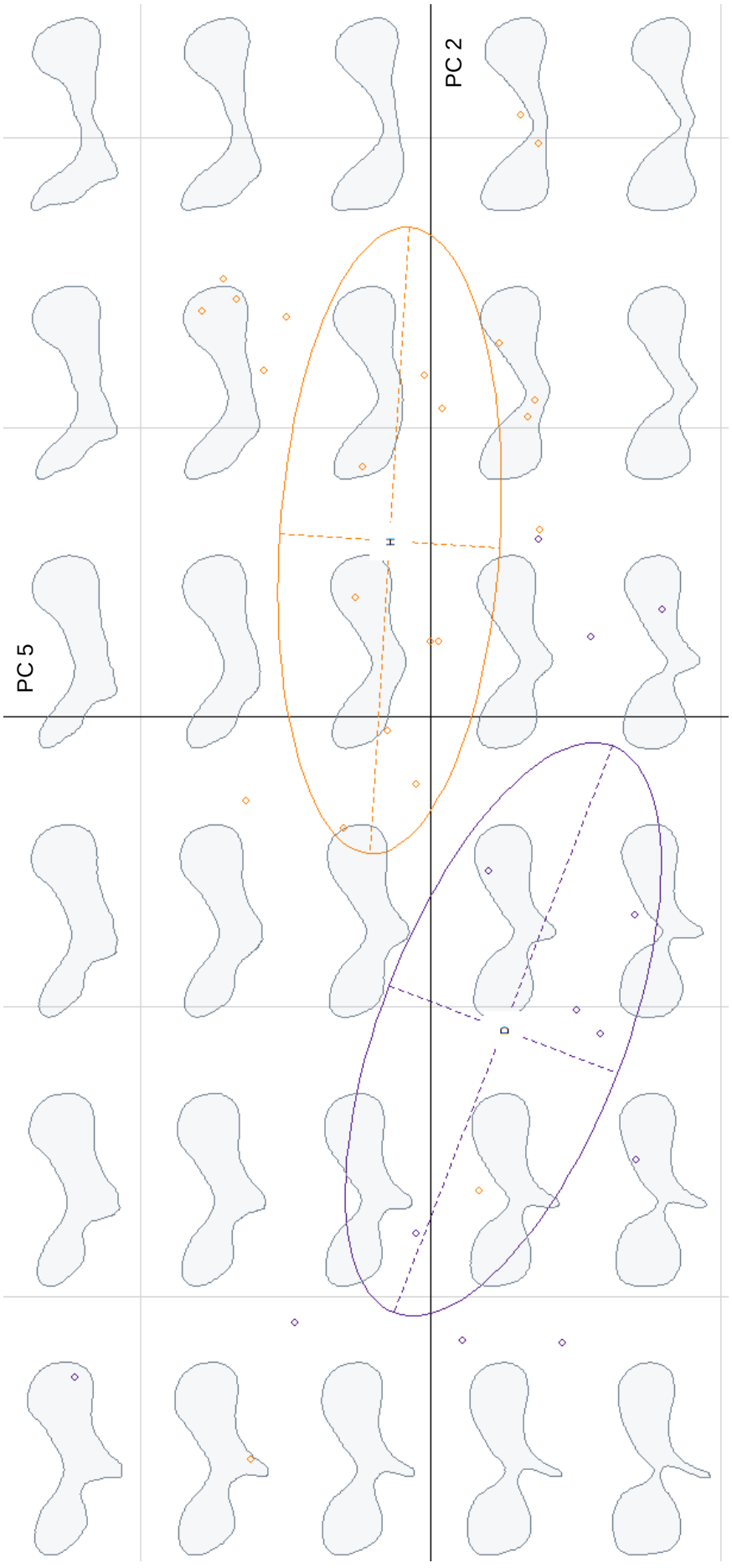


Figure 4.21 – PCA scatter plot from shape analysis.

4.6.3 – Shape Analysis Summary

Shape analysis and outline-based analysis are similar in many ways; the main difference is the use of harmonics in the former to reconstruct the data coordinates. Furthermore the use of eFourier analysis is markedly different from other GMM. The most outstanding advantage of using the Momocs package, as opposed to outline-based GMM in the geomorph package, is the ability to display the reconstructed shapes in a PCA plot. This allows the researcher to easily relate the location of the data points to the reconstructed shapes without having to evaluate the degree of changes along the two axes and assuming the shape of the data located further away from the axes. In other words, it is not necessary to consider the hypothesised region for each species. The clustering of data points can be explained by the shapes demonstrated on the PCA plot and interpreted independently from the standard data set.

4.7 – Chapter Summary

In this chapter, four different GMM-based methods have been proposed to quantitatively analyse the morphological differences of the lower molars between two domestic equid species – namely, horses and donkeys. All four methods were reasonably successful in separating horses from donkeys. Unfortunately, molars from mules were not available for the present study; it remains to be demonstrated that the latter can be discriminated using morphological traits in lower check teeth. However, all four methods agree on a number of aspects:

i. Horses have a very wide variation in their dental morphology.

ii. Previously postulated morphological differences in the cheek teeth (Armitage and Chapman, 1979; Davis, 1980; Eisenmann, 1986; Uerpmann and Uerpmann, 1994) of horses and donkeys are mostly valid.

iii. All methods indicate that the bucco-lingual distance is a more reliable trait than others in the separation of horses and donkeys (and thus possibly of mule). The lingual valley shape is largely determined by the shape of the metaconid and the metastylid, but both are vulnerable to non-metric variations (e.g. zigzag slope in some individuals, e.g. Figure 4.2). On the other hand, the bucco-lingual distance is extremely sensitive to the tooth wear stage, and there is a marked difference between premolars and molars in horses. Therefore, it is advisable to keep these limitations in mind when carrying out a taxonomic determination of the species based on lower dental morphology.

The application of these four geometric morphometric methods not only further confirms previous claims of differences in lower dental morphology between horses and donkeys, but also indicates that further uses of GMM in other skeletal elements can be developed to compensate for the limitation of conventional biometric approaches, which rely mainly on a few measurements and, therefore, cannot provide a comprehensive description of the element's shape. Nevertheless, this is not to say that GMM will not suffer from some of the same problem as conventional biometric analysis. In fact, the same issues with inter-specific variation and representativeness of the modern samples remain. In addition, issues with image acquisition may also impair the accuracy of GMM. As mentioned in section 4.2, not all images are taken under the same setting to optimize the sample size under limited resources. As a result, bias caused by inter-observer errors and lens distortion may exist in this pilot analysis. In addition, although it was argued that the view angle should not impact species determination in current application (section 4.2), the occlusal surface of the lower molar is not completely level; it may be tilted due to the misalignment of the

teeth, and so it may cause a problem when deciding how the occlusal image should be viewed. These problems have never been considered before, since the determination has been based on purely qualitative observations of the morphological traits. However, they can be a crucial factor when attempting to analyse the traits quantitatively. As observed in this chapter, several samples are determined as "outliers" although they can be clearly determined as horse or donkey through visual determination, but this is still a small price to pay for developing a quantified analytical method that can provide more objective results.

The initial results suggest that the accuracy of all four methods is similar for the distinction of horses and donkeys. Some individuals seem to have a higher tendency to be misidentified as a different species, and this is likely to be associated with the degree of the tooth wear, as well as with other non-metric variation in the dental enamel fold patterns that are not species-specific. However, the nature of these different methods makes some of them more useful than others for the taxonomic determination of specimens of unknown affiliation (e.g. archaeological specimens). The direct use of the angle and the bucco-lingual distance measurements makes the Angle Analysis approach seemingly easier to employ than the others, but the apparent disadvantage is that only two traits are considered. The landmark-based method is probably the least ideal method for the present aim because landmarks are difficult to assign on the featureless lower dental pattern. Both outline-based and shape analysis can be viewed as using different approaches to interpret the same concept. However, the software package for shape analysis makes it better fitted for the present aim of determining the species of "unknown" specimens. All four methods have their own advantages and weaknesses; thus, they are all be used to determine the possible species of archaeological equid molars in the following chapter.

Chapter 5 - Identification of Zooarchaeological Equids

5.1 – Introduction

This chapter will deploy methods described in previous chapters, to determine the taxonomic affiliation of archaeological equid specimens in order to establish the ratios of different domestic equids in a number of different types of Romano-British sites. The taxonomic determinations will allow the species frequency for different domestic equids in various site types to be established as well as provide the basis for the isotopic analysis presented in Chapter 7. As a result, this chapter contains two sets of analytical outcomes:

1. Results of biometric analyses of post-cranial elements, which are used only for establishing the ratio of different domestic equids species that can be further analysed to understand the acquisition of domestic equids in different site types.
2. Results from geometric morphometric analyses of dental morphology of lower molars for species determinations, mainly used for interpreting the results of isotopic analysis (Chapter 7).

The postcranial elements will be interpreted based on the two biometric techniques evaluated in Chapter 3 (DFA and the Davis method) and the lower molars will be classified using the various GMM approaches discussed in Chapter 4.

It is acknowledged that species determinations based on biometric techniques are not as accurate as one would hope; this is due to a number of factors discussed in the previous chapters, e.g. issues with the representativeness of the modern domestic equid specimens. Nevertheless, an attempt to determine the species of archaeological specimens is still crucial because it not only produces a rough species frequency estimation of different domestic equids, but also provides additional information to compare with the identification based on morphological criteria. This chapter will first present the species of

archaeological specimens predicted by DFA, followed by the examination of archaeological equids' first phalanges using the Davis method. After that, the lower molars will be analysed through the use of GMM. The aim of this chapter is not only to calculate the ratio of different domestic equids from selected sites and provide species determination for further interpretation, but also to provide a more comprehensive view of the consistency of different methods.

5.2 – Archaeological Material

In the selection of archaeological equid specimens, Romano-British sites with relatively abundant equid remains were targeted. This would increase the likelihood of dental remains being available for taxonomic determinations through GMM, isotopic, and aDNA analyses. Furthermore, with a greater abundance of domestic equid remains, the possibility of having more relatively complete post-cranial elements for morphological assessment would also be higher. Ideally, sites with a military nature should be preferred over civilian sites. This is because, according to historical sources, the Roman army used large quantities of both mules and horses and, therefore, the chance of both species being represented should be higher than at civilian sites, where mules may have been too costly for most 'ordinary' people (Laurence, 1999). However, it was soon realised that too strong a focus on military sites would be impractical, since there is a general lack of domestic equid remains from military sites in Roman Britain.

In contrast to their use of cattle, the only other domestic mammal of a similar size, the Romans rarely consumed the flesh of domestic equids. This claim is supported by the general lack of butchery marks on most surviving horse bones and their overall

completeness in contrast to those of cattle bones, which are highly fragmented (Maltby, 2010). If the Romans did not usually consume the meat of domestic equids, then to dispose of its carcass would have been extremely troublesome; indeed, even a pony-size equid (12 hands, 122 cm) can easily weigh up to 250 kg. Nowadays, when a veterinarian states that a horse's death is inevitable and should occur in the near foreseeable future, it is quite common for the owner to walk the horse to the designated place (such as a pit or on a truck depending on the regulations for dead livestock in different countries) and let it die there. However, weight is not the only obstacle that needs to be overcome when disposing of a horse carcass. If a quick burial is necessary for sanitation reasons, then, preparing the burial pit and burying the carcass is also very labour-intensive. If the carcass is buried after the onset of *Rigor mortis*, it will be impossible to be bent and fit into a smaller burial pit, unless the carcass is disassembled. Although *rigor mortis* will gradually dissipate after a day, it is still strenuous to manipulate the carcass to fit into the pit. One interesting horse burial from the early twentieth century was found in Whitby; the carcass was carefully dismantled and packed in a small grave (circa 180 x 96 cm) (Daulby and Baker 2003). This shows discreet planning to save labour by not digging an unnecessarily large pit. As a result, it is quite common to find horse skeletons in abandoned well backfills or in remote locations of ditches. For owners in urban areas or rural settlements, such a location may not be difficult to find. It is very likely that Roman veterinarians were capable of offering suggestions to the owners of dying horses to prepare for their death by sending such horses to secluded outskirts. Unfortunately, abandoned wells are not commonly found in Roman forts, and the defensive fort ditches were functional and so were less likely to be used for disposing of dead animals. Dixon and Southern (1997) suggested that there might have been a standard procedure in the Roman military to dispose of horses. Whilst unsuitable horses may have been sold to civilians, the dead horses could be further utilised for the production of leather and bone objects. Horse remains are also argued to have had a major

role in funerary rituals in the Germania Inferior province of the Roman Empire (Groot, 2008), but it is not clear whether these horses were specifically killed for the ritual. An alternative way to dispose quickly of a dead animal would be to cremate it, but very few cases of domestic equid cremation have been recorded (Cool and Bond, 2004). In any case, equine remains in Romano-British sites are scattered and limited.

Adding to the difficulty of their scant presence, the frequency of equine remains in Romano-British military sites is below the average for Romano-British sites overall. Maltby (2010, p269) pointed out that horse remains are more commonly found in suburban sites than in any other types (e.g. fort, villa, urban settlement). This has further restricted the possibility of selecting materials exclusively from Romano-British military sites. This is a good point to consider when reflecting on the reasons behind the general lack of equine remains from military sites, even though the Roman army is known to have relied heavily on domestic equids. Perhaps it can be best thought as an example of the "*osteological paradox*" questioning the assumed direct relationship between skeletal materials and paleodemography (Wood *et al.*, 1992). Put simply, the general lack of equine remains in military sites can be explained by the same reason that skeletons of soldiers are rarely found in military forts: they are useful to the army only when alive. The Roman army, with little doubt, was definitely the largest user of domestic equids in terms of the number of animals per person. Considering the horse-to-human ratio of a cavalry unit and a normal household, it can be assumed that at any given time, there would be more horses – and very probably mules – in a fort with a cavalry unit than in any rural, villa, or small urban settlement (although large urban areas, such as Rome or London would have had more domestic equids, which were involved in activities like transport, trading, chariot racing, etc.). However, the Roman army would only have been interested in domestic equids that are capable of carrying out their duties and, therefore, any livestock unable to work would

be retired from military service and removed from forts. Unless they died in military action as warfare casualties, by accident, or as victims of a sudden outbreak of disease, equids in the Roman army were more likely to have been retired from military service and to have spent the rest of their life elsewhere. They could have been sold to villas where they were still capable of carrying out less demanding work or sold back to stud farms, where they may have served as stallions. In the case of an outbreak of disease, there would have been a large quantity of dead livestock to deal with. It is less likely that the Romans would have allowed a pile of dead horses exposed near the fort, and perhaps burning them would have been a logical solution. As a result, only the occasional unexpected death of healthy individuals may have allowed equine remains to be preserved as a whole. Since most retired or unsuitable domestic equids were more likely to have ended up in villa or rural settlements, it is reasonable to suppose that the horse death rate was much higher in these settings than in a military fort.

Another question that pertains to military equine remains: can we really distinguish warhorses from civilian equivalents in archaeological context? If the remains of military equids could end up in civilian sites admixture with “civilian equids”, how can we tell one from the other based on their skeletal remains? And can we still refer to a horse as a warhorse once it had been retired to civilian life? As a result, it was not practical for the present research to restrict itself to the limited material available from military sites. Additionally, the inclusion of non-military sites in the study allows the ratio of local and non-local domestic equids to be compared on different types of site (Chapter 7).

Domestic equid remains from five Romano-British sites were studied (Map 5.1). The sites were selected on the basis of their availability (access to the material), and – crucially – on

the basis that all five sites contained remains that were identified previously as either possible donkeys or suspected mules. These remains are ideal for this study in the application of the species-determination methods discussed and to conduct isotopic analyses in order to investigate equid procurement strategies.

All measurements (as described in section 3.2.3) of post-cranial elements were taken by the current author with a Mitsutoyo CD-12”C digital calliper and all images were taken using a Nikon D80 camera with a Sigma 17-70mm lens and were measured using the procedure described in Chapter 4. The following sections will provide basic background information regarding these five sites. It should be noted that additional measurements from other Romano-British sites were obtained either from their original faunal reports or from Johnstone’s thesis (2004) (Table 5.1). The inclusion of these specimens allowed a broader overview of the domestic equids in Roman Britain. Details of these additional sites will not be described in this chapter, as they can be found in the original faunal reports.

No	Site	Reference
1	Alcester*	Chuang, unpublished data
2	Beddington Sewage Farm	ABMAP database
3	Castleford	Johnstone, 2004
4	Chaucer House, Southwark	ABMAP database
5	Chichester Cattlemarket	Levitan, 1989
6	Coldharbour Farm	Johnstone, 2004
7	Danebury	Grant, 1984
8	East London RB Cemetery	Johnstone, 2004
9	Elms Farm	Johnstone and Albarella, 2002
10	Haddon	Johnstone, 2004
11	Haydon Fort	Johnstone, 2004
12	Healam Bridge*	D. Jaques, in prep.
13	Ilchester, Church St.	Levitan, 1994
14	La Sagesse	Bourdillon, 1990
15	Longthorpe II	King, 1987
16	Lutton/Huntingdon	Johnstone, 2004
17	Market Deeping	Albarella, 1997b
18	Newstead Fort	Johnstone, 2004
19	Norman Cross	Albarella, 1997a
20	Orton Hall Fort	King, 1996
21	Ribchester*	Stallibrass and Nicholson, 2000
22	Scole-Dickleburgh	Baker, 1998
23	Southwark	Bendrey, 1999
24	Thorley	Johnstone and Jaques, 1999
25	Thornhill Farm, Fairford	Levine, 2004
26	Thorpe Thewles	Rackham, 1985
27	Tort Hill West	Albarella, 1997a
28	Winchester*	Maltby, 2010
29	Winchester Palace	Johnstone, 2004
30	Wroxeter Baths Basilica	Johnstone, 2004

Table 5.1 – List of sites from which measurements were obtained.
* - sites which measurements were taken by the current author. While the remaining data are taken from Johnstones (2004), original publications are listed if available.

Molar teeth for the geometric morphometric analyses in the second half of this chapter were also obtained from the same five sites with an additional four images from two Serbian sites (Pirot and Viminacium, Vukovic, pers. comm.). All images were taken under the same camera setting described in section 4.2 except the Serbian samples and two possible donkey molars from Fairford. These four Serbian molars from two different individuals were identified as mules based on their morphology (S. Vukovic, pers. comm.) and, therefore, it was considered useful to test whether GMM would be able to distinguish them from other domestic equid teeth. These molars were also used for isotopic analysis, as discussed in the following chapter, as a way to represent domestic equids in continental Roman sites. Molars from complete mandibles as well as isolated teeth were included for image analysis. The separation of premolars and molars was carried out using Payne's (1991) method. However, it should be noted that this method was mainly developed to separate the premolars and molars of horses; the accuracy of this method in other domestic equids has not been evaluated. In the process of separating archaeological premolars and molars in the current thesis, it is speculated that the scattering of premolars and molars has a high linear correlation. Some known molars (from complete mandibles) overlap with the premolars in Payne's data. As a result, specimens for the current study were mainly from complete mandibles or teeth associated with other distinguishable teeth (i.e. second premolar or third molar). However, some loose teeth were also included. Although a precautionary measure was taken to distinguish between premolars and molars, the possibility of premolars being included cannot be entirely ruled out among these loose teeth. Additional material used for either aDNA or isotopic analyses will be presented in the relevant chapters.

Map 5.1 – Romano-British sites in current thesis

5.2.1 – The Roman Site of Healam Bridge, North Yorkshire

The Roman settlement of Healam Bridge is located alongside of the Roman Dere Road between two Roman urban centres: Aldborough and Catterick. Based on the archaeological finds, Healam Bridge was considered an isolated roadside *vicus* mainly for agricultural production. The site was occupied from the mid-1st century AD and possibly extended into the early 5th century AD in its last phase. Evidence of a military presence in the early stage of occupation suggests the site may have started as a fort, which faded in the later phase while the *vicus* remained and evolved into a rural settlement, which extended into the early Medieval period (D. Jaques, forthcoming). A substantial quantity of equine remains has been identified from this site. It is believed that equids were bred in the vicinity as the site may have served as a roadside station in a major road network. The majority of the equid bones were found in the earlier phases of the site including a near complete skeleton, which was identified as a mule (D. Jaques, forthcoming.).

5.2.2 – Northern Suburb and Western Suburb, Winchester, Hampshire

Two sites were chosen from the Winchester area: the Northern Suburb (Victoria Road, Hyde Abbey, New Road) and the Western Suburb (Crowder Terrace). It is perhaps not appropriate to describe them both as one single archaeological site, because the areas excavated for both "sites" were extensive and, therefore, should perhaps be referred to as a "site complex". As a result, not all sites within the site complex are included in the current thesis. Some sites showed higher equine ratios and in some relatively complete equid skeletons were recovered. The selection of sampled sites was based on these two considerations. According to Maltby (2010, p.270), Victoria Road, Hyde Abbey, New Road, and Oram's Arbour either have a substantially high frequency of "horse" remains, relatively complete skeletons, or both. Since the frequency is based on the cattle to horse

ratio, and cattle normally predominate in Roman faunal assemblages, a high horse to cattle ratio can be considered as a high horse ratio overall. However, during the visit to Winchester Museum Services, the author realised that locating individual sites from the collection was extremely difficult because all materials are boxed as a whole and sorted according to phases, which are not given fully in the faunal report. As a result, under the limited time constraint of this thesis, not all boxes were examined. Furthermore, the faunal material from Oram's Arbour could not be located.

Although the faunal reports of these sites were only published, in combination with other studies, in 2010, the excavations actually took place between 1972 and 1985 (Maltby, 2010). The majority of the faunal material was studied during the early to middle 1970s, before Armitage and Chapman (1979) had published their discovery of the first Roman mule in Britain. It is, therefore, not surprising that "no attempt was made during recording to differentiate equid bones into horse, mule, or donkey" (Maltby, 2010, p.203). Therefore, revisiting this site might help further understanding, not only of the mule to horse ratio in a major Roman urban settlement with high frequency of equine remains, but also the material can be used to examine if all domestic equids were local or whether some were imported from elsewhere (see Chapter 7).

5.2.3 – The Roman site of Thornhill Farm, Fairford, Gloucestershire

The site of Thornhill Farm, Fairford was excavated from 1979 to 1989 in response to a potential threat from the construction works for Cotswold Water Park. The project was undertaken by Oxford Archaeological Unit (now Oxford Archaeology) with the co-operation of the Amey Roadstone Corporation. An area of approximately 40.5 ha. was excavated. Archaeological evidence suggests that the site was occupied by an agricultural

settlement with a specific function related to the management of large herbivore herds, such as horses and cattle, to exploit the local rough pasture (Jennings *et al.,* 2004). However, the faunal remains are not as abundant as at other large settlement sites. In addition, the condition of the faunal remains is not ideal. Most skeletal elements are fragmentary and heavily eroded, and only very few complete or relatively complete limb bones were recovered. Fortunately, teeth remains for isotopic analysis are more resistant to taphonomic damage and the dental morphology of the lower molars could still be used for species identification.

Although not mentioned by Maltby (2010), the ratio of equine remains in the Fairford site is relatively high (equids : cattle = 303 : 1025, based on Levine, 2004). The site was once regarded as a stud farm (Miles and Palmer, 1990), but Levine (2004, p.128) rejected this interpretation on the basis of the lack of juvenile equid remains. Nevertheless, the association between a high ratio of juvenile remains and a stud farm has never been clearly established. According to Maltby (2010), the frequency of equid remains in rural settlements is normally higher than in other types of sites, and thus it is not clear, based on current faunal evidence, whether or not equid breeding may have taken place at Fairford. However, this is the only site in the current study where a "definite" identification of two donkeys (early phase) has been made (Levine, 2004). If the teeth identified as donkey were available for isotopic analysis, this would have rendered the site of crucial importance in examining the "localness" of these domestic equids. Unfortunately, this was not the case. As mentioned above, the condition of the preservation of the materials is less than ideal; in addition, further breakage and damage of the material occurred during the transport and handling in post-excavation activities. Furthermore, some materials had been removed and sampled for a different project (Julie Hamilton, Thames Valley Isotope Project, Sampled 2008). Subsequently, the identified donkey teeth could not be located during the process of

sample collection. Fortunately, the original photographs of the identified donkey molars were kindly provided by M. Levine (pers. comm.), thus allowing GMM to be carried out. Regrettably, the actual molars identified as being from donkeys were unavailable for isotopic analysis.

5.2.4 – Bremetenacum, the Roman fort of Ribchester

The Ribchester site was first excavated in 1980, but the majority of the materials originate from the second phase of excavations, which took place in 1989 and 1990 (Buxton and Howard-Davis, 2000). The site is located on the remains of a known Roman fort and, therefore, its association with the fort can be clearly established. Like most other military sites, the equid remains from Ribchester are not abundant. However, two phases (phase 2.2 and phase 3) showed unusually high ratios of equid remains because of the discovery of partial equid skeletons (Stallibrass, 2000; Stallibrass and Nicholson, 2000). These two phases are regarded as being associated with the rebuilding of the site with stone material replacing its original wooden structure. All equine elements were identified as horses with no mention of the possibility of mules or donkeys being present. This renovation work can be unambiguously dated to AD 120, therefore, the chronology of these two phases can also be dated to the period in between 79 and 120 AD (Stallibrass, 2000) while the fort was still in use.

Equine remains from Ribchester were ideal for this project since they were from contexts associated with a military nature (fort) originating within a relatively short time span. In addition, they were superbly preserved due to the nearly waterlogged conditions.

5.2.5 – Bleachfield Street, Alcester

This site was commercially excavated around 2005, and the faunal material was identified by the present author (Chuang, unpublished report). Although the site extended well into post-Roman periods, it still can be clearly separated into Early and Late Roman phases based on pottery typology and coins (Craddock-Bennett, 2008). Previous researchers have argued that the site sits on a putative Roman fort (Booth and Evans, 2001). However, the faunal assemblage does not appear to be consistent with this claim; not only is the species representation frequency similar to that of a nearby extramural settlement (Maltby, 2001), but also the low frequency of equine remains found from the Bleachfield Street site is typical for both Roman urban and military sites. The lack of complete limb bone elements has also restricted the possible identification of mules based on qualitative morphological criteria. Nonetheless, the fact that there should have been a military fort at or near the site and that there were numerous teeth available for isotopic analysis, including one specimen that seemingly fit the morphological criteria described by other scholars as being characteristic of mules, made this site a suitable selection for the current study.

5.3 – Outcomes of Biometric Analysis

In this section, the results of the two biometric analyses discussed in Chapter 3 will be explained and interpreted. The ratios of different domestic equids species – horses, donkeys, and mules – are estimated for each method separately. However, since there are some specimens that are analysed using both methods, all data will be combined in the last section to provide the overall ratio estimation.

5.3.1 – Predicting Roman Equids Using the Modified DFA Method

Since Johnstone (2004) had already used biometrical methods to identify the species of a large number of Roman equids, it could be argued that it would be redundant to run the process again. However, as demonstrated in Chapter 2, the modified DFA method is based on a different approach in addition to using a larger and somewhat more refined dataset and, therefore, it is necessary to see if the outcomes differ significantly from Jonhstone's. As a result, in addition to the archaeological specimens collected for the current thesis, the data from other Romano-British sites that Johnstone collected as part of her thesis will also be tested. Furthermore, data available from the Animal Bone Metrical Archive Project (ABMAP, http://archaeologydataservice.ac.uk/archives/view/abmap/, accessed 03/02/2015) was also used, if not already included in Johnstone's (2004) work. It should be remembered that because the modified version of DFA uses a "simultaneous estimation" approach, which can include only samples with all measurements available, the number of samples suitable for prediction is, therefore, significantly reduced. This is because several measurements are not commonly measured by faunal specialists using the von den Driesch measurement scheme (1976). For example, most archaeological specimens are missing HTc in humeri, and the greatest depth of distal articular facet (DFd) in radii, and the greatest lateral length (Ll) in all elements is sometimes neglected in the reports. Thus, due to the lack of available measurements, humeri will be not included in the current thesis.

An evaluation system with three levels of identification similar to Johnstone's was used for determining the prediction of specimens in the current analyses: definite, probable, and possible identification. The main difference between the current system and Johnstone's is the use of the M-dist. The M-dist from the predicted specimens to the predicted group centroid of the species is considered as a criterion in Johnstone's work (2004, p.150).

Nevertheless, this criterion seems to make very little logical sense, especially when the probabilities of group membership are based on the M-dist. That is to say, the M-dist is already represented in the probability and, therefore, it is redundant as a separate criterion. According to Johnstone's system, a probable individual has either a low probability but with a small M-dist (within 1 standard deviation of the average) or has a high probability, but with a relatively large M-dist. The former case can happen if the group centroids are close to each other and the specimens fall between them, but the second scenario will happen only when the specimen is extremely far from all group centroids and, therefore, the probability is very likely to be comparatively high because the M-dist between this specimen and the other group centroids will be even greater. Hence, there are some archaeological specimens termed "super-mule" or "super-horse" considered to be "probable mule" or "probable horse" in previous research (Johnstone, 2004). Individuals with unusually high M-dist should be considered only as a "possible" determination, since the high M-dist is actually implying that such specimen may not belong to any of the groups (or possible errors in the measurements). As a result, the M-dist were not disregarded for the predictions (i.e. not directly as a value, but they were inevitably considered in the calculation of probabilities). In order to be classified as a "definite" identification, the specimen needs to have a probability of predicted membership greater than 80%. A "probable" identification is defined as a specimen that has a probability of between 50% and 80%. Such specimens will be indicated with an asterisk (*). Finally, if a sample has a probability of less than 50%, it will be considered to be "possible" identification, which is indicated by a question mark (?). Since horses are expected to be more common in Romano-British faunal assemblages than mules and donkeys, this section will focus mainly on those determined to be non-caballine equids. All outcomes are listed in Appendix II.

5.3.1.1 Radius

Nearly all of the available archaeological radii are missing the measurement of the distal articular facet depth (DFd) (as this measurement is not listed in von den Driesch's measuring scheme). As a result, only ten of the archaeological specimens examined had all the required measurements available for analysis (Figure 5.1). The majority are determined to be definite horse or probable horse (n=7). However, there is one probable donkey as well as a definite mule and a probable mule. The prediction of the probable donkey is more problematic than that of the mule, since this radius (Z001) is from a relatively complete skeleton (Sk.682, Winchester) with both radii available, and the other radius (Z002) has a contradictory prediction as a probable horse. The issue of contradictory predictions of different elements from the same individual is one aspect that the current thesis aims to examine. As for this case, the largest difference between the two radii is that one has a slightly longer greatest length (7 mm in difference), and surprisingly, the longer radius is the one being predicted as a probable donkey.

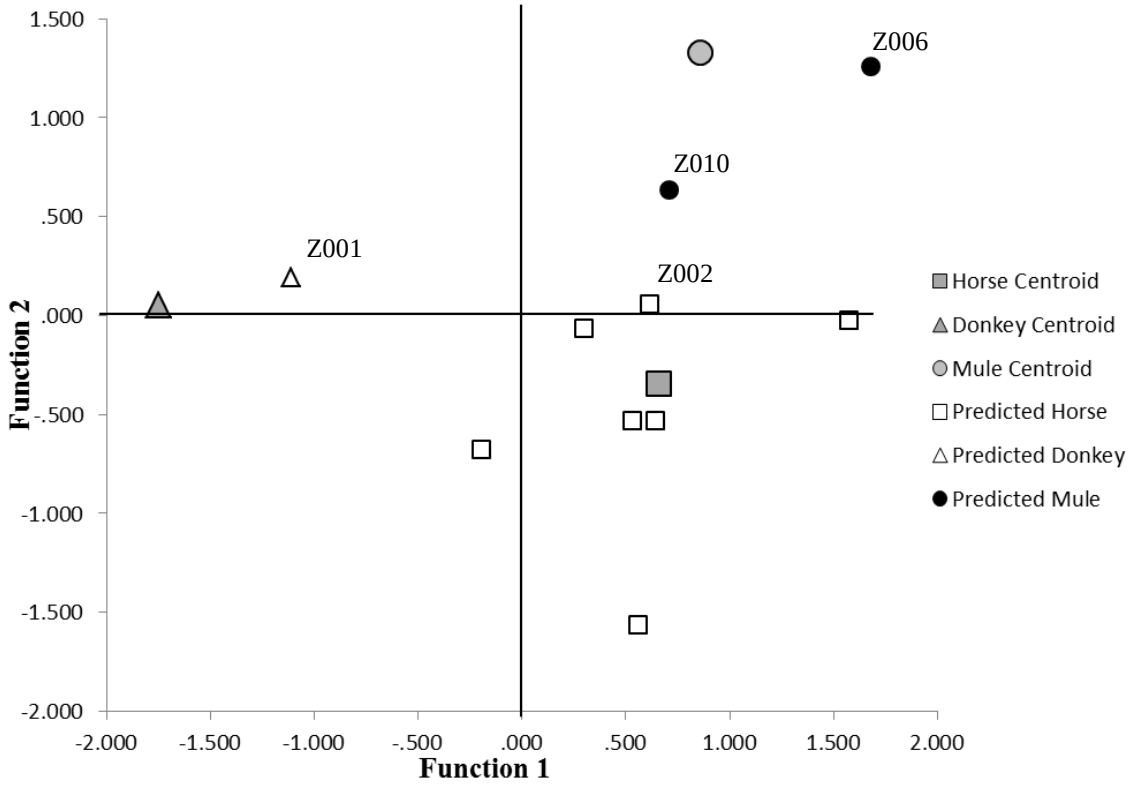


Figure 5.1 – DFA scatter plot for archaeological radii

5.3.1.2 Metacarpal

Among 46 archaeological samples, 7 mules were predicted, and the rest were determined to be horses with different levels of probability (Figure 5.2). Two definite mules are identified, one from Orton Hall Farm (King, 1996) (Z036) and the other from Longthorpe II (King, 1987) (Z033). Both specimens are also determined as definite mule and possible mule respectively in Johnstone's work. Both metacarpals are among the largest, but are not necessarily the most slender when considering the smallest shaft width (SD). One interesting specimen worth mentioning is the "probable donkey" from Iron Age Danebury determined by Johnstone. This specimen (Z026) is identified as a "probable mule" in the current analysis. What is interesting about this specimen is not the discrepant result from different analyses, but the fact that this specimen has unusual measurements that make it stand out from the rest of the archaeological metacarpals. Being one of the longest metacarpals, with a GL of 230 mm (largest from the site), it has an unusually small proximal and distal breadth and a narrow smallest shaft width. The general profile described by these unusual measurements is much closer to those of metatarsals instead. Unfortunately, these measurements are all taken from published reports (Grant, 1984) and, therefore, it cannot be verified whether this discrepancy resulted from a misprint in the original report. As a result, this specimen was excluded from further assessment. The other "probable donkey" identified by Johnstone from the same site is identified as a "definite horse" in the current analysis (Z023).

There is yet another case where the identification of a specimen in this study disagrees with a published "donkey" identification. The metacarpal from Hunt's House, Southwark (Z039) is from the articulated forelimb of a partial skeleton identified as a donkey based on the morphological features of the radius and on the log ratio method for metacarpals

(Bendrey, 1999). However, it was determined as a "probable horse" in the previous DFA (Johnstone, 2004) and as a "definite horse" in the current one. While this metacarpal is the shortest among all archaeological metacarpals, it is not the most slender when the smallest shaft width (SD) is considered. The reason it is more "horse-like" in the biometric analysis may reside in the unusually wide distal articular end distorting the general proportions. No evident pathological condition can be observed in this bone (Bendrey, pers. comm.) and, therefore, it is not certain whether the unusual broadening of the distal end is caused by heavy labour through life or any other living conditions of this individual.

The four other predicted mules are from three other sites. No further comment can be made regarding the probable mules and the possible mules from Baths basilica, Wroxeter, since the measurements appear to have been obtained from records achieved from excavations after the known site report had been published (Barker and Armour-Chelu, 1997). One of the remaining two predicted mules is from Healam Bridge (Z052). While the probability of this element being from a mule is considerably low(45.04%), it is worth noting that this specimen is from a partial skeleton (HB-7613) and is suspected to be from a mule based on the morphological characteristics of several elements.

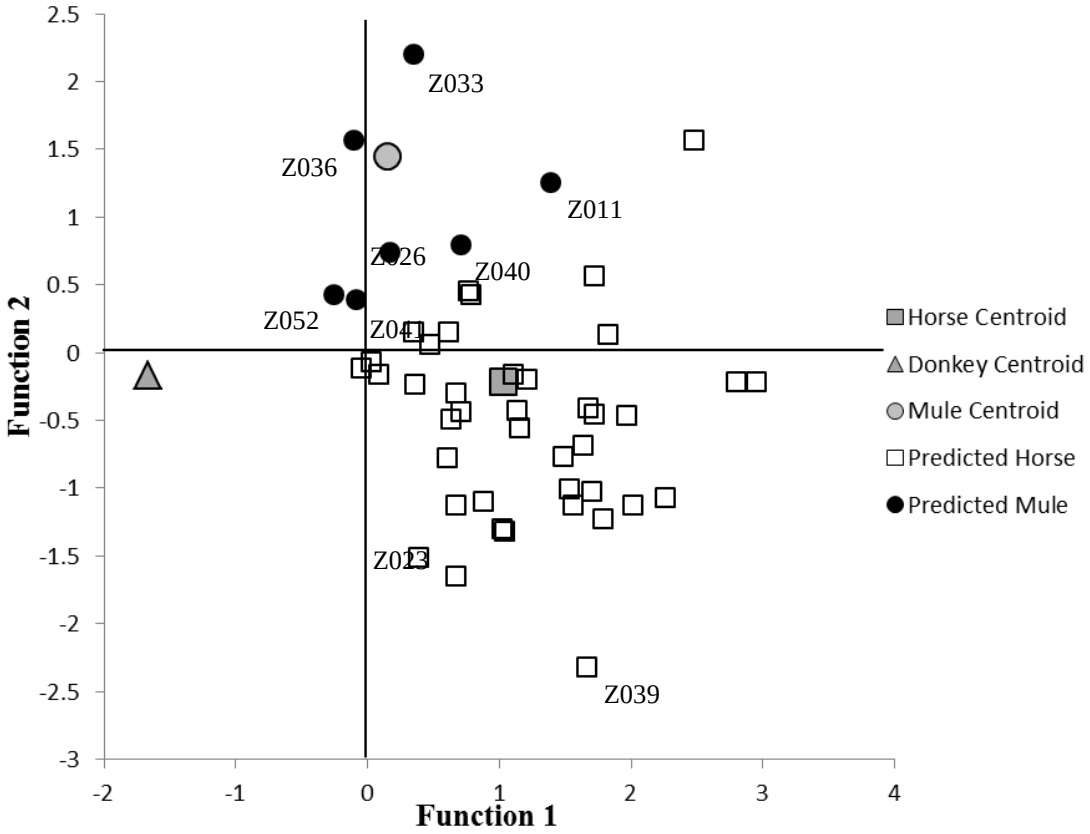


Figure 5.2 – DFA scatter plot for archaeological MC.

5.3.1.3 Femur

Three of the six archaeological femora are also used in Johnstone's (2004) DFA analysis, and all three were determined to be non-caballine equids. Interestingly, the same predictions are made by the current study for these three cases, but with relatively low probabilities (all are determined to be probable identifications). As a matter of fact, all specimens have relatively low probabilities for their respective prediction (the highest being 65%). Considering that the accuracy of using the femur in DFA has already been questioned based on the results involving specimens of known species, it is perhaps best to avoid the femur as an element for species determination. In other words, if the determination from another element of the same individual contradicts that from the femur, it is recommended to consider the determination of the other element as the more likely.

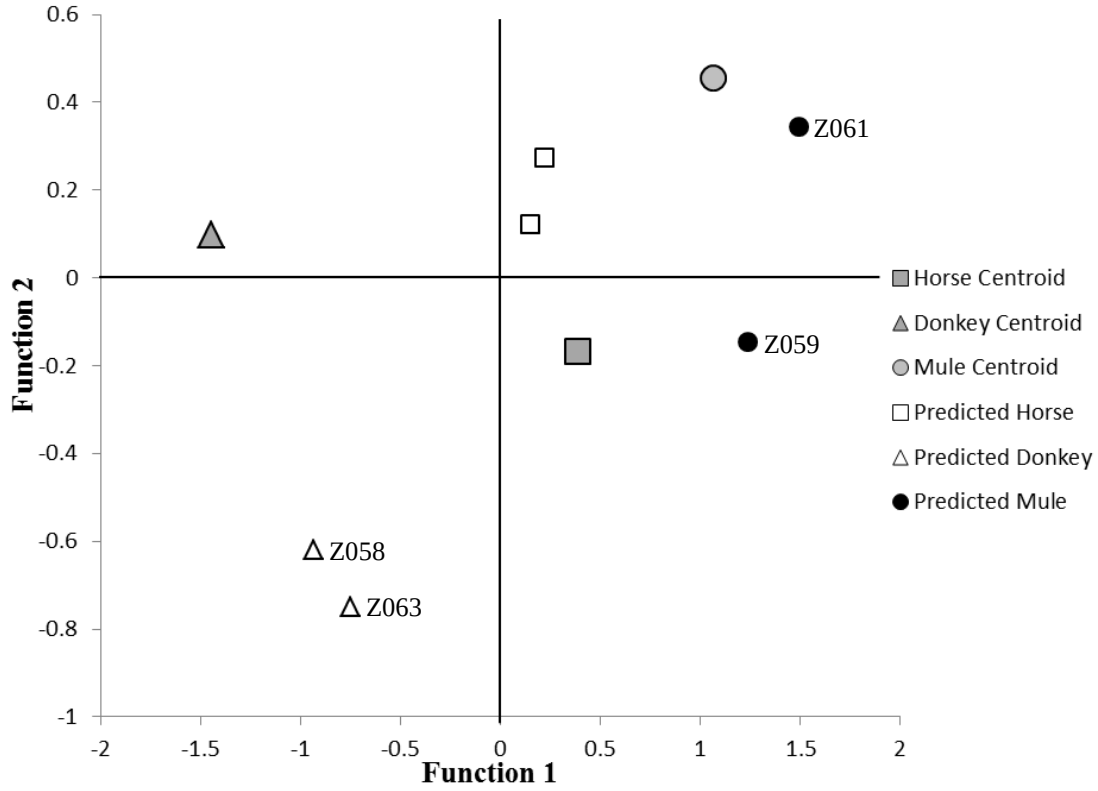


Figure 5.3 – DFA scatter plot for archaeological femora.

5.3.1.4 Tibia

Out of all 21 archaeological specimens, 1 probable donkey and 8 mules (with varying probabilities), were determined using the modified DFA. Twelve of these specimens are also listed in Johnstone's work (2004), but only five of them were determined in her study, since seven specimens were lacking a value for the lateral length, which is not considered as a DFA variable in the present modified version of the method.

An extremely high ratio of mules was determined from Orton Hall Farm. Four out of five specimens were determined to be mules (three definite, one probable). In addition to the definite mule metacarpals from the same site, Orton Hall Farm has 5 mules out of 19 mule determinations so far. It is not certain whether these measurements were all from different individuals or derived only from a few individuals, but it seems that Orton Hall Farm had an unusual domestic equid population. However, it should be pointed out that, in the

original faunal report (King, 1996), the shaft width measurement was actually taken at mid-shaft (MD), which is different from the smallest shaft-width (SD) used in most other reports. The difference between the two measurements is normally very small (usually less than 3 mm), but it still may cause the Orton Hall Farm individuals to appear more robust than other specimens (see Appendix II). Paradoxically, these predictions are in contradiction to the commonly held assumptions on the morphological differences between equid species. According to these assumptions, both donkeys and mules should have more slender limbs, i.e., they should have relatively smaller shaft-widths than horses of a similar size, though the tibiae have never been used specifically to support such a claim.

The remaining four mules are from Chichester Cattle market (M*, Z065), Longthorpe II (M*, Z070), Ribchester (M?, Z079), and Chaucer House (M*, Z083). The probable donkey is from Healam Bridge (Z081); it belongs to a partial skeleton and has an articulating femur (Z062) that was determined as a "possible" horse in the previous section, as well as a metatarsal (Z126) and two first phalanges (Z172 and Z173).

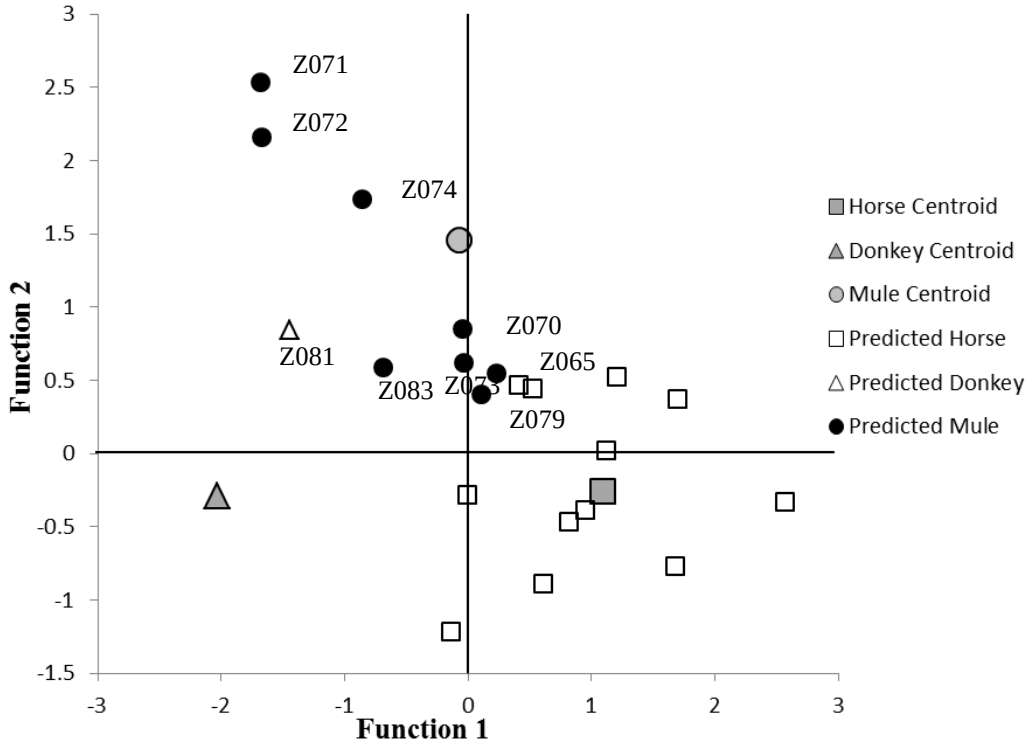


Figure 5.4 – DFA scatter plot for archaeological tibiae

5.3.1.5 Metatarsal

Unlike the metacarpals, no morphological criterion in metatarsals has been suggested for the separation of domestic equid species, and the overall classification rate in the current method is lower than in metacarpals. Nevertheless, the biometric analysis of this element, one of the most commonly found horse remains, is still essential. Forty-two archaeological specimens were included in the current analysis; of these, twelve were determined to be mules with varying degree of probability. Compared to the metacarpals, the larger number of mule determinations in metatarsals may be due to the higher risk of more horses being misidentified as mules. It should also be noted, however, that several pairs of specimens are from the same individuals, and thus the "raw" mule-horse ratio should not to be taken at face value. The metatarsal of the partial skeleton from Healam Bridge (HB-7294) is determined as a definite horse (Z126), but the final determination of this individual will be discussed in the summary section of the DFA results.

Two definite horses are located quite far away from the group centroid (Figure 5.5). These two specimens seem to have unusual measurements that require further investigation. One specimen from Ilchester (Z088) seems to have its SD and Dd measurements reversed, while a specimen from Orton Hall Farm (Z109) has an extremely short GL, which could be a misprint (215 mm instead of 251 mm) or a misplaced metacarpal recorded as a metatarsal. Both specimens are determined as definite horses with extremely high probabilities (99.68% and 99.91%, respectively), but the M-dist from the centroid of the predicted species is also extremely high. Given that the reason for the unusual measurements cannot be determined at present, these two samples are excluded from further discussions.

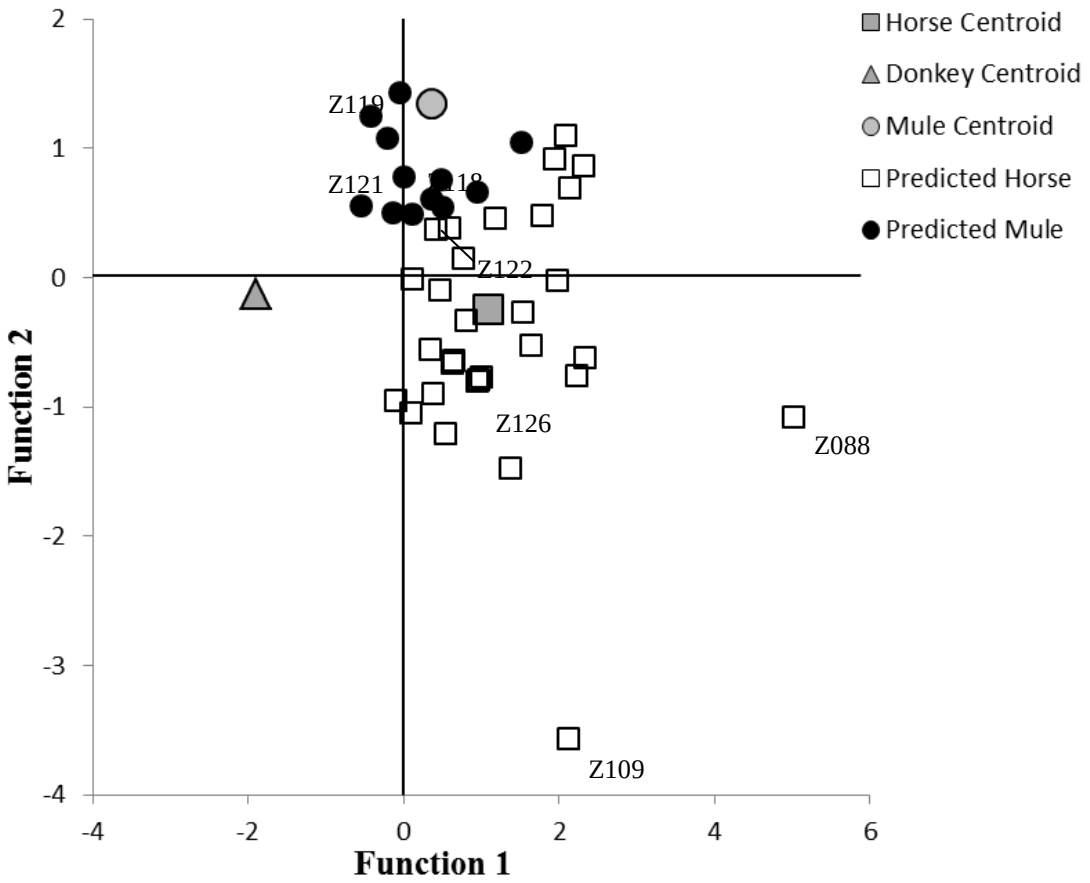


Figure 5.5 – DFA scatter plot for archaeological MT

5.3.1.6 First Phalanx (PH1)

Although it has been argued that it is possible to separate anterior first phalanges from the posterior ones based on morphological differences, it is not the norm for such information to be included in faunal reports. In addition, the results of the combined DFA analysis (anterior and posterior) do not differ significantly from the results when anterior and posterior phalanges are analysed separately. As a result, the anatomical position of the first phalanges is disregarded in the present study. Only 2 out of 43 archaeological PH1 were predicted to be mules, and this produced the smallest mule-horse ratio of all elements. Further examination of the misclassification rate in the dataset indicates that although the tendency for mules to be misidentified as horses is relatively high (16.7%), the misclassification rate of horses as mules is even higher (21.9%). Such phenomena cause an outcome similar to that of the metatarsal, which over-estimates the number of mules. However, this does not seem to be the case here. Both mule identifications are from

Winchester, but one of the two specimens (Z161) has an extremely low probability rate (50.91%) that nearly equals its probability of being a horse (49.04%). The consistency of results from the first phalanges using different techniques will be discussed later in this chapter.

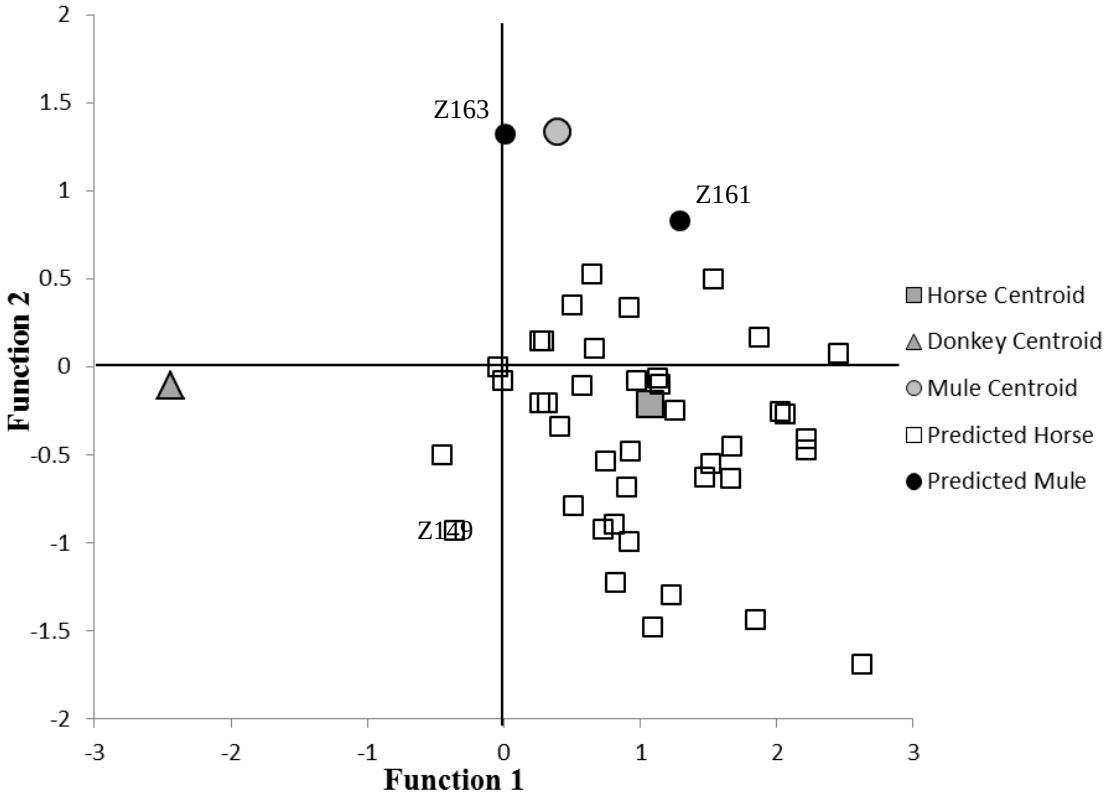


Figure 5.6 – DFA scatter plot for archaeological PH1. Note Z149 is suspected as a donkey under qualitative determination and will be discussed in the next sections (section 5.3.3)

5.3.2 – DFA results and their implications

Based on the outcomes of the current findnigs, it seems robustness and slenderness do not play a decisive role in the determination of species in current biometric approaches, at least, for discriminating horses and mules (see Appendix IV for SD-GL indices). Contrary to the general assumption of mule bones being more slender than most horses, the majority of predicted mules in the current DFA outcomes do not appear to be more slender than horses. In fact, most of the calculated SD-GL indices of predicted mules are within the range of horses (except tibia and MC, the issue with tibia has already been mention in section

5.3.1.4). The question regarding whether castrated horses may be misidentified as mules is less likely to be a main issue because: 1, the castration of horse in Roman time took place after the limb bone is completely fused, and 2, slenderness and robustness do not dominate the determination of species in the current DFA method.

Table 5.2 summarises the number of species determinations of archaeological specimens using modified DFA. The femur has the most unusual horse-donkey-mule ratio of 1:1:1. Considering that the femur also shows the lowest accuracy rate in the "control dataset" of specimens of known taxonomic affiliation, such a result is very likely to be inaccurate and, therefore, it was considered best to exclude it from further interpretation. As a result, only the outcomes from archaeological radii, metacarpals, tibiae, metatarsal, and first phalanges are considered for the determination of species frequencies based on DFA. In addition, since the probability of "possible" identifications is lower than 50%, they are also excluded from further assessment. In other words, only "definite" and "probable" identifications are taken into account in the discussion of species representation (Table 5.3).

	Radius (n=10)	MC (n=47)	Femur (n=6)	Tibia (n=21)	MT (n=40)	PH1 (n=43)
Horse	3	29	0	7	13†	23
Horse*	4	10	1	5	14	17
Horse?	0	1	1	0	1	1
Donkey	0	0	0	0	0	0
Donkey*	1	0	2	1	0	0
Donkey?	0	0	0	0	0	0
Mule	1	2	0	3	1	1
Mule*	1	2‡	2	4	9	1
Mule?	0	2	0	1	2	0
H:D:M	7:1:2	39:0:6	2:2:2	12:1:8	28:0:12	41:0:2

Table 5.2 – Summary of DFA determination.
Note that "†" in definite horse in MT indicates that two potential erroneous specimens have been excluded from the total. "‡" in the probable mule in MC indicates that one potential erroneous specimen has been excluded from the total.

	Radius (n=10)	MC (n=44)	Tibia (n=21)	MT (n=40)	PH1 (n=43)	Total
Horse	3	29	7	13†	23	75
Horse*	4	10	5	14	17	50
Donkey	0	0	0	0	0	0
Donkey*	1	0	1	0	0	2
Mule	1	2	3	1	1	8
Mule*	1	2**	4	9	1	18
H:D:M	7:1:2	39:0:4	12:1:7	27:0:10	40:0:2	125:2:25

Table 5.3 – Summary of DFA determination excluding femora and "possible: identifications. Note that "†" in MT indicates that two potential erroneous samples have been excluded from the total.

After the exclusion of femora, the questionable specimens (Z026, Z088, and Z109), and all possible identifications, a total of 152 archaeological specimens remained to be assessed. If the numbers of "definite" and "probable" identifications are combined, then the horse-donkey-mule ratio is 125:2:25 and leads to a 5:1 horse-mule ratio. Whilst both accounted donkey identifications (Z001 and Z081) are "probable" identifications, it should be noted that the one from Healam Bridge (Z081) has a relatively low probability (56.54%), i.e. not far from its calculated probability of being a mule (40.72%) while the second identification is a probable donkey radius (Z001), which belongs to a partial skeleton (Sk.682, Winchester) with contradictory identifications from this individual's other elements.

This is a good moment to stress that those specimens deriving from the same complete or partial skeleton should be considered as one in order to avoid over-estimation. However, it must also be noted that the predictions are not always consistent for different elements of the same individual, and thus we should have an established and consistent method to assess the final species determination. For such a purpose, it is recommended to evaluate the predictions by the classification rate of the element rather than considering them

equally. For example, the classification accuracy for the metacarpals is considerably higher than for the radii; and, the misidentification rate for the former is significantly lower than that of the latter. Thus, more weight should be given to the determination based on metacarpals rather than giving equal values to both elements. Considering the reliability of these elements in both the present and Johnstone's DFA analyses, the assessment ranking for the elements should be MC > PH1 > MT ≥ Tibia > Radius (> Femur).

The probability value should also be taken into consideration if different sides of the same element have a different species prediction. For example, the two radii from the partial skeleton, Sk.682 (Winchester), are determined to be different species. However, the right radius (Z001) is determined as a probable donkey (75.95%) while the left radius is determined as a probable horse (65.09%). If the two radii were the only specimens available for this individual, then it should be determined as a probable donkey. No objective scoring system is developed for settling the inconsistent predictions between different elements, since it involves complex calculations of the representativeness for each species and elements for very little gain.

Based on the results from the modified DFA, the current thesis suggests that species determination should emphasise the accuracy ranking of the element before calculating the total number of determined species from different elements. In other words, for example, a horse identification determined from a metacarpal should be considered more accurate than both radii of the same individual being determined as mules. Nevertheless, for the elements considered to have a similar accuracy ranking, i.e., tibiae and metatarsals, the value of the probabilities should be considered. The simplest way is to average the probabilities from two elements and determine the species based on the highest average probability. For

example, partial skeleton (HB-7294) has a femur (Z062), a tibia (Z081), and a metatarsal (Z126). They are determined as possible horse, probable donkey, and definite horse respectively. As mentioned above, femora should be avoided due to their low accuracy. Thus, the species identification will be determined by two elements with a similar accuracy rate, namely, tibiae and metatarsals. The average probabilities for each species from these two elements are 46.18% (horse), 28.91% (donkey), and 24.91% (mule). As a result, this individual should be considered as a horse. It should be noted that a simple calculation of means of probabilities is not statistically sufficient to determine the likelihood of species. An approach which considers multivariates involved the probability should be used. However, since there are only five individuals are known to have more than one element being used in DFA (Table 5.4), no special effort is made to develop such approach. The prediction given by the element with the highest assessment ranking decides the specific determination of the individual.

Site Context	MC	PH1	MT	Tibia	Radius	Femur	Determined Species
Winchester SK-682	H, H	-	-	-	H*, D*	-	H
HB 7613	M?	-	M*, M*	H*	H*		M*
HB 7294	-	-	H	D*	-	H?	H
Ribchester 3663	-	H, H	M*, M	-			H
Winchester NR-561	-	H*	M*	-	-	-	H*

Table 5.4 – Species determination of different elements from the same individual

Assuming that there are no more individuals with more than one element being used, the 141 archaeological specimens have a horse-mule ratio of 120:21 (5.7:1) (and no donkey identified by DFA). Specimens measured are all from Roman Britain, but data was also available from Iron Age specimens (e.g. Danebury and Coldharbour Farm) as well as other sites (the latter contains no determined mules). Since the present study focuses on Roman Britain, Iron Age specimens are excluded in the calculation of species frequencies. This gives 101 horses and 21 mules determined by modified DFA (horse: mule ≈ 4.9:1).

All 21 sites with Roman domestic equid remains were each assigned to one of six different site types: Urban, Military, Rural, Small Town, Villa, and Cemetery (Table 5.5). Assigning a site type to each assemblage is an exceedingly challenging task because some of the sites were continuously occupied over a long period of time, and thus the functions of the site may have changed through time. For example, Thorpe Thewles is probably better known as an Iron Age site, but it was continuously occupied throughout Roman times as well (Heslop, 1987). While most of the animal remains have been dated to the Iron Age, there are still a few that belong to the Roman phases. Likewise, attempts to divide the specimens into different Roman phases will complicate the issue. First, not all sites can be further divided with the same precision and temporal resolution. Some sites existed for only a short time span and have a clear chronology, such as Ribchester (Buxton and Howard-Davis, 2000), but others are comparatively poorly dated – for example, Fairford (Jennings *et al.*, 2004; Levine, Pers. Comm.). As a result, site types are only assigned on the basis of the general description given in the excavation reports; no further division is made for Roman phases.

The East London Roman Cemetery is the only cemetery site, and it is not certain how domestic equids in cemetery sites represent the use of domestic equids, although Groot (2008) argued that horses were involved in Roman funerary rituals. It also has been argued that horse remains in cemetery sites may be results of re-deposition (Foster, 2012). Similarly, Orton Hall Farm is the only site that can be classified as a Roman villa and, therefore, it may not be representative of other sites of this type. In addition, as mentioned above, the system of measurement used in the study of the faunal remains from Orton Hall Farm is slightly different from those at other sites and, therefore, the species determinations may be problematic. Nevertheless, the large number of mule determinations is still worthy further examination in the future. Among the four remaining site types, military sites have the highest ratio of mules (1 mule in every 4.6 domestic equids) in comparison to the mule ratio of non-military sites (excluding cemetery and villa, 1 mule in every 7.75 domestic equids). This result agrees with the preference for using mules as pack animals in the Roman military forces (Roth, 1999, p.206).

A sharp contrast was expected to be observed between urban and rural settlements. However, whilst the urban settlements have a relative high mule:horse ratio, the use of mules for delivery through *cursus publicus*, which would normally have employed mules as pack animals, would be more intensive in urban areas, as would the use of mules for drawing the carts of the Roman elites who lived in these urban centres (Laurence, 1999). This is not to argue that rural settlements were not part of the *cursus publicus*, but it could merely reflect differences in the volume of traffic and the level of wealth between these two site types. However, under the current analysis, the ratio between these two site types differs little (horse to mule for urban is 5.33:1, and for rural is 6.75:1). The reason for the unexpected high mule:horse ratio in rural area is due to the higher frequency of mules from

Healam Bridge, which is suspected to have had a military influence in its early phase (D. Jaques, forthcoming).

In comparison to urban sites, as reflected in the consumption of different domestic species, populations in rural settlements were considered to be less "Romanised" (King, 2001), and this may imply that the use of mules may have been a cultural phenomenon. Although mules are known to be associated with agricultural production today, it has been suggested that domestic equids did not reach their full potential as farm animals before the invention of proper haulage equipment much later (Langdon, 1986). Even if they had been used in agricultural production, it would have been too expensive for ordinary farmers in Roman Britain to own this infertile animal for labour merely for a decade or two.

To summarise, the species determined by DFA using five different elements (radii, metacarpals, tibiae, metatarsals, and first phalanges) suggests that mules are only found in Roman contexts, but not at Iron Age sites. In addition, no donkeys can be confidently determined. Mules are more likely to be associated with military sites, and if they are found in a non-military context, they are very likely to be found in major urban settlements. Although mules do not seem to have been as abundant as many historians have claimed (Peddie, 1997), the overall ratio indicates that there should be at least one mule for every six domestic equids found in Roman Britain.

Site Type	Site	Horse	Mule	H:M Ratio
Urban	Beddington Sewage Farm	3	1	32:6 (5.33:1)
	Chichester Cattlemarket	3	2	
	Ilchester, Church St.	1	0	
	Winchester	23	2	
	Wroxeter Baths basilica	2	1	
Military	Castleford	3	1	11:3 (3.67:1)
	Longthorpe II	3	2	
	Ribchester	5	0	
Rural	Fairford	4	1	27:4 (6.75:1)
	Healam Bridge	12	3	
	Lutton/Huntingdon	3	0	
	Norman Cross	1	0	
	Thorpe Thewles	5	0	
	Tort Hill West	2	0	
Small Town	Alcester	2	0	22:2 (11:1)
	Chaucer House	0	1	
	Elms Farm	14	0	
	Scole-Dickleburgh	5	1	
	Southwark	1	0	
Total		92	15	92:15 (6.1:1)
Villa	Orton Hall Farm	6	6	6:6 (1:1)
Cemetery	East London RB Cemetery	4	0	2:0
Grand Total		102	21	102:21 (4.9:1)

Table 5.5 – Frequency of domestic equids from different site types

5.3.3 – Species Determinations using the Davis Method

In Chapter 3, it was shown that, while the Davis method may not be effective for the separation of mules and horses, the method can still efficiently distinguish donkeys from the other two species and, therefore, is able to offer additional support in the determination

of archaeological specimens. Forty-seven first phalanges missing the required measurements for the modified version of DFA can nevertheless be included in an analysis, using the Davis method. As is clearly shown in Figure 5.7 – which uses the index (BFd/GL) and SD – only a few specimens are located outside of the overlapped areas. This indicates that similar clustering may be expected for modern and archaeological specimens. The majority of specimens are clustered within the range of known horses (indicated by the hashed line); only one specimen falling in the range of modern donkeys and outside the overlap area with horses.

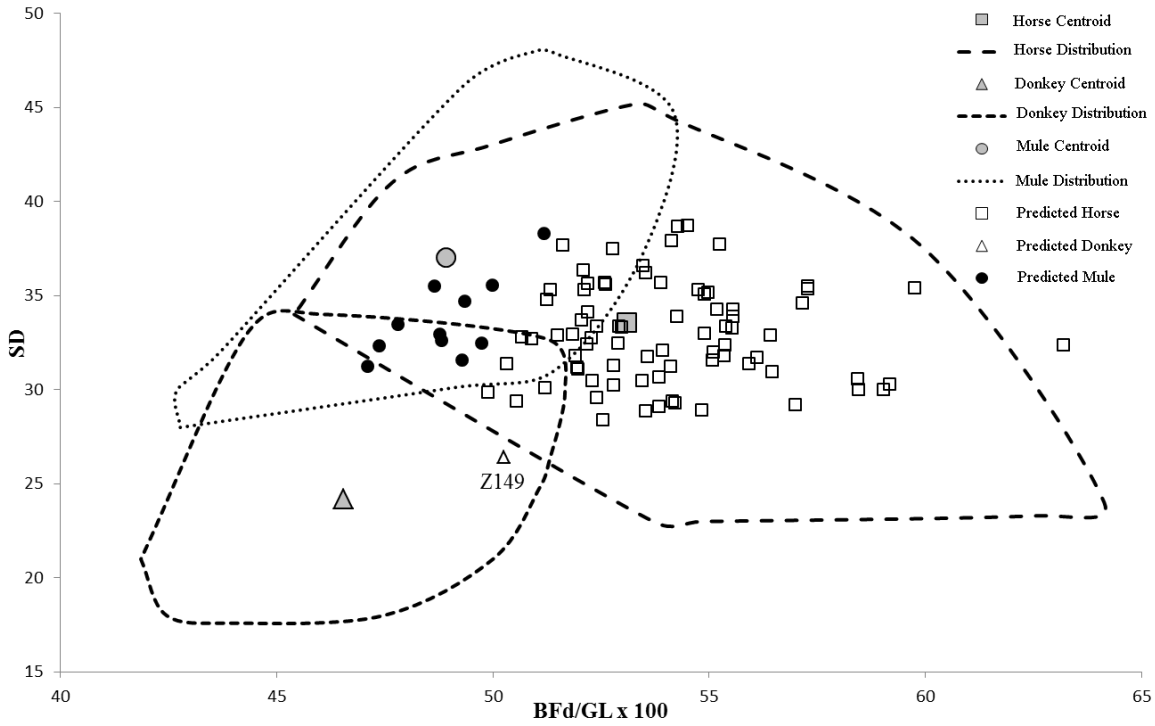


Figure 5.7 – BFd/GL index and SD scatter plot with archaeological specimens
Numerous archaeological horses are scattered on the right side of the diagram which indicates their similarity to modern ponies.

The one specimen (Z149) that is clearly located in the donkey range (where no overlap occurs) belongs to a posterior first phalanx from Fairford. It can be confirmed as a posterior first phalanx because it is associated with the other hind limb element from the same side including a tibia, an astragalus, and a calcaneus; the metatarsals are regrettably

missing, and the tibia is too incomplete for sufficient measurements to be taken to be used in DFA analysis. The modified DFA indicated that this first phalanx is likely to be a "probable" horse. However, based on the observation of qualitative morphological criteria (Figure 5.8), this specimen more resembles a donkey than a horse. Since the presence of donkeys at Fairford is suggested by the discovery of teeth bearing an asinine morphological patterns (Levine, 2004), the identification of this specimen as a donkey seems reasonable. Furthermore, the results from the cross validation of the dataset using the M-dist in the Davis method, which attest that no other species are misidentified as donkeys (see section 3.3.3.2), further support this determination.

Figure 5.8 – Z149 Comparison to reference collection.
Z149 is more similar to the donkey in the reference collection, but it does appear to be slightly more robust than the donkey (132).

The extensive overlapping of domestic equids is to be expected, as shown in the study of specimens with known species affiliation. The solution proposed to solve the dilemma and to determine the species quantitatively relies on the comparison of the M-dist of each specimen to the group centroid of all three species. The determination is made based on the

shortest distance calculated among the three group centroids. Unfortunately, unlike the calculation of probabilities in DFA, this method is not able to evaluate further the level of probability, and thus identifications cannot be classed as either “possible” or “definite”. Among the 90 specimens, 78 were determined as horses, one as a donkey, and eleven as mules. The results of only 4 out of the 43 first phalanges are inconsistent with the determinations made using modified DFA: one is determined as donkey and three as mule instead of all being determined as horses in DFA. All four conflicting cases are determined to be probable identifications in the DFA with relatively low probabilities (average=58.92%). The differences between the M-dist for the determined donkey (Z149) and one of the three determined mules (Z165) are more significant and, therefore, will be considered as probable donkeys and probable mules respectively, while the remaining two determined mules (Z136 and Z158) will be considered as possible horses and so excluded from the ratio calculations.

As mentioned in section 5.3.2, some of the specimens come from the same individuals, and thus they need to be removed to avoid overrepresentation. For example, the partial skeleton from Healam Bridge (HB-7614) has three of its four first phalanges analysed by the current method. All three are determined to be mule, which agrees with the species determination made from the metatarsals through DFA. As for all other first phalanges from the same individuals (i.e. Winchester NR-561 and Ribchester 3663), there is also no discrepancy found between the species determinations from different elements of these individuals. Among these 83 different individuals, 75 are determined as horses, one as a donkey, and seven as mules. Six of the determined horses are dated as Iron Age according to either previous work or the original reports. As a result, the Roman domestic equids ratio based on the Davis method is 69:1:7 (horse:donkey:mule). The ratio of mules is estimated to be

much lower than that obtained using DFA (1 mule in every 11 domestic equids; DFA suggests 1 mule in every 5.9 domestic equids).

Most sites already have their site type assigned in the previous section. However, there are two new sites that remain ambiguous: Winchester Palace and Haddon. Winchester Palace, Southwark, is believed to be a Roman building complex that was used for military purposes (Yule, 1989). While some evidence suggests that it was occupied by military personnel, the building complex seems to have been used only for administrative functions rather than for other military activities. As a result, it is assigned here as "other" instead of "military". The other Roman site is more problematic. The data from the Roman site of "Haddon" are listed in Johnstone's thesis (2004). However, the full reference of this site is not given and, therefore, it is only assumed to be the Roman bathhouse site at Haddon, Cambridgeshire (Upex, 1994). The site has been assigned as "other" in Johnstone's work (2004) and, therefore, will also be considered as the same category in the current analysis. The number of determined species from each site is summarised in Table 5.6. Sites assigned as "cemetery" and "others" will be excluded from further discussion since the meaning behind the presence of livestock at these sites is unclear.

The mule:horse ratio, again, is higher for military sites (1 mule per 5 domestic equids) than in a non-military context (1 mule per 12.8 domestic equids). Urban sites have the highest mule ratio among non-military sites followed by rural sites. The determination of the only donkey from a rural site is worth noting. According to historical studies regarding Roman livestock, donkeys were more commonly used as agricultural labour animals than were either horses or mules (Roth, 1999, p.205, and references within). Thus, it should not be surprising that the only donkey is from a rural site. However, this scenario refers mainly to the Roman heartland, the Mediterranean region, and perhaps, the near East provinces of the

Empire, where donkeys were used as a cheap substitute for horses (Roth, 1999). The archaeological evidence of donkeys is scarce in the north-western part of the Empire, and there is no evidence showing that they were more common in rural sites, although it must be remembered that faunal reports from rural sites are very much a minority. Given that both donkeys and mules were either new introduction before or after Roman invasion, the native population were less likely to employing donkeys and mules largely in agricultural activities, the presence of donkeys in rural sites rather than in villa sites is peculiar.

Site Type	Site	Horse	Donkey	Mule	Ratio
Urban	Chichester Cattlemarket	2	0	1	19:0:3 (6.3:0:1)
	Winchester	16	0	2	
	Wroxeter Baths basilica	1	0	0	
Military	Ribchester	1	0	1	4:0:1
	Hayton Fort	2	0	0	
	Newstead Fort	1	0	0	
Rural	Fairford	0	1	0	19:1:2
	Healam Bridge	12	0	2	
	Norman Cross	1	0	0	
	Thorley	1	0	0	
	Thorpe Thewles	2	0	0	
	Tort Hill West	3	0	0	
Small Town	Elms Farm	13	0	0	20:0:0
	Scole-Dickleburgh	7	0	0	
Total		62	1	6	62:1:6
Other	Haddon	2	0	1	3:1
	Winchester Palace	1	0	0	
Cemetery	East London RB Cemetery	4	0	0	4:0
Grand Total		69	1	7	69:1:7

Table 5.6 – Species determination using the Davis method

5.3.4 – Species representation of domestic equids based on post-cranial elements

A total of 216 post-cranial elements are included in the biometric analysis; 126 are analysed using only DFA, 47 are analysed using only the Davis method, and 43 are

analysed using both methods. Of all specimens, only ten are determined as either "possible horse" or "possible mule", and these will be excluded from further discussion. In addition, results using femora (n=6) will be excluded because, as previously mentioned, predictions based on this element are deemed to be insufficiently accurate. In order to prevent the overestimation of certain species, only one determination is given to each individual regardless of how many elements of that individual are used in the biometric analysis. Five near complete or partial skeletons, comprising a total of 25 specimens, were included in either the DFA or Davis method, or analysed using both. For these individuals, it is necessary to assess all outcomes and assign a single species determination that best describes each of them. A similar assessment for these five individuals has been carried out using DFA (section 5.3.2) and, as was mentioned in the previous section, no intra-individual disagreement is found between the different specimens in the Davis method as well as no contradictory species determination between the two methods. Table 5.7 provides a summary of the determination species of each of the five individuals.

Site Context	MC	PH1	PH1 Index	MT	Radius	Determined Species
HB 7613	M?	-	M, M, M	M*, M*	H*	M*
HB 7294	-	-	H, H	H	-	H
Winchester SK-682	H, H	-	H, H	-	H*, D*	H
Winchester NR-561	-	H*	H	M*	-	H*
Ribchester 3663	-	H, H	H, H	M*, M		H

Table 5.7 – Species determinations of the individuals with multiple elements analysed

After excluding uncertain and adjustments made for partial/almost complete skeletons, 179 specimens were determined by either one or both methods. Twenty-three of these

specimens were dated from the Iron Age; no determinations of mules or donkeys were made for any of them. The ratios of domestic equids from the remaining 156 Romano-British specimens of different sites are listed in Table 5.8.

Site Type	Site	Horse	Donkey	Mule	Ratio
Urban	Beddington Sewage Farm	3	0	1	35:0:7
	Chichester Cattlemarket	5	0	3	
	Ilchester, Church St.	1	0	0	
	Winchester	23	0	2	
	Wroxeter Baths basilica	3	0	1	
Military	Castleford	3	0	1	13:0:4
	Longthorpe II	3	0	2	
	Ribchester	4	0	1	
	Hayton Fort	2	0	0	
	Newstead Fort	1	0	0	
Rural	Fairford	3	1	1	39:1:5
	Healam Bridge	23	0	4	
	Lutton/Huntingdon	3	0	0	
	Norman Cross	1	0	0	
	Thorley	1	0	0	
	Thorpe Thewles	5	0	0	
	Tort Hill West	3	0	0	
Small Town	Alcester	2	0	0	26:0:2
	Chaucer House	0	0	1	
	Elms Farm	16	0	0	
	Scole-Dickleburgh	7	0	1	
	Southwark	1	0	0	
Total		113	1	19	113:1:18
Villa	Orton Hall Farm	6	0	6	6:0:6
Other	Haddon	2	0	1	3:0:1
	Winchester Palace	1	0	0	
Cemetery	East London RB Cemetery	8	0	0	8:0:0
Grand Total		130	1	25	130:1:25

Table 5.8 – Species representation of domestic equids identified using DFA and Davis method by site.

Species representation from this final determination process differs little from using either analysis. A ratio of 1 mule to every 8.2 domestic equids is estimated for non-military sites (i.e. urban, rural, and small town), while the grand total suggests one mule in every 6.24 domestic equids. This is a sharp contrast to the almost total absence of specimens identified as donkeys in the assemblages; only one donkey (Z149, Fairford) was determined. Although DFA suggests that this specimen is a probable horse with a low probability rate it clearly clusters with the modern donkeys when using the Davis method.

Although mules are still in the minority, they are commonly found at the different sites selected for the current study. According to the taxonomic determinations presented above, mules can be found in 12 out of 24 of the sites, and are particularly common in urban and military sites. The mule-horse ratio is also much higher in military sites than in any other non-military sites with the exception of the only villa site included in the present investigation. The outcomes give rise to two important questions:

(1) If donkeys are as rare as the results suggest, would there have been a sufficient donkey population in Roman Britain not only to maintain a continuous supply of donkeys (i.e. local reproduction), but also to establish local mule breeding?

(2) Given that it seems mules are more commonly associated with urban and military sites (with a possible association with villa sites as well), does this indicate that the use of mules was restricted within Roman culture and not adapted by or familiar with local “native” populations?

These questions will be discussed in a latter chapter, when results of isotopic analysis are examined.

5.4 – Species determination of lower molar dental morphology

A total of 55 lower molars from 36 individuals were used in all four GMM analyses described in the previous chapter (Chapter 4). As briefly mentioned previously in section 5.2, the identification of most molars can be confirmed as such, despite the fact that some specimens were not part of 'intact mandibles', mainly due of the presence of other adjacent teeth (premolars or third molar). Although Payne (1991) argued the first and second molars could be separated from the third and fourth premolars by comparing two measurements from the occlusal surface, the method seems to be inconclusive, as several known molars overlapped with the premolars in Payne's work. Nevertheless, the method was still used to exclude teeth that are unlikely to be molars.

Thirteen molars from nine individuals were deemed by other scholars and the present author as showing dental morphological traits atypical for horses (Table 5.9). Given that the identification of horses is less problematic, and they are also expected to be more common than donkeys and mules, more emphasis is put onto those suspected as non-caballine equids in the following discussion of the results of the four GMM analyses. The M-dist are calculated for every analysis to check the correlation between specimens and group centroids of modern specimens of known species. However, it should be remembered that since mule samples are lacking from the modern control, the M-dist are, therefore, considerably less useful in the current GMM analyses for the identification of this taxon. Thus, the determination of mules can only be based on the hypothesised expectations, as explained in the previous chapter.

No	Site	Context	Tooth	Qualitative Determination*
T001	Healam Bridge	HB-7614	Left M_1	Mule
T002	Healam Bridge	HB-7614	Right M_1	Mule
T010	Winchester	VR-405	Left molar	Mule
T018	Winchester	VR-481	Right M_1	Mule
T024	Fairford	FTF2084	Left M_1	Donkey
T025	Fairford	FTF2084	Left M_2	Donkey
T026	Fairford	FTF2459	Right molar	Donkey
T036	Ribchester	RB-728	Left M_1	Mule
T037	Ribchester	RB-728	Right M_1	Mule
T038	Ribchester	RB-728	Left M_2	Mule
T039	Ribchester	RB-728	Right M_2	Mule
T049	Alcester	ALC-3002	Left molar	Mule
T052	Serbia	Viminacium	Right M_1	Mule
T053	Serbia	Viminacium	Right M_2	Mule
T054	Serbia	Pirot	Left M_1	Mule
T055	Serbia	Pirot	Left M_2	Mule

Table 5.9 – Teeth with atypical caballine dental patterns.
*- the qualitative determination is based on dental morphology described by previous researchers (e.g. Armitage and Chapman, 1979, Eisenmann, 1986, Uerpmann and Uerpmann, 1994, etc.) summarised in Johnstone (2004).

5.4.1 – Angle analysis

The majority of specimens (n=37) fall with in the distribution of modern horses, while the M-dist indicate that 44 specimens are likely to be horse rather than donkey. Only 4 specimens fall within the donkey range, whilst 12 are determined as donkeys based on the M-dist.. Unfortunately, as pointed out previously, there are no available mule samples for comparison, nor is the M-dist used here able to provide probabilities for further evaluation. However, some of the specimens do sit in the hypothesised mule region (Fig 5.9). All four molars from the Serbian specimens identified as mules by S. Vukovic (pers. comm.) (T052 to T055) fall into the hypothesised mule region. This suggests that, if dental morphological traits were reliable for species identification, then the current method should be able to distinguish them objectively. Nevertheless, some specimens that were suspected in

previous studies to be mules do not fall into this hypothesised region. For example, the partial skeleton from Healam Bridge was identified as a mule based on several qualitative morphological features (D. Jaques, pers. comm.), and the results of the biometric analysis presented in the previous section are consistent with this determination. However, both the left and right first molars of this individual (T001, T002) fall into the distribution of donkeys, suggesting that while the lingual valley is more V-shaped, the bucco-lingual distance does not resemble the characteristics thought to be typical for mules. An individual from Ribchester was purported to be a mule based on the fact that all of its available four lower molars (T036-T039) show "mule" morphological traits: i.e. deep penetration of the buccal valley and a V-shaped lingual valley. Even though all molars from this individual are located in the bottom left corner of the horse range, they sit beneath the 0.05 cm cut-off (dashed-line in Figure 5.9). A first molar (T006) positioned in the horse/(hypothesised) mule overlapping zone is paired with its second molar (T007), which sits within the horse range. These two molars belong to a partial skeleton from Healam Bridge (HB-7294), which was also determined as a horse in DFA.

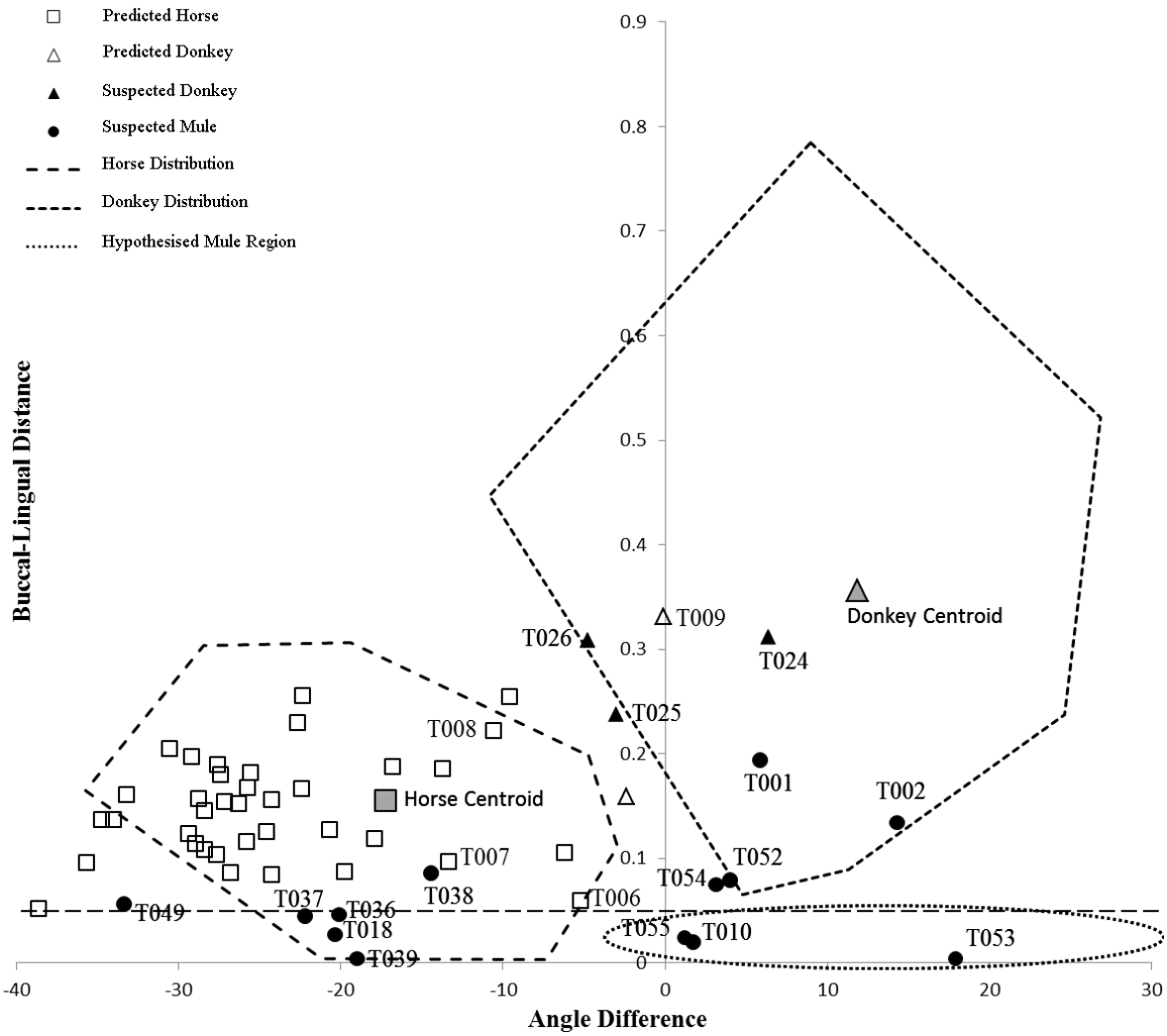


Figure 5.9 – Scatter plot of archaeological lower molars based on lingual valley angle and bucco-lingual distance.
The dashed-line marks the bucco-lingual distance at 0.05cm. Nearly all suspected mule molars are based on the short bucco-lingual distance, but this does not always appear with a narrow angle of lingual valley.

The determination of donkeys concurs with the taxonomic identification based on qualitative morphological traits. Three donkeys were identified from Fairford. Two of these are from a relatively complete mandible (T024 and T025) and have been previously identified by Levine as donkey (Levine, pers. comm.), albeit one of them is slightly outside the donkey range. However, whether the remaining tooth (T026) is a molar or premolar cannot be fully confirmed since it is a loose tooth and is slightly larger than typical molars, but it is still included for its resemblance to two other donkey molars (T024 and T025). Four of the five specimens that fall within the donkey range are suspected by previous

researchers of being either donkey (T024, T026) or mule (T001, T002) based on qualitative morphological traits. However, the remaining specimen (T009) shows a discrepancy between different molars of the same individual. T009 is a second molar from the same mandible as a first molar (T008). While the actual distance between these two molars is not unreasonably far apart on the scatter plot, they are clearly in different distributions; the M-dist undoubtedly support this separation. The crown height of this individual as well as its un-erupted third molar suggests that it is about 4-5 years of age, and the inconsistent determination is very probably due to the different wear stage between first and second molars. Although this is the only young individual that was used in the current analysis, it is still important to remember that other than premolar-molar distinction, age differences should also be taken into account for species determination using dental morphology. The possibility that this young individual is, indeed, a mule also cannot be ruled out.

Since mules cannot be confidently identified, the ratio of the three domestic equids cannot really be calculated. Of the 35 individuals from Romano-British contexts, only five were determined as non-caballine domestic equids. However, it also seems that the degree of variation in equid dental morphology is much greater than hypothesised and, therefore, likely to be more substantial than expected.

5.4.2 – Landmark-based GMM

Before discussing the results of landmark-based GMM, it is necessary to provide a hypothesised scatter plot predicting the location where each species is most likely to fall. The previous chapter has already provided an interpretative framework for the modern 'control' dataset with reconstructed thin-plate spline meshes showing the shape of each end

of the axis. The reason for providing a new plot here is that every time a new set of landmark coordinates is introduced into the matrix, it will affect the outcome of the Procrustes fitting and, therefore, ultimately alter the PCA. As a result, the PCA plot in the previous chapter represents only how the different sets of landmark coordinates would scatter if they were the only dataset. Based on the reconstructed thin-plate spline on each end of both axes, the three different domestic equids species are more likely to be located in the hypothesised region shown in Figure 5.10. The further left along the x-axis (PC1) the shorter the bucco-lingual distance will be and *vice versa*. Similarly, the higher up the y-axis (PC2) the more round the metastylid will be and vice versa. As a result, donkeys are more likely to be located in the upper right corner and horses are likely to be located in the bottom-left corner (slightly overlapping the centre), whilst the upper left corner is the hypothesised area for mules to cluster.

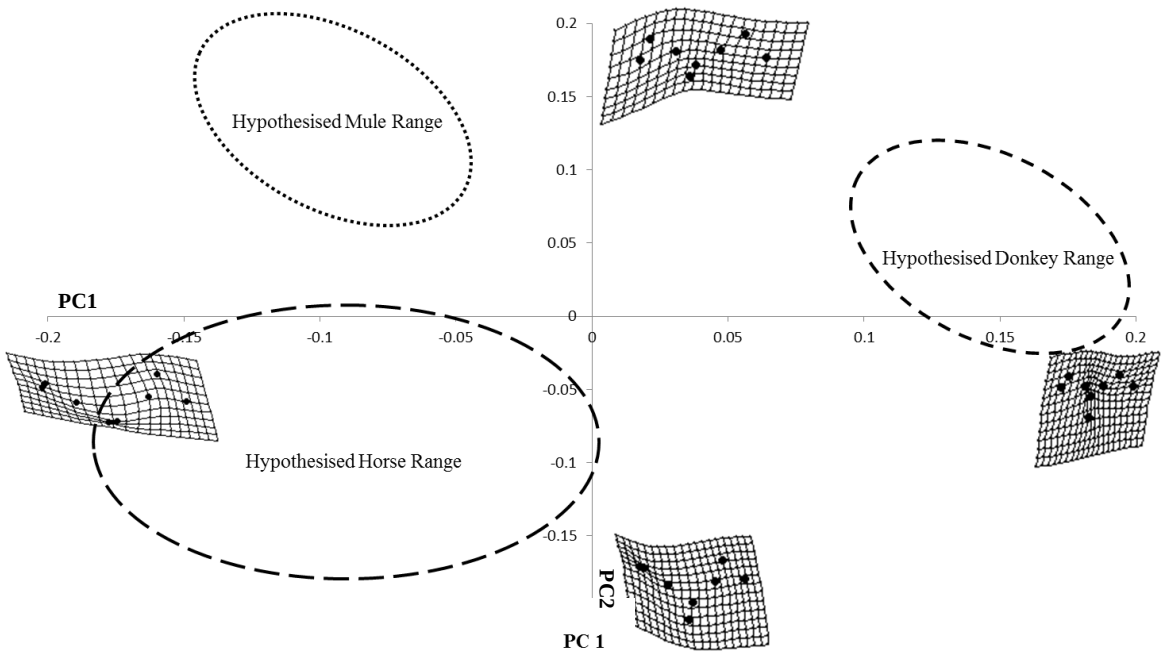


Figure 5.10 – Hypothesised region for each species.

It is rather surprising that the majority of the specimens fall near the hypothesised region for horses, but none falls into the expected region for donkeys (Figure 5.11). This may be

due to the first landmark point (LM1) being defined as the most anterior point in the metastylid and, in practice, the determination of this point can be very close to the second landmark point (LM2) despite the shape of the metastylid. As a result, many suspected donkey specimens fall into the bottom right quartile of the plot, indicating that they have large bucco-lingual distance, but LM1 and LM2 still sit close together. This includes all three specimens determined as donkeys in the Angle Analysis (T024 to T026).

On the other hand, although several specimens fall nicely into the hypothesised mule distribution, most of them are not the same specimens as in the previous analysis. Three of the four suspected mule molars from Serbia (T052, T054, and T055) are located closer towards the origin. In addition, a suspected mule molar from Winchester (T010) falls into the hypothesised mule distribution in both analyses, suggesting that it is likely to have the morphological characteristics that fit the description of a mule. Other possible mule suggested by this analysis are T018 (Winchester), T036 and T039 (Ribchester), and T049 (Alcester). It should be pointed out that T036 and T039 are from the same individual, from which two other molars are included (T037 and T038), but both fall near the expected horse region.

Even though the landmark-based analysis is able to point out the likelihood of several possible mules, it is not able to further confirm the determination of donkeys. A possible cause for having no donkey identifications, in contrast to the previous method, may be related to the three suspected donkeys showing an atypical metaconid shape. Instead of having a rounded metaconid, as occurs in most domestic equids, a “zigzag” slope occurs in all three suspected donkey molars. This non-metric variation may affect how the general shape is interpreted in all geometric morphometric analyses.

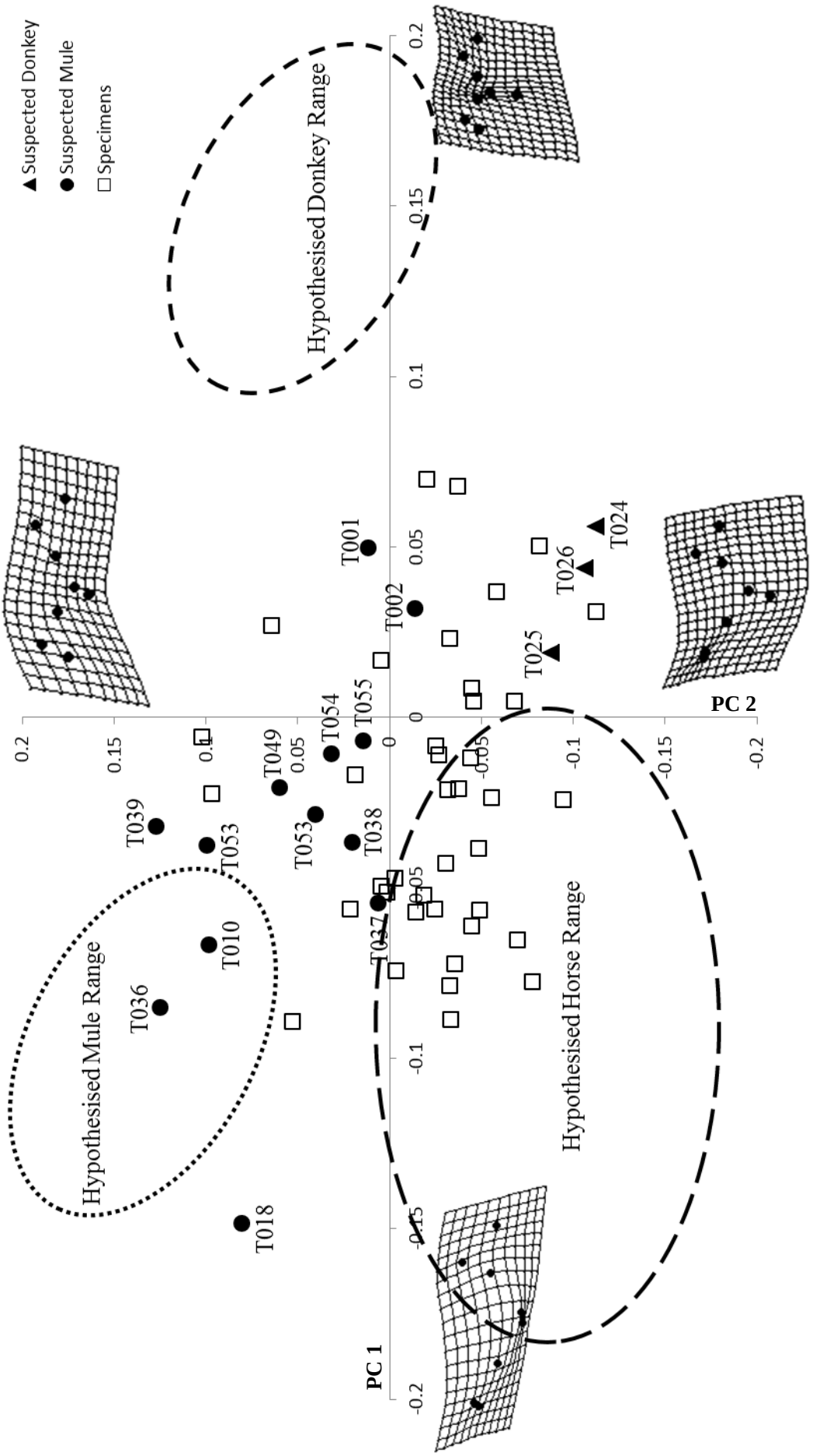


Figure 5.11 – PCA scatter plot of archaeological specimens using landmark-based GMM.

5.4.3 – Outline-based GMM

Similarly to the landmark-based GMM, the clustering and thin-plate spline needs to be recalculated when new sets of coordinates were included for the Procrustes fitting. As a result, a new PCA scatter plot was produced to include the new data. Based on the shape of the thin-plate spline on each end of the axes, PC1 (x-axis) determines the symmetry of the metastylid and the metaconid and seems to be associated with the shape of the lingual valley. Conversely, PC2 (y-axis) is dominated by the bucco-lingual distance. Based on these observations, it can be assumed that mules will fall into the upper right corner and donkeys into the bottom right whereas, in contrast, horses will occupy the central area (Figure 5.12). However, the known horse samples fail to meet this expectation. Not only do the three known horses samples cluster with those of donkeys after the new Procrustes fitting, but also the majority of samples are spread evenly on both sides of the x-axis – when it was expected that they would mainly fall on the left of the plot (Figure 5.13).

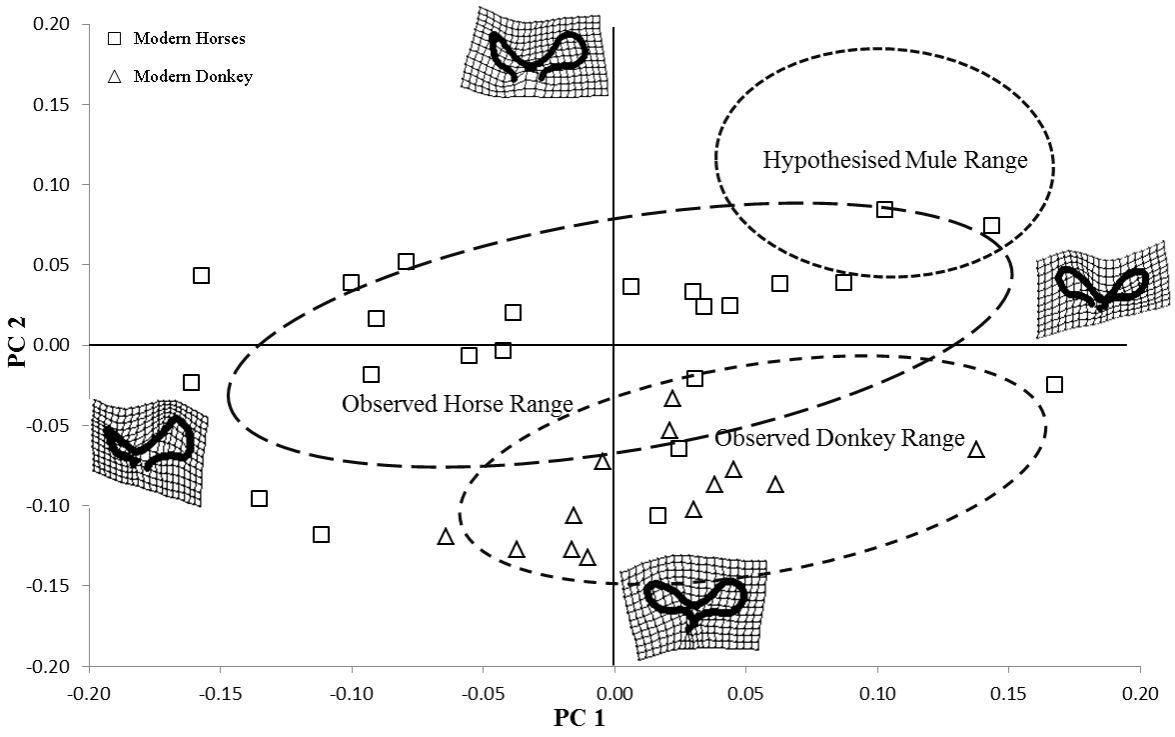


Figure 5.12 – Hypothesised Region of each species.

As a result, while those specimens suspected as donkeys (T024 to T026) are still located in the overlap area (donkey/horse), none of the suspected mules fall in the hypothesised mule region (Figure 5.13). Instead, about half of the suspected mules are located closer to (T001, T002, T010, and T052) or within (T049) the observed donkey distribution, while the other half fall within the observed horse range (T018, T036 to T39, T053, T054, and T055).

The outcomes of outline-based analysis are unsatisfactory and may be inadequate for species determination since the PCA fails to demonstrate any clear grouping of known morphological differences. A possible cause could be the high variety in dental morphology observed in the horses, which overlaps with most of the archaeological specimens, and leads to substantial uncertainty in taxonomic determinations. Further refinement of both landmarks and semi-landmarks may be able to resolve this predicament. The other possible cause for this clustering is the misinterpretation of the thin-plate spline along each axis. That is, the software is only able to provide the reconstructed thin-plate spline images of the two ends of both axes; it is difficult to confirm how the thin-plate spline shape changes progressively between these points. A possible solution to this is to reconstruct a thin-plate spline for each specimen and then to compare them to the mean shape of the “modern control” dataset. However, since there is no mule control dataset, this solution cannot satisfy the needs of the current thesis.

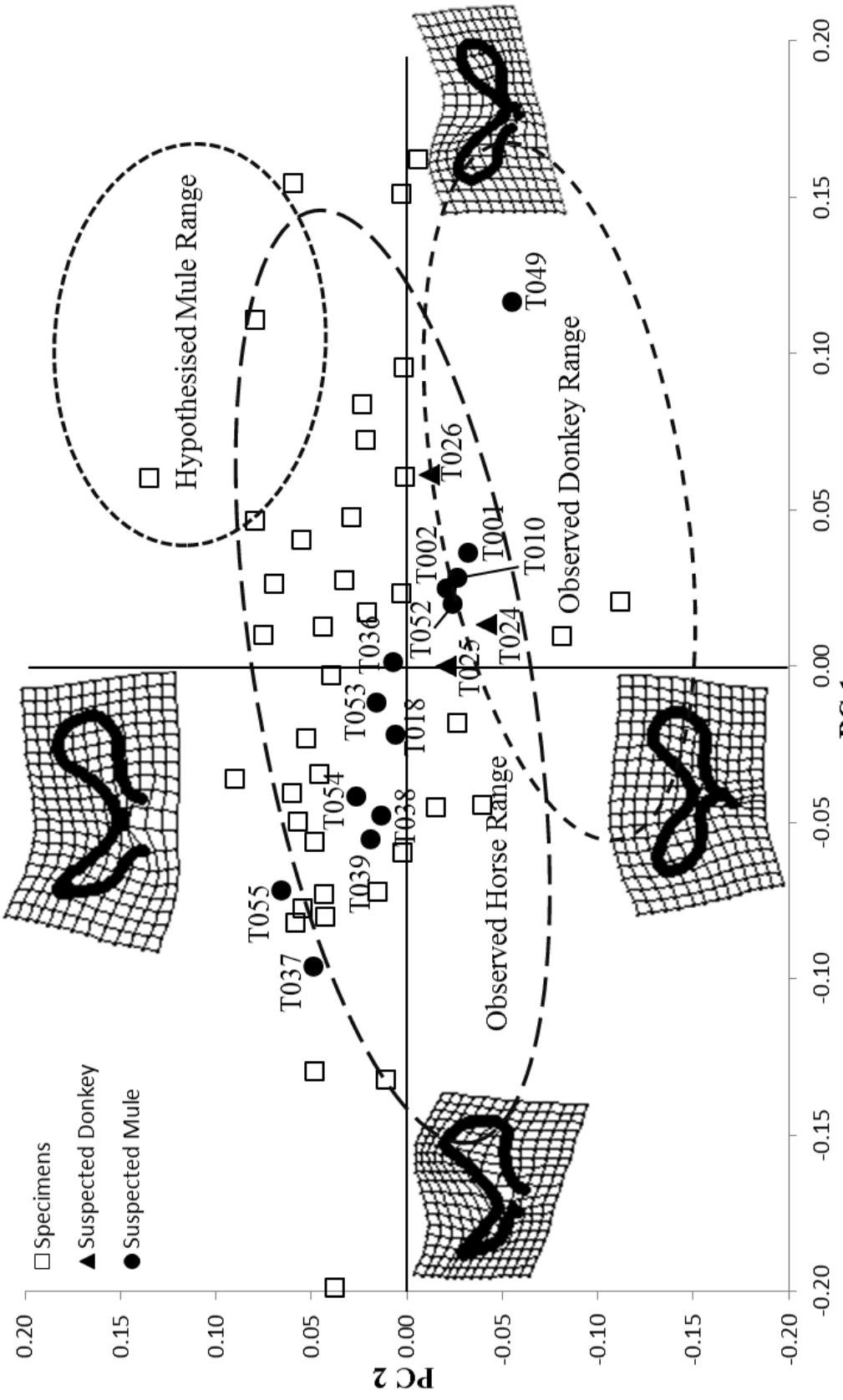


Figure 5.13 – PCA scatter plot of archaeological specimens using outline-based GMM.

5.4.4 – Results of shape analysis

The outcomes of the shape analysis of the 55 archaeological specimens demonstrate some level of clustering of suspected mules (Figure 5.14). As mentioned in the previous chapter, PC2 and PC5 are used as the x-axis and y-axis respectively to plot the data points; PC2 is an indicator of the bucco-lingual distance (with the larger distance on the left), and PC5 is associated with the lingual valley shape and the symmetry of the metaconid and the metastylid (symmetrical on the lower part and asymmetrical on the top). As a result, mules should be located in the lower right corner with symmetric metaconids and metastylids, in addition to extremely short bucco-lingual distances. However, while the majority of suspected mules (black dots in Figure 5.14) are located in the lower right quartile; they are much closer to the centre point than expected. In addition, a sharp contrast between two suspected mules, T010 and T018, requires further examination. T010 sits perfectly in the location expected for mules (lower right corner), but T018 is located in the upper right and clusters with the other specimens that are assumed to be typical horses. Examination of the original dental pattern indicates that this sharp contrast is very likely to be caused by the symmetry between the metaconid and the metastylid. T018 is less “mule-like” than T010 from this perspective, although both have an extremely short bucco-lingual distance.

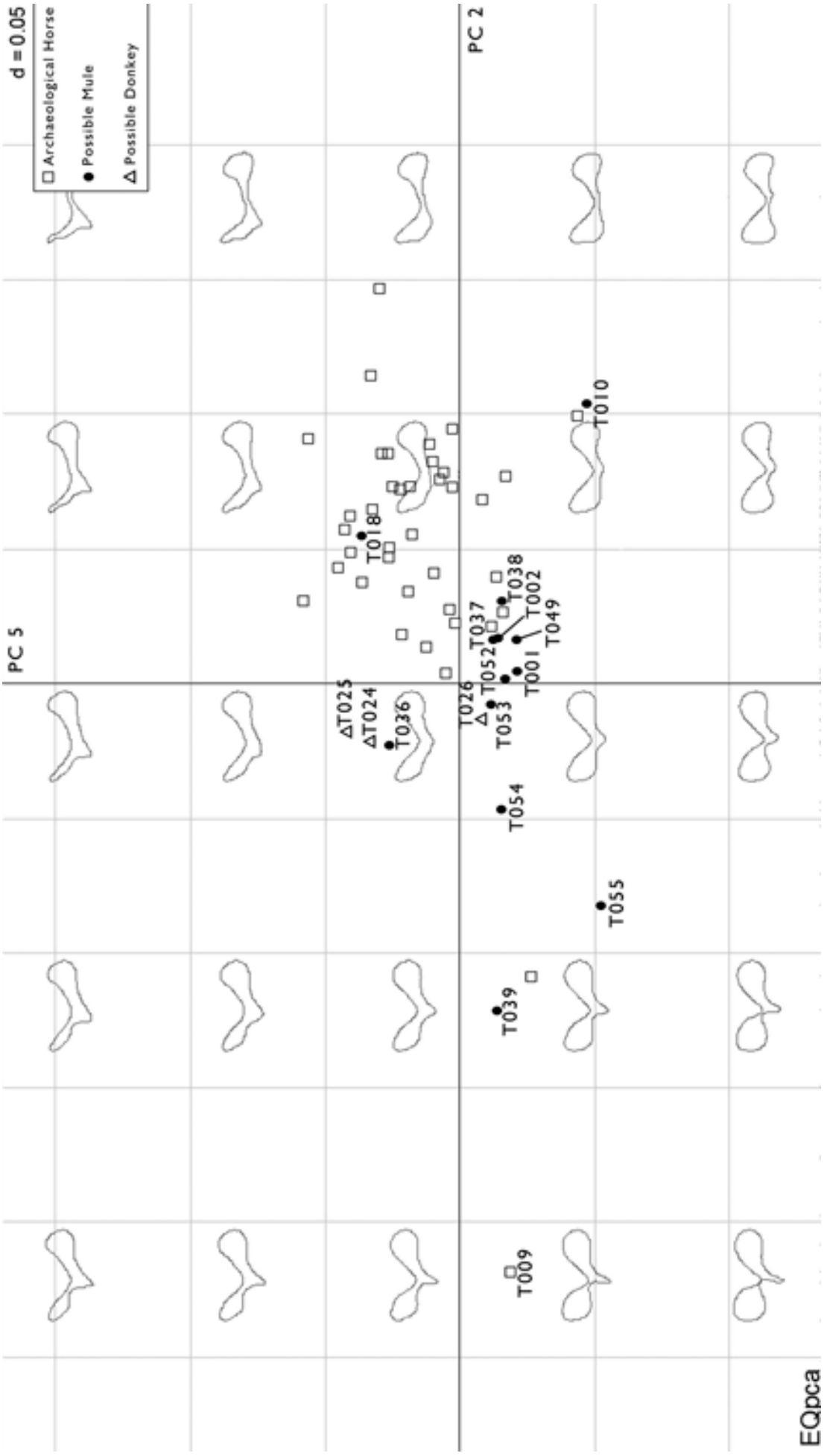


Figure 5.14 – PCA scatter plot using shape analysis with Momocs

The three suspected donkeys (T024 to T026) fall into the left side of the plot indicating that their bucco-lingual distances are indeed larger than the majority; however, the non-metric variance of the zigzag slope found in all three teeth evidently affects their location on the plot. Instead of being located on the lower left quartile, two of them sit in the upper left quartile, indicating a less symmetrical pattern between the metaconid and the metastylid. Only two specimens, which are not suspected of being either mules or donkeys, are also located on the right side of the plot. Both specimens (T009 and T021) are the second molar articulating the first molars (T008 and T020). As mentioned in section 5.5.1, both individuals are considered to be younger individuals based on the crown heights and, therefore, they may be at a different wear stage compared to the other teeth.

Finally, the significant differences between teeth from the same individual are rather alarming. Four molars from the same suspected mule from Ribchester (T036 to T039) are spread far apart in three different quartiles. While two are clustering with the majority of suspected mules near the origin point, the remaining two are somewhat closer to those of donkeys. In general, the shift of suspected mule data points towards the left can be explained by the fact that, other than the bucco-lingual distance, PC2 is also influenced by the lingual valley shape (V-shape on the right and U-shape on the left). However, the location discrepancy of the same individual can seriously impair the accuracy of this method since different outcomes (mule or donkey) may be interpreted for different teeth.

5.4.5 – Results comparison for all GMM analyses

All interpretations of the analytical results for suspected mules and donkeys are listed in Table 5.10. Although it seems that the outcomes of all four analyses are highly inconsistent, they still provide some support for the determinations based on qualitative criteria. The

intention of developing these geometric morphometric methods is not to argue against the claim or application of qualitative observations, but to provide objective and quantified support for it. After all, as subjective as it might be, the use of qualitative morphological traits is still the most direct and economical method for species determinations. However, the quantitative analyses of these traits seem to indicate that these qualitative traits may not be as reliable as previously claimed.

Species frequencies can be estimated using the current methods, although the sample size and the number of available sites are significantly smaller than for the biometric methods. Among the 32 individuals from Romano-British sites (excluding two individuals (T052 – T055) from Serbia), 5 mules, 2 donkeys, and 25 horses were determined. This leads to a mule-donkey-horse ratio of 5:2:25, indicating that there is 1 mule for every 6.4 domestic equids, a result that is quite close to the previous results based on biometric analyses. It should be reiterated that numerous teeth with atypical caballine dental pattern are excluded because some were thought more likely to be premolars, according to Payne's (1991) method, and others suffer from either irregular wear or pathological conditions, which affects the occlusal surface and, therefore, prevents any clear GMM analysis. The small sample size makes ratio estimation by site types, or even as a whole, insufficient for a further meaningful discussion and thus it is mentioned only for reference here.

No	Site	Qualitative Determination	Angle Analysis	Landmark-based	Outline-based	Momocs
T001	Healam Bridge	Mule	D	D	D	M
T002	Healam Bridge	Mule	D	D	H	M
T010	Winchester	Mule	M	M	D	M
T018	Winchester	Mule	M?	M	H	H
T024	Fairford	Donkey	D	H	D	D
T025	Fairford	Donkey	D	H	D	D
T026	Fairford	Donkey	D	H	D	D
T036	Ribchester	Mule	M?	M	H	D
T037	Ribchester	Mule	M?	H	H	M
T038	Ribchester	Mule	H	H	H	M
T039	Ribchester	Mule	M?	H	H	D
T049	Alcester	Mule	H	H	D	M
T052	Serbia	Mule	M	H	D	M
T053	Serbia	Mule	M	H	H	D
T054	Serbia	Mule	M	H	H	D
T055	Serbia	Mule	M	H	H	D

Table 5.10 – Species determination for teeth with atypical caballine dental patterns.
Same individuals are highlighted in grey (T001-002, T024-T025, T036-T039, T052-T053, and T054-T055).

In the process of developing methods, issues such as intra-species variation (e.g. a Shetland pony (604, University of Southampton) with deep V-shaped lingual valley and an unexpectedly short bucco-lingual distance compared to other horses) and non-metric variations in the dental patterns unrelated to species determination (e.g. zigzag sloping of the metaconid in donkey molars (132, University of Southampton)) all appear to have affected the species determination of archaeological specimens. As a result, it is still necessary to evaluate some of these issues below.

The first and most notable issue is the inconsistency between methods. Other than visually determined typical horses, none of the 16 teeth gives consistent results from all four

methods. An interesting case here is the partial skeleton from Healam Bridge (HB-7613), represented here by teeth T001 and T002. This individual was suspected to be a mule because of certain traits in both cranial (i.e. dental) and post-cranial (tibia and metacarpal) were regarded as atypically for horse (D. Jaques, pers. comm). The biometric analyses of its post-cranial elements suggest this individual is more likely to be a mule, but three of four GMM results suggest the dental morphology is closer to that of a donkey than of a mule. Unfortunately, the cause of such inconsistency may reside in the absence of modern mule control dataset, which ultimately can lead to the underestimation of the overlap between species. In addition to the inconsistency between methods, discrepancies also exist between different molars of the same individuals. Among the five individuals with more than one analysed molar, only the suspected donkeys from Fairford (T024-25) and one possible mule from Serbia (T054-55) have consistent results for both their M_1 and M_2. The four molars from the individual from Ribchester have extremely inconsistent results. Not only does M_1 have different outcomes from M_2, but also the results for the right molars are different from the left ones. The implication of this observation is that it is not only the inter-specific variation that may induce misidentification, but also intra-tooth variation may produce false results. Even though it would still be feasible to make further refinements to the methods by assessing which molar is the more accurate for species identification, this will not be a practical development in real terms, as the separation of molars from premolars in isolated teeth is challenging enough.

As a hybrid, it is also possible that a mixture of the different traits in the parent species occur in the offspring, such as the case of the offspring of wild and domestic pigs which one tooth resemble the father while another is more similar to the mother (Evin *et al.*, 2015). It is hypothsised here that if similar situation is to be observed in mule, then the inconsistency of traits in different molars of hybrid will be represented as a large distance

between two teeth in the scatter plot (assuming one is more donkey-like and the other more horse-like). In other words, it is expected to see the first and second molar of horses or donkeys to cluster closer than those of mules. In order to test this assumption, the squared Euclidean distances (d^2) between M_1 and M_2 are calculated for 17 individuals with both teeth available (one individual has M1 and M2 from both sides available). While the shortest distance of all four methods all belongs to either horse or donkey, only one possible mule (T037-T039) has the largest distance of all four methods. The current result indicates that while it is still possible that hybrid has a mixture of traits from both sides of parent, this is not observed in M_1 and M_2.

No	Site	Context	Q.D.	Angle Analysis	Landmark-Based	Outline-based	Momocs
T003-T004	Healam Bridge	HB00D	H	20.2613	0.0127	0.0054	0.0052
T006-T007	Healam Bridge	HB00B	H	66.1308	0.0046	0.0107	0.0129
T008-T009	Winchester	VR3136	H	110.4930	0.0044	0.0088	0.0587
T014-T015	Winchester	NR113	H	58.7984	0.0009	0.0085	0.0043
T020-T021	Winchester	VR1280	H	171.0086	0.0041	0.0074	0.0174
T022-T023	Winchester	VR440	H	3.4523	0.0020	0.0018	0.0017
T024-T025	Fairford	FTF2084	D	88.1776	0.0019	0.0006	0.0001
T027-T028	Fairford	FTF2052	H	23.6129	0.0051	0.0166	0.0016
T033-T034	Fairford	FTF369	H	1.3888	0.0012	0.0001	0.0005
T036-T038	Ribchester	RB1728(L)	M	32.1505	0.0133	0.0025	0.0062
T037-T039	Ribchester	RB1728(R)	M	10.2929	0.0151	0.0026	0.0192
T040-T041	Ribchester	RB1766	H	206.2968	0.0002	0.0056	0.0036
T042-T043	Ribchester	RB9926	H	0.9567	0.0053	0.0010	0.0006
T045-T046	Ribchester	RB743	H	3.4523	0.0020	0.0080	0.0073
T047-T048	Alcester	ALC1147	H	0.8684	0.0068	0.0188	0.0007
T050-T051	Alcester	ALC838	H	84.5120	0.0029	0.0136	0.0125
T052-T053	Serbia	SERhi4	M	193.8277	0.0036	0.0026	0.0006
T054-T055	Serbia	SERsvs	M	3.8285	0.0003	0.0024	0.0018

Table 5.11 – Squared Euclidean distance (d^2) between M_1 and M_2. Q.D.– Qualitative Determination

The second issue is image acquisitions. The GMM used in the current thesis is mainly restricted to 2D images. However, as mentioned previously, the occlusal surface of molars is never a simple flat surface. Under visual inspection, a tooth can be rotated to the best orientation suitable for the observer; this angle may vary between teeth. However, in order to objectivise a GMM method, a fixed angle is required for taking photographs of different teeth. As a result, slight damage or uneven surfaces, which can be avoided or ignored in a visual observation, may influence 2D images and significantly affect the outcomes. Although the use of 3D imagery may resolve this issue, it is neither economical nor practical to employ such technology at the present stage. Moreover, the actual problem is that the comparison of these morphological traits in most archaeological literature is by text-description and (probably exaggerated) drawings of typical molars, but never the actual photo of molars from the mandibles of known species, particularly mules. Photographs of complete mandibular teeth of domestic equids are available from Eisenmann's website, including not only the three species studied here, but also the teeth of hinnies (Figure 5.15). Examination of the two photographs of mules makes it clear that that the molars are quite different. While both molars in the second photograph resemble the description of typical mules in the literature, the molars in the first photo would be more "donkey-like" according to the description (i.e. no buccal valley penetration observed). If the level of overlap between different species cannot be understood, then it is probably still too early to use GMM to distinguish different dental patterns of domestic equids.

In summary, it is unfortunate that current outcomes are not robust enough to be used as strong support for confident identifications. At most, they are only suggesting that these specimens were suspected as possible donkey/mule teeth for a good reason. Therefore, these teeth will be viewed as possible donkey and mule teeth when interpreting their isotopic values in the Chapter 7.

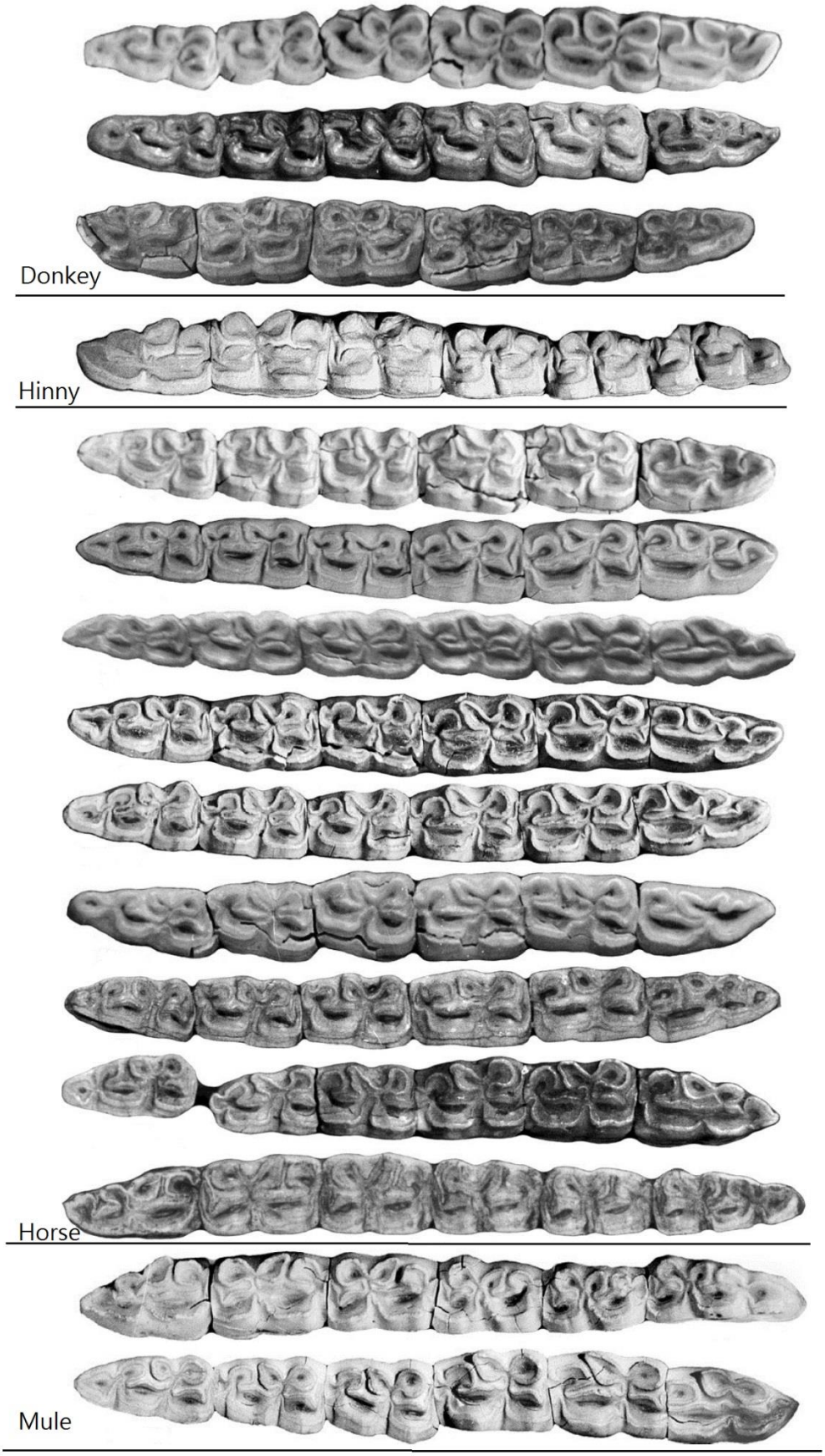


Figure 5.15 – Dental Pattern of different domestic equids from Eisenmann's database. Images are taken directly from Eisenmann's website and are merged to fit into one page for comparison.

5.5 – Chapter Summary

This chapter presents the results from different species determination methods with the aim of not only providing estimated domestic equid frequencies, but also to determine possible non-caballine domestic equids for isotopic analysis in Chapter 7. The consistency and accuracy of each method have also been evaluated. It should not be surprising to find conflicting results from applying different methods to evaluate the same elements, as well as using the same methods on different elements of the same individual as has already occurred in the modern control dataset. After all, other than the uncertainty in variations related to a wide variety of breeds, these domestic equids not only resemble each other in appearance, but also, as labour animals, have a similar life style. Thus, how one should evaluate the conflicting results and give a species determination poses a significant challenge. Different considerations are required for each method depending on its nature: the accuracy rates for different elements and species are considered when determining the outcomes from DFA, M-dist are calculated to provide further support in the the Davis method, and cross comparison is made for all four GMM, as will be discussed now in more detail.

Taxonomic determinations in this chapter were made with different considerations given for each method. For DFA, the accuracy for different skeletal elements was evaluated for cases where multiple elements were available for a single individual. A ranking for the accuracy in species determination for the different elements was given: MC>PH1>MT≥Tibia >Radius[>Femur]. The humerus was not included in the analysis due to the lack of specimens in the archaeological assemblage. Only a few discrepancies were observed among the individuals with multiple elements used in DFA, and all can be

determined by using the ratio of determined species, which can further be evaluated by the accuracy ranking of these elements.

The M-dist is used as a method of species determination in both the Davis method and the Angle Analysis in GMM. The calculation of this distance allows the distance of each data point to different group centroids to be quantified. The conflicting results for the first phalanges between DFA and Davis method are assessed based on both the probability of membership in the former and the M-dist in the latter. Since all four conflicting specimens are considered as probable identifications using DFA, the M-dist between the group centroids in the Davis method needs to be taken into consideration. Two horses (Z136 and Z158) are determined as "possible" (H?) and so are excluded from further discussion. On the other hand, the remaining two are determined as a donkey (Z149) and a mule (Z165) respectively based on the significant difference in their M-dist.

It is unfortunate that the level of inconsistency in all four GMM approaches is considerable; this is due, at least in part, to the lack of modern mule samples to use as 'controls' to set up a standard, and thus this has limited the possibility to develop a systematic approach to evaluate the accuracy. Although the results cannot be used directly to confirm species affiliation of specimens with qualitative morphological traits regarded as 'non-caballine', they do provide support to the contention that these specimens are different from those deemed typical horses. As a result, they will be viewed as possible donkeys or mules in Chapter 7, when their "localness" is investigated through isotopic analyses.

Chapter 6 - Recent Advances on Identification – aDNA

6.1 – Chapter Introduction

While putative mules and donkeys have been identified in the past using both qualitative and quantitative techniques, as shown in the previous chapters, species determinations are not always consistent in every case using different techniques. A number of causes may be behind these inconsistencies; e.g. insufficient number of control samples (i.e. mules) or inadequate modern controls (e.g. the use of specialised breeds); errors in original measurements in published site reports (e.g. Danebury MC-MT), or possible life-long intensive labour reflected in bone modification (e.g. the Southwark donkey, Bendrey, 1999). Such inconsistency continues to cast doubt on the reliability of existing methods, either qualitative or quantitative. That said, it is not the intention of the current thesis to disregard previous identifications made from existing methods, or to argue that none of these methods can accurately distinguish horses, donkeys, and mules and thus they should all be generalised as domestic equid identification in faunal reports given as *Equus sp.*. In contrast, the present thesis aims to draw attention to the importance in distinguishing different domestic equid species, since their social-economic importance is reflected by their procurement strategies. However, in order to properly examine the acquisition of domestic equids in the past, one must be able to accurately distinguish between different domestic species. As demonstrated and argued in previous chapters, the use of a number of methods in the present thesis, and comparisons in their consistency may lend credence to some taxonomic determinations with high levels of plausibility. However, the only approach to confidently distinguish between domestic equids is through the use of ancient DNA (aDNA hereafter) analysis. This short chapter will review previous works in aDNA analysis on equid species identification, and discuss the role aDNA analysis plays in the current study through a pilot project which is still in progress.

6.2 – The use of aDNA for equid species identification

Compared with other approaches for species determination, aDNA is the most absolute method to unambiguously identify archaeological specimens with unknown species affiliation. Despite its relatively high financial costs, aDNA analysis has become more affordable in recent years. Additionally, the power of the technique has increased dramatically, while the processing/sequencing time of specimens has decreased. Still, this method is not routinely applied in zooarchaeological research. While it would certainly be wasteful to have every bone fragment identified by molecular techniques (e.g. aDNA, ZooMS (see below)), the unambiguous taxonomic determination of some "special" specimens could provide important insights, to confirm the presence of species that cannot be securely identified using conventional methods, and to cross-validate uncertain morphological traits. ZooMS (Buckley *et al.*, 2009) is a recently developed biomolecular method, which uses collagen for species identification. Similar to aDNA analysis, this novel molecular technique allows species to be identified regardless of the presence of visible morphological traits and only requires about 1 mg of powdered sample (Buckley *et al.*, 2009).

aDNA analysis is not an unfamiliar method in zooarchaeological research related to horses. Several horse-related projects have used aDNA analysis as their primary method with great success (Jansen *et al.*, 2002; Di Bernardo *et al.*; 2004; Cieslak *et al.*, 2010; Gurney, 2010; Lira *et al.*, 2010; Svensson *et al.*, 2012; Warmuth *et al.*, 2012; Hovens and Rijkers, 2013; Orlando *et al.*, 2013; etc.). However, most studies either focus on horse domestication (e.g Jansen *et al.*; 2002; Warmuth *et al.*, 2012) or the genetic divergence between modern breeds (e.g. Lira *et al.*, 2010; Hovens and Rijkers, 2013). Only a handful of researchers are

addressing the subject of species identification. In this section, some cases of aDNA analysis related to domestic equids will be reviewed.

6.2.1 – The Pompeii "hybrid" equid

The most interesting case using DNA as tool for taxonomic identification is, perhaps, a relatively recent publication on the identification of Pompeii equids (Gurney, 2010). In 2004, Di Bernardo *et al.* published their work on five complete equine skeletons excavated from Pompeii in 1987. The original purpose of their paper was to examine the relationship of these Roman equids to modern ones through the analysis of mitochondrial DNA. However, one of the five skeletons examined showed a DNA sequence not only different from the other four, but also different from known modern horse breeds. Based on this discovery, Bernardo *et al.* stated that that skeleton belonged to an extinct horse breed that was unrelated to any modern breed. However, Gurney (2010) noticed that the published sequence for that particular individual was uncommon, and that this may have been due to a technical mistake. Gurney discovered the individual with uncommon equine DNA sequence showed a combination of both horse and asinine DNA sequence. In other words, the sequence indicated that the individual was a "hybrid" of two species; this "hybrid", however, was an artificial combination of two incomplete DNA sequence (technical error, e.g. during processing of samples or during DNA amplifications), and did not represent the DNA sequence of the actual hybrids such as mules or hinnies. Gurney (2010), then, re-analysed this individual to reveal it was in fact a donkey rather than an extinct horse breed. It must be noted that, apparent morphological differences between this individual and the four other equid skeletons found in the same stables were not noticed in these near complete skeletons.

6.2.2 – Validating lingual valley shape through aDNA analysis

A previous attempt had been made to confirm the lower dental morphological differences between *E. caballus* and *E. asinus* using aDNA analysis in an unpublished M.A. dissertation (Hite, 2008). This MA dissertation is the only known study on such subject. In her dissertation, Hite (2008) examined the lower dental morphology of *E. caballus* and *E. asinus* and used mitochondrial DNA (mtDNA hereafter) to cross-validate the known criteria. Although the sample size is small (n=3), Hite concludes that V-shaped and U-shaped pattern as well as the length of buccal fold are characteristic enough to separate donkeys from horses. Unfortunately, several important factors were overlooked in this attempt, such as differences between molars and premolars or how age and surface wear may affect the determination. The differences between premolars and molars were not established when discussing the dental morphology in Hite's work (2008). From the pictures used in her dissertation (Figure 2.2 in the current thesis), it is quite clear that the tooth demonstrating U-shape in horse was a premolar based on the buccal valley and the use of Payne's method (1991). In addition, no age information is given for all the samples determined to species level. As already pointed out in Chapter 2 and by previous researchers (Levine, 2004, Johnstone, 2004), teeth wear can alter the shape of enamel folds. For extremely young or old equids, or even equids with uneven occlusal surfaces, the differences between "V-shaped" and "U-shaped" can be difficult to discern. The same factor will also affect the length of buccal fold, especially when no specification is made on whether specimens are molars or premolars.

As a result, although Hite (2008) argued that the aDNA analysis confirms the morphological traits observed in the lower teeth, the results did not clarify the differences

between molars and premolars. Moreover, her aDNA analysis was based on mtDNA and, therefore, the possibility of detecting hybrid species was unfeasible.

6.3 – aDNA analysis for hybrid species: the basic principle

The application of DNA analysis is so embedded into today's society that people are very familiar with what it is used for and is capable of doing, but are less clear on the specific requirements and on the implications of the results. The use of aDNA analysis in archaeology has a very wide application, from identifying diseases that had similar bone lesions (e.g. tuberculosis caused by different bacteria, Mays *et al.*, 2001) to the determinations of the coat colour of past horse (and other species) individuals (Svensson *et al.*, 2012). Not only can it be used for taxonomic and sex identifications, it can also be used to understand evolutionary processes of a species (Orlando *et al.*, 2013). For the present study, the primary aim is to determine the taxonomic status of specimens through aDNA analysis to validate existing morphological criteria used in the taxonomic identification of domestic equids, ultimately allowing mules and donkeys to be distinguished from horses.

It should not come as a surprise that differences in DNA sequences exist between different equid species, making it is possible to identify them genetically. In most cases identifications can be carried out by comparing the abundant mtDNA; unfortunately this is not the case for the identification of hybrids (e.g. mules). There are two types of DNA: mtDNA and nuclear DNA (nuDNA hereafter). The mtDNA of an individual is a direct replicate of the mother's mtDNA without it being rearranged to form a new DNA sequence (though mutations still occur from time to time). The nuDNA, on the other hand, will be rearranged to form a new DNA sequence. It contains a half set of each parent's

chromosomes, and creates a new sequence for the progeny. For the purpose of species identification, mtDNA will be sufficient since it will differ from species to species (i.e. sheep *vs*. goats). In addition, the fact that mtDNA in a cell is more abundant than nuDNA (which has only one nucleus per cell) and thus has a greater likelihood of being extracted and amplified, has made the former a better candidate for ancient DNA analysis. However, in the genetic analysis of hybrids, the use of mtDNA is inadequate. If using this type of DNA, horses and mules would be indistinguishable from each other, as would donkeys and hinnies. Using the Pompeii equids mentioned above as an example: analyses of their mtDNA can only reveal that four individuals had horses as mothers, whereas one has had a donkey as a mother; it cannot be determined though mtDNA whether the four individuals were mules or horses, or whether the individual whose taxonomic assignation was revised to "donkey" was in fact a donkey or a hinny.

Such complexity has set a high technological threshold for the preservation conditions of selected samples. The moment a creature dies, the DNA in the cell starts to decay and, in general, the more time elapsed since death the more fragmentary the DNA (though rates of decay vary according to macro- and micro-environmental conditions). In addition, there seems to be a very complicated correlation between the abundance of surviving mtDNA and the availability of nuDNA (Campana *et al.*, 2012). As a result, there is no guarantee that if a lot of mtDNA survived, then, nuDNA will be more likely to survive as well, and *vice versa*. Given this, and the relatively smaller amounts of nuDNA in the cell compared to mtDNA, the successful extraction rate of the former from archaeological samples is expected to be low. Adding to the relatively low success rate of nuDNA extraction, the availability of suitable samples, the required infrastructure (facilities), as well as costs of the analyses are all issues that pose challenges to validating known methods for distinguish domestic equids using genetic techniques.

6.4 – Identifying archaeological mules: a pilot project in progress

At the initial stage of the current thesis planning, using aDNA analysis to resolve the ambiguity of both qualitative and quantitative identification methods was one of the main aims. To achieve this aim, numerous specimens were collected and aDNA was extracted from a number of specimens for Sanger sequencing (also known as conventional sequencing or chain termination approach, Gupta and Gupta, 2014, see next section) by the present author in cooperation with the Centre for Geogenetics at the Natural History Museum (University of Copenhagen), Denmark. Unfortunately, due to several factors, the project had to be postponed and it did not resume until recently. Although the current thesis is unable to provide the full details of this on-going project, the initial results are still worth discussing here as they may provide a general direction for future work. In this section, the method will be briefly explained, followed by a general description of the material, and a discussion of the implication of the available results.

6.4.1 – Method: from Sanger Sequencing to NGS (Next-Generation Sequencing)

Following the initial attempt based on Sanger sequencing in 2013, a next-generation sequencing (NGS) approach is becoming more commonly applied in genetic research and was considered to be more cost-efficient for the current thesis than the previous approach. The main difference between Sanger sequencing and NGS method is the order of defining the target (Gupta and Gupta, 2014). For the Sanger sequencing, a short strand of nucleic acid sequence (known as a “primer”) of the targeted species will need to be added to the prepared samples to extract the DNA of the targeted species before being amplified them using polymerase chain reaction (PCR) (Gupta and Gupta, 2014; Brown and Brown, 2011). PCR is a process designed to trigger DNA synthesis by amplified fragmented DNA strands that has been extracted by specific primer used in the extraction. The synthesised DNA

then can be used in sequencing, in current case, for taxon identification. NGS, on the other hand, uses a different approach. To simply put it, instead of adding a primer to the extractions and then amplifying a target species, NGS method will amplify every DNA fragment still surviving in the archaeological specimens and detect whether any of these DNA fragments belongs to the target species (Gupta and Gupta, 2014). The advantage of the latter method is that it is much faster than Sanger sequencing, but this does not increase the success rate for extracting nuDNA from archaeological specimens.

6.4.2 – Material for aDNA analysis

A total of forty specimens were selected for aDNA analysis. The selection of specimens is based on the availability of material and the presence of identified mules. As a result, the specimens from Healam Bridge and Dangstetten were chosen over other sites for two reasons: the abundance of doesmtic equids specimens including the presence of (near) complete mule skeletons and the availability of material for desctructive analysis. The first twenty specimens were exclusively from Healam Bridge and were processed in Copenhagen by the present author at the beginning of 2013. However, while a few specimens were thought to contain aDNA, no endogenous sequences were obtained in subsequent sequencing and thus these forty specimens are not included in the present thesis. Towards the end of 2013, an additional twenty specimens were sent to Centre for Geogenetics, to have their DNA extracted and, if present, sequenced using NGS. Five of these specimens came from Healam Bridge and the remaining fifteen were from Dangstetten, Germany (Table 6.1). The reason for choosing these two sites are based on that both sites have near complete skeletons identified as mule and also the availability of material for aDNA analysis.

The Roman site of Dangstetten is located near modern day Küssaberg, Germany (at the border between Germany and Switzerland). It was a military camp with a short occupation span (Uerpmann and Uerpmann, 1994; Uerpmann, in prep.) This camp was established in 15-12 BC, and abandoned after the death of Drusus in 9 BC. The site was excavated during 1968 to 1982, but the faunal report is still yet to be completed. A relatively large number of complete or almost complete equid skeletons were found at the site. Uerpmann's taxonomic identifications of these skeletons were based on qualitative morphological dental traits (Uerpmann and Uerpmann, 1994). The completeness of these equine skeletons has allowed sampling from elements other than teeth. This preserves the teeth for further morphological observation and isotopic analysis while using aDNA analysis from other elements to validate the results. However, while permission for carrying out aDNA analysis was kindly granted by Prof. Uerpmann, isotopic analysis of the same site is already under way in a separate project. Since the current thesis aims to focus on only the procurement strategies of domestic equids in Roman Britain, the material from Dangstetten was used with the sole aim of validating qualitative morphological criteria through aDNA analysis.

Specimens of post-cranial elements from fifteen equid skeletons from Dangstetten were sampled for the present study. These skeletons have been identified as horses or mules by Prof. Uerpmann (pers. com.) based on qualitative dental morphological criteria. Table 6.1 shows the material from Dangstetten and Healam Bridge sampled for aDNA analysis.

No.	Sample	Site	Element	Qualitative Identification
1	DA-1144	Dangstetten	Mandible	Mule
2	DA-479	Dangstetten	Maxilla	Mule
3	DA-358	Dangstetten	Mandible	Mule
4	DA-504	Dangstetten	Maxilla and mandible	Mule
5	DA-479	Dangstetten	Maxilla	Mule
6	DA-820	Dangstetten	Radius, L	Mule
7	DA-999	Dangstetten	Maxilla	Mule
8	DA-1080	Dangstetten	Mandible	Mule
9	DA-1165	Dangstetten	Humerus, R	Horse
10	DA-1104	Dangstetten	Femur, L	Horse
11	DA-1151	Dangstetten	Scapula, L	Horse
12	DA-1165	Dangstetten	Maxilla	Horse
13	DA-217	Dangstetten	Metapodial 2 or 4	Mule
14	DA-959	Dangstetten	Metapodial 2 or 4	Mule
15	DA-1157	Dangstetten	Scapula	Mule
16	HB-5069	Healam Bridge	Lower dp3, L	Mule?
17	HB-5031	Healam Bridge	Lower P3, L	Mule?
18	HB-5561	Healam Bridge	Lower P3, L	Horse
19	HB-6821	Healam Bridge	Lower M1, R	Horse
20	HB-2814	Healam Bridge	Lower M1, R	Horse

Table 6.1 – Material selected for aDNA analysis using NGS.
Identifications of Dangstetten skeletons carried out by Uerpmann (pers. com.) based on qualitative dental traits. Identifications of Healam Bridge specimens made by the present author based on qualitative dental traits.

6.4.3 – Initial results of aDNA analysis using NGS

Attempt has been made to differentiante modern horses, donkeys, and their hybrid offspring using genetic analysis (Zhao *et al.*, 2005). Their genetic differences between these species have been demonstrated in both mtDNA and nuDNA. The palaeogenetic analysis is still ongoing (Schubert *et al.*, in prep.), but preliminary results are available and are presented below. They are based on personal communication from Prof. L. Orlando, Centre for GeoGenetics (Natural History Museum, Copenhagen University).

The use of high-throughput screening (HTS) allows the decoding of DNA sqeuncing to process at much faster speed than Sanger sequencing (Mannocci *et al.*, 2008). It is a method commonly adopt in NGS. In current study, HTS libraries were successfully built

from 5 out of the 20 samples: DA-1080; DA-1165; DA-1104; DA-959, and DA-217 (all from Dangstetten). However, sequences could only be obtained from three of these: DA-217, DA-959 and DA-1104. As Table 6.1 shows, these three specimens were identified as mule, mule and horse respectively on qualitative morphological grounds (Uerpmann, pers. comm.).

Despite the sequencing efforts (from 5,314,650 to 104,928,339 and 107,799,314 sequences), only a limited portion of both genomes, mitochondrial and nuclear, were covered. Expected damage patterns were found: they showed an increase of C→T changes towards read starts, an increase of G→A towards read ends, and an excess of As and Gs at the genomic position preceding sequence starts (Orlando, pers. comm.). This indicates that the data are real.

A series of analyses to evaluate the odds of the samples being mules (or any hybrid, for that matter) were carried out. Here the idea was to compare the sequence information of the Dangstetten specimens to that of equid species for which sequences at the whole genome level are available. These analyses included: PCA, Admixture and F3-stats. These are analyses commonly used in genetic studies to determine the likelihood of group membership. F3-stats is one of the F-statistics used regularly in genetic analysis. F3 is considered as outgroup analysis which is used to determine the membership of unknown specimen (Peter, 2015). Further detaild of the outcome will be available when the project report is ready.

Results show that the only specimen identified genetically as a mule is R14DA_959, where the admixture shows about 20% of the genome clustering with non-caballines (i.e. *E. asinus*).

Although the sample size is small, these preliminary results contradict only one of the species identifications based on qualitative morphological traits. Thus, DA-1104 is indeed a horse; and DA-959 can also be confirmed as a mule. However, preliminary results strongly suggest that DA-217 (determined as a mule based on its morphological characterisitc) is in fact a horse. This indicates that determinations made from qualitative morphological traits may not always be reliable.

No	Specimen	Element	aDNA result	Qualitative result
10	DA-1104	Femur, L	Horse	Horse
13	**DA-217**	**Metapodial 2 or 4**	**Horse**	**Mule**
14	DA-959	Metapodial 2 or 4	Mule	Mule

Table 6.2 – Specimens identified by aDNA analysis.
Contradictory identification highlighted in grey.

The photograph of both the maxillary and mandibular tooth row for DA-959 is available from Uppermann and Uppermann (1994, p.355, Fig1 and Fig2). While the determination of DA-959 as a mule is based on both maxillary and mandibular dental morphology, the current thesis will focus only on the morphological criteria of the mandibular teeth since they are more commonly used by researchers. Judging from the description in Uerpmann and Uerpmann (1994, pp. 355-6), this individual had been determined as a mule based on the lingual valley in all mandibular teeth are “V”-shaped and the somewhat shorter bucco-lingual distance in all mandibular teeth (Figure 6.1). However, comparing the images of

some of other suspected mules in the current thesis, the qualitative criteria in the molars of DA-959 are not as "typical" as others (e.g. Ribchester, Figure 6.2). Unfortunately, mandibular teeth images for DA217 and D1104 are not available for comparison and, therefore, the aDNA results cannot be used to validate the dental morphology of these two individuals.

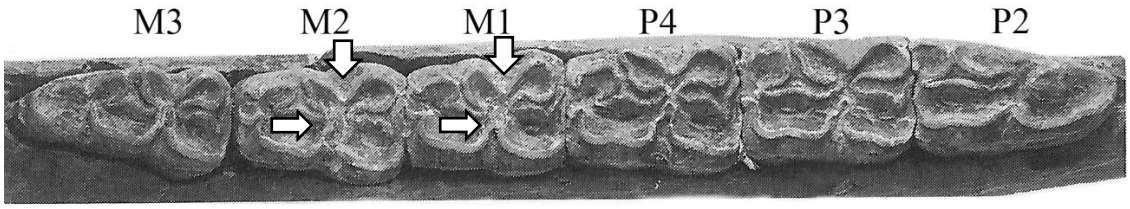


Figure 6.1 – Mandibular teeth of DA-959. (Image taken from Uerpmann and Uerpmann, 1994)
Note that, while the lingual valley of both first and second molars is more-or-less "V"-shaped and the metastylid and the metaconid are quite symmetrical, the lingual-buccal distance of the first molar is clearly larger than that in "typical" mules. Uerpmann and Uerpmann (1994) used the "V"-shaped lingual valley and the elongated buccal valley in the third premolar as well as morphological traits in the maxillary teeth to argue for mule identification.

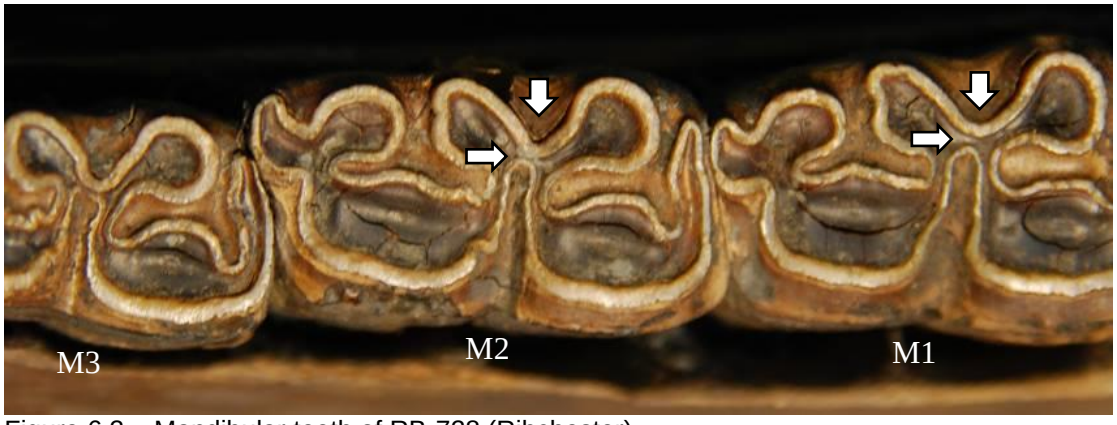


Figure 6.2 – Mandibular teeth of RB-728 (Ribchester).
Note the V-shaped lingual fold, the symmetrical roundness of the metaconid and the metastylid, and the short bucco-lingual fold distance, particularly in M2.

6.4.4 – Indication of current aDNA findings

Due to the low success rate of extracting nuDNA from archaeological material, the sample size from the initial results is considerably small (n=3). The contradictory identification of DA-217 reveals that qualitative evaluation of dental morphology may not reliably distinguish different domestic equids. This suggests that the variability in dental

morphology in horses is much greater than has been previously assumed. In other words, when examined for their qualitative traits, mandibular teeth in some horses can appear "mule-like". Conversely, it could also be possible that some mules are more "horse-like", based on the characteristics of the same elements. However, for the current case, when the available image of DA-959 is re-examined, it seems that while some morphological traits are typically mule (V-shape), some other traits (bucco-lingual distance) may not be typical in all mules. As a result, before completely rejecting the reliability of morphological criteria, the current outcomes imply that qualitative identification can be subjective and need to be reconsidered. Thus, it would be wise to apply quantitative methods suggested in the present thesis to confirm any suspicion regarding the presence of non-caballine equids.

As mentioned above, this is an on-going project; additional specimens are still being analysed and further analysis of putative mules and donkeys will be able to provide a better estimation of the reliability of dental morphology and post-cranial morphological criteria.

6.5 – Chapter Summary

In this short chapter, the use of aDNA analysis for the identification of domestic equids is discussed. Previous aDNA studies have mostly focused on the evolution of equids and only a few of them have dealt more directly with taxonomic identifications. A previously unpublished Master's dissertation (Hite, 2008) focused on validating claimed dental traits for equids by using aDNA analysis. However, in addition to the small sample size, several aspects of the research design were unsuitable for the detection of hybrid species (i.e. work only focused on mtDNA). Thus, the validity of morphological traits for the detection of mules is still in doubt.

Technological advances have increased the processing speed and the resolution of outcomes in aDNA analysis. Similarly, the success rate of aDNA extraction and analysis has increased as well, and the cost of such investigations has also become, relatively speaking, more affordable. This has increased the opportunities for the identification of hybrid species in archaeological assemblages. However, success rates are still relatively low judging from present results (3 out of 20 specimens). This is mainly due to the fact that the abundant mtDNA commonly used in aDNA analysis is insufficient in the genetic characterisation of hybrids. The success rate in the extraction and sequencing of nuclear DNA, which is required in the study of mules and other hybrids, is considerably lower.

The initial results from this on-going project reveal that a specimen which was previously identified as mule based on qualitative evaluation of its dental morphology is, in fact, a horse. Whilst this seems to question the reliability of morphological traits as criteria for taxonomic identification of hybrids, it actually also emphasises the essential problem of qualitative criteria: i.e. subjectivity. The images of specimen DA-959 mentioned above show rather ambiguous characteristics that are neither “typically” horse, nor “typically” mule. As a result, in addition to whether these morphological criteria are reliable, the subjectivity of the qualitative method should also be questioned and further explored using quantitative approaches.

Even though the small sample size from the initial results of this on-going project is insufficient to warrant firm conclusions, it does indicate that determinations based purely on qualitative methods can be misleading. Therefore, it is advised to include quantitative methods to further support the species determination as suggested in the current thesis.

As mentioned above, first results of the analysis of ancient DNA from equid samples from Dangstetten strongly suggest that morphological traits are not always reliable in the identification of mules. However, given the limited nature of this preliminary palaeogenetic study, the extent of the overlap in the morphological variability in mules and horses it is still unclear, and should be a subject for a more thorough investigation.

Chapter 7 - Isotopic Analyses: Method, Material, and Outcomes

7.1 – Introduction

This chapter will present all the aspects of isotopic analysis of the current research. The first part of this chapter will review the basic concept of isotopic analysis and build a hypothetical model for the different procurement strategies for domestic equids. The rationale behind the sample selection will be explained and lists will be given of the specimens used for isotopic analysis. This will be followed by the details and a summary of the outcomes from the analyses, as well as their interpretation. This chapter will then end with a discussion of the significance and implications of the results from isotopic analyses.

7.2 – Stable Isotopic Analyses of Mobility and Migration: A Brief Overview

The use of stable isotopic analysis in archaeological studies allows new information to be obtained from skeletal remains and contributes new perspectives on interpreting past human behaviours. Whilst isotopic analysis is more commonly associated with studies on the dietary patterns of past populations, the method can also be used to detect their movements. Mobility and migration are important aspects of human behaviour, which ultimately resulted in the current human occupation of the globe and the similarity as well as the diversity of different cultures. Use of strontium and oxygen isotopes has made detecting some of these movements possible by comparing the isotopic values from skeletal remains against the local isotopic range (Brown and Brown, 2011). This allows archaeologists to detect and interpret human movements based on direct evidence. While it is difficult to demonstrate whether the presence of an object is evidence of trade, the result of spreading technology, or the movement of people, analysis of strontium and oxygen isotopic is able to show if the environment an individual grew up in is different from the

place he/she was buried. In addition, the style of artefacts can be learned and imitated, but evidence in bones and teeth is generally unintentional and, therefore, can directly better represent actual past mobility. A similar method can be applied to animals to determine whether the presence of a new species could be an indication of continuous importation of that species as food or evidence of the introduction of the animal to a new habitat.

Isotopes are the same element in alternate forms – with a different number of neutrons and hence different masses. Through food and water consumption, these isotopes will be incorporated into different body tissues (teeth, bone, hair, muscle, etc.) of all creatures because they are involved in the process of tissue formation (Brown and Brown, 2011). As a result, different ratios of isotopes, such as carbon, oxygen, and nitrogen, will reflect not only the diet, but also the environment surrounding the organism.

Unlike determining the diet of an individual using carbon and nitrogen isotopes from bone, which gives an average diet assessment over a long period, understanding mobility requires isotopic records that represent a shorter time span, so tooth enamel is predominately used. This is because, in order to study the mobility of an individual through a developmental period, it is necessary to compare the isotopic value representing a known age of the individual against the defined local range of the site where the individual is found. As a result, teeth are more suitable than are bones for examining purposes such as past mobility and migration. Whilst bones are more abundant than are teeth in most archaeological cases, the isotopic value derived from bones is less representative of a location than teeth because bones are constantly remodelling. In other words, bones are constantly forming throughout a lifetime. This means the minerals in bones will undergo a complete turnover after a certain period, and different bones will have a different turnover

rate. As a result, isotopic values from bones will provide only an average of whatever was consumed in this period. The enamel in teeth, on the other hand, will not remodel once formed and thus can be used as a proxy to represent the dietary catchment of an individual's developmental years. Furthermore, the ages for the complete formation of enamel and the eruption of each tooth are generally better understood than the remodelling rate of bones.

Various studies have used isotopic analysis to address questions regarding mobility and migration in the past, mostly of humans (for example, Price *et al.*, 2002; Bentley *et al.*, 2004; Fischer *et al.*, 2007; Prowse and Schwarcz, 2007; Eriksson *et al.*, 2008; Schroeder *et al.*, 2009; Giblin *et al.*, 2013; Gregoricka, 2013; etc), but the same method can also be used to discuss animal mobility and migration as a result of human behaviour (Pearson *et al.*, 2007; Bendrey *et al.*, 2009; Berger *et al.*, 2010; Towers *et al.*, 2010, 2011; Thornton *et al.*, 2011; Henton, 2012; Madgwick *et al.*, 2013; Minniti *et al.* 2014; etc.). Among these studies, Bendrey *et al.* (2009) had a similar aim to the current research, as they attempted to examine the local supply of horses in southern Britain during the Iron Age by using strontium isotopic analysis on two horses. The results revealed different origins for these two horses, but there was not enough evidence to conclude whether local Iron Age tribes were breeding their own horses or captured and tamed wild/feral horse populations. Another similar study is that published by Berger *et al.* (2010) which discusses the mobility of a putative mule from Weißenburg, Germany. The study used oxygen and strontium isotopic values from different sections of the lower fourth premolar (P_4) as well as its mandible to represent different periods throughout its life and concluded that the studied mule may have travelled through the Alps, but results were inconclusive regarding its place of birth. Other studies, such as Towers *et al.* (2010), also used strontium isotopic

analysis to discuss the localness of the cattle and aurochs used in funerary rituals in Bronze Age Britain.

Several different elements can also be used to detect localness based on their association with changes in the surrounding environment, such as lead and neodymium, but the former is more commonly found in metal or ceramic artefacts (e.g. Iñañez *et al.* 2010) whereas the latter is more commonly used on fossil material in palaeoecological studies (e.g. Janz and Vennemann, 2005). However, two different stable isotopes are more commonly employed than others in archaeological research for determining mobility: strontium and oxygen. The basic concepts of their application in archaeology are relatively well understood and, therefore, only the basic premise of their application and use will be described here. That said, it must be stressed that, at present, most results of stable isotopic analyses cannot be used on their own as a tool to trace origins. This is because isotopic values are rarely unique and location-specific. In other words, different places that are far away from each other may have the same local isotopic signature. Nevertheless, in most cases, isotopic analyses are able to provide enough evidence, which can be used to examine local versus non-local origin.

As mentioned above, oxygen and strontium are two elements frequently used for studies on mobility and migration. For the current study, oxygen isotopic analysis was chosen as the main method to analyse all available specimens. The main reason for this was financial. Secondly, oxygen isotopic analysis was regarded as being more suitable than strontium isotopes to provide evidence of the import of animals from the continent for the present study (see section 7.2.1). As a result, strontium isotopic analysis was performed only on a small number of specimens to obtain complementary results to help shed light on the

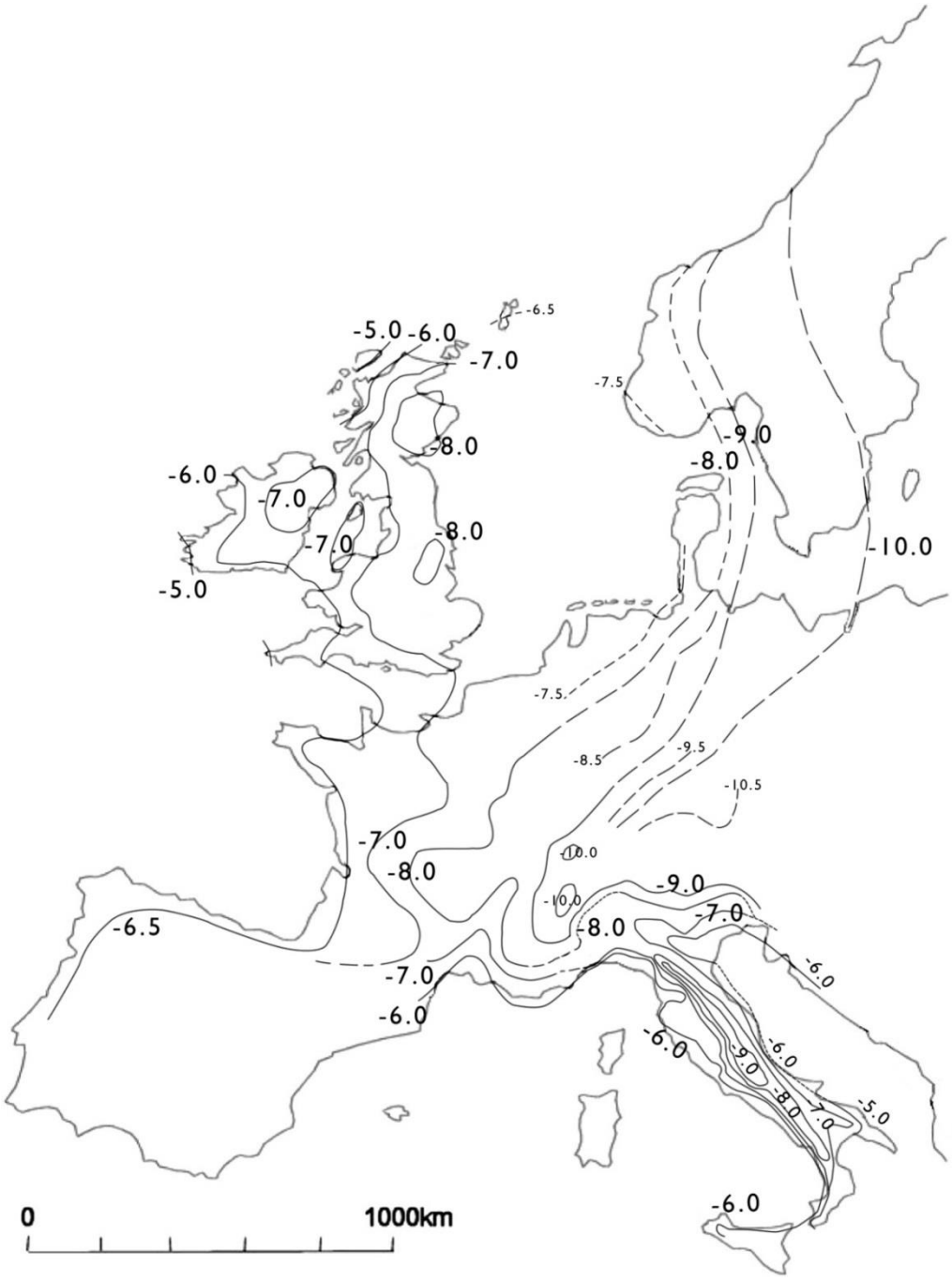
possibility of tracking 'origins' of tested samples. To further explain why oxygen isotopic analysis is more useful to the current study, it is necessary to understand the differences between these two isotopic analyses.

7.2.1 – The Basic Principles of Oxygen Isotopic Analysis

The use of oxygen isotopic analysis is common in studies of mobility in archaeology (e.g. Prowse and Schwarcz, 2007; Schroeder *et al.*, 2009; Brown and Brown, 2011), so only a simplified version of the basic principle involved is offered.

In nature, oxygen has three isotopes, ^{16}O, ^{17}O, and ^{18}O. The ratio between ^{18}O and ^{16}O ($^{18}O/^{16}O$, or expressed relative to a standard as $\delta^{18}O$) in natural water is different from region to region depending on factors such as temperature, latitude, altitude, and distance to shore. In other words, the local evaporation rate and precipitation will determine the local $\delta^{18}O$ values. Local drinking water, which includes several sources of natural water such as rainfall or input from melted ice or snow, and which is generally assumed to be similar to the mean of local precipitation, will, then, reflect different local $\delta^{18}O_{\text{Drinking Water}}$ (hereafter $\delta^{18}O_{DW}$) values. Therefore, animals drinking the same local water source will have similar $\delta^{18}O_{DW}$ values in their body tissues. Nevertheless, the $\delta^{18}O_{DW}$ value is not unique to a specific region because regions with a similar climate and geography will also have a similar $\delta^{18}O_{DW}$ value even if they may be far from each other in actual distance. Map 7.1 is a demonstration of modern $\delta^{18}O$ values in different regions of Europe. Note that the $\delta^{18}O$ value is distributed in a gradient because the distance to shore is the main factor for the evaporation rate and precipitation. Subsequently, $\delta^{18}O_{DW}$ values change mainly in a southwest-northeast gradient, but are complicated by a steep Mediterranean gradient inland

from the Mediterranean coast, and distinctive values near the Alps where the altitude is high.



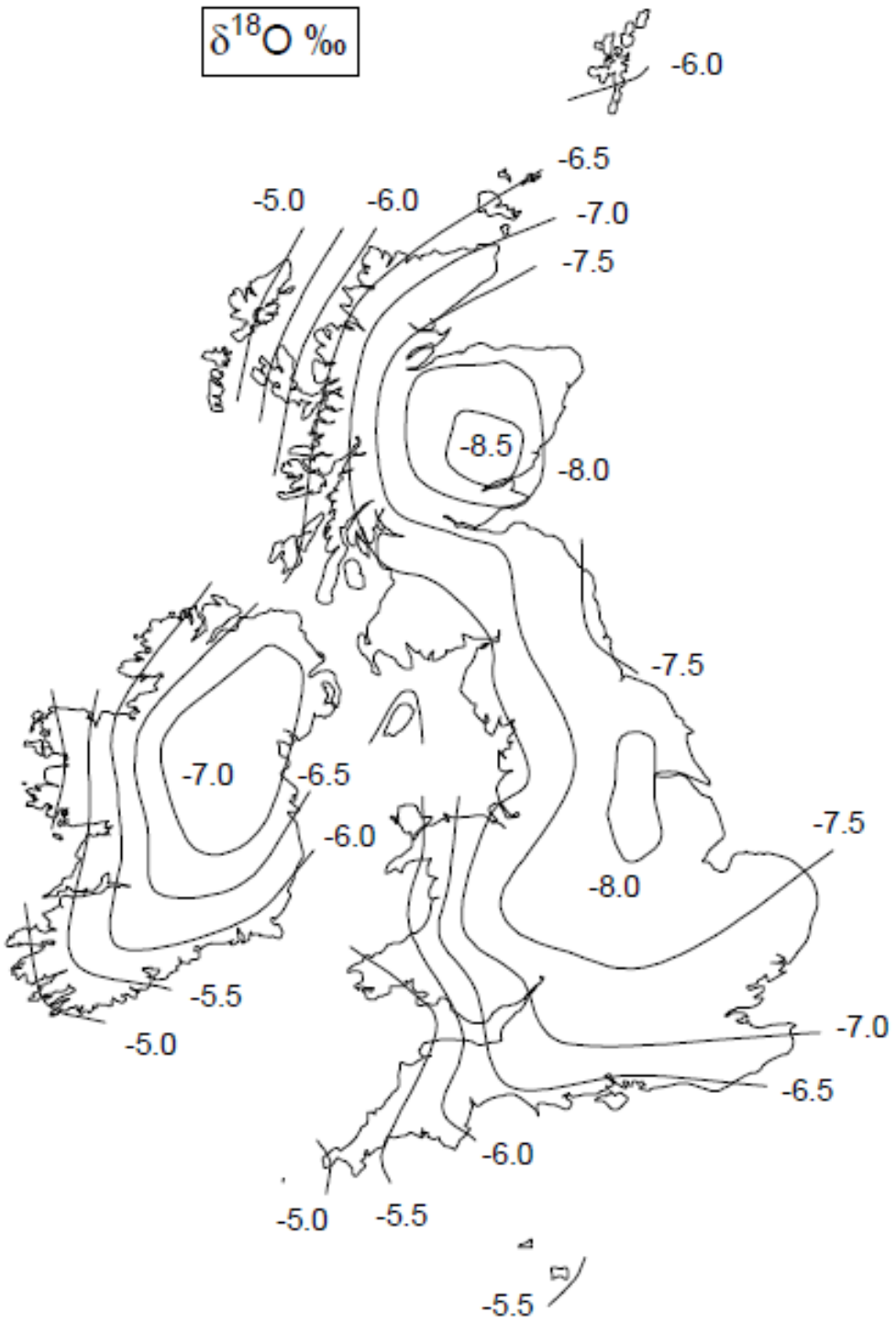
Map 7.1 – $\delta^{18}O_{DW}$ value range from mean annual precipitation for western Europe (adapted from Hughes *et al.*, 2014 and Schwarcz *et al.*, 2010)

A more detailed $\delta^{18}O_{DW}$ gradient map is available for Britain from the work of Darling *et al.* (2003, Map 7.2). This map is based on modern groundwater and can be used to represent the $\delta^{18}O_{DW}$ range for Roman Britain under the assumption that there has been no

dramatic climatic change (McCormick *et al.*, 2012). From this map, it is clear that the $\delta^{18}O_{DW}$ value decreases in a west-east direction. This is because the North Atlantic Drift from the southeast is the major factor for the weather in Western Europe. The differences between $\delta^{18}O_{DW}$ values, then, can be used as an indicator of the location of origin of an individual. Given that $\delta^{18}O_{DW}$ values change progressively over the landscape, it is possible to deduce the location of where the specimen is more likely to have originated. For example, if a specimen that is known to be of British origin has a $\delta^{18}O_{DW}$ value of between -8.0‰ and -8.5‰, then it is very possible for this specimen to be from eastern Scotland or central England (part southeast Yorkshire and northwest East Midlands). If a specimen has a more positive $\delta^{18}O_{DW}$ value, between -3.0‰ and -4.0‰, it would be reasonable to exclude this specimen as being of British origin since no region within the UK has a $\delta^{18}O_{DW}$ value this positive. In addition, in this case, it would even be possible to speculate that the specimen may have originated from the southwest coast of the Iberian Peninsula or Northern Africa.

It is also important to know that there are some shortcomings to oxygen isotopic analysis that may affect the efficiency of the results. Because $\delta^{18}O_{DW}$ is climatic/temperature sensitive, it is affected by seasonal changes.

The formation of teeth takes place incrementally over a long period, and this is crucial for the development of an appropriate sampling strategy (see section 7.4.1). In addition to seasonal differences, the source of drinking water (particularly for domesticated animals) and the metabolic differences between species and body mass are all possible factors affecting $\delta^{18}O_{DW}$ value. This issue can only be resolved with more comprehensive studies and larger datasets.



Map 7.2 – $\delta^{18}O_{DW}$ range based on modern groundwater (from Darling *et al.*, 2003).

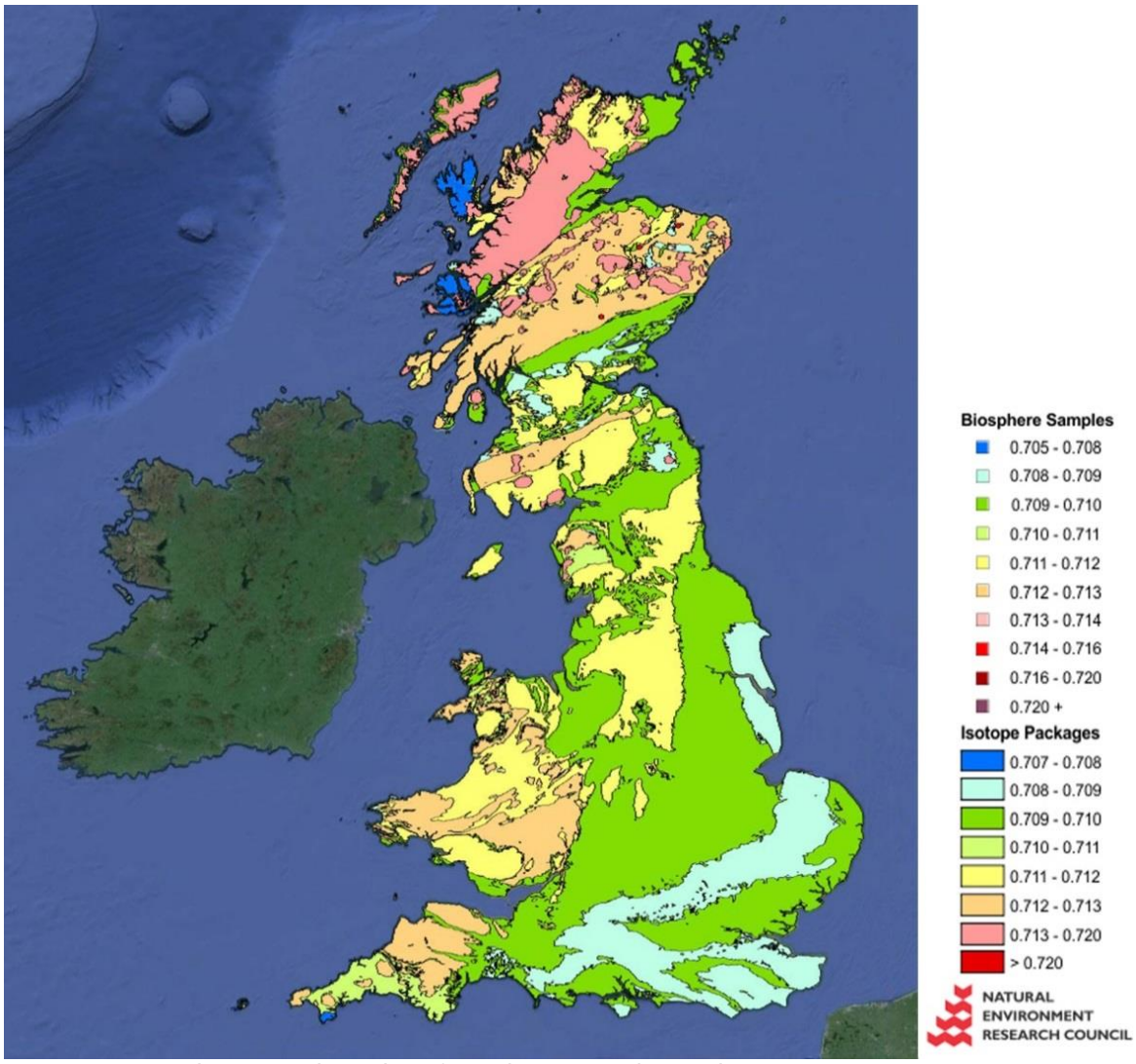
7.2.2 – The Basic Principles of Strontium Isotopic Analysis

Strontium Isotopic analysis is, perhaps, by far the most common method used for discussing mobility and movement in archaeology. The reason for its popularity is that unlike oxygen, strontium isotopic analysis is determined only by the soil type of a region

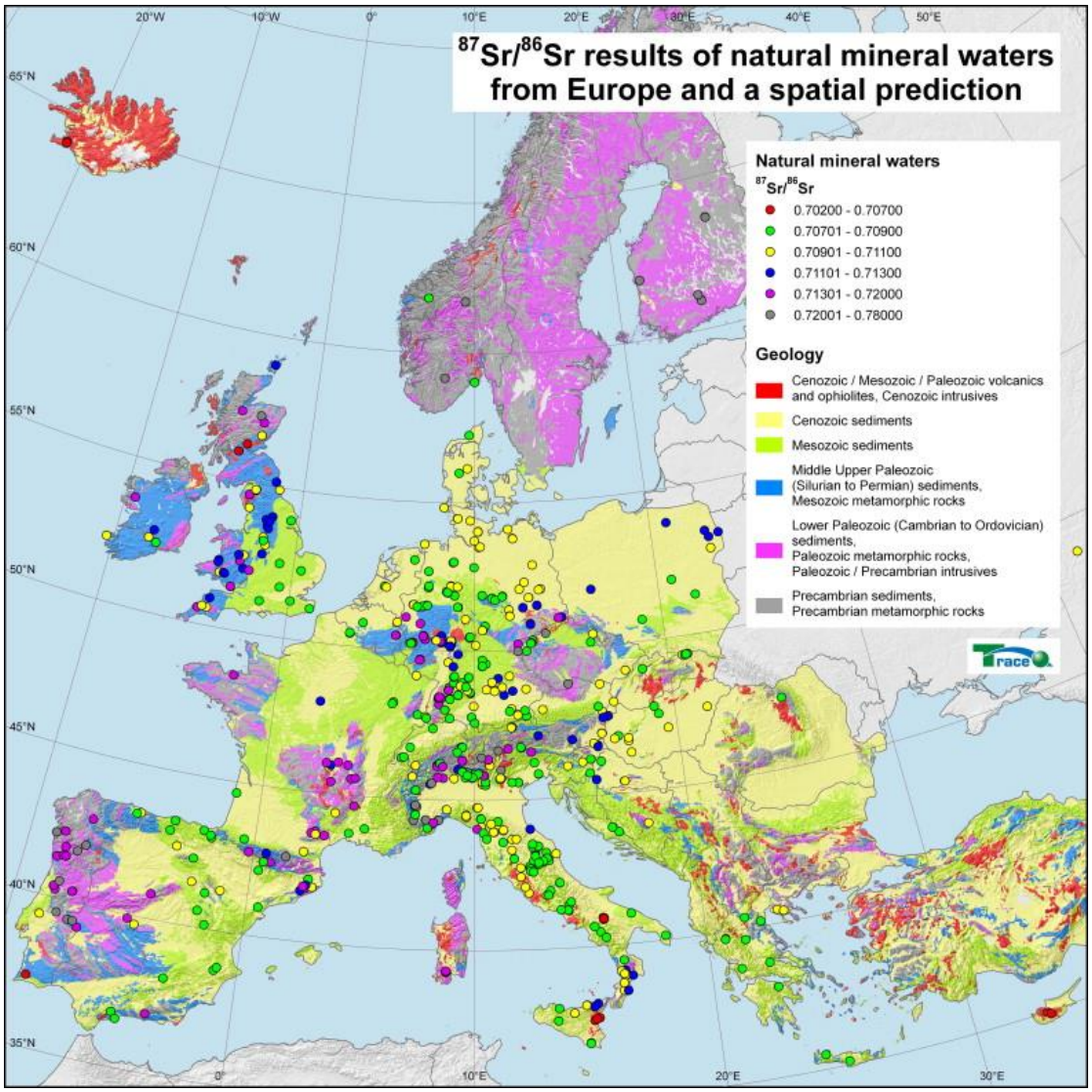
and is not affected by numerous other factors such as possible minor climatic/temperature changes or differences in metabolic systems. Strontium (Sr) has four different isotopes existing in nature: ^{84}Sr, ^{86}Sr, ^{87}Sr, and ^{88}Sr. Of these four, three are stable, and ^{87}Sr is formed from the radioactive decay of ^{87}Rb (rubidium). The ratio of ^{87}Sr to ^{86}Sr ($^{87}Sr/^{86}Sr$, refers to as the strontium isotopic ratio in this thesis) is related to the geological age of the bedrock and, consequently, to the surface soils composed mainly from the weathered bedrock (Bentley, 2006; Brown and Brown, 2011; Slovak and Paytan, 2012). Both water and plants will show the same strontium isotopic ratio as the soil type, and the same ratio will persist in creatures that consume the local water and plants. Thus a comparison of strontium isotopes in tooth enamel with a non-local dietary catchment can be distinguished from the local ones.

In contrast to oxygen isotopic values, the strontium isotopic ratios do not change in a gradient through the landscape. As a result, the same logic for determining the possible region of origin using oxygen isotopic values cannot be applied for strontium isotopic values. That is, if a $\delta^{18}O_{DW}$ value is out of the local range, it is still often possible to attribute the specimen to further inland or closer to the shore; but such a rationale will not work for strontium. It is, therefore, imperative to have a method for establishing the possible location where the strontium isotopic ratio could have originated. A geological map with detailed $^{87}Sr/^{86}Sr$ information for the UK was produced by Evans *et al.* (2010, Map 7.3). This map includes data obtained from spring water and plants, as well as from skeletal material from archaeological sites and, therefore, it is ideal for the current study. From this map, it is not difficult to see that there is no observable pattern in strontium isotope values. Not only can similar isotopic values exist in different parts of the island, but they also exist in the continental landmass (Map 7.4). For example, chalk soil ($^{87}Sr/^{86}Sr$ between 0.708 and 0.709) is the main soil type for South East and East England, but it is

also the most common soil type in continental Europe. As a result, if all samples can be confirmed to have originated within a given region, then strontium isotopic ratios will be able to not only discriminate between locals and non-locals, but will also be able to detect the possible origins of non-local individuals. However, when the geographical region of origin cannot be confirmed, strontium isotopic ratios can only determine if the samples are local or not.



Map 7.3 – Strontium Isotopic Ratios of UK. (Evans *et al.*, 2010)



Map 7.4 – Strontium Isotopic Ratios of Europe based on mineral water. (Taken from Voerkelius *et al.*, 2010.)

7.2.3 – The Basic Principles of Carbon Isotopic Analysis

Traditionally, carbon isotopic analysis is not used as a tool for examining migration or movement, but rather is used as a representation of diet. This is because carbon isotopic values mainly reflect the plant types being consumed by different individuals. Unlike humans with the ability to alter local vegetation by introducing new plant species through domestication and other agricultural activities, for grazing herbivores, the food resource is determined mainly by the local vegetation. Thus, if the vegetation is significantly different in one region from that in others, carbon isotopes may indirectly reflect the origin of the

animal. Before explaining how carbon isotopic values can be used to determine localness, it is necessary to provide a basic background of how carbon isotopic analysis works.

^{12}C, ^{13}C, and ^{14}C are the three carbon isotopes that can be found in nature. Among them, ^{12}C and ^{13}C are stable isotopes, and their ratio varies according to the photosynthesis path adopted by the plants. In a temperate climate, plants usually adopt the "Calvin-Benson cycle" (or C_3 carbon fixation) as the photosynthetic pathway and produce a pair of 3-carbon molecules for the further production of energy (e.g. glucose and other sugars) (Simpson, 2010). This type of plant is generally referred to as a C3 plant. In contrast to C3 plants, plants in hot and arid climates have adopted a different photosynthetic pathway, which has a two-staged process, and they produce 4-carbon molecules instead of 3-carbon ones. As a result, this type of plant is known as a C4 plant. These two different plant types have different rates of absorbing ^{12}C and ^{13}C from the atmosphere and, therefore, have different ^{13}C to ^{12}C ratios ($\delta^{13}C$).

Since climate is the dominating factor in whether a region favours C3 or C4 plants, the availability of plant types can be used as a proxy for the environment. For example, C4 plants are more abundant in continental Europe (e.g. the Balkans) than in Britain and, therefore, it would be extremely unusual for a British local horse to have a high ratio of C4 plant intake. However, the resolution provided by carbon isotopic evidence is much lower than that of oxygen and, therefore, can be used only as a rough guide, i.e., to indicate unusual diets. Furthermore, it is uncertain what percentage of diet for a domesticated species, such as horses, is provided by humans (fodder) and how much is derived from exploiting surrounding pastures.

7.3 – Using Isotopic Analysis to Determine Equid Procurement Strategies

In previous sections, the advantages and limitations of different isotopic analyses were discussed along with the basic concept for their application in archaeology. In this section, different models will be hypothesised to represent various equid procurement strategies. Before setting up the possible scenarios, it is necessary to reiterate the main research questions for this part of the current thesis:

(1) Is there a correlation between different procurement strategies and site types? For example, do military sites have the same procurement strategy as urban or rural settlements?
(2) Based on Roman historical records, there should be three different types of domestic equids commonly used: horses, donkeys, and mules. Do different domestic equid species have different supply sources? Do they all come from the same breeding ground (whether local or non-local), or were there different breeding centres that specialised in breeding certain species?
(3) Given the challenges of donkey-keeping and mule-breeding in Roman Britain as discussed previously (see Chapter 1), is it possible that some of these animals were imports from the continent or other parts of the Roman Empire? In order to answer these questions, different models need to be hypothesised for different scenarios.

Domestic equids are highly mobile animals, but their mobility is restricted if they are sold and purchased as commodities. Many of these animals are bred for the purpose of exploiting their labour and, therefore, are assumed to be kept under human management until they are ready to carry out designated tasks. As a result, the comparison of isotopic signatures from the early period of an individual's life and the local range, i.e. where it was discovered, may provide insights into its procurement, in other words, may show whether

the individual was brought from a different region or was born and raised within a local area. However, since a comparison can only be made between the early life of an individual and the place of discovery, all journeys, long or short, that this individual experienced are simply undetectable. That is, even a locally bred horse can be sold to a very distant region and can work there over a long period, then be sold back to its breeding ground. In cases like this, it is impossible for the current method to detect such transactions, and we can only determine that this horse was apparently procured locally while, for its last owner, it was a commodity purchased from afar. This limitation is worth noting, since the life history of labour animals may be extremely complicated, especially for horses and mules, which are known to have participated in military operations at frontiers.

Having pointed out the blind spot of the current hypothesis, it may be redundant to state that all hypothetical models assume that all individuals lived in only two locations at most: the breeding ground and the place of death. Therefore, for the current research, it is assumed that if an individual's isotopic value falls in the local range, it is determined as having been procured locally wherever it may have been during its life time, and vice versa. Although the exact origin of specimens cannot be determined by isotopic values, the pattern will be able to show whether different specimens may have had the same origin. This is because if a herd of domestic animals grew up in the same environment, then their isotopic value (strontium or oxygen) will be similar to that of other members of the same herd, and yet dissimilar to that of individuals that grew up in a different area where the environmental setting differed in one way or another (soil composition and/or different climate). As a result, the animals from the same region (supplying source) should have similar isotopic values, and these values should be different to those of individuals that originated in a different region. Therefore, we can determine whether there are only a few supply sources or multiple and random acquisition sources based on the clustering of

isotopic data. In other words, if the majority of domestic equids are supplied from a certain breeder while only a few are procured elsewhere, then there will be a concentration of isotopic data indicating the local range of the breeding ground along with a few scattered data points reflecting the other independent breeding locations (similar to Pattern A in Figure 7.1). Following this logic, the procurement strategy can be broadly divided into three general patterns: specific local supply, specific non-local supply, and no specific supply.

For specific local supply, it is assumed that a site only procures domestic equids from one or a few specific breeders within the local region. This would be represented by a narrow cluster of isotopic data falling in the local range (Pattern A in Figure 7.1). However, if the location of the site is near the border of different geological or climatic features (i.e. different soil types or different $\delta^{18}O_{DW}$ range on average), then it is possible that specimens are scattered in different zones but they will still form a narrow range. This type of pattern is likely to occur in rural settlements where the demand for domestic equids can be met locally without the need to import from afar. Similar to the first scenario, it is possible that all domestic equids will be procured from a single or a few breeders that are outside of the local region. In such a scenario, the isotopic data will still be scattered closely in cluster(s), but will not be within the local range (Pattern B in Figure 7.1). This type of procurement strategy might be atypical considering how common domestic equids are used on a daily basis. Nevertheless, it may represent unusual cases, such as battlefields and temporary forts, where the conquest is in progress before the armies have had a chance to secure the local horse supply. Once the fort is established and surrounding areas have been controlled, it is likely that the procurement strategy for a military fort during peace time would resemble that of a rural settlement (i.e. specific local supply). However, the Roman military remount (replacement horse) supply had its own regulation and would have been controlled by

central officials (Hyland, 1990; Dixon and Southern, 1997); bulk purchase or the purchase through authorised breeders was only the possible alternative. As a result, it is possible that the data will cluster much closer to each other than those from rural settlements. The other possible site that may have such a pattern would be stables of circuses where racehorses are likely to have been imported in large amounts for a specific purpose. In contrast to the two scenarios above, perhaps the most common procurement strategy would be no specific supply for domestic equids. This would be represented by a relatively random distribution of isotopic data with some local domestic equids and others from non-local regions (Pattern C in Figure 7.1). Large urban settlements or "*mansio*" sites are likely to have this type of distribution pattern. This is because of the high volume of trading activities occurring in these types of sites, which will have attracted domestic equids from different regions, either travelling through (and dying) or being sold to locals. Because of these hypothesised patterns, it is possible to examine the general procurement strategies of different sites by roughly estimating the number of supply sources and possible locations for breeding (local versus non-local).

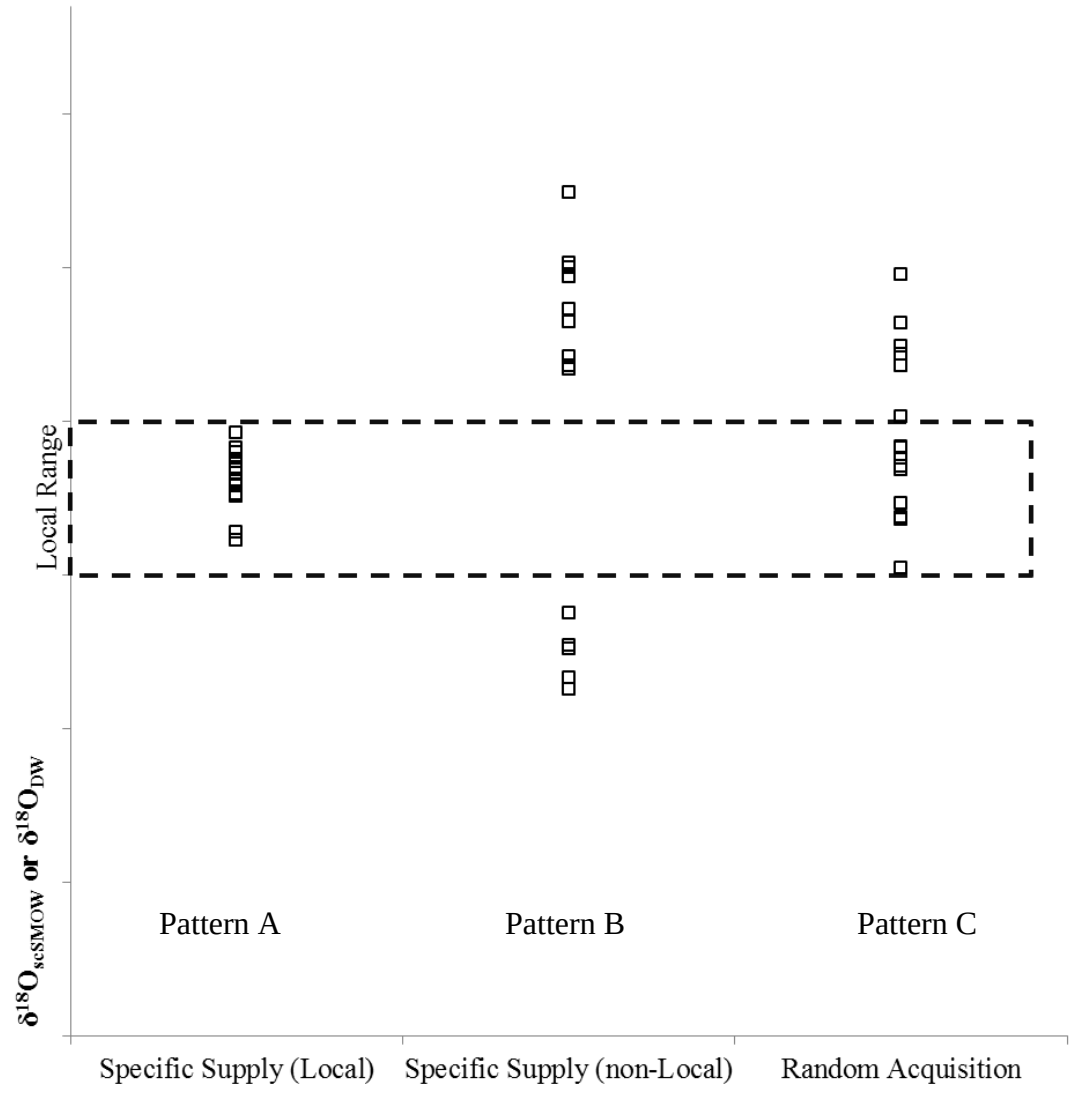


Figure 7.1 – Hypothesised distribution patterns for different procurement strategies.
The area within the dashed-line represents the hypothetic local range. Similar patterns can be argued for strontium isotopes.

7.4 – Material

A total of 40 teeth from 5 different sites were selected for stable oxygen isotopic analysis. This is a relatively small proportion of all the samples collected for the current research and it is, therefore, necessary to explain further the rationale behind the selection of material.

7.4.1 – Material Selection

As explained at the beginning of section 7.2, teeth are more suitable than bones for studying the mobility of past populations. Therefore, only the lower premolars and molars were chosen for isotopic analysis. The selection of which teeth to include is based on two main considerations besides availability. Firstly, the species of the tooth specimen has been successfully determined based on the dental morphology either from the specimen itself or from other teeth of the same individual (see Chapter 5). Secondly, the selected tooth specimen is completely formed before the individual reaches the age at which it will be considered suitable for work and, therefore, might be sold and transported away from its breeding ground. The breaking in of foals usually takes place when they have reached at least three years of age, and most of the time, four years of age is recommended (Hyland, 1990). This is mainly with the aim of extending their working life because most limb bones and vertebrae are still largely unfused before this age and will deform if worked under pressure (Bennett, 2008b). Indeed, the Romans seem to have applied the general same standard for breaking in foals (Hyland, 1990). While it is still possible for yearlings to be sold, this is rather unusual for labour animals because buying a young animal that cannot be used for several more years is simply uneconomical.

As a result, it is essential to evaluate which tooth is more suitable than others for the current research by establishing the time of eruption and formation for each tooth. Table 7.1 is a summarised chart for eruption time and mineralisation of different equine lower teeth (Amorosi, 1989; Hoppe *et al.*, 2004). Although the information is based on horses, in the absence of research arguing any noticeable differences among different domestic equids, the same dental development is assumed to apply to all other domestic equids. The mineralization of teeth, that is, their formation, will be much earlier than their eruption; in

particular, equine teeth are hypsodont, which means they have a much taller crown and so will continuously be worn down through life. It also means the crown may continue to form after eruption. Based on previous research, teeth formed before three years of age (Figure 7.2 and Table 7.1), including the second and third premolars (P_2, P_3) and the first and second molars (M_1, M_2), are most suitable as samples, as they contain isotopic data that can represent the birth place where a domestic equid theoretically spent its first three years of life. However, it should be noted that breast milk affects the oxygen isotopic value because breast milk contains mainly body water, which has been metabolically fractionated (Wright and Schwarcz, 1998). As a result, only the later forming portion of both M_1 and M_2 should be used, i.e., post suckling. Regarding the lower fourth premolar (P_4) and third molar (M_3), although they continue to form after four years of age, the early formed half (i.e. the lower half) can still indicate whether the equid is from the local population or from elsewhere. For the current thesis, P_2, and P_3 are used if available and only the suitable part of P_4, M_1, and M_2 are used if no other teeth are available ($P_4 > M_2 > M_1$); however, the use of M_3 is completely avoided.

It is also important to note that seasonality also affects $\delta^{18}O$ because the water evaporation rate is strongly associated with temperature, which is ultimately tied to precipitation. Therefore, while the average $\delta^{18}O$ can be obtained from sampling evenly throughout the tooth, for herbivore mammals with high-crowned teeth (hypsodont herbivores), it is also possible to easily divide a tooth into several sections to compare seasonality differences (e.g. Berger *et al.*, 2010; Henton, 2012). This may be of particular importance for examining different herd management patterns in the past. For example, wealthy Roman breeders may have been able to afford to have had the horses taken into the mountains during the summer to exploit the free mountain pasture and save nearby pasture for winter (Hyland, 1990). The benefit is more than just using rich mountain pasture efficiently, since

the trip can also serve as training for the foals to harden their hoofs (Hyland, 1990). However, this type of herd management may affect the $\delta^{18}O$ values in these individuals. More sophisticated techniques, such as laser ablation (LA) or strontium isotopic analysis, can also be used on smaller teeth to obtain data from different time periods during tooth formation (e.g. Passey and Cerling, 2006). However, for detailed microsampling, it is essential to have a full understanding of enamel formation which allows the data to correspond to age (or season). Unfortunately, while the age of teeth formation in horses is well-studied (Hoppe *et al.*, 2004), the growth rate of teeth may not remain constant throughout the formation process (Bendrey *et al.*, 2014; Zazzo *et al.*, 2012). As a result, all samples in the current thesis are bulk-sampled either as a whole (P_2 and P_3) or from sections that were formed before the age of three. Since domestic equids foal in late spring or early summer, most foals will have experienced approximately equal numbers of summer and winter seasons by the time they reach the age of three. This means that the outcomes will be the average isotopic value of each tooth during the time of formation (roughly two or three season cycles excluding the nursing period). Furthermore, it should be stated that analysed samples contain only enamel because, as previous research has suggested, dentine is more likely to be affected by diagenesis (Kohn *et al.*, 1999).

	Eruption			Enamel Formation
Tooth	Schmid (1972)	Silver (1969)	Sisson and Grossmam (1966)	Hoppe *et al.* (2004)
Premolar 2 (P_2)	2.5 years (30 months)	2.5 years (30 months)	2.5 years (30 months)	12 – 33 months
Premolar 3 (P_3)	2.75 years (33 months)	2.5 years (30 months)	3 years (36 months)	13 – 38 months
Premolar 4 (P_4)	3 years (36 months)	3.5 years (42 months)	4 years (48 months)	15 – 54 months
Molar 1 (M_1)	1 year (12 months)	Present by 12 months, but have a wide variation	9 – 12 months	Before birth to 26 months
Molar 2 (M_2)	2 years (24 months)	2 – 2.5 years (24 – 30 months)	2 years (24 months)	6 – 39 months
Molar 3 (M_3)	3.5 years (42 months)	3.5 – 4.5 years (42 – 54 months)	3.5 – 4 years (42 – 48 months)	18 – 58 months

Table 7.1 – The eruption and mineralisation of lower premolars and molars in horse.

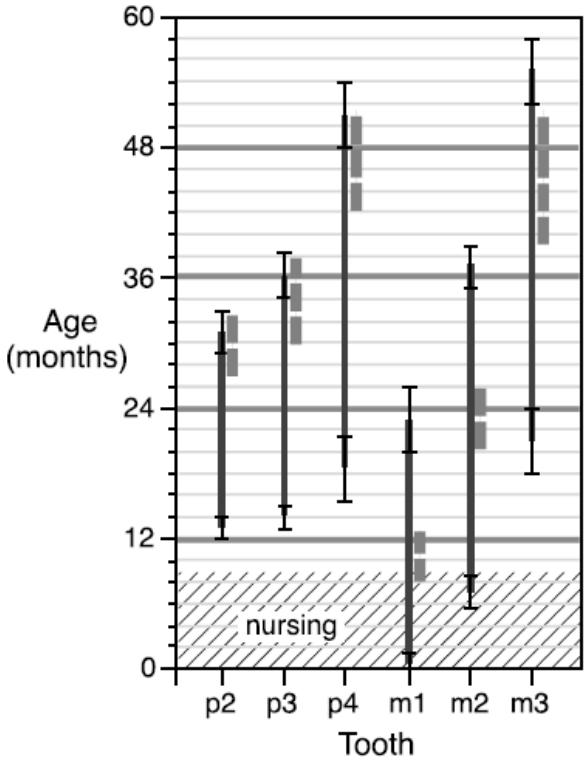


Figure 7.2 – The age of formation and eruption for premolars and molars in horses. (from Hoppe *et al.*, 2004).
The black lines represent the time of teeth formation and the thick grey dashed line represent the age of teeth eruption.

7.4.2 – Selected Material

After applying the above considerations and criteria to select the suitable samples, only 40 teeth that are available for access were considered suitable for use in the current research. The majority of these specimens were determined to be horses (n = 31) with seven possible mules and two possible donkeys determined using methods and interpretation discussed in the previous chapter. Although the main aim of the current thesis is to examine the procurement of domestic equids in Roman Britain, it should be noted that four specimens (one horse, one possible donkey, and two possible mules) from two Roman sites in Serbia are included for two reasons. First, they can be used to represent contemporary isotopic values of domestic equids from the continental Roman Empire, and secondly, to compare the procurement strategies between British and continental Roman sites. Table 7.2 summarises the number of samples from each site and their species.

Site	Horse	Possible Donkey	Possible Mule	**Total**
Winchester	13	0	2	**15**
Alcester	3	0	1	**4**
Ribchester	7	0	1	**8**
Fairford, Thornhill Farm	8	1	0	**9**
Serbia	1	1	2	**4**
Total	**32**	**2**	**6**	**40**

Table 7.2 – Number of samples from selected sites.

Whilst strontium isotopic analysis can also help to determine the localness of archaeological samples in question, the cost of this analysis is significantly higher than that of oxygen isotopic analysis. For this reason, only 16 specimens were selected for strontium isotopic analysis to gain more insight by combining the results with their oxygen isotopic values. Given that several studies involving strontium isotopic analysis are based on Roman material from the Hampshire region (Bendrey *et al.*, 2009; Evans *et al.*, 2006;

Eckardt *et al.*, 2009; Evans *et al.*, 2012a), the majority of these 16 specimens (n=12) were selected from Winchester in order to make a comparison with known strontium isotopic values. An additional three were selected from Alcester to further define the local oxygen isotopic range (see below), and the only possible donkey specimen from Fairford was also included for further examination.

7.4.3 – Methods

All samples were prepared by the author in the Isotopic Lab at the Department of Archaeology, University of Southampton. Conventionally, powders are ground directly from the tooth after the removal of the surface dirt and calculus. However, to avoid contaminating the powder with loose dirt and calculus particles, a vertical slice was cut from the tooth with dentine and the covered cementum removed from the enamel. This left only the enamel for grinding into powder. The enamel slices were placed in ultrasonic cleaner to remove all loose particles (soaked in RO water, for 380 seconds, twice). After the slices had been dried, roughly 10 to 15 mg of enamel powder was ground from each specimen using a dental burr. Since the current analysis aims to obtain an average isotopic value of the entire tooth, particular attention was paid to grinding the powder equally from the enamel. For the oxygen isotopic analysis, the prepared powder was placed in a microcentrifuge tube and then washed with 10% acetic acid three times. RO water was added to remove the acetic acid after each wash. The powders were then placed in the vacuum oven to dry (45°C under 75 mbar for an hour or until dried). For the strontium isotopic analysis, another thin layer of the surface was removed before grinding the powders for analysis to remove the effects of diagenesis.

Powders for oxygen and carbon isotopic analysis were sent to the University of Bradford and 16 samples for strontium isotopic analysis were sent to the National Oceanography Centre.

7.5 – Results

Ideally, the interpretation should be made from direct comparison of raw data from an individual species from a known location. However, since there is no known oxygen isotopic data for domestic equids to define the local isotopic values, it was necessary to convert the current raw data values into the oxygen isotopic value representing local drinking water ($^{18}O_{DW}$) for further interpretation. This was a two-step conversion for the current thesis because the analysis is done using structure carbonate from enamel ($^{18}O_{scSMOW}$) and needed to be converted into a calcium phosphate value ($^{18}O_{PO4}$) before being transformed into the value equivalent to drinking water. While a different technique could measure $\delta^{18}O$ in calcium phosphate directly, there are several clear benefits for using structure carbonate instead of phosphate (Bryant *et al.*, 1996). First, structure carbonate is much easier and cheaper to analyse compared to phosphate. Secondly, it has greater precision than analysis using phosphate. In addition, it will also produce $\delta^{13}C$ values, which may also bear some information on local vegetation.

Since every species has a different metabolism and diet pattern, the converting equation should be species-specific. However, since most of the research in this field has targeted wild equids before domestication, which are difficult to identify to species level and are assumed to behave similarly, the available equations were all designed to be applied to all equid species, wild or domestic. The first equation was developed by Bryant and Froelich

(1995) and additional datasets were integrated by Kovács *et al.* (2012) to produce the following new equation:

$$\delta^{18}O_{PO4} = 0.97 \times \delta^{18}O_{scSMOW} - 7.94 \quad (R^2 = 0.99) \qquad (1)$$

This differs slightly from the original equation (Bryant *et al.*, 1996):

$$\delta^{18}O_{sc}(\pm 1.3) = 1.02(\pm 0.04) \times \delta^{18}O_{PO4} + 8.3(\pm 0.7) \quad (R^2=0.986) \qquad (2)$$

and a different equation proposed by Iacumin *et al.* (1996) for all species:

$$\delta^{18}O_{PO4} = 0.98 \times \delta^{18}O_{scSMOW} + 8.5 \quad (R^2=0.98) \qquad (3)$$

The equation from Bryant *et al.* (1996) could not be applied; since the data were not published in full, it was not possible to inverse or transpose the equation for the calculation of $\delta^{18}O_{PO4}$. While there is only a slight difference between conversions produced by equations (1) and (3) (roughly 0.3 after conversion), equation (1) is used in the current thesis as it was specifically developed for equids.

The second step was to convert the $\delta^{18}O_{PO4}$ value into $\delta^{18}O_{DW}$ equivalent. Similar to the previous conversion, there should be a species-specific equation to precisely describe $\delta^{18}O_{DW}$ in different species, but this was not available due to practicality and sample availability. Different scholars have suggested several different equations for this conversion (see discussion in Pryor *et al.*, 2014). Most of the dataset used to derive equation (1) included a wide range of equine species for the benefit of palaeontologists, who do not always know the species of the fossil under study and require data outside of domestic equids. Even though it has been argued that most of these equations differ slightly from each other (Delgado Huertas *et al.* 1995) and are often used without associating the original dataset with the studied dataset, when tried with current outcomes from the current thesis, it was found that the differences could be greater than 1‰. Such

differences could have a serious impact on the interpretation. For example, when using the equation suggested in Pryor *et al* (2014), nearly all converted values were lower than -8.0‰, thus indicating that none of the analysed specimens are local to their site location while the other equations argued differently. One possible cause for the large difference may be that these equations are mainly applied to faunal fossils found before the Pleistocene period for the purpose of palaeo-environmental temperature reconstruction. As a result, it was necessary for the current research to use a more species-specific equation since the current thesis focuses specifically on domestic equids in the historical era, which may have behaved quite differently from their wild relatives. Nevertheless, it is suggested that animals reared under domestic settings tend to produce less reliable isotopic values (D'Angela and Longinelli, 1990; Bryant *et al.*, 1994; Sánchez Chillón *et al.* 1994). The following equation is proposed by Sánchez Chillón *et al.* (1994) using mainly *Equus caballus* (feral and domestic) as well as a few *Equus asinus* and, therefore, it is considered more adequate for the current research than other equations with datasets that include zebras:

$$\delta^{18}O_{PO4} = 0.7369(\pm 0.083) \times \delta^{18}O_{DW} + 22.04\ (\pm 0.604)\ (R^2=0.95) \quad (4)$$

Similar to equation (1) above, this equation needs to be transposed to calculate the $\delta^{18}O_{DW}$ value. Fortunately, it had been transposed by Skrzypek *et al.* (2011) from an original dataset as follows:

$$\delta^{18}O_{DW} = 1.29 \times \delta^{18}O_{PO4} - 28.7 \quad (R^2=0.95) \quad (5)$$

It is important to keep in mind that each equation used has its own uncertainty and, therefore, the more conversions there are, the greater the uncertainty will be. As mentioned in the beginning, it is best to compare the results directly, that is, to compare $\delta^{18}O_{scSMOW}$ with $\delta^{18}O_{scSMOW}$ to avoid the loss of accuracy in data conversion. Unfortunately, this can be done only if the data are from the same species and expressed with the same unit as in

the published data. Isotopic research on historic/domestic equids or animals in general is relatively rare compared to research on humans. As a result, only a handful of sources allow a direct comparison of raw data. In the following section, raw data are compared directly whenever possible, and only when attributing the outcomes to geological regions is the conversion made by using above equations.

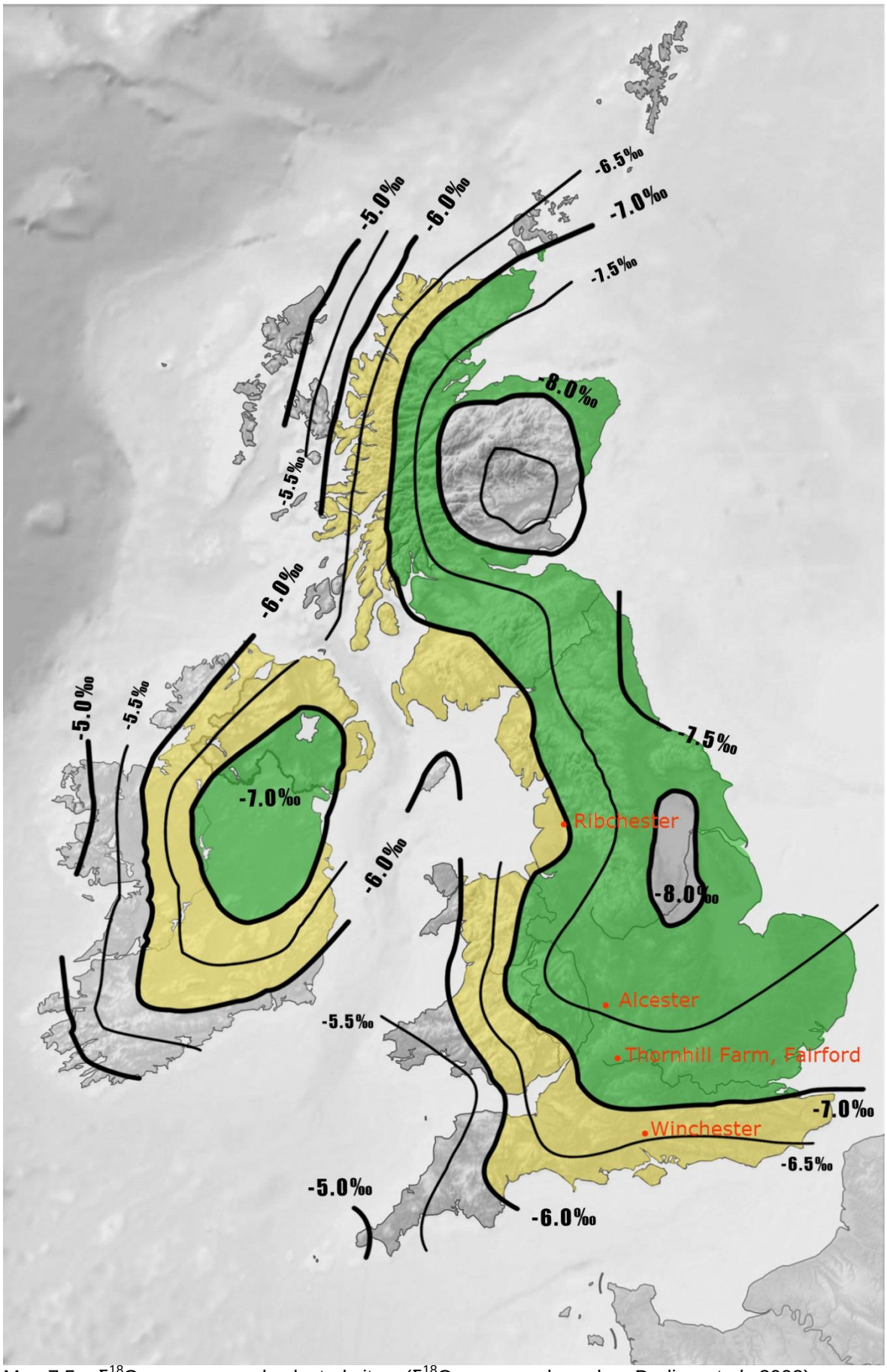
There is no need for the outcomes of strontium isotopic analysis to be converted and, therefore, the raw data from strontium isotopic analysis can be compared directly between individuals and with the local range.

The $\delta^{13}C$ values produced with oxygen isotopic analysis are also measured on structural carbonate and, therefore, need to be converted into a value that can represent palaeovegetation. It is suggested that there is a constant offset of 14‰ between the two values (Kohn and Cerling, 2002) and, therefore, the conversion is made by applying the following simple equation:

$$\delta^{13}C_{PV} = \delta^{13}C_{SC} - 14(‰) \quad (6)$$

In order to determine the localness of any specimens, it is necessary to first define the local range. The challenge for defining the local range is that the area considered as "local" can fluctuate depending on the subject and scale, not to mention the limitation for the type of isotopic analyses applied. For the current thesis, the determination of localness was largely determined by the oxygen isotopic values, and the strontium isotopic ratio was used to confirm the localness suggested by its oxygen value. The immediate local area defined by the current thesis was represented by the area within 10 kilometres of the site in question

while a larger catchment area with a radius of 50 kilometres was also considered since domestic equids are more mobile than other livestock. Using Winchester as an example, the $\delta^{18}O_{DW}$ range for most of the immediate local area is between -6.5‰ to -7.0‰ and the range would extend to between -6.0‰ to -7.5‰ when considering a larger catchment area. Previous studies have argued that the determination of a local $\delta^{18}O$ range for the UK using archaeological specimens can be problematic because of the possible errors resulting from different conversion equations (Evans *et al.*, 2006; Eckardt *et al.*, 2009; Müldner *et al.*, 2011; Chenery *et al.*, 2012; detailed in Chenery *et al.*, 2010). As a result, to determine an individual as local, researchers often rely on combining the strontium isotopic ratio with the comparison of $\delta^{18}O_{PO4}$ values from samples known to be local. Unfortunately, no existing domestic equid data are available for the current thesis to compare the results with, and thus the local $\delta^{18}O_{DW}$ range in this thesis is based on the map from Darling *et al* (2003). However, as pointed out in Evans *et al.* (2012b), since values above -4.5‰ are limited to a certain region, the $\delta^{18}O_{DW}$ range considered to be local for UK in current thesis is between -9.0‰ to -5.0‰.



Map 7.5 – $\delta^{18}O_{DW}$ ranges and selected sites. ($\delta^{18}O_{DW}$ ranges based on Darling *et al.*, 2003). Note that the green belt (-7.0‰ to -8.0‰) and the yellow belt (-6.0‰ to -7.0‰) occupy the majority regions in the UK.

7.5.1 – Results of Oxygen Isotopic Analysis by Site

7.5.1.1 Winchester

Being the most equid-rich Roman site in the current thesis, 15 teeth were selected from the Winchester site complex. Based on the dental morphology (see previous section and Table 7.2), there are 13 horses and 2 possible mules. Nearly all domestic equids fall within the modern local drinking water range, except one individual (VR-1594), which had a lower oxygen isotopic value indicating it was from a colder or drier environment (Table 7.3 and Figure 7.3). Both possible mules are grouped relatively closely, indicating that they were from a similar climate. However, the horses had a much wider oxygen isotopic range.

Winchester is the most southern site in the current thesis and is located in the -6.5 to -7.0‰ zone based on the $\delta^{18}O$ value for modern groundwater (Map 7.5). Theoretically, its immediate local oxygen isotopic range should be within this value range. Given that Winchester is near the border line between two gradient zones, most of the outcomes fit the local values quite nicely, suggesting that domestic equids in Roman Winchester were likely to be from surrounding areas either north (-7.0 to -8.0‰, the green belt) or south (-6.0 to -7.0‰, the yellow belt). The individual with a low $\delta^{18}O$ value (-8.50‰) would have been from an area such as eastern Scotland if not from the continent.

The two possible mules also have similar $\delta^{18}O$ values indicating that they were also from a similar environment. However, it should be noted that the oxygen isotopic value alone cannot fully represent the definitive origin of the individual since the $\delta^{18}O$ value represents only the environment the individual lived in during tooth formation.

ID Context	Species	Tooth	$\delta^{18}O_{scSMOW}$	Std. dev.	$\delta^{18}O_{DW}$
VR-3136	Horse	P_2	26.13	0.15	-6.24
VR-440	Horse	P_2	25.18	0.18	-7.43
HA-75	Horse	P_4	25.63	0.21	-6.87
NR-495	Horse	P_2	25.78	0.07	-6.68
VR-410	Horse	$M_{1/2}$	25.41	0.07	-7.14
VR-2608	Horse	$P_{3/4}$	25.36	0.09	-7.21
VR-1594	Horse	$M_{1/2}$	24.33	0.08	-8.50
VR-1280	Horse	M_1	25.17	0.10	-7.45
HA-99	Horse	$M_{1/2}$	25.70	0.05	-6.79
HA-13	Horse	$M_{1/2}$	25.87	0.06	-6.57
NR-113	Horse	M_1	25.49	0.08	-7.04
NR-557	Horse	$M_{1/2}$	25.81	0.17	-6.65
CT-225	Horse	$M_{1/2}$	24.94	0.07	-7.73
VR-481	Possible Mule	P_2	25.55	0.06	-6.97
VR-405	Possible Mule	$M_{1/2}$	25.14	0.21	-7.48

Table 7.3 – $\delta^{18}O$ values of Winchester specimens

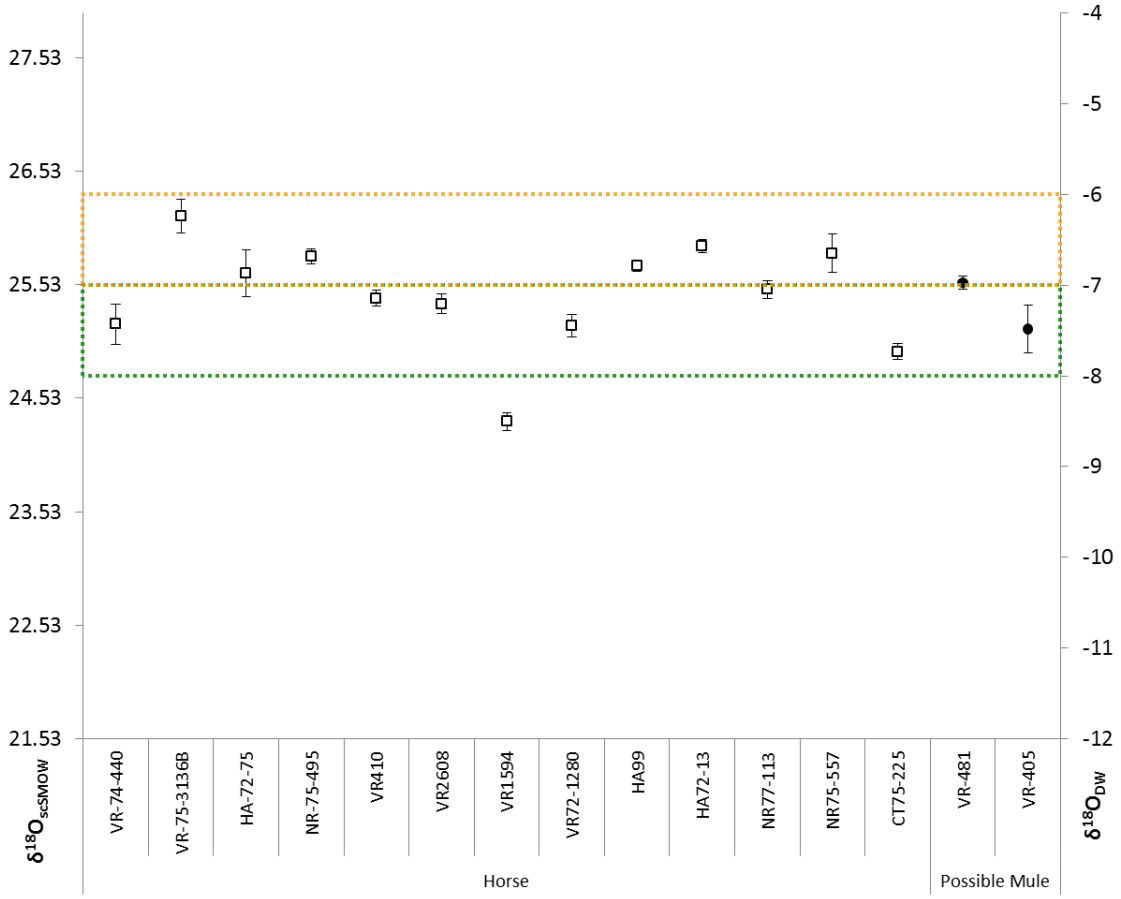


Figure 7.3 – The $\delta^{18}O$ distribution of Winchester specimens.
The dashed yellow and green box represents two different zones: -6.0 to -7.0‰ (yellow) and -7.0 to -8.0‰ (green) in Map 7.5.

7.5.1.2 Alcester

Of the four equid teeth from Alcester, three were identified as horses and one as a possible mule. The three horses from the site have a very narrow oxygen isotopic range while the possible mule has an elevated value that implies a warmer or wetter origin (Table 7.4 and Figure 7.4). All three horse individuals are located within the -7.0 to -8.0‰ zone, which is very close to the immediate local range of -7.5 to -8.0‰, suggesting that all three horses were likely to have been obtained from the nearby area. Such uniformity of the $\delta^{18}O$ values may also imply a single supply source for horses, which is different from the possible mule. Furthermore, the $\delta^{18}O$ value of the possible mule is markedly different from that of the possible mules from Winchester, indicating that there were perhaps at least two different sources supplying mules.

ID Context	Species	Tooth	$\delta^{18}O_{scSMOW}$	Std. dev.	$\delta^{18}O_{DW}$
ALC-5175	Horse	$P_{3/4}$	25.35	0.05	-7.23
ALC-1020	Horse	P_2	25.21	0.03	-7.40
ALC-1147	Horse	P_2	25.05	0.03	-7.60
ALC-3002	Possible Mule	$M_{1/2}$	26.38	0.04	-5.94

Table 7.4 – $\delta^{18}O$ values of Alcester specimens

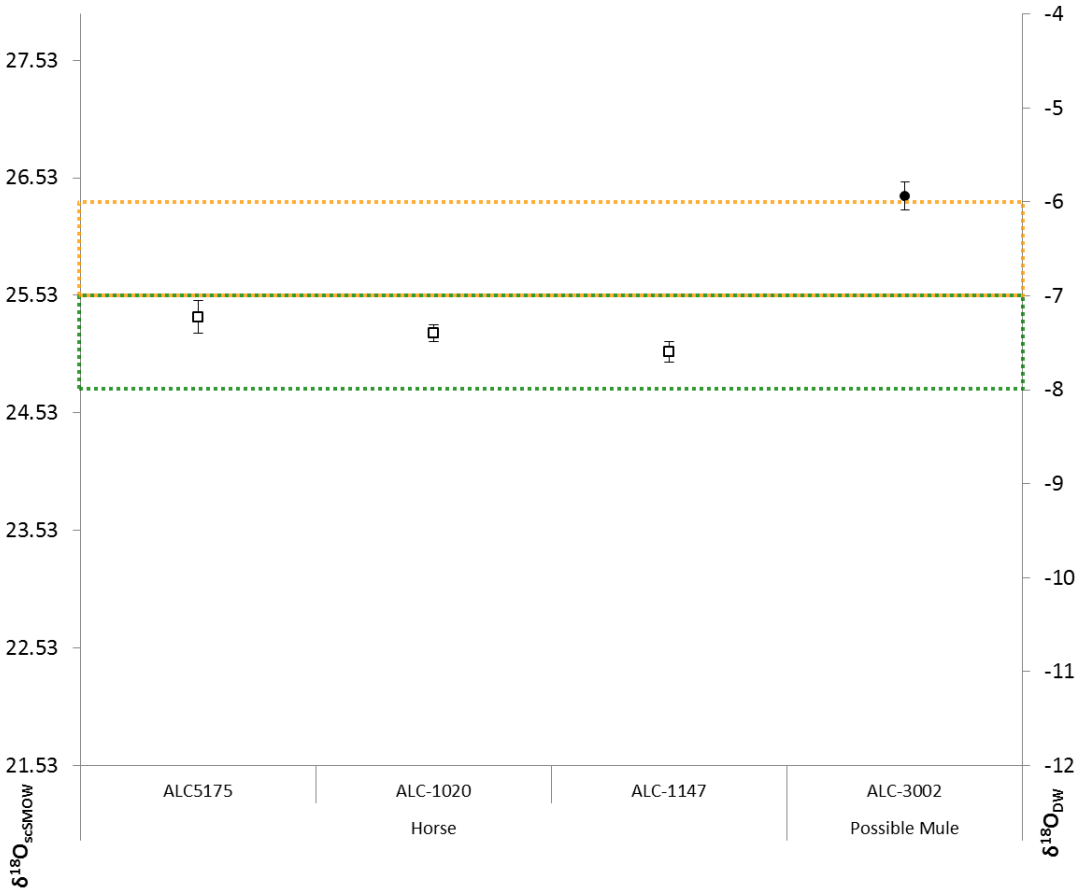


Figure 7.4 – The $\delta^{18}O$ distribution of Alcester specimens.

7.5.1.3 Ribchester

The Ribchester site is represented by seven horse teeth as well as one from a possible mule. Compared to the Winchester samples, samples from Ribchester form a narrower cluster (Figure 7.5); indicating that these domestic equids were likely to have been bred in a similar environment. The possible mule has a $\delta^{18}O$ value similar to those identified from the Winchester assemblage (Table 7.5), but different from that of Alcester.

ID Context	Species	Tooth	$\delta^{18}O_{scSMOW}$	Std. dev.	$\delta^{18}O_{DW}$
RB-259	Horse	P_2	24.73	0.04	-7.99
RB-743	Horse	P_2	25.20	0.04	-7.40
RB-989	Horse	$M_{1/2}$	25.22	0.04	-7.39
RB-254	Horse	P_3	25.38	0.07	-7.19
RB-9069	Horse	M_2	25.55	0.09	-6.97
RB-8078	Horse	P_2	25.67	0.07	-6.83
RB-5053	Horse	$P_{3/4}$	24.65	0.08	-8.09
RB-728	Possible Mule	P_2	25.10	0.04	-7.54

Table 7.5 – $\delta^{18}O$ values of Ribchester specimens

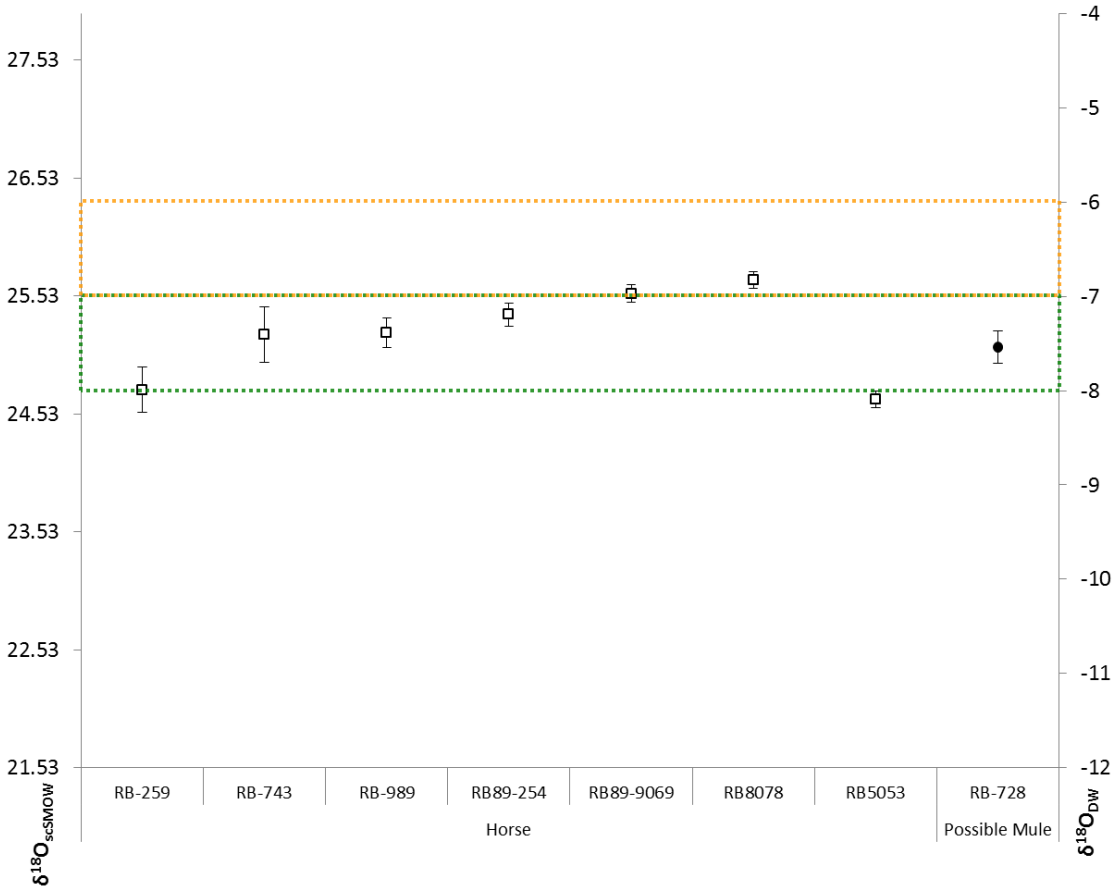


Figure 7.5 – The $\delta^{18}O$ distribution of Ribchester specimens.

7.5.1.4 Fairford, Thornhill Farm

Nine equid teeth were selected from Fairford including the only identification of a donkey. The oxygen isotopic value of this donkey is rather surprising as it suggests an origin with less rainfall or from a more inland region rather than a warmer region such as the coastal Mediterranean (Table 7.6 and Figure 7.6). This low $\delta^{18}O$ value nearly falls outside of the lower limit for modern Britain's groundwater values which may imply that this individual had been imported. A $\delta^{18}O$ value this low would have been available in only a limited region within the Roman Empire including the mountain regions, such as the Alps or Pyrenees, or an inland region, such as southern Germany (Map 7.6). It is generally assumed that donkeys were more commonly used and, therefore, bred in coastal Mediterranean regions where the $\delta^{18}O$ value would have been much higher. Other factors cause such a low $\delta^{18}O$ value, such as differences in the metabolic system or the general liquid intake of the animal (amount of water or the source of water), but the question cannot be answered with only the current data.

The horses, on the other hand, seem to have a comparatively narrower range with the exception of one individual (FTF-2229), which has an enriched $\delta^{18}O$ value implying a warmer/coastal origin. Other than this outlier, the remaining seven horses are scattered in a closely clustered pattern that is relatively similar to Ribchester. Such a pattern suggests that the horses at Fairford were supplied mainly by a single source; but that a few individuals were acquired from different sources.

ID Context	Species	Tooth	$\delta^{18}O_{caSMOW}$	Std. dev.	$\delta^{18}O_{DW}$
FTF-2052	Horse	P_3	25.23	0.08	-7.38
FTF-369	Horse	P_3	25.03	0.09	-7.62
FTF-14	Horse	$M_{1/2}$	24.66	0.10	-8.09
FTF-857	Horse	$M_{1/2}$	25.38	0.09	-7.18
FTF-1039	Horse	$M_{1/2}$	25.05	0.07	-7.60
FTF-2229	Horse	M_1	26.31	0.06	-6.02
FTF-250	Horse	$M_{1/2}$	25.18	0.09	-7.43
FTF-3124	Horse	$M_{1/2}$	24.70	0.07	-8.03
FTF-2459	Possible Donkey	$M_{1/2}$	23.98	0.11	-8.93

Table 7.6 – $\delta^{18}O$ values of Fairford specimens

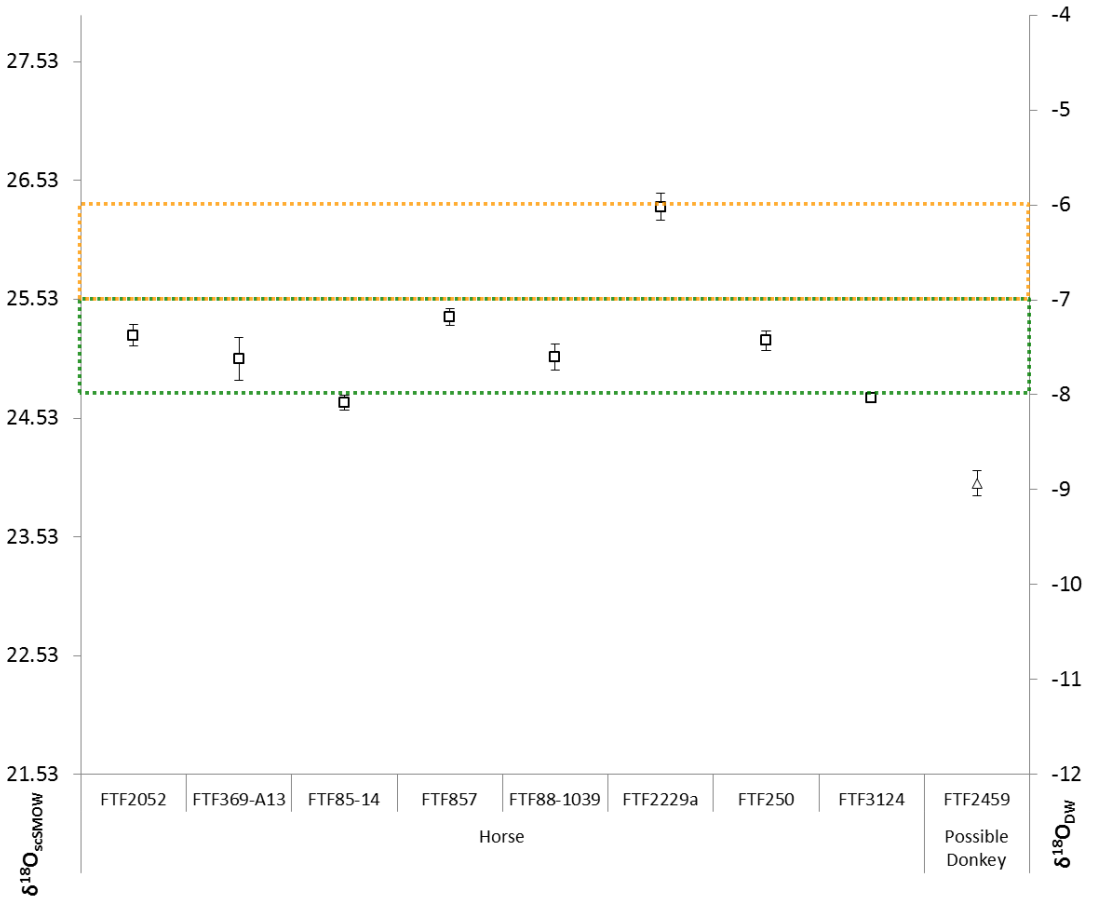
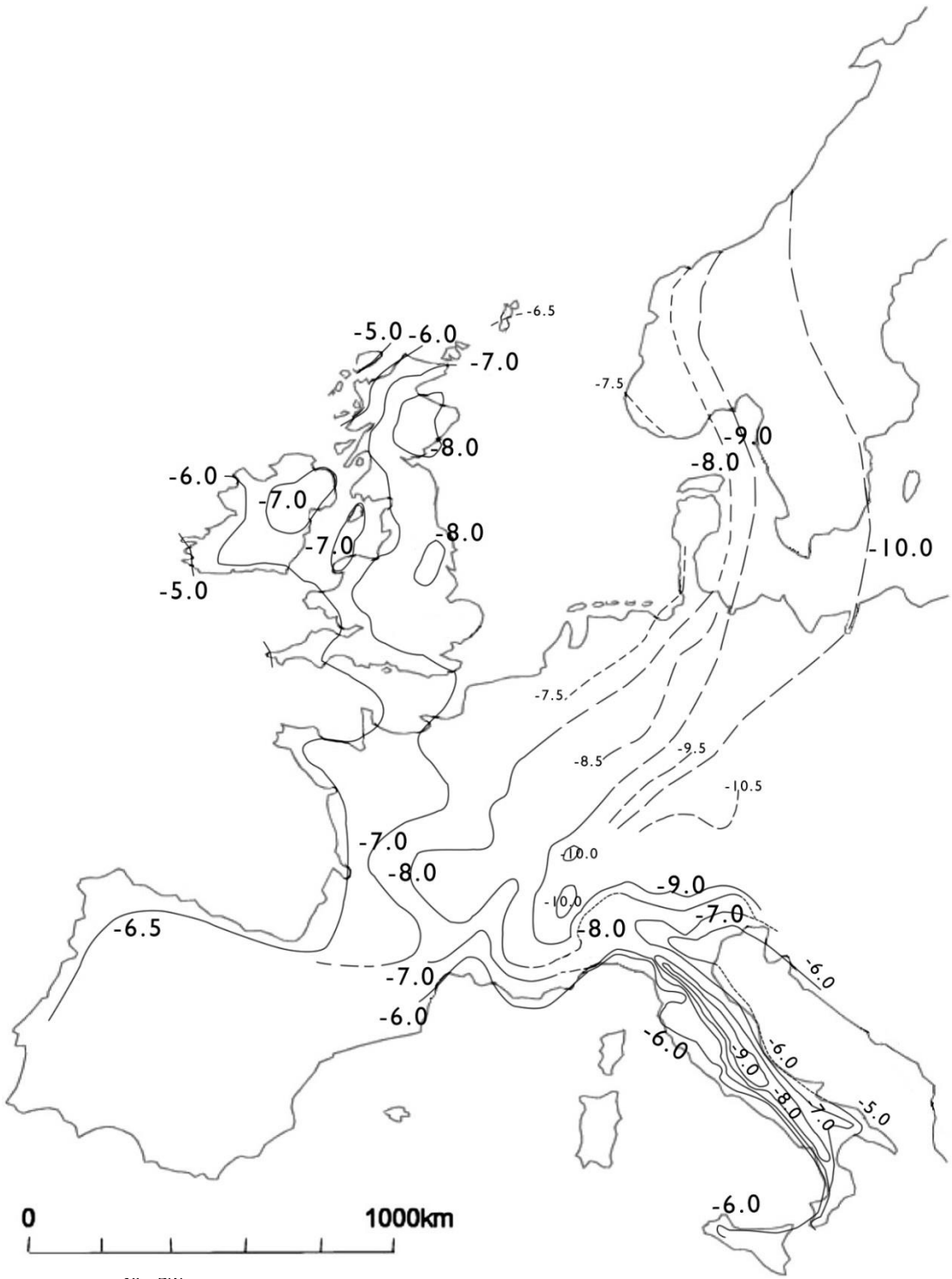


Figure 7.6 – The $\delta^{18}O$ distribution of Fairford specimens.



Map 7.6 – $\delta^{18}O^{DW}$ contour map of Europe (adapted from Hughes *et al.*, 2014 and Schwarcz *et al.*, 2010)

7.5.1.5 Serbian sites

The oxygen isotopic values for all three species of domestic equids from Serbian sites seem to suggest a unique origin of their own, as they are separated from each other (Table 7.7 and Figure 7.7). The modern local drinking water range for Serbia is assumed to be

slightly higher than the range for Britain (-7.0 to -9.0‰, according to Map 7.6). While both mules are within this value range, the tooth of the donkey and horse resulted in lower values, indicating a more inland or colder origin. The horse, in particular, has an extremely low oxygen isotopic value, which suggests an origin that is further east in the Caucasus mountain region or from the Alps in the north-west.

The $\delta^{18}O$ values of the non-caballine domestic equids from the Serbian sites are similar to those found in Roman Winchester and Ribchester. That is, both mules fall into the -7.0‰ to -8.0‰ range. Interestingly, the Serbian donkey also has a surprisingly low $\delta^{18}O$ value in the -9.0‰ to -10.0‰, range which indicates that it was also from an inland region with a high altitude environment. This is contrary to the common impression of donkeys being commonly used and bred in the warmer Mediterranean region especially since Serbia is relatively close to the Mediterranean coast.

ID Context	Species	Tooth	$\delta^{18}O_{caSMOW}$	Std. dev.	$\delta^{18}O_{DW}$
SERB01	Horse	P_2	21.91	0.14	-11.53
SERB03	Donkey	P_3	23.60	0.04	-9.42
SERB02	Possible Mule	M_2	25.39	0.12	-7.17
SERB04	Possible Mule	P_4	25.05	0.08	-7.60

Table 7.7 – $\delta^{18}O$ values of Serbian specimens

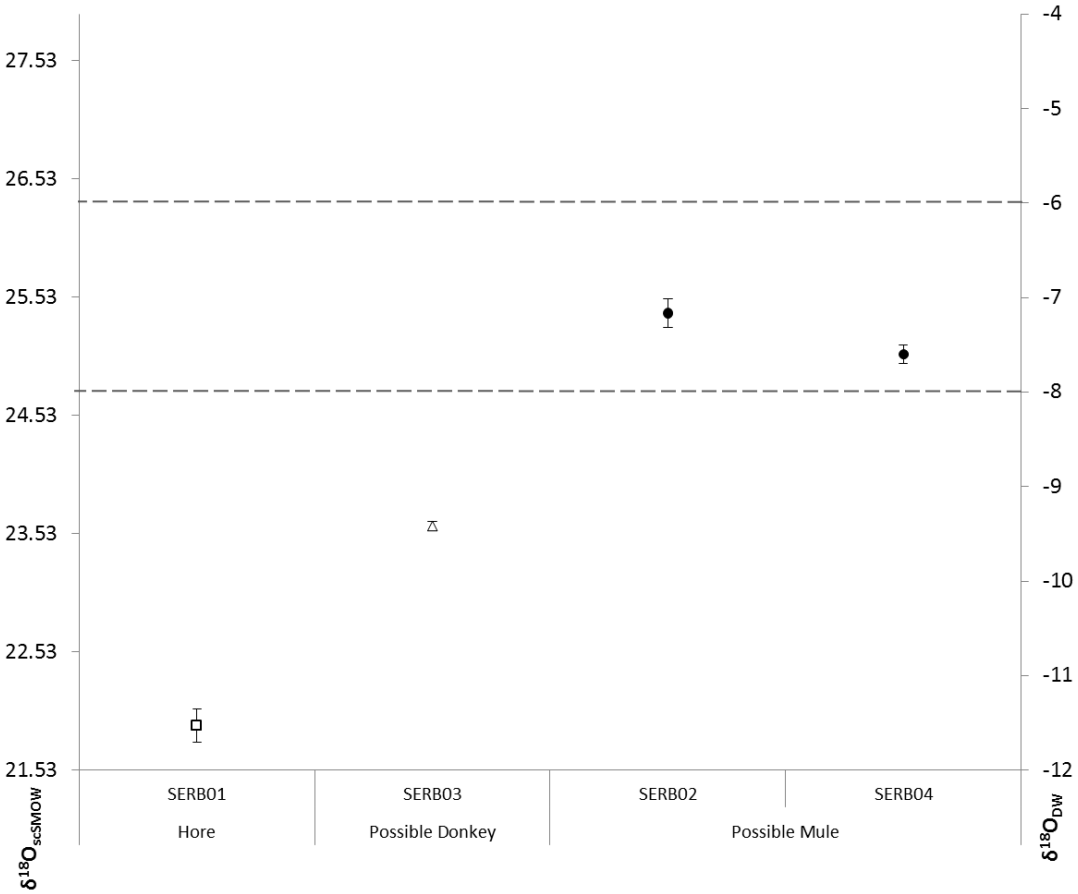


Figure 7.7 – The $\delta^{18}O$ distribution of Serbian specimens.

7.5.1.6 Comparison between Oxygen Isotopic Data

In addition to these five Roman sites (four British and one Serbian), two additional archaeological sites with published $\delta^{18}O$ values for domestic equids from a similar time period (one Roman and one early medieval) were included to observe possible patterns that might reveal some evidence for different domestic equid procurement strategies. Unfortunately, as mentioned above, very little isotopic analysis has been done on archaeological domestic equids and, therefore, not all published sites have been analysed with the same isotopes or lists made of the raw data. As a result, both $\delta^{18}O_{scSMOW}$ and $\delta^{18}O_{DW}$ are used as the axis in the figure allowing a comparison to be made. In addition, the time range for additional sites is no longer restricted to the Roman period so that more archaeological domestic equids can be included for comparison.

Four horses with published $\delta^{18}O_{scSMOW}$ values from an early medieval site of Velim-Velištak, Croatia, were available from a study on water consumption of the region (Lightfoot *et al.*, 2014). All four horses are from the early medieval phase of the site and have relatively "typical" $\delta^{18}O$ values for Mediterranean coast of between -4.9‰ to -7.5‰. As well as these four horses, the lower fourth premolar (P_4) of one Roman mule (identified based on physical morphology) from Weißenburg, Germany was analysed in longitudinal sections to represent its life history (Bergers *et al.* 2010). Although a whole series of data were obtained from different parts of the tooth (as well as the alveolar and mandibular bone), only the average $\delta^{18}O$ values from enamel are used for comparison. This is because the current study focuses on the environment before the age of three which can best represent the breeding ground. The average $\delta^{18}O_{DW}$ value from enamel is -8.1‰, which is within the local range of the site but also overlaps with most inland continental regions.

When considering all domestic equids regardless of the species, the distribution range of each site differs from that of others (Figure 7.8). Among Romano-British sites, Fairford has the widest distribution range of oxygen isotopic values while Ribchester has the narrowest range. However, as noted in the previous section, the wide variation in the Fairford assemblage is caused mainly by having one horse with an extremely enriched $\delta^{18}O$ value and one donkey with a markedly low $\delta^{18}O$ value. All the other horses seem to scatter relative closely in between these values. Thus, the distribution range would change if only the results on horses were used. Meanwhile, the distribution of domestic equids from Serbian sites significantly exceeds that from all British sites. Despite consisting of only four samples representing two different sites, the level of dispersion is still significantly greater than for Roman Britain in general. Furthermore, this wide distribution range for Serbian domestic equids is also observed in a different continental site. The oxygen isotopic values of four domestic equids (presumably all horses) from the early

medieval site of Velim-Velištak, Croatia also demonstrate a similar type of wide distribution range. This difference in distribution range may indicate that there were fewer domestic equid supply centres for Britain than in the northern Balkans, where the catchment area for domestic equids would have included a much wider geographical region.

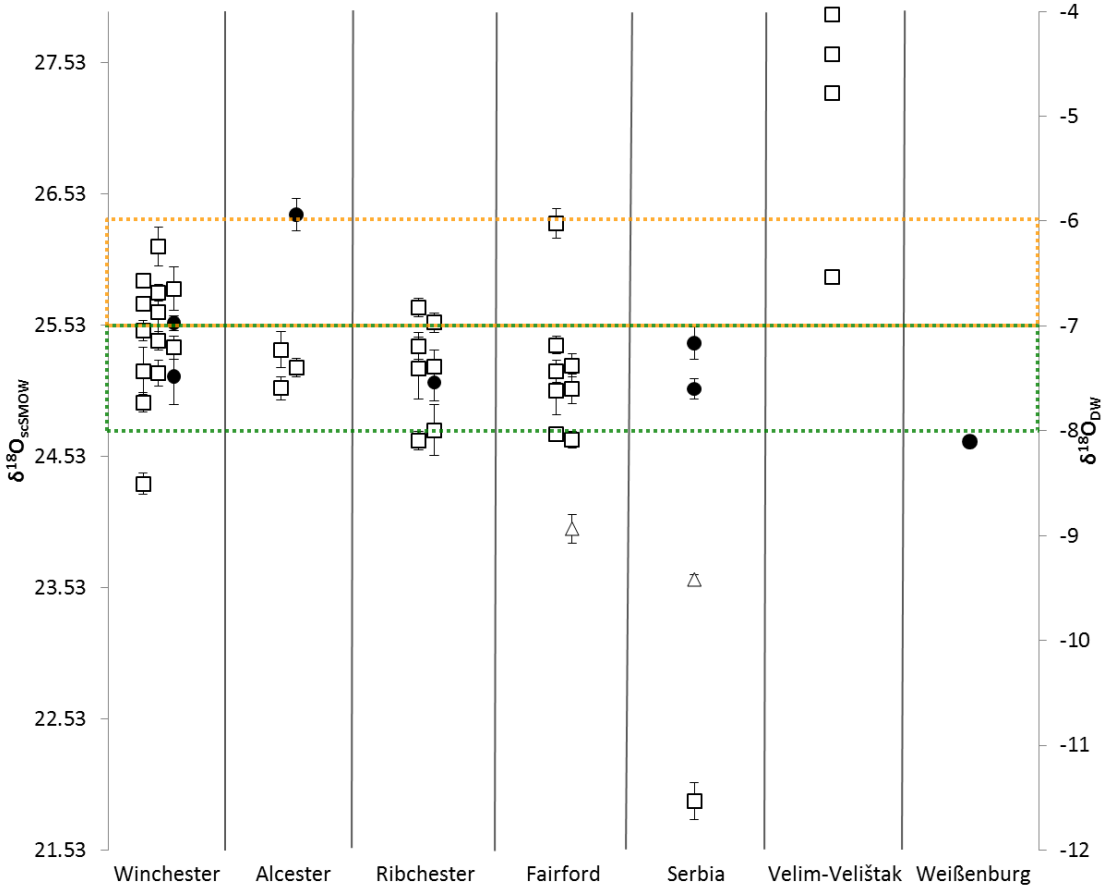


Figure 7.8 – Distribution of $\delta^{18}O$ values by sites.
Horses are represented by squares, possible donkeys are represented by triangles, and possible mules are the black dots.

Since there are only a few donkeys and mules from the assemblage, it was thought it might be more meaningful to exclude them from further comparison. It should be reiterated that there is still a chance that some of these mules are, in fact, horses. However, even if they all turned out to be horses, it would only affect the pattern for the Alcester and the Serbian sites since the possible mules from other sites all tend to scatter with the horses. After the removal of the other two domestic equid species, Winchester has the greatest range for oxygen isotopic values, instead of Fairford (Figure 7.9), while the three horses from

Alcester form a closely scattered array representing the narrowest range of all four UK sites. The contrast between these two sites may be due to the difference between their site function, and the patterns fit well with the hypothesised scenarios described at the beginning of this chapter. Winchester is known to have been an urban settlement in Roman times (Maltby, 2010), and Alcester is argued to be a putative fort based on a few military-related finds (Booth and Evans, 2001). As an urban settlement, the level of human activities will be much more complicated than for rural settlements or military forts. Nevertheless, the limited land space will have restricted any large-scale animal reproduction taking place within the urban range. As a result, in order to fulfil the large demand of livestock for meat and labour, it was probably necessary to extend the catchment area to include more possible supply sources. A similar conclusion is implied by the strontium isotope analysis on the Iron Age and Roman cattle from Owslebury site (Minniti *et al.*, 2014).

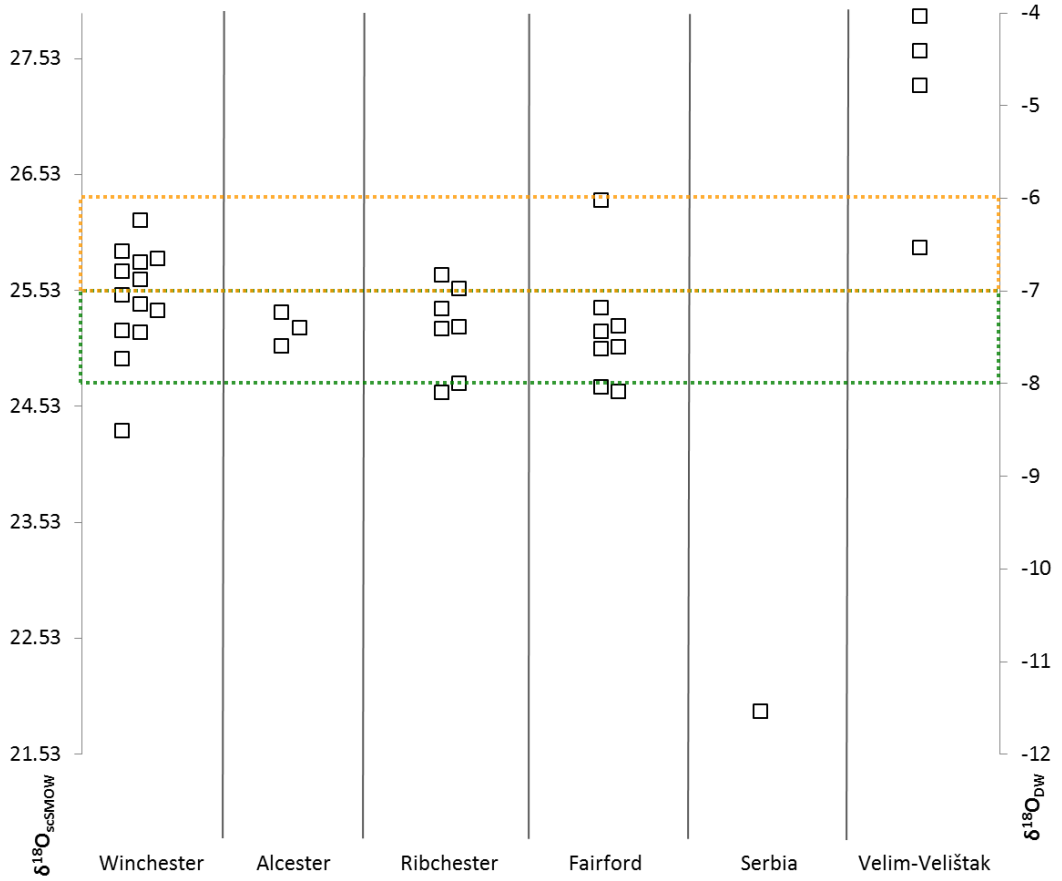


Figure 7.9 – The $\delta^{18}O$ distributing patterns of horses by sites.
Note that Winchester equids demonstrate a wider range of catchment area.

In contrast to Roman Towns, military sites were function specific and so had fewer non-military activities. Although it is nearly impossible to determine any archaeological horse remains as warhorses, it is still interesting to see that the narrow range of $\delta^{18}O$ values seems to suggest a more restricted horse-supply scheme for both military sites. A further indication of such a pattern is that the procurement of military horses may have been limited to a few authorised suppliers. The Roman legal documents, such as *Codex Theodosianus*, have specific sections on the high standard that needed to be fulfilled for a qualified military horse and the penalty for any horse examiner accepting bribes for passing unqualified horses (Hyland, 1990; Dixon and Southern, 1997). This is somewhat supported by comparing Winchester to both Alcester and Ribchester. Ribchester is a known military fort site. Similar to Alcester, the data distribution of Ribchester horses is also narrower than that of Winchester. However, subtle differences exist between the procurement strategies of Alcester and Ribchester. All Alcester horses have $\delta^{18}O$ values that fit with immediate surrounding while this is not the case with the horses from Ribchester. One possible reason is that, according to Map 7.5, the changes in $\delta^{18}O$ values near Ribchester are more rapid than Alcester due to geological/climatic factors; thus, the chances of acquiring horses from an area with a different $\delta^{18}O$ value will be higher. Furthermore, Ribchester has a longer history as a military fort compared to Alcester. It is possible that these horses represent different phases of the fort. The non-local horses may have been acquired before the army had secured a local source.

However, as mentioned in the previous chapter, Fairford is not known to have been associated with a military context. It is merely a rural settlement with continuous occupation over a relatively long period. It is also suspected to have been a stud farm in the late Iron Age (Miles and Palmer, 1990), even though the lack of foetal and immature equine remains seems to argue against this hypothesis (Levine, 2004). The presence of

donkeys may imply that there may have been some attempts at local mule breeding at Fairford, which is also suggested by Levine (2004, p.129).

The different clustering of data from each site reveals procurement strategies that may correspond to the speculated functions of the sites. However, it is also important to examine whether differences exist between the procurement strategies for these three domestic equids. If the data are arranged so that the isotopic values are grouped by species (Fig 7.10), it is clear that the distribution of horses indicates that they were not from any one particular supplier. Although the distribution pattern of possible mules seems to cluster into two or three groups, the clustering does not correspond to the sites. In other words, individuals from the same site do not cluster together and, therefore, they were not likely to have been from the same source.

In contrast, the $\delta^{18}O$ values obtained from two possible donkeys are somewhat unexpected. As mentioned above, donkeys are generally assumed to be more frequently used in the coastal Mediterranean region where the local $\delta^{18}O$ range would be more positive than in continental inlands. The considerably low $\delta^{18}O$ values of both Roman donkeys imply that both donkeys were likely to have been raised in a region either with a relatively high altitude (>1,500 metres), near a stream where water is mainly supplied by melted snow from the mountains, or from inland on the continent. Nevertheless, as mentioned previously, the conversion to $\delta^{18}O_{DW}$ is based on two equations used mainly for equids in general, which does not account for the possible differences in body size and metabolism between species. Among the three domestic equids, donkeys would be the smallest when considering the relative sizes by modern standard. Therefore, using the same equation for individuals with different sizes may create a systematic offset for those above or below the

average. However, such a possibility is beyond the range of the current thesis and can be raised here only as a possible explanation for the unexpected outcomes.

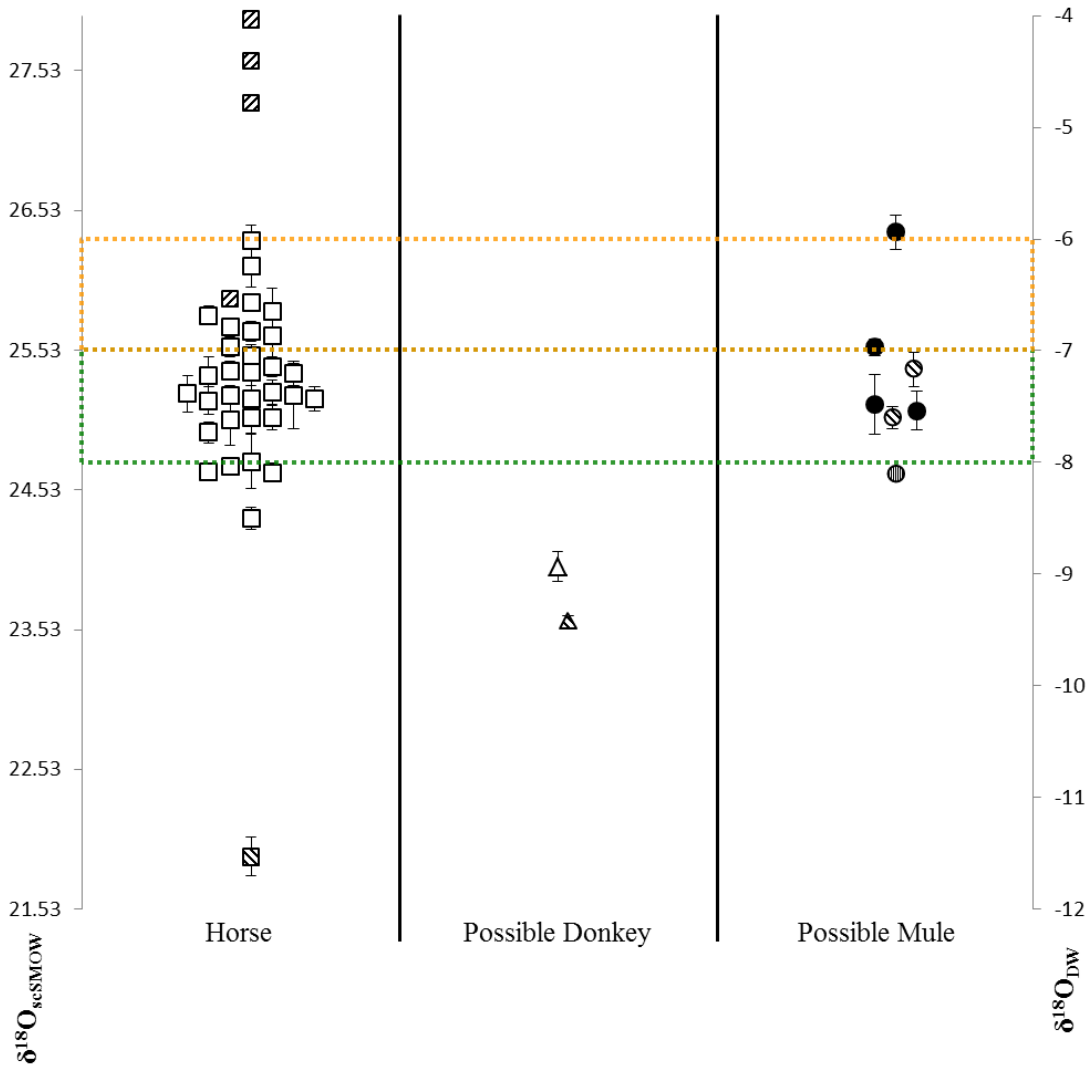


Figure 7.10 – The $\delta^{18}O$ distributing patterns by species.
Note the narrow clustering of British horse samples. Four horses from Velim-Veliš̌tak, Croatia are located at the top (with a backward slash pattern). Samples from the two Serbia sites shows different isotopic oxygen signals for each species (one horse, one possible donkey, and two possible mules, with a forward slash pattern). The Weißenburg possible mule (grey dot) has a different isotopic oxygen value compared to the other possible mules..

7.5.2 – Overview of Carbon Isotopic Results

Carbon isotope ratios from skeletal remains are not usually used to determine the movement and mobility of populations because they represent only the amount of C3 and C4 plants consumed by an individual. However, since the percentage of C3 and C4 plants over the landscape is somewhat related to the climate, possible divergence still may be detected between an area predominated by C3 plants and area where C4 plants are more abundant (MacFadden *et al.*, 1999). For example, there are more C4 plant species in central and southern Europe than in Britain (Pyankov *et al.*, 2010; Collins and Jones, 1986). Thus, it is possible that the percentage of C4 plants intake will differ between continental domestic equids and British ones. For that reason, comparison between $\delta^{13}C$ values is still relevant to the current thesis and the correlation between $\delta^{18}O$ and $\delta^{13}C$ would also be an interesting subject for investigation. Furthermore, the $\delta^{13}C$ values are measured for the same sample as the oxygen isotopic analysis using structure carbonate and, therefore, all samples that have undergone an oxygen isotopic analysis would also have a $\delta^{13}C$ value without any additional cost.

Since it is meaningful only to compare the $\delta^{13}C$ differences between sites, the focus of this section will be detecting the differences between British and continental sites rather than discussing the subtle differences within each site in detail. In order to compare the $\delta^{13}C$ values on a continental scale, the two additional continental sites used for comparing oxygen isotopic values were also included. All data are listed in Table 7.8.

The average of the three continental sites is more positive than all four British sites and a clear separation can be seen in the distribution of $\delta^{13}C$ data (Figure 7.11). This fits with the assumption that the domestic equids from continental sites may have consumed more C4 plants since they are more abundant in central and southern Europe than in Britain.

Individuals with a more negative $\delta^{13}C$ value were found both in continental and British sites, but individuals with a higher $\delta^{13}C$ value were found only in continental sites. It is also interesting to point out that the identified mule from Weißenburg has a series of $\delta^{13}C$ values derived from its premolar (Berger *et al.* 2010) and although the average used here shows no difference from British sites, there are four constant $\delta^{13}C$ values from the dentine of roots, presumably during its four to seven years of age, closer to the continental average (Berger *et al.* 2010, Table 5). However, no reliable conclusion can be made based on this observation since there are many other possible factors that would affect $\delta^{13}C$ particularly for domestic animals which may be fed on fodder. Furthermore, the significant difference between the $\delta^{13}C$ values of the two possible donkeys indicates they are less likely to have had the same origin. In addition, the similarity between their $\delta^{18}O$ values should be further investigated.

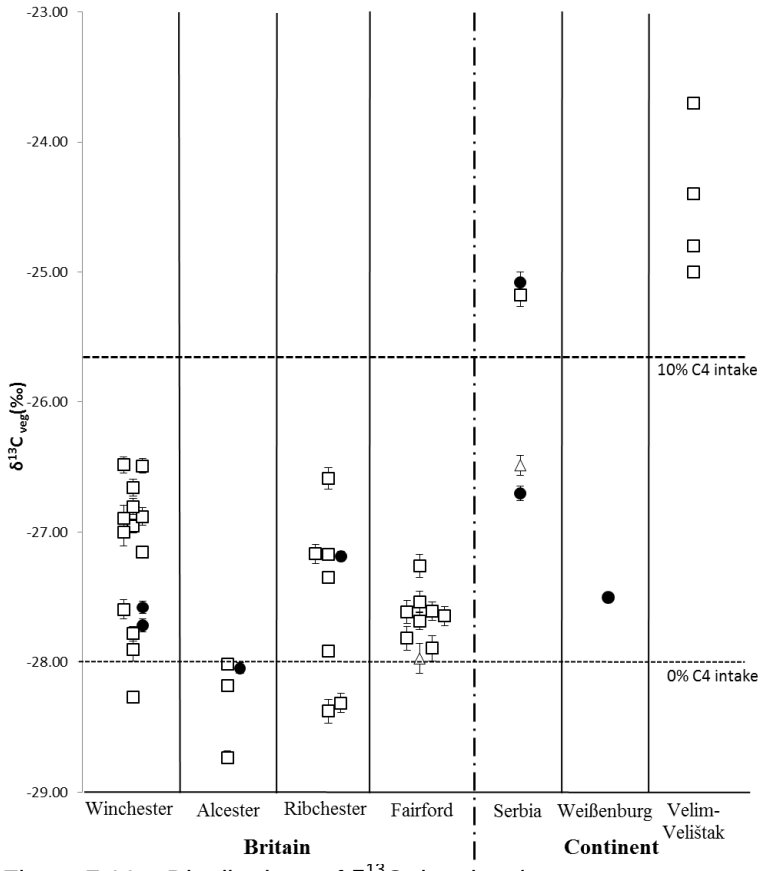


Figure 7.11 – Distributions of $\delta^{13}C$ data by sites.
Horses are represented by squares, possible donkeys are represented by triangles, and possible mules are the black dots
The isotopic values have been converted to represent the palaeovegetation. The black dashed line indicates roughly 10% of intake of C4 plants (estimation based on O'Regan *et al.*, 2008).

No	Context	Species	$\delta^{13}C$ (‰)	No	Context	Species	
1	VR-3136	Horse	-12.95	37	SERB01	Horse	-11.18
2	VR-440	Horse	-13.78	38	SERB02	Possible Mule	-12.70
3	HA-75	Horse	-14.27	39	SERB03	Donkey	-12.49
4	NR-495	Horse	-12.48	40	SERB04	Possible Mule	-11.08
5	VR-410	Horse	-13.90	41	Weißenburg	Possible Mule	-13.5
6	VR-2608	Horse	-12.66	42	Velim-Velištak	Horse	-9.7
7	VR-1594	Horse	-12.89	43	Velim-Velištak	Horse	-11
8	VR-1280	Horse	-12.88	44	Velim-Velištak	Horse	-10.4
9	HA-99	Horse	-13.60	45	Velim-Velištak	Horse	-10.8
10	HA-13	Horse	-12.80				
11	NR-113	Horse	-13.15				
12	NR-557	Horse	-12.49				
13	CT-225	Horse	-13.00				
14	VR-481	Possible Mule	-13.58				
15	VR-405	Possible Mule	-13.72				
16	ALC-5175	Horse	-14.73				
17	ALC-1020	Horse	-14.02				
18	ALC-1147	Horse	-14.18				
19	ALC-3002	Possible Mule	-14.05				
20	RB-259	Horse	-13.91				
21	RB-743	Horse	-13.35				
22	RB-989	Horse	-13.17				
23	RB-254	Horse	-14.32				
24	RB-9069	Horse	-14.38				
25	RB-8078	Horse	-13.17				
26	RB-5053	Horse	-12.59				
27	RB-728	Possible Mule	-13.19				
28	FTF-369	Horse	-13.62				
29	FTF-2052	Horse	-13.54				
30	FTF-14	Horse	-13.89				
31	FTF-857	Horse	-13.82				
32	FTF-1039	Horse	-13.65				
33	FTF-2229a	Horse	-13.68				
34	FTF-250	Horse	-13.26				
35	FTF-3124	Horse	-13.61				
36	FTF-2459	Donkey	-13.97				
Romano-British Sites Mean = -13.52				Continental Roman Sites Mean = -11.43			

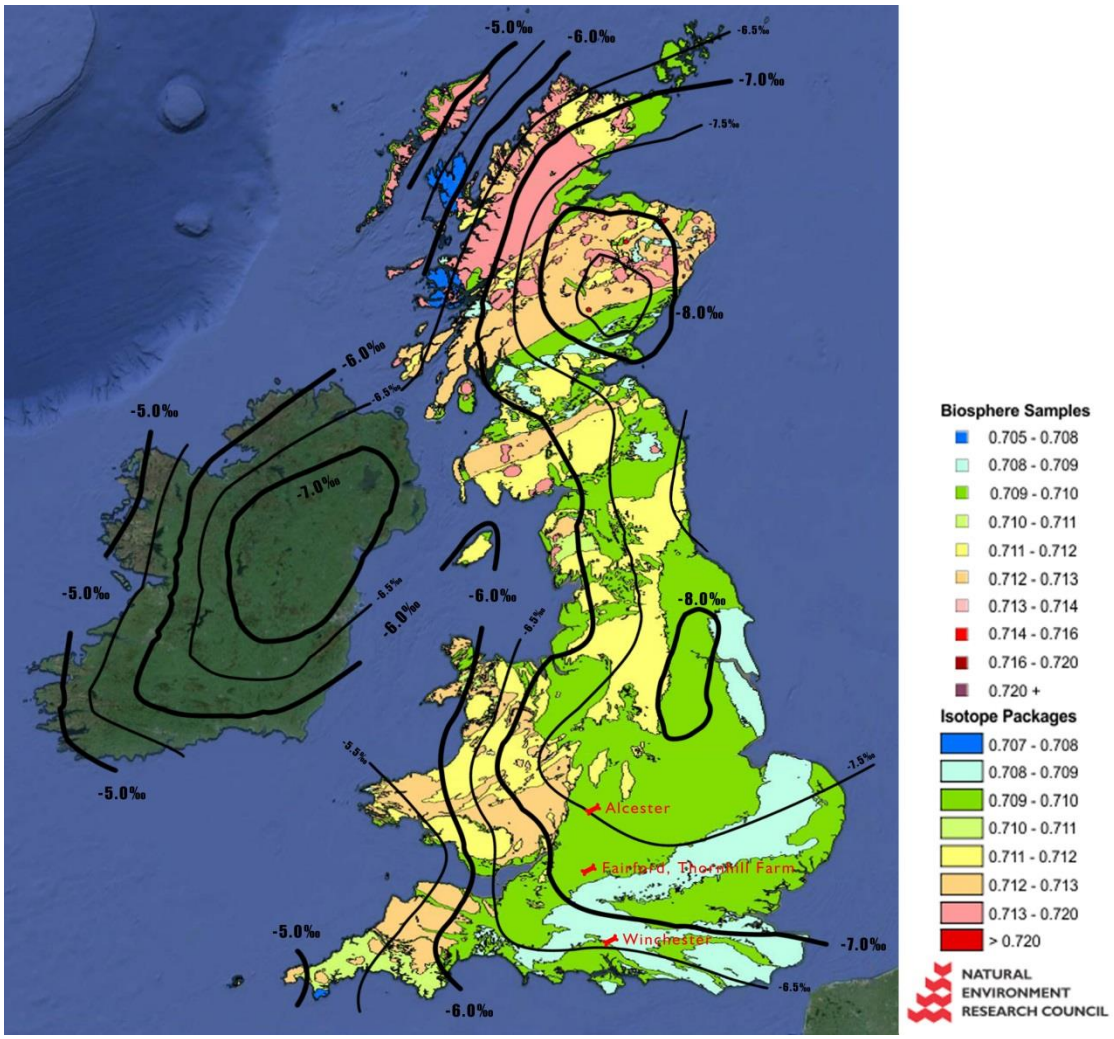
Table 7.8 – $\delta^{13}C$ data of current specimens and published data (Bergers *et al.*, 2010, Lightfoot *et al.*, 2014)

7.5.3 – Results of Strontium Isotopic Analysis

As mentioned earlier, although the strontium isotopic analysis has a clear advantage for understanding the mobility and movement of past populations, it is more accurate for determining the localness of individuals within a known region of origin. For example, an $^{87}Sr/^{86}Sr$ value of between 0.709 and 0.710 can indicate regions including most of southeast Britain, central and northeast Germany, the northwest of the Italian peninsula, and other scattered locations throughout Europe (Map 7.4). However, if the oxygen isotopic value is considered, it is possible to exclude some of these areas not only to increase the accuracy for determining the localness of the samples, but also to narrow down the range for the possible origin. Whilst adding the strontium isotopic analysis to the current thesis provides a better understanding of domestic equid acquisition in Roman Britain, the high cost of the method restricts its application. As a result, only 16 specimens from 3 sites were selected for strontium isotopic analysis (Table 7.9 and Map 7.7), and the results are used to further verify the localness of these 16 specimens as determined by previous oxygen isotopic analysis and to provide further information about their possible origins.

No	Context	Species	Tooth	$\delta^{18}O^{DW}$	$^{87}Sr/^{86}Sr$	±2 std. dev.
1	VR-3136	Horse	P_2	-6.24	0.709777	0.000016
2	VR-440	Horse	P_2	-7.09	0.711864	0.000016
3	HA-75	Horse	P_4	-6.69	0.708448	0.000015
4	NR-495	Horse	P_2	-6.56	0.708609	0.000014
5	VR-410	Horse	$M_{1/2}$	-6.89	0.708296	0.000013
6	VR-2608	Horse	$P_{3/4}$	-6.93	0.709629	0.000014
7	VR-1594	Horse	$M_{1/2}$	-7.87	0.708485	0.000015
8	HA-99	Horse	$M_{1/2}$	-6.63	0.709304	0.000015
9	NR-113	Horse	M_1	-6.82	0.709389	0.000017
10	CT-225	Horse	$M_{1/2}$	-7.31	0.709986	0.000015
11	VR-481	Possible Mule	P_2	-6.76	0.715700	0.000013
12	VR-405	Possible Mule	$M_{1/2}$	-7.13	0.708550	0.000016
13	ALC-1020	Horse	P_2	-7.07	0.710272	0.000016
14	ALC-1147	Horse	P_2	-7.21	0.710947	0.000015
15	ALC-3002	Possible Mule	$M_{1/2}$	-6.02	0.711513	0.000015
16	FTF2459	Possible Donkey	$M_{1/2}$	-8.18	0.710207	0.000016

Table 7.9 – $^{87}Sr/^{86}Sr$ value of the selected 16 specimens.
Listed with converted $\delta^{18}O_{DW}$ values. Specimens that fit the local isotopic signature of the site are highlighted in grey.



Map 7.7 – Locations of selected sites with both oxygen and strontium isotopic analyses.

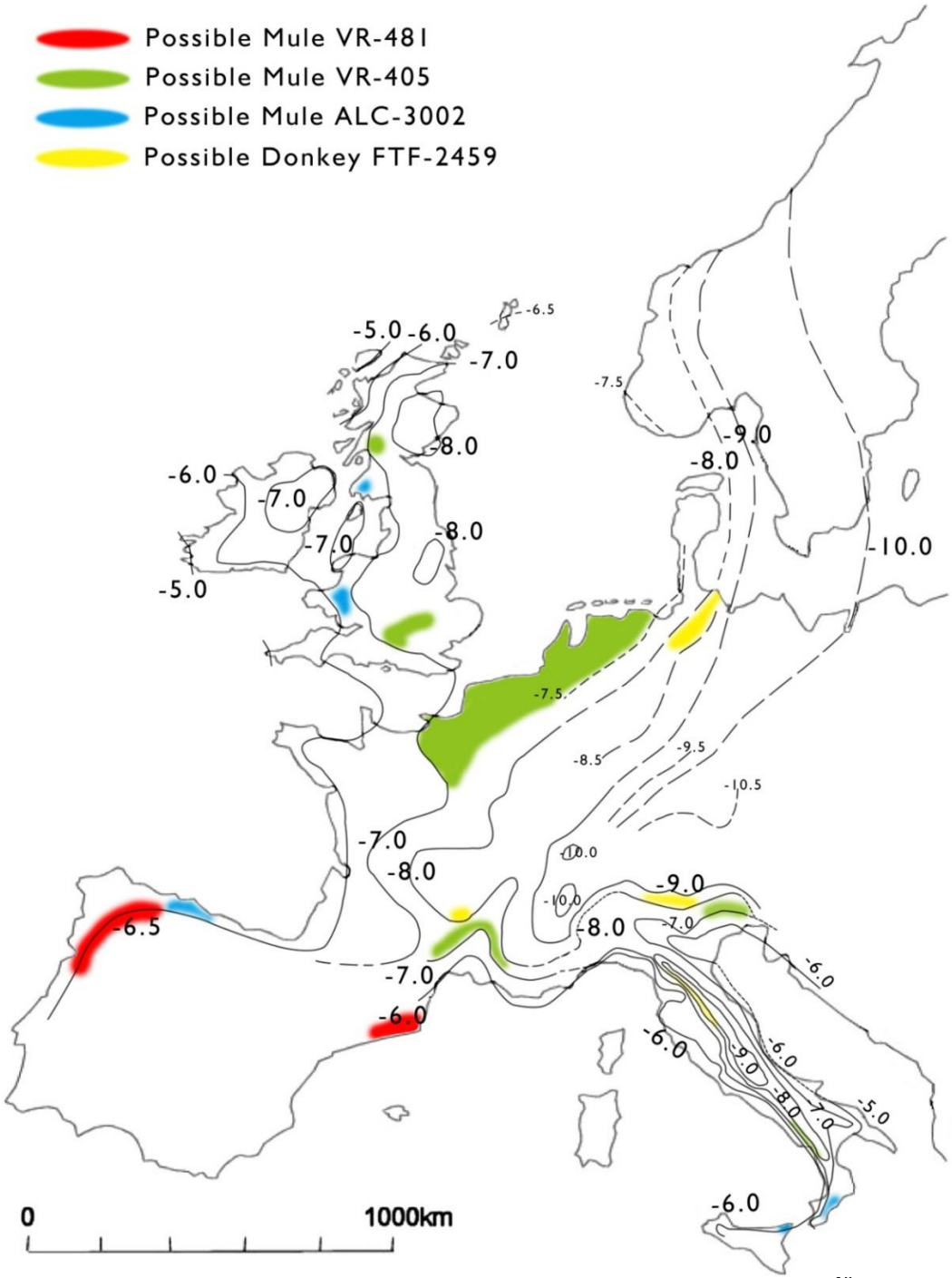
A total of 12 specimens were analysed from Winchester. The results indicate that these 12 specimens are from four different $^{87}Sr/^{86}Sr$ zones: 0.708-0.709, 0.709-0.710, 0.710-0.712, and 0.715-0.715. The local isotopic signature for Winchester has a $\delta^{18}O_{DW}$ range of between -6.0 and -7.0‰ and an $^{87}Sr/^{86}Sr$ range of between 0.708 and 0.710. Areas with a similar isotopic signature can be found only along the same longitude with Winchester, as well as a few scattered areas in Wales, the northwest coast, the northern Orkney Islands of the British Isles, and possibly regions near Rome of continental Europe. Seven of the Winchester horses fit this isotopic signature, and unless evidence can be found supporting the claim that there was large-scale importation of horses from these regions, the Winchester samples with this isotopic signature can be confidently determined as local. On

the other hand, the remaining three horses were likely to have had different origins since their isotopic signatures are not akin to one another. The isotopic signatures of both possible mules also suggest different origins. VR-481 has an $^{87}Sr/^{86}Sr$ value which is atypical for British samples and, therefore, can be determined as a foreign import (Map 7.8). The other possible mule, surprisingly, has an isotopic signature that could be quite local, but it should be noted that this isotopic signature is also common in Europe since it can also be found in most parts of the coastal region of northwest Europe (France, Belgium, Netherland, etc., see Map 7.8)

According to Map 7.7, the local range $^{87}Sr/^{86}Sr$ ratio of Alcester is between 0.709 and 0.710. However, the average strontium isotope ratio of 20 human remains from Wasperton, a Roman and Anglo-Saxon cemetery site only about 20 km to the east of Alcester, suggests that the local strontium ratio range is more likely to be between 0.710 to 0.711(Montgomery *et al.*, 2009). Both of the Alcester horses' isotopic signatures fall into this local range and thus can be determined as local. In contrast, the possible mule has an enriched oxygen isotopic value that places its possible origin to central Wales or the northern coast of the Iberian Peninsula.

Strontium isotopic analysis was also carried out on the only possible donkey from Roman Britain. Its oxygen isotopic value clearly indicates that this individual was more likely to have been an import. This can be further confirmed with its $^{87}Sr/^{86}Sr$ value. Although the $^{87}Sr/^{86}Sr$ value (0.710207) does not directly imply a foreign origin as the atypical one found in one of the possible mules from Winchester, areas with such a strontium isotopic ratio cannot be found in regions with an oxygen isotopic value lower than -8.0‰ in Britain.

However, this isotopic signature is more commonly found in west central Europe (central-south France and southern Germany) and the central Italian Peninsula.



Map 7.8 – Possible locations of origin of the four non-Caballine equids. Both $\delta^{18}O_{DW}$ and $^{87}Sr/^{86}Sr$ value are used.

Figure 7.12 presents the scatter-gram of all sixteen specimens from the current thesis that have both $\delta^{18}O$ value and $^{87}Sr/^{86}Sr$ ratio as well as the identified mule from Weißenburg. When compared to the expected local range for Roman Britain, the outcomes seem to infer that all the horses from Winchester and Alcester were procured locally within Britain while at least one possible mule (VR-481) and the only possible donkey were clearly procured from outside of Britain. Most horses fit the local isotopic signature of their respective site. Only three horses from Winchester are determined to be non-local. Adding strontium isotopic values further strengthens the previous interpretation that the horse procurement strategy differed according to site types.

If all possible mules are in fact mules, as suggested by their dental morphology and their isotopic signatures being different from that of the horses, then the current results demonstrate several interesting observations. First, both strontium and oxygen isotopic analyses point that all the mules (n=4, three possible mules from the current thesis and one from Weißenburg) were from different geological regions which, therefore, implies that mule production was localised in different parts of the Roman Empire. If we focus only on the results from the oxygen isotopic analysis, it would seem that mules were bred in only two or three different environments: the warm Mediterranean coastal region and regions that are various distances further inland. The former is represented by only one specimen from Alcester (ALC-3002) with the highest $\delta^{18}O$ value among all domestic equids under study. However, its' strontium isotopic value seems to argue against most of the Mediterranean region except southern Italy (Map 7.7) as its breeding ground. Other possible mules from the Romano-British context all point to a region that is slightly inland ($\delta^{18}O_{DW}$ between -7.0 and‰ -8.0‰) as their breeding ground, and the identified mule from Weißenburg seems to have originated slightly further inland (or higher altitude). On the other hand, the strontium isotopic ratios of the four mules represent the range of at least

three different geological regions as their place of origin ($^{87}Sr/^{86}Sr$ ratio ranges: 0.708 – 0.709, 0.711 – 0.712, and 0.715 – 0.716). The dispersed isotopic values show that mule breeding may have been practised on a local basis rather than monopolised by a few breeding centres. Nevertheless, the outcomes also suggest that, at least for Roman Britain, the breeding of horses and of mules seem to have been independent from each other.

This takes us to the second implication: two possible mules have both their strontium and oxygen isotopic values within the expected British local range indicating that there is a possibility that these mules (VR-405, Winchester and ALC-3002, Alcester) were locally bred within Roman Britain. If this were the case, then it would also imply that donkeys would have been locally available for the practice of mule breeding. Unfortunately, donkeys are extremely rare in Roman faunal assemblages, as indicated by the results in the previous chapters, and the only donkey specimen in this part of the current thesis (from Fairford) does not have a local signature. As indicated by Map 7.7, the isotopic signatures for both possible mules can also be found in continental Europe. As a result, the local breeding of mules in Roman Britain should remain a possibility that requires further evidence.

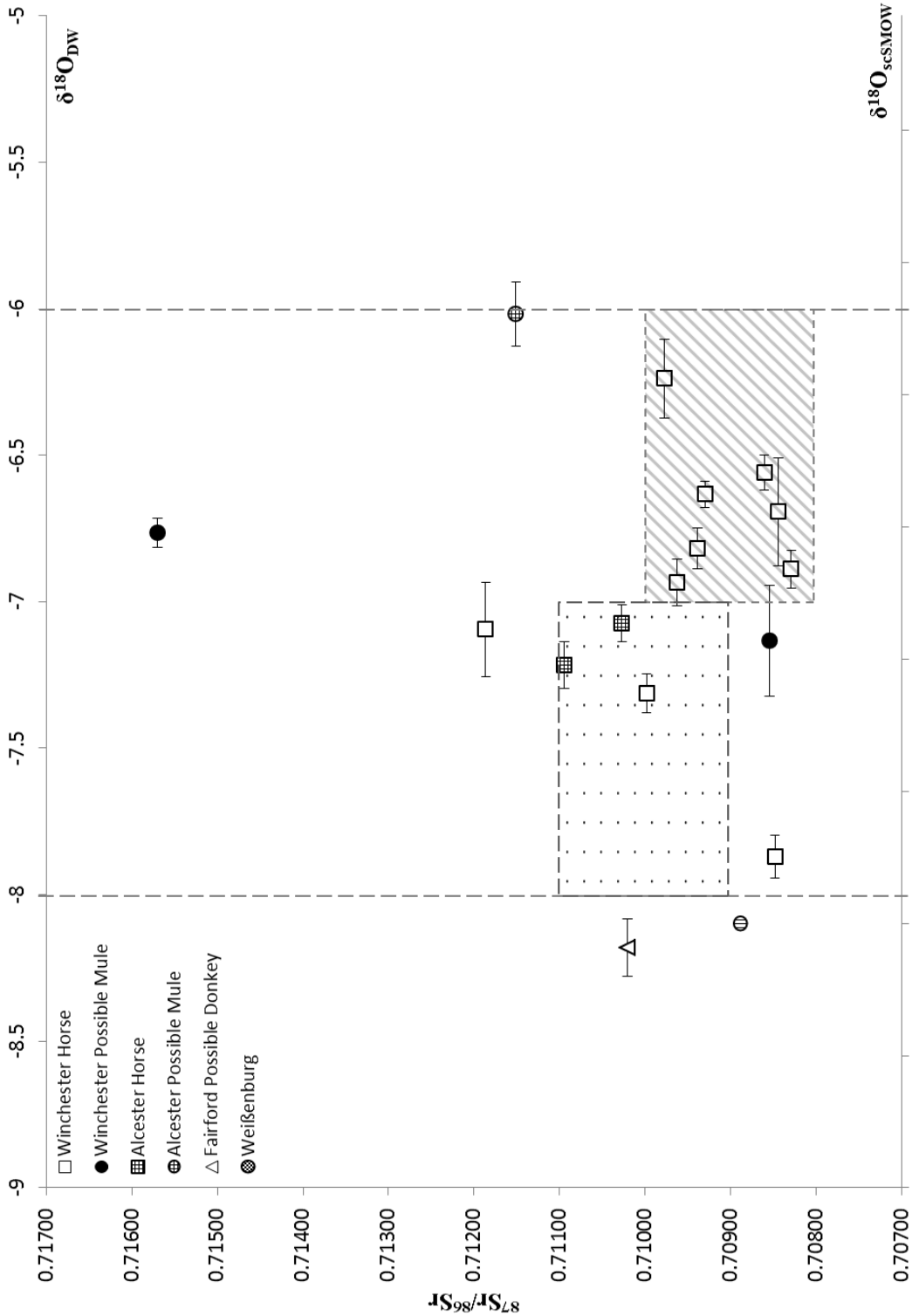


Figure 7.12 – Combination of $\delta^{18}O$ and $^{87}Sr/^{86}Sr$ data.
The box with backward-slash indicates the local range for Winchester and the box with dotted pattern indicates the local range for Alcester.

7.6 – Summary and Conclusion

In this chapter, the localness and possible origins of 40 domestic equids have been examined using isotopic analyses for discussing domestic equid procurement strategies in Roman Britain. The significance of the outcomes from various isotopic analyses is that it provides valuable direct evidence to support the claim regarding the importation of domestic equids into Britain during the Roman occupation. The importation of material goods, such as coins, pottery, and glassware from outside of Britain, can of course to be attested directly. However, evidence for the importation of livestock is more indirect and ambiguous. In contrast to introducing an exotic species (such as donkeys or camels), the importing of livestock species that were indigenous to Britain is be extremely difficult to detect, not only because direct evidence is not easily observable, but also because the relative number of individuals being imported would have been small. It is generally believed that one of the main reasons for importing livestock species that can also be found locally is to improve the local breed and, therefore, only a selected few specimens are imported to initiate the improvement process. Subsequently, the importation of livestock is often speculated upon based on indirect evidence, such as increase in size (Albarella *et al*, 2008). The current findings show that not all domestic equids from Romano-British sites were procured locally within Britain. At least one individual from the current study, which may possibly be a mule, can be confirmed to have had a foreign origin based on its strontium isotopic ratio. The other specimen with a greater possibility of being an imported animal is the possible donkey from Fairford (FTF-2549). However, since both possible donkeys (FTF-2549 and SERB03) are represented by relatively low $\delta^{18}O$ values, which contrasts with the impression that donkeys were commonly used in Mediterranean region, it is also possible that the outcomes are merely reflecting an unknown inter-species difference caused by metabolism or livestock management (e.g. amount or source of water and dietary intake or metabolic differences). Nevertheless, both possibly imported

individuals are also very likely to be non-caballine domestic equids based on their dental morphology, a discovery that may provide further insights for answering the question of whether mules and donkeys were bred locally in Roman Britain. Based on the current isotopic evidence, two possible mules (VR-405 and ALC-3002) could have been locally bred since their oxygen and strontium isotopic values failed to prove that they were of non-British origin, but current outcomes are equally insufficient to argue that they were bred in Britain. In addition, the unusually positive $\delta^{18}O$ value of the Alcester possible mule (ALC-3002) makes it more likely to be a foreign import.

The procurement strategy for Winchester as indicated by both the strontium and oxygen isotopic analyses matches nicely with the hypothesised scenario for urban settlements – that is, a large catchment area for domestic equids, mostly from the surrounding regions along with a few possible imported individuals. A similar pattern would probably be found when examining large Roman urban centres such as London and York. Although the number of samples available for Alcester is less satisfactory, the outcomes from the oxygen and strontium isotopic analyses still both support the view that the horses were likely to have been from the same origin, which is different from the case of the possible mule. As mentioned earlier, the location of the Alcester assemblage is speculated to have been a fort, and the procurement strategy indicated by the isotopic analysis fits the hypothesised specific local supply scenario. Logically, this type of pattern represents a self-contained rural economy where local demand was met by local production. As mentioned above, this type of strategy may also have been found in military establishments during peace time. In contrast to the specific local supply model observed in Alcester, Ribchester is in between a "specific local supply" and a "specific non-local supply". This is because the location of the site is at the intermediate zone between two gradient $\delta^{18}O_{DW}$ ranges, which makes it rather difficult to determine what is local and what is not. The

distribution of data from Ribchester suggests that horses were procured from specific sources regardless of the localness of their origins. The compact distribution fits the hypothesised model for military sites, although it is slightly different from Alcester. Fairford is also represented by a specific local supply scenario and, to a certain extent, resembles the distribution of the Ribchester samples. It does not fit perfectly with the hypothesised scenario for rural settlements, and yet it appears very differnt from the random acquisition model of urban settlements. The possibility of Fairford being a stud farm may explain the outliers from other regions, but unless all horses are from the same generation (e.g. catastrophic killing), the possibility is slim. The other explanation would be that Fairford may have served as a *mansio*, with local horses stationed for service as well as the occasional death of horses travelling in from other regions. However, the fact that the location of Fairford is not associated with a major road network largely weakens this possibility.

From a wider geological perspective, the distribution patterns of domestic equids from British sites are more compact than those from continental Europe. The two Serbian horses with non-local $\delta^{18}O$ values make a sharp contrast to British sites that procure horses mostly from the surrounding regions. The exploitation of local horses is a logical strategy for an island environment, but further explanations are required for those imported individuals. Unfortunately, the small sample size restricts the possibility of investigating potential changes in the procurement strategy over time. It is conceivable that the longer it was under Roman occupation, the fewer domestic equids needed to be imported in Britain. For military logistics, it may have been more essential to obtain a stable local supply for remount than to secure imports. This is because local horses are much better adapted to the surroundings than imported foreign horses. For other labour tasks, on the other hand, it would make no economic sense to continuously import a species that is locally available.

As for donkeys and mules, while the evidence does suggest their presence in Roman times, current outcomes suggest that some of them were imported, but cannot fully confirm the local production of either non-caballine species, particularly donkeys. In summary, the outcomes from the isotopic analyses indicate that most horses were procured within Roman Britain, but the procurement strategies varied depending on the function of the sites. In addition, a relatively high ratio of imports is observed among the non-caballine domestic equids although the sample size is small.

Chapter 8 - Discussion and Conclusion

8.1 – Introduction

One of the main aims of the current thesis is to examine the procurement strategy of domestic equids in Roman Britain. This area of research has not yet been fully explored using archaeological material. This is mainly due to the fact that the socio-economic importance of domestic equids has not been fully recognised, but also because of the lack of conclusive methods to identify taxonomically archaeological equid specimens. As a pilot study, the current thesis has investigated the topic of procurement strategy from two perspectives: the types of domestic equids that were used and in which frequencies, and where they were acquired from. In order to consider both aspects, the first part of the thesis deals with the application of different methods (biometric, geometric morphometric, and genetic) for distinguishing different domestic equid species. The second part of the thesis, then, takes the species determination based on dental morphology and compares the localness of different domestic species through isotopic analyses. The results indicate that there are potential differences between the procurement strategies of the three domestic equids in Roman Britain, in addition to different strategies between site types.

8.2 – Summary of current findings

Both species representation frequency and localness are used to interpret the procurement strategies of selected Roman sites in Britain. These outcomes were derived from different methods and not all samples were analysed using every method. In other words, post-cranial elements were not used in the isotopic analyses and, therefore it is necessary to present the results separately before integrating the interpretation in a more comprehensive discussion.

8.2.1 – Species Representation

The most intriguing and, perhaps, contentious argument from the biometric analyses is the determination of the mules. Twelve archaeological specimens have been "identified/determined" as mules by previous researchers mainly through DFA (n=10, see Table 1.2 and discussion in section 2.5). Conversely, a total number of 26 mules (minimum number of individuals) were determined from post-cranial elements in the current thesis (Chapter 5). Among these, only three are determined as mules in both Johnstone's work and the current thesis. Five additional mules are determined from Johnstone's original sample using the modified DFA in the current thesis (three out of five were "possible" horses in Johnstone's original determination), and two mule determinations are rejected (Appendix II). The main cause of the differences is the inclusion of the first phalanges and the exclusion of femora. The notable increase in the number of mule determinations in the material used in the present study is due to the inclusion of a number of sites where the presence of mules was suspected, particularly Healam Bridge in Yorkshire. In contrast, all three cases determined as donkey in Johnstone's work are rejected using the modified version of DFA, although all these samples were from Iron Age contexts. The only donkey determined by the current study is a first phalanx from Fairford – a site in which the presence of both donkey and mules has previously been suspected (Levine, 2004).

The horse-donkey-mule ratio of 130:1:25 was calculated based on all 156 post-cranial bones from 24 different Romano-British sites. While this lends further support to the notion of donkeys being strikingly uncommon in archaeological faunal assemblages of that period, it also suggests that mules may have been largely unrecognised due to the considerable difficulty in distinguishing them from horses. Due to the almost total absence of donkeys, it is impossible to discuss its frequencies distribution at different site types.

However, the outcomes suggest that the frequency of mules is associated with site function. A higher frequency of mules was observed at military sites as well as from large urban settlements. The mule-horse ratio in military sites is 1:3.25, while the ratio for civilian sites is 1:7.14. In addition, among the civilian sites, large urban centres have a higher mule-horse ratio (1:5) than small towns (1:13). Mules are not frequently found in rural settlements (1:7.8) when compared with towns (1:6.8); this implies that the use of mules may be associated more with the cultural aspect of the settlement. While the local population may have acknowledged the superiority of mules as labour animals, they may not have had access to one, or have developed any need for this foreign animal.

8.2.2 – Localness of Domestic Equids

Two different isotopic analyses (oxygen and carbon) were carried out on 40 archaeological specimens, and strontium isotopic analysis was carried out on 16 of them. While no direct evidence can be drawn from the carbon isotopic values, both oxygen and strontium isotopic values reveal interesting patterns regarding procurement strategies. It was hypothesised that the catchment area of domestic equids in large urban settlements would be much larger, involving multiple sources of supply (random acquisition model). On the other hand, rural settlements and small towns would have had a much smaller catchment area for their domestic equid acquisition, because the local demands would have been lower than the local supplies. As a result, a specific local supply model would be the best fit for rural settlements and small towns. In contrast to civilian sites, the sources of domestic equids for military sites should be more complicated and may differ depending on the history of the site. In times of peace, a steady supply from specific breeders through bulk purchase, along with some additional individual recruitment, is more likely to have been the main procurement strategy. However, in times of war, the procurement of domestic equids could have been extremely random, from emergency recruitment (local or

non-local) to capturing enemy mounts. Domestic equids are more likely to be either killed in action or retired from the military and sold for civilian use. As a result, it is more difficult to predict what procurement model would fit a military site without knowing its precise history. Nevertheless, since bulk purchase would probably have been the main method of acquisition (Laurence, 1999), it could still be suggested that, regardless of its origin, procurement strategies of domestic equids in most military sites would tend to be similar and thus it is suggested that they should show similar patterns when isotopic results are analysed.

Setting possible non-caballine samples aside, isotopic results from the horses from Winchester are scattered both within and outside of the immediate local range, indicating a "random" procurement strategy, which suggested a relatively large catchment area. This shows a sharp contrast to Alcester, where all three horses are clustered tightly together within the local range. Isotopic analysis from the horses at Ribchester imply there were two supply sources; one within the local range, the other from a colder or more inland region possibly outside Britain. The horses from Fairford show a similar scattered pattern as do those from Ribchester, with the majority of horses originating from a narrow local catchment area but with an additional few from elsewhere.

Although, according to their isotopic signatures, the majority of domestic equids were seemingly obtained locally, a few individuals have isotopic signatures that do not match the estimated Britain range; therefore, these are more likely to have originated outside Britain. Taking into account the results of both the oxygen and strontium isotopic analyses, most of the suspected non-caballine individuals – the possible donkey from Fairford (FTF2459) and two possible mules (VR-481, Winchester and ALC-3002, Alcester) – are

likely to have their origin outside Britain. In contrast, a single horse from Winchester has an isotopic signature that indicates a foreign origin. Judging from these results, it is evident that the ratio of suspected non-caballine individuals with non-British isotopic signatures is significantly higher. It is also important to iterate that while one possible mule (VR-405) from Winchester shows an isotopic signature that seems to match the local range, it is equally possible that it originated from another location with the same signature (Map 7.8). In addition, considering that the isotopic signatures of mules do not cluster closely with each other, it is much less likely that mules were bred in only a few centralised facilities, as previously assumed (Hyland, 1990; Johnstone, 2004). As indicated by the oxygen isotopic values, Roman mules were bred in warm coastal regions as well as in places further inland.

8.2.3 – Recommendation for future equids identification

Since the current thesis has utilized several different techniques to identify domestic equids to species level, there are some thoughts and recommendations that the current author would like to share and comment for future related researches. Many of these suggestions or observations are mentioned in previous chapters, this section will summarise them in bulletin points.

1. Morphological criteria should be reconsidered and questioned. Although the qualitative evaluation of morphological criteria for identifying the species of domestic equids has been suggested and practised for a long period of time, many issues have also been overlooked in the past. For example, can modern specimens be representative for the identification of archaeological equids? The interspecific variation in a taxon which has been intensively selective bred to manipulate the size and conformation has been largely underestimated. Moreover, the claims of post-cranial morphological traits in mules are based on a relatively small number of modern mules that may have the same

or closely related parents. The accuracy of the dental morphological criteria in wild/extinct equids populations has recently been challenged based on aDNA analyses outcomes (Geigl and Grange, 2012). In addition, the current thesis also gave an example of an archaeological horse being misidentified as a mule based on the dental morphology (Section 6.4). Therefore, it is wise to avoid rely specie identification based on morphological criteria along. The use of other methods, such as qualitative approach or biomolecular analysis is recommended.

2. Qualitative evaluation can be subjective. Many cases of donkey or mule identifications are based on the visual observation of "small" or "slender" limb bones (see Table 1.2) or based on the "relative" shape of dental pattern. However, these are subjective description of specimens that may differ from one observer to the next. Furthermore, the qualitative evaluation approach tends to pay very little attention on explaining the presence of mixture traits. For example, the presence of both asinine "V"-shaped lingual fold and a caballine trait of moderate bucco-lingual distance (partial penetration of the buccal fold). This may be particularly important for identifying hybred as observed in the offspring of wild boar and domestic pigs (section 5.4.4, Evin *et al.*, 2015). A recent study has shown that inter-observer differences do exist when evaluating the dental criteria of equids (Twiss *et al.*, 2016). Therefore, it is recommended to use quantitative analysis to verify the qualitative observation.

3. Be aware of the limitation of each method. As discussed in previous chapters, contradictory results from the same element under different methods or different elements of the same individuals all indicate that these methods can only be used to provide a base to evaluate the probability of species determination. Not to mention, it is still uncertain if interspecific differences do exist and can be identified using either

qualitative or quantitative method. For example, the degree of overlap between horse and mule observed in DFA suggests that these two species are quite similar in their limb bone proportion and, therefore, DFA can only provide a probability to the determination of species. The current thesis has put together a dataset combining both Johnstones work (2004) and Eisenmann (http://www.vera-eisenmann.com) along with few additional specimens from other collections (Table 3.1, Appendix I). The dataset (Appendix I) is uploaded in a Dropbox folder for people to utilize for future species determination using either DFA or Davis' method. (https://www.dropbox.com/sh/a2ogi48ezv934qc/AABYXvfzTWZRmrcdxEci6EhYa?dl=0). It is hoped that more specimens with detail background (such as parent breeds for mule offspring and sex of specimens) can be added to increase the accuracy of DFA method. It is also recommended to employ GMM approach to other elements in order to explore alternative criteria.

To carry out various quantitative analyses for a few equids remains is probably not cost-efficient for most faunal specialists who need to identify the species or taxon of thousands of animal remains. But, other than recording all standard measurements, more detailed descriptions or photographs should be provided when suspecting the presence of donkeys or mules.

8.3 – The "Making" of Mule and Donkey-Keeping in Roman Britain

Mule breeding was, without question, one of the most lucrative business ventures in the Roman world (Laurence, 1999). The demand for this beast of burden remained high throughout Roman history, as the price for mules was strikingly high (Laurence, 1999). Even as late as colonial times in Central America, the cost of mules was still markedly

higher than that of horses, not to mention of common donkeys (Konard, 1980). It was also believed that before Vespasian became Emperor of Rome, he invested in a mule-trading business to recover his wealth after serving in North Africa (and thus presumably thus earned his nickname, "*Mulio*"), although this has been recently questioned by Bosworth (2002). A more contemporary example is George Washington, who had been much credited for his resolute pursuit of ideal donkeys to ultimately improve the quality of mules in the United States (Powell, 1969). Although one could question the actual influence that his two imported donkeys had on present donkey and mule populations in the United States, Washington's visionary plan made the mule breeding a fruitful industry that not only increased agricultural productive power, but also made a profit by exporting the mules later during the WWI (Smith, 2008).

Nonetheless, mule breeding is not an easy business that can be established effortlessly. The challenges of successfully breeding a mule were described in Chapter 1, and it is clear that the Romans were aware of, and able to overcome, some of these problems. Yet, while such knowledge was acknowledged, and presumably circulated among stud farm owners through works of Varro and Columella, it is somewhat surprising that the current isotopic results suggest that most mules were of non-British origin. Based on the results of current species determination, mules are found in most military and large urban sites included in the present thesis (although due to the nature of this study – e.g. sites with relatively large equid frequencies – the choice of sites may be biased towards locations with a higher probability of mules being present). The site types associated with mules, i.e. major urban settlements and military sites, as mentioned above, are almost exclusively "Roman" in essence. Nevertheless, regardless of the number of sites where mules were determined, the number of these hybrids per site is still a mere token compared to the number of horses. This indicates that there was a minimal demand for mules in certain sectors of the Roman

population of Britain, perhaps to perform a "social" role that could not be carried out by local ponies. Nonetheless, it is curious that the Romans did not establish any local mule breeding to satisfy the local demand, no matter how small.

The first challenge for establishing local breeding would have been the availability of jacks. As mentioned in Chapter 1, specific criteria have to be met for a jack to be used for mule breeding, including raising it as a horse to eliminate its natural instinct of rejecting mares and increasing its chance of being accepted as a "horse" by the mare. However, at present, no evidence of local donkeys in Roman Britain has been established. The number of donkeys known from this period does not suggest the existence of a breeding population. As reasoned by Leighton:

> *It is oftentimes necessary to use different jacks to perpetuate the ass species than are used to copulate with mares, because jacks that are allowed to mate with she-asses often refuse to mate with mares. Consequently, in a complete mule-breeding establishment, it may be necessary to maintain three separate divisions; jacks and jennets (she-asses) to be mated for the production of jacks used in mule breeding and for the perpetuation of the ass species; horses and mares to be mated to obtain the mares to be used in mule breeding; and a third division composed of jacks and mares so produced which are mated for production of the desired mules. (1969, p.50)*

As a result, in order to produce mules, a similar or even more numerous donkey populations to the mule population must exist to support and ensure the continuous production of mules. Nonetheless, the ratio of donkey remains to the other two species does not indicate the existence of such a donkey population. Moreover, the only donkey specimen with isotopic analysis results appears to be non-British in origin.

Even though some evidence from previous studies and the present thesis suggests that donkeys were present in Roman Britain, they cannot be directly associated with "mule breeding". As mentioned in Chapter 1, there are specific requirements for a mule-breeding jack. According to Roman authors, the ideal mule-breeding jack should be the first generation offspring of a jennet and a wild ass. Following this logic, to ensure the mule-breeding jack is of the best quality, a continuous supply of wild asses would need to be established. This is very unlikely to have been the case in real life. Nevertheless, even if mule-breeding jacks were purchased from elsewhere instead of wild asses being imported directly, the cost would probably not have differed much. According to Varro (R.R. 2.8.3), the price of a mule-breeding ass from *Reate* would have been between 300,000 to 400,000 *sesterces* while a small farm owned by Pliny, the elder was worth only a third or a quarter of this (Letters 6.3, as translated in Lomas, 1996). However, such a seemingly unreasonable price may actually imply that mule breeders were not willing to encourage more competitors in this lucrative venture.

Several other possible causes could have contributed to the possible reluctance of Romans to produce donkeys locally, even against the potential gain from a new market for these foreign pack animals. First, the idea of breeding locally an animal species that originated from other parts of the Roman Empire may even have violated the Roman ideology of nature. Before the age of enlightenment, "nature" was still largely explained by the elemental and humoral theory, which had an enormous impact on agricultural activities (Sykes, 2014, Jones *et al.*, forthcoming). It is equally possible that to the Romans, a creature that inhabited a mostly hot and dry region should not have been bred in a cold and wet environment. The Romans may not have understood the specific habitats for different species with the details on annual precipitation or local vegetation as modern ecologists do, but they could have interpreted what was suitable for one region and what was not by

applying the elemental theory. Thus, it is possible that Romans may have thought the local production of donkeys would yield an imbalanced output and would probably require additional effort to bring it into equilibrium; from a modern perspective, a huge human input would be required through the provision of shelter, clothing, and food supplements for their welfare and survival.

In addition to the additional intensive livestock management required in an unsuitable habitat, the prevailing attitudes of Roman citizens toward donkeys may also have kept them from establishing a local donkey population on this remote island. Despite their common use as agricultural and pack animals, donkeys were never strongly associated with Roman culture. Neither donkeys nor mules were used exclusively by the Romans and, therefore, they lack the uniqueness to represent Rome compared to the Aquila in the Roman legion or the she-wolf associated with the founding of the city. To most Romans, donkeys were low status labour animals with no outstanding quality to make them indispensable (Tonybee, 2013). Extremely hilly terrains and the narrow paths in vineyards are the only circumstances that can truly demonstrate the donkey's virtue of sure-footedness and its petite but durable body. Neither were common features of Roman Britain. Without any noticeable benefit, in the addition to the extra cost of keeping donkeys and possible taxes for their importation, there would have been no immediate urge to introduce the donkey and establish a stable local breeding population of the species in a region with a sufficient supply of other domestic equids.

A foreign species may also be introduced if they have other social implications. Fallow deer (*Dama dama*) is an example. Recent studies have demonstrated the complexity of introducing this species into Britain (Sykes, 2004, 2007, 2010; Sykes *et al.*, 2013).

Originally, scholars believed that this taxon was introduced by the Romans (Chapman and Chapman, 1975; Lister 1984, Yalden, 1999). However, a thorough examination of the archaeological data reveals that several cases of early *Dama* identification were either misidentifications or were possible intrusive (Sykes, 2004). Based on the available material, it was concluded that the present fallow deer populations in Britain descend from the introduction of this species – possibly from Sicily – by the Normans (Sykes, 2004, 2010). Later, a further confirmed identification of fallow deer from the Fishbourne Roman Palace with a local isotopic signature (Sykes *et al.,* 2006) clearly demonstrated that the Romans did in fact introduce fallow deer when they occupied Britain and managed to establish local breeding population (Sykes *et al.,* 2006; Madgwick *et al.,* 2013; Miller *et al.,* 2014). Nevertheless, the species seems to have died out after the end of Roman rule in Britain (Sykes, 2010). Based on the material gathered for the current thesis, the number of Roman fallow deer in Britain exceeds the suspected number of donkeys in the same period. Although fallow deer are not a domestic labour animal and do not seem to have any well-recognised economic importance, this wild species was closely associated with Diana, the goddess of healing (Sykes, 2014; Miller *et al.*, 2014), and its antlers may have been used for medical purposes (Sykes, 2010). The religious symbolism in combination with the medical value of its body parts (i.e. antlers and bones) induced the Romans to either bring part of their remains to Britain (Miller *et al.,* 2014) or keep them alive in the country (Sykes *et al.,* 2006) despite the costs. After all, it is difficult to put a price on religious belief and health. Unfortunately, the only religious tie for donkey is as one of the sacred animals of Dionysus, who is not known to have been widely worshipped in this part of the Roman Empire. Interestingly, although fallow deer – in contrast to donkeys – can survive under British climatic conditions without human management, they do not seem to have developed a feral population after the Roman occupation on the scale of the present population in southern England. This may imply that the number of fallow deer introduced

alive was very limited, even though fallow deer remains in Roman faunal assemblages seem to have been more abundant than donkeys.

Even though similar arguments can be made for mules as for donkeys, it should be noted that while mules are the offspring of donkeys, they command a much higher social prestige as labour animals, which was reflected in their price. Mules were as insignificant as were donkeys as a religious symbol since they were not sacred animals representing any deities, but perhaps, they were able to signal their owners' superior social ranking in a more subtle way. For instance, the implication of a higher social ranking can be drawn from the fact that mules are more commonly depicted on Roman coins (Figure 8.1) than donkeys, and this hybrid creature is also often associated with kings in Old Testament stories (e.g. King Solomon in 1 Kings: 1:33-34, King David in Kings: 1:38). Moreover, as mules were expensive and mostly, if not exclusively, employed by military and government officials, the presence of mules in large urban settlements and military sites implies that they were imperial property and were either still working on official duties or retired into the hands of affluent civilians as a sign of their connections to government officials. Either case would have indicated that the cost of importing this foreign species was not a major concern. In contrast, for the local gentry, it may have been an extreme privilege to own a two-wheeled carriage pulled by imported mules just as people today own limited edition luxury cars. As a result, the local breeding of this hybrid would have undermined the sense of "superiority" of their owners, and, as the only social group that had the financial power to establish local breeding, they might even have deliberately maintained the rarity of mules in Britain.

Figure 8.1 – Roman coins showing mules pulling two-wheeled carriage (carpentum).
Images from Josh Illingworth, NGC Ancients Grader.
(https://www.ngccoin.com/news/viewarticle.aspx?NewsletterNewsArticleID=1340)

8.4 – Mule Supply in Roman Britain

Results in this study indicate that mules were significantly more abundant than donkeys in Roman Britain, and thus point to two seemingly conflicting facts: (i) mules were found to have been more closely associated with military sites and large urban settlements; and (ii) both donkeys and mules were not locally bred, at least not in any significant numbers. While the former suggests there was a definite demand for mules in Roman Britain, the latter rejects the possibility of a local supply. Therefore, without a sufficient local source, the demand for mules, which existed in Roman Britain, would have to have been satisfied through other means. Before addressing the issue directly, it would be useful to first look at the example of the domestic equid market in late Victorian Britain.

Moore-Colyer (1995) published an article reviewing the breeding and supply of horses in Victorian Britain, which summarised the rise and fall of the horse-breeding industry in Britain. According to his review, Britain did not develop as a major horse-breeding region for two reasons. First, the risk involved in horse breeding for individual breeders (i.e. local farmers) was too high. Horses can only be branded and sold by three years of age. Prior to that, they exploit the same pasture and land space that can be used to raise livestock, such as sheep, pigs, or even cattle, which can be sold for profit in a relatively shorter time span. Second, in the 1860s, in order to decrease maintenance costs, the British military, the biggest buyer of local horses, began purchasing only horses that had reached four years of age. This act further increased the costs for horse-breeders and, therefore, the number of individual breeders decreased. The remaining breeders started to focus on the quality of the horses instead of the quantity. Fortunately, according to Moore-Colyer, the successful introduction of exceptional horse breeds such as Clydesdale Suffolk, and Shires, pushed British local horse breeding into its golden age; in their heyday, horse breeders in Britain

made glittering profit from exporting these horses to foreign countries. However, the British government did not react to the high demand from foreign markets, and due to the excessive exporting of local horses, not only did the selling price for horses within Britain increase dramatically but also the production of ordinary horses no longer met local demand. As a result, local farmers (who required horses as draught and pack animals for agricultural production), as well as the transport industry (which needed horses to pull their carts) were forced to use inferior breeds or broodmares, and even to import second-rate foreign horses, many of which were descendants of exported British breeds. The British horse market for these specific breeds soon crashed due to the rise in American mule production and the introduction of lighter carriage horses, and finally, the development of the railway system further crushed any hope of a revival of local horse breeding.

However, the demand for horses and mules from the British military never decreased; as a matter of fact, it increased between the last quarter of the 19th century and the first half of 20th century. By the mid-19th century, Britain had earned its reputation as "the empire on which the sun never sets", with colonies all over the world. To maintain order within the empire, settling local disputes and rebellions had become a common issue for the British military. Many of these battles were fought in regions where the use of horses and mules was essential to victory. Even when facing such crucial demands from its own military, British officials were still optimistic about the falling horse supply from the British homeland, simply because

> *"... as long as our navy is efficient we can draw our supply of remounts in wartime from all over the world at prices with which the English farmer cannot possibly compete, and it is hardly worth their while to breed horses in order to be in the*

> *market in the event of our navy failing to keep the waterways open*." (Eden, 1900, as quoted in Moore-Colyer, 1995)

As a result, Britain spent a substantial amount of money purchasing mules from the United States and Canada to cover the demand in battlefields abroad. It is difficult to judge from partial evidence how beneficial it would have been for the British administration at the time to change its policy and support the local breeding of horses and mules. It may have saved the money spent on purchasing foreign equine supplies, but it may have equally caused losses in other agricultural production, which was more essential for most local citizens.

For the Romans, although mule breeding was probably operated mainly by affluent estate owners, the government's attitude might have considerably affected the decision regarding its production since the Roman military was the largest buyer of mules. A military campaign to conquer the whole of Britain was never a top priority of Roman emperors. After the initial "invasion" by Caesar and the following Claudian conquest campaign, most military operations were related to the pacification of local rebellions and there was nearly no further expansion in Britain after the construction of Hadrian's and Antonine Wall. This suggests that Roman emperors had little interest in aggressively taking over the whole of Britain and therefore, there might have been a smaller demand for domestic equids in Roman Britain, which could be sufficiently met by the local supply. In addition, the Roman trade network, utilising both the road networks and maritime routes, was well established; regardless where the mules were bred, they could be quickly sent to the frontier. Were a Roman official to have made a statement regarding a situation similar to that expressed by the British official above, it might have been as follows:

> *As long as our army is efficient, we can draw our supply of remounts in wartime from all over the empire of a quality with which the British breeds cannot possibly compete, and it is hardly worth anyone's while to introduce donkeys to breed local mules in order to supply the military in the event of our legions failing to keep the trade networks open.*

8.5 – Conclusion

The current thesis has examined the procurement strategies of domestic equids within Roman Britain first by comparing the ratio of different species used in different site types and their localness. In order to achieve this research aim, the current thesis evaluated current methods for the determination of equid species, suggested modifications to some of them, and suggested new alternatives. It also utilised, in a pilot study, aDNA analysis in an attempt to validate the qualitative criteria and quantitative analyses used in taxonomic determinations. Furthermore, isotopic analyses were utilised to investigate the localness of domestic equids.

While previous studies have argued that some qualitative features, such as the slenderness of long bones, can be useful for the separating the different domestic equid species, the subtle differences between taxa can be distinguished only through quantitative analyses. As a result, several biometric and geometric morphometric analyses have been developed to provide the basis for species determination of the archaeological material used in the present study. Although previous studies have employed similar methods, none has cross-validated its determinations using additional methods. The current thesis has demonstrated that there are significant inconsistencies not only different between methods, but also

between different elements of the same individual. Therefore, it is important to consider the reliability of the method(s) being applied and the skeletal element under investigation before a taxonomic determination of an equid specimen is made.

The results from different analyses in the current thesis reveal that donkeys were almost absent from Romano-British sites and, while mules were small in numbers but not uncommon, the evidence suggests that they were more likely to have been imported instead of locally bred. Available evidence indicates that the Romans did in fact introduce donkeys and mules into the British Isles, but there is not sufficient evidence to support the case that they established a significant local tradition for the breeding of these animals.

The current thesis does not argue, however, that local breeding never occurred in Roman Britain; instead, as indicated by the result of the oxygen isotopic analyses, it argues that mules from other parts of the Roman Empire were bred from regions with similar oxygen isotopic range to that of Britain. However, based on both economic and cultural considerations, the local breeding of these newly "introduced" animals must not have been intentional or systematic. The effort and cost required for keeping donkeys would have exceeded the benefit of keeping them in an unsuitable habitat. Local ponies, which were more familiar to the local population, could have easily been used to replace donkeys as beasts of burden for nearly all local agricultural activities. Furthermore, unlike fallow deer, donkeys and mules are not known to have had any important religious significance or practical medical use, and thus they lacked intimate ties with Roman civilians in Britain. Although their abilities as pack animals may have been appreciated by the military, the decision regarding logistics of supplies was often made by a few officials who had other considerations. As a result, when the Romans began their occupation of the British Isles,

donkeys were not included as part of the "Roman package" that was systematically introduced into the newly conquered land.

Unquestionably, the Romans left a rich legacy that has extended beyond their time in the form of infrastructure (e.g. road networks) or cultural behaviours (e.g. diet), but localised donkey and mule breeding in Britain was not likely to be a tradition that they should be credited with. While numbers of donkeys and mules are recorded in the Doomsday Book, these animals were still little known throughout the medieval period. Scattered literary or graphic evidence and a confirmed archaeological donkey finding (Baxter, 2002) indicate that these two species were of meagre importance, contradicting their popularity in Victoria times either as a tourist attraction (i.e. the beach donkey-ride) or as labour animals (Dent, 1972). From the case of European fallow deer mentioned above, it is clear that the "introduction" of a species may not be a clear single event. The value of animals changes through time, cultures, and technological innovations. Whilst there is no doubt that people in Britain were acquainted with these animals through a Christian context, in addition to their low "social status", it would also have been impractical for peasants to replace sturdy local ponies with a high-maintenance foreign species. However, the value of the humble donkey seemed to have shifted after Henry VIII declared his ambition to improve the size of horses in England. While the law seemingly affected only horses, it may actually have altered the decision regarding the choice of labour animals. For peasants, small local ponies were an excellent choice for cheap labour animals because they did not require as much food as larger horses and could carry nearly as much as a donkey. However, if ponies were no longer an option because they were excluded from the commons since the Horse Act 1540 forbid stallions under 15 hands (about 152 cm) and mares under 13 hands (about 132 cm) to graze in common land, donkeys would have been the next most suitable option as cheap labour animals. As non-caballine equids, no size restriction would be

forced on donkeys. There was no need for any concern that they would affect the size of horses because these two species are not naturally attracted to each other. More importantly, even in the unlikely event of a natural cross-breeding occurring, the offspring may have been an even more valuable creature: the mule. As a result, while the main purpose for setting up a minimum size limit was to improve the quality of horses, it may have encouraged peasants to seek out solutions in other species. Moreover, this seems to have coincided with the increase in the number of donkey remains from British archaeological sites after the 17th century (Baxter, 2002).

Through carefully reviewing the existing methodologies on species determination of domestic equids, the current study has developed more objective and accessible approaches for future work. It has also utilised aDNA analysis to explore the validity of qualitative criteria used in the identification of domestic equid taxa and isotopic analysis to explore in a systematic manner the probable importation of domestic equids. The outcomes obtained from these analyses can be regarded as the foundation upon which future research into procurement strategies for domestic equids in Roman Britain can be based.

The current thesis provides a first overview of how domestic equids were procured in Roman Britain. Nonetheless, it also points out potential directions for further studies, such as the use of aDNA to test the reliability of both qualitative and quantitative identification methods. The purported simplicity of the domestic equid procurement pattern hypothesised for Britain is mostly due to the isolated island setting, which limits supply sources from continental Europe. The oxygen isotopic values for four horses from Velim-Veliš̌tak, a Croatian early Medieval site (Lightfoot *et al.*, 2004), indicate a relatively diverse supply source compared to the Romano-British sites. Thus, the data from continental Europe may

reveal a different procurement pattern. In addition, the proposition made in this study which uses Henry VIII's Horses Act of 1540 as the dividing point for the actual localisation of donkey production requires further evidence both from further historical and archaeological studies. Considering the lack of records regarding these humble beasts, it may also be possible to tackle this question using molecular approaches and to test their genetic diversity despite the lack of any well-established local donkey breed in Britain.

Scholars have long questioned whether the lack of donkeys and mules in Romano-British faunal assemblages was due either to the difficulties of separating domestic species or to not being sufficiently aware of their possible presence. However, while subtle differences may pose a challenge for distinguishing mules from horses, this research both donkeys and mules do not appear to have been present in significant numbers during the Roman occupation. This was probably due to the substantial efforts that would have been required to establish a local donkey breeding population and the practicalities of replacing the local ponies. Through the use and development of quantitative methods and the utilisation of a number of isotopic analyses, it is hoped that the current thesis provided a different perspective to interpret past human-animal (equid) relationship that go beyond the historic evidence, which might only depict a part of the bigger picture.

Appendices

Appendix I.I – Measurements of Modern Control Data (Humerus)

		Measurements					DFA	Probabilities		
ID	Sp./Breed	GLl	SD	Bd	BT	HTC	Determination	Horse	Donkey	Mule
C001	Przewalski	262.8	28.2	77.8	69.6	33.2	Horse	95.03%	4.77%	0.20%
C002	Przewalski	257.6	33.7	75.4	66.4	32.1	Horse	77.82%	21.59%	0.59%
C003	Przewalski	256.4	30.6	69.1	66.4	31.5	Horse	57.26%	40.20%	2.55%
C004	Przewalski	273.7	32.5	78.6	79.6	35.9	Horse	93.08%	6.84%	0.08%
C005	Przewalski	282.7	32	82.8	71.8	36.4	Horse	86.09%	0.58%	13.33%
C006	Przewalski	265.5	34.8	71.8	65.9	31	Horse	51.91%	37.85%	10.24%
C007	Przewalski	261.8	32.7	74.4	64	32.6	Horse	75.16%	17.30%	7.54%
C008	Przewalski	273	35.4	76.3	69	33.4	Horse	75.37%	11.37%	13.26%
C009	Przewalski	276.1	32.9	74.8	71.1	34.1	Horse	71.35%	8.20%	20.44%
C010	Przewalski	263.2	31.9	77.8	68.4	35.7	Horse	90.80%	8.32%	0.88%
C012	Przewalski	255.7	31.6	79.4	68.3	33.8	Horse	93.13%	6.82%	0.05%
C013	Przewalski	264.4	35.5	76.1	70.4	36	Horse	81.63%	16.57%	1.79%
C015	Przewalski	270.1	34.9	77.4	68.8	32.9	Horse	85.98%	7.09%	6.93%
C016	Przewalski	272.9	34.4	78.1	79.2	34.9	Horse	94.16%	5.63%	0.22%
C017	Przewalski	283.2	38.5	83	73.6	37	Horse	87.89%	2.42%	9.69%
C018	Pony	219.3	26.6	62.7	55.8	28.6	Donkey	9.74%	90.26%	0.01%
C019	Pony	244	27.1	66.9	60.8	30.3	Donkey	56.46%	41.52%	2.02%
C020	Pony	288	38.3	80.8	74.9	36.2	Horse	57.99%	1.50%	40.51%
C021	Pony	257.6	33.4	72.6	67.6	33.4	Horse	62.65%	36.45%	0.91%
C022	Pony	284	36.6	80.8	73.6	35.8	Horse	83.63%	3.35%	13.02%
C023	Pony	268.2	37.1	78.3	65.3	33.8	Horse	76.39%	17.13%	6.48%
C024	Pony	298	34.2	80.9	72.1	36.4	Mule	51.61%	5.07%	43.32%
C025	Pony	275.5	34	81.1	71.2	35.6	Horse	93.92%	2.66%	3.42%
C026	Pony	288	36.2	83.1	75.4	36.2	Horse	89.79%	1.57%	8.65%
C027	Pony	257.7	28.8	70.9	62.5	32.2	Horse	67.62%	12.99%	19.39%

Measurements of Modern Control Data (Humerus, cont'd)

		Measurements					DFA	Probabilities		
ID	Sp./Breed	GLl	SD	Bd	BT	HTC	Determination	Horse	Donkey	Mule
C028	Pony	275	32.6	78.1	75.4	39.7	Horse	88.86%	1.74%	9.39%
C029	Pony	300	35.6	78.4	73.9	37	Mule	5.60%	0.25%	94.15%
C030	Pony	266.5	28.2	74.8	71	33.9	Horse	93.13%	4.72%	2.15%
C031	Pony	253	25.8	67.4	61.8	32.2	Horse	22.38%	77.29%	0.33%
C032	Pony	250.5	30.6	66.4	61.6	31.9	Donkey	36.88%	53.49%	9.62%
C034	Arab	316	31	88.6	78.2	40.4	Mule	9.49%	0.01%	90.51%
C035	Arab	328	38.6	89.6	82.8	43.4	Mule	4.79%	0.02%	95.20%
C036	Arab	311	33.3	81.2	87.5	36.2	Horse	89.52%	1.79%	8.69%
C037	Arab	312	36.8	87	79.6	42.5	Mule	63.77%	1.47%	34.77%
C096	Race Horse 123 Left	348	41.75	96.96	89.36	43.58	Mule	56.70%	0.31%	42.99%
C097	NF Pony 137	275.54	37.88	74.86	73.53	37.91	Horse	51.14%	45.18%	3.69%
C098	Shetland 604 left	203.34	22.99	52.53	51.6	25.3	Donkey	1.02%	98.98%	0.00%
D001	Donkey	225.4	27.9	61	58.2	29.2	Donkey	10.62%	89.32%	0.06%
D002	Donkey	231.5	22.8	60.5	52.7	21.6	Donkey	29.42%	68.85%	1.73%
D003	Donkey	214.5	27.1	60.5	53.9	26.7	Donkey	6.15%	93.84%	0.01%
D004	Donkey	210.5	28.4	58.4	54.3	25.4	Donkey	0.92%	99.08%	0.00%
D005	Donkey	202.1	24.2	56	51.7	26.8	Donkey	2.08%	97.92%	0.00%
D006	Donkey	240.2	28	62.9	61.7	31.5	Donkey	15.96%	83.65%	0.39%
D007	Donkey	227.1	28.2	63.2	57.8	32.2	Donkey	15.02%	84.87%	0.11%
D008	Donkey	218.6	26.8	57	51.1	24.6	Donkey	4.63%	95.21%	0.17%
D009	Donkey	222	27.9	57.2	55.5	28.3	Donkey	2.90%	97.06%	0.05%
D010	Donkey	262.4	31.9	74.7	70.2	35.8	Horse	81.54%	17.54%	0.92%
D011	Donkey	214.1	25.8	55.1	54.7	26.4	Donkey	3.06%	96.92%	0.02%
D012	Donkey	250.8	28.5	70	65.2	32.7	Horse	50.25%	49.50%	0.25%

Measurements for Modern Control Data (Humerus, cont'd)

		Measurements					DFA	Probabilities		
ID	Sp./Breed	GLl	SD	Bd	BT	HTC	Determination	Horse	Donkey	Mule
D013	Donkey	246.4	39	71.5	64.1	31.8	Donkey	18.25%	81.67%	0.08%
D063	Donkey 131 Left	215.43	23.66	54.55	49.91	25.24	Donkey	2.18%	97.77%	0.05%
D064	Donkey 132 left	233.35	31.75	63.52	59.98	30.2	Donkey	11.60%	88.26%	0.14%
M001	Mule	293	32.4	75	69.1	34.8	Mule	0.67%	0.02%	99.32%
M002	Mule	282.6	30.2	74	65.1	34.9	Mule	6.76%	0.68%	92.56%
M003	Mule	288	35.2	75.6	70.9	35.9	Mule	13.42%	1.62%	84.95%
M004	Mule	299	26.2	80.3	70.8	35	Mule	18.06%	0.12%	81.82%
M006	Mule	352	45.6	101.6	89	45.3	Mule	4.13%	0.00%	95.87%
M007	Mule	285.3	33.5	76.4	69.1	36.3	Mule	16.39%	1.22%	82.39%
M008	Mule	304	40.2	84.7	80.8	40.9	Horse	32.40%	0.31%	67.29%
M009	Mule	344	37	89.1	81.5	40.3	Mule	0.10%	0.00%	99.90%
M010	Mule	344	45.1	97	90.4	43.4	Mule	29.27%	0.05%	70.68%

Appendix I.II – Measurements of Modern Control Data (Radius)

		Measurement							DFA	Probabilities		
ID	Sp./Breed	GL	Bp	BFp	SD	Bd	BFd	DFd	Determination	Horse	Donkey	Mule
C002	Przewalski	314	74.7	69.3	33.2	69.1	57.8	35.4	Horse	80.14%	2.43%	17.43%
C004	Przewalski	305	73.7	66.1	33.7	65.5	56	33.9	Horse	85.08%	10.58%	4.34%
C005	Przewalski	328	81.6	70.9	38	75.3	62.7	38.7	Horse	66.44%	31.38%	2.17%
C006	Przewalski	325	79.3	73	35.3	71.6	61.3	38.2	Horse	95.37%	0.41%	4.23%
C007	Przewalski	305	72.3	65.2	36.1	67.4	56	32	Mule	35.31%	18.18%	46.51%
C008	Przewalski	317	73.7	66	34.3	66.7	55.3	35.4	Horse	63.25%	29.62%	7.13%
C009	Przewalski	314	76.4	68.9	39.8	71.6	60	34.6	Mule	46.14%	4.39%	49.48%
C010	Przewalski	319	76.2	70.5	37.5	70.5	59.4	33.3	Mule	28.27%	0.59%	71.15%
C011	Przewalski	316	78	71.9	35.2	72.7	61.3	36.7	Horse	86.67%	1.04%	12.30%
C012	Przewalski	318	77.7	70.4	38	74.1	51.4	35.6	Donkey	22.59%	58.71%	18.70%
C013	Przewalski	302	73.2	65.8	35.2	71.1	59.8	35.6	Horse	56.78%	27.96%	15.26%
C014	Przewalski	314	76.6	69.2	37	71.7	60.7	36.2	Horse	77.84%	5.50%	16.67%
C015	Przewalski	310	76.6	69	38.6	69.8	57.6	33.8	Horse	68.55%	5.41%	26.04%
C016	Przewalski	322	77.9	68.8	37.9	71.4	58.1	36	Horse	58.47%	31.45%	10.08%
C017	Przewalski	324	82.8	73.5	41.1	77.6	65.5	36.5	Horse	70.33%	3.41%	26.26%
C018	Pony	242.7	59.3	54.1	28.8	54.5	47	27.6	Donkey	47.83%	49.61%	2.56%
C019	Pony	284	67.1	61	31.4	62.7	52.1	31	Donkey	43.35%	44.35%	12.30%
C020	Pony	329	81.3	73	40.9	78.3	66.3	36.2	Mule	28.48%	2.00%	69.52%
C021	Pony	296	75.4	68.6	34.7	68.6	54.7	34	Horse	88.94%	6.39%	4.67%
C022	Pony	319	80.9	75.4	37.6	76	62.5	34.7	Mule	45.66%	0.20%	54.15%
C023	Pony	312	73.3	66.1	37.9	67.6	55.8	33.5	Mule	42.73%	13.48%	43.79%
C024	Pony	317	79.7	70.1	31.7	75.8	62.1	36.7	Donkey	41.21%	57.26%	1.54%
C025	Pony	310	77.9	70.9	35.1	70.3	60.4	36	Horse	95.50%	0.97%	3.54%
C026	Pony	322	82	72.4	40	77.3	64	35.7	Horse	60.98%	11.45%	27.57%
C027	Pony	296	69.4	63.5	30.5	61.2	51.9	31.5	Horse	79.59%	12.65%	7.77%

Measurements for Modern Control Data (Radius, cont'd)

		Measurement							DFA	Probabilities		
ID	Sp./Breed	GL	Bp	BFp	SD	Bd	BFd	DFd	Determination	Horse	Donkey	Mule
C028	Pony	332	83	74.4	36	76.1	62.5	35.3	Horse	73.53%	5.87%	20.60%
C030	Pony	286	69.4	62.1	28.8	64	52.3	28.7	Donkey	20.42%	73.92%	5.66%
C031	Pony	324	72.4	66.7	31.2	66.4	56.6	34.7	Horse	61.43%	10.10%	28.46%
C032	Pony	296	67.1	62.2	33.6	62.5	52.5	32.9	Horse	54.60%	12.07%	33.34%
C033	Arab	386	91	81.2	41	82.8	71.4	43.2	Horse	77.80%	0.69%	21.52%
C034	Arab	374	86.5	79.8	37.7	78.3	65.2	40.1	Horse	52.46%	0.24%	47.30%
C035	Arab	377	93.2	82.8	39.1	83.5	67.4	42.1	Horse	92.94%	1.81%	5.25%
C036	Arab	354	83	76.6	36.2	77.8	65.8	34.7	Mule	7.86%	0.17%	91.97%
C037	Arab	349	87.6	79.4	37.9	80.3	67.7	39.5	Horse	88.81%	0.39%	10.80%
C041	Tarpan	315	73	64	36	68	57	35	Donkey	23.58%	69.67%	6.75%
C044	Shetland	270	67	61	30	58	48	29	Horse	80.78%	16.82%	2.40%
C045	(Horse)	408	99	90	45	93	76	44	Mule	15.42%	0.03%	84.55%
C046	(Horse)	371	91	81	42	84	68	42	Horse	76.75%	2.30%	20.94%
C048	Shetland	287	71	63	32.5	64	56	31	Horse	69.17%	25.77%	5.06%
C049	Grand	378	101	89	48	95	77	46	Horse	92.14%	0.27%	7.59%
C050	Poney	187	51	48	25	48.5	44	26	Horse	80.32%	19.42%	0.27%
C054	Poney	244	60	56	24	54	47.5	27	Horse	79.03%	19.14%	1.84%
C055	Welsh	270	63	56	30	60	49	28	Donkey	3.81%	93.91%	2.29%
C056	Poney	194	53	50	26	50	45	25.5	Horse	86.84%	12.51%	0.65%
C057	Poney	285	69	63	32	63	52	29	Horse	51.29%	21.17%	27.54%
C058	Grand	355	88	81	42	83	69	40	Mule	41.06%	0.08%	58.87%
C059	(Horse)	358	84	78	40	80.5	60	40.4	Mule	25.05%	1.47%	73.48%
C067	Hannover	395	104	91	50	99	82	49	Horse	91.01%	0.24%	8.75%
C068	Hannover	380	101	93	51	91.2	79	46	Horse	87.37%	0.00%	12.63%
C076	Arabe	358	84	79	37	77.5	66	36	Mule	11.22%	0.02%	88.77%

Measurements for Modern Control Data (Radius, cont'd)

		Measurement							DFA	Probabilities		
ID	Sp./Breed	GL	Bp	BFp	SD	Bd	BFd	DFd	Determination	Horse	Donkey	Mule
C077	Poney	305	73	67	34	66.5	57	34	Horse	82.35%	3.27%	14.38%
C078	Mongol	330	79	72	37	75	62	37.5	Horse	60.85%	4.27%	34.88%
C079	Mongol	310	77.5	73	35	70	61	37	Horse	95.58%	0.05%	4.38%
C080	Mongol	320	82	75	40	78	64.3	39	Horse	85.77%	0.62%	13.61%
C081	Tarpan	336	80.5	70.5	39	75	59	35	Donkey	18.74%	56.44%	24.82%
C082	Arabe	355	84	78	40	79.5	70	40	Mule	33.13%	0.04%	66.83%
C084	(Horse)	340	82	75	39	79.5	64	35.6	Mule	8.99%	0.94%	90.07%
C086	(Horse)	405	106.5	94.5	49	94	78	48	Horse	98.24%	0.01%	1.76%
C089	Exmoor	308	75	70	32.5	69.5	58	34	Horse	77.07%	1.41%	21.52%
C090	Islande	250	72	67	35	65	53	32.5	Horse	99.34%	0.23%	0.44%
C091	Fjord	345	88	78	44	82	67	37.5	Mule	47.05%	1.89%	51.06%
C092	Islande	328	82	74	43	75	63	37	Horse	67.75%	0.61%	31.64%
C094	Welsh cob	344	86.1	77.82	42.85	81.1	66.39	36.66	Mule	21.90%	0.43%	77.68%
C095	Pony 3158 right	284.25	67.09	60.8	31.52	62.92	51.19	29.91	Donkey	25.90%	59.06%	15.04%
C096	Race Horse 123 left	392	102.1	88.87	45.46	93.35	77.64	46.4	Horse	96.92%	0.48%	2.60%
C097	NF Pony 137 left	324.5	81.01	74.1	33.78	73.92	60.32	37.76	Horse	95.03%	1.59%	3.38%
C098	Shetland 604 left	238.03	56.55	50.9	26.12	49.78	42.23	26.04	Donkey	15.97%	83.68%	0.35%
D001	Donkey	269.7	64.6	57.6	31.8	60.1	49	29.5	Donkey	15.19%	82.07%	2.74%
D002	Donkey	284.1	60.1	52.7	27.5	55.3	47.3	27.7	Donkey	0.90%	98.42%	0.68%
D003	Donkey	261.4	62.9	54.8	28.6	57.4	45.6	27.1	Donkey	1.77%	98.08%	0.16%
D004	Donkey	247.4	58.2	52.5	26	52.2	43.5	25.7	Donkey	10.77%	88.45%	0.78%
D005	Donkey	247.7	54	49.9	24.9	49.4	41.6	24.3	Donkey	6.75%	89.87%	3.38%
D006	Donkey	279.6	67.1	59.2	29.4	62.7	52.2	30	Donkey	9.87%	88.89%	1.24%
D007	Donkey	269.9	66.2	58.1	31.3	61.8	49.9	29.4	Donkey	6.95%	92.25%	0.80%
D008	Donkey	270.1	60	51	27	56.1	44.6	25.3	Donkey	0.05%	99.91%	0.04%

Measurements for Modern Control Data (Radius, cont'd)

		Measurement							DFA	Probabilities		
ID	Sp./Breed	GL	Bp	BFp	SD	Bd	BFd	DFd	Determination	Horse	Donkey	Mule
D009	Donkey	263	58.7	53	27.1	53.8	44	25.2	Donkey	3.58%	93.68%	2.74%
D010	Donkey	296	72	63	32.8	69.3	55.6	31	Donkey	4.76%	92.01%	3.23%
D011	Donkey	296	71.1	62.1	32.6	67.9	55.1	30.8	Donkey	4.55%	92.56%	2.89%
D012	Donkey	317	74.4	64.8	34.4	70	55.2	32.6	Donkey	3.82%	92.73%	3.45%
D015	Olduvai	256.1	61.7	55	28.8	57	42.7	28.5	Donkey	3.15%	96.67%	0.18%
D016	Syrie	298	65.5	58.5	31.5	60	49	29	Donkey	5.85%	83.70%	10.46%
D017	(Donkey)	225	60	55	30	61.5	46	26.5	Donkey	6.78%	90.89%	2.33%
D018	Afrique	269	65	58	32.5	60	49	30	Donkey	23.36%	73.88%	2.76%
D019	(Donkey)	268	61	55	31	58	47	28	Donkey	5.80%	88.50%	5.70%
D022	(Donkey)	287	68	60	32	62	51	30	Donkey	14.37%	82.58%	3.05%
D023	Nubie	305	69	61	30	65	52	31	Donkey	2.90%	94.85%	2.25%
D025	Zoo	289	67	59	32	64	50	29	Donkey	1.57%	95.89%	2.55%
D026	(Donkey)	272	62	55.5	29	55	46	28	Donkey	14.54%	83.42%	2.04%
D029	Ane Blanc	330	71.1	60.8	33.4	67.3	54.5	35.3	Donkey	0.48%	99.22%	0.30%
D030	Ane Blanc	313	74.7	64.8	34.2	69.5	55.4	33.3	Donkey	6.29%	92.08%	1.63%
D031	(Donkey)	233	53	47	23.5	47	39	24	Donkey	1.29%	98.66%	0.05%
D032	(Donkey)	272	59	53	29.5	55.5	45.5	27	Donkey	2.23%	94.04%	3.73%
D045	(Donkey)	273	66	60.5	30	63	53	32.5	Horse	63.11%	32.31%	4.59%
D056	(Donkey)	281	68.5	61.5	32	63.5	53.2	34	Horse	62.19%	36.34%	1.47%
D059	sans crâne	275	60	54	28	55.5	44.5	26	Donkey	1.91%	94.83%	3.26%
D060	sans crâne	235	58	50	26.5	51	42	24.5	Donkey	1.64%	98.33%	0.03%
D061	Donkey 3349	265.15	56.96	49.25	27.82	53.21	44.86	26.61	Donkey	0.28%	99.59%	0.13%
D062	Donkey 546 left	278.18	64.48	58.24	29.61	60.37	49.16	27.28	Donkey	9.52%	78.60%	11.88%
D063	Donkey 131 left	263.18	56.82	50.84	25.58	50.13	42.57	25.43	Donkey	3.06%	96.19%	0.75%
D064	Donkey 132 left	278.79	67.3	60.07	31.69	61.86	52.96	30.68	Donkey	44.09%	51.21%	4.71%

Measurements for Modern Control Data (Radius, cont'd)

		Measurement							DFA	Probabilities		
ID	Sp./Breed	GL	Bp	BFp	SD	Bd	BFd	DFd	Determination	Horse	Donkey	Mule
M001	Mule	332	73.8	67.7	34.7	70.5	56.7	34.7	Mule	14.28%	12.92%	72.80%
M002	Mule	321	74	65.9	31.6	65	57.2	32	Horse	61.24%	23.78%	14.98%
M003	Mule	341	77.1	71.2	38.2	73.4	60.1	35	Mule	5.95%	0.76%	93.29%
M004	Mule	339	78.6	71.2	39.5	75	61.1	34	Mule	4.90%	1.91%	93.20%
M005	Mule	320	76.9	69.9	36.2	71.5	62	34.8	Horse	60.00%	2.50%	37.50%
M007	Mule	341	76.7	68.2	37.9	72.1	60.2	35	Mule	13.58%	20.60%	65.82%
M008	Mule	366	85.1	79	40.2	79.1	66.2	35.8	Mule	3.09%	0.02%	96.89%
M009	Mule	406	89.7	81.4	41.9	83.7	67.2	41	Mule	3.20%	0.29%	96.51%
M010	Mule	396	98	88.7	47.7	96.9	77.1	44.4	Mule	4.81%	0.05%	95.14%
M012	NY 204211	400	93	84	43.5	88	71	40	Mule	2.20%	0.11%	97.69%
M013	NY 14116	349	92	82	43	82.5	65.5	38	Horse	85.33%	0.64%	14.03%
M019	MCZ 1655	316	78	70	37	72	58	32.5	Mule	42.52%	12.73%	44.75%
M020	MCZ 1656	366	85	78	36	79	66	38	Mule	28.39%	0.64%	70.96%
M021	(Mule)	362	84	80.5	42.3	85	70	43	Mule	4.42%	0.01%	95.57%
M022	Gen 753/69	338	81	75	38	78.5	65	39	Mule	42.54%	0.71%	56.75%
M023	HL mlt 5	293	77	69	42	74	59	34	Horse	55.45%	8.50%	36.06%

Appendix I.III – Measurements of Modern Control Data (Metacarpal)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C001	Przewalski	218	49.8	33.8	29	47.3	36.1	Horse	86.05%	2.32%	11.64%
C002	Przewalski	216	44.8	32	29.5	46.8	33.4	Horse	94.36%	0.68%	4.96%
C003	Przewalski	215.9	47.7	29.7	31.6	43.4	34.4	Mule	9.94%	19.00%	71.06%
C004	Przewalski	217.8	46.6	30.6	31.5	43.8	33	Mule	12.12%	18.72%	69.15%
C005	Przewalski	220	50.6	35.1	33	46.8	37.1	Mule	19.48%	1.92%	78.60%
C006	Przewalski	223.8	49.5	34.3	33.4	47.9	37.2	Mule	42.10%	0.94%	56.96%
C007	Przewalski	197	45.6	30.9	32.7	44.1	31.5	Mule	46.00%	7.87%	46.13%
C008	Przewalski	214.2	47.1	31.1	30.3	43.3	33.4	Mule	14.43%	22.76%	62.81%
C009	Przewalski	216.1	49.3	30.9	33.2	47.3	34.3	Horse	58.38%	6.55%	35.08%
C010	Przewalski	216.7	47.7	31.9	32.2	46.2	34.4	Horse	48.86%	4.72%	46.42%
C011	Przewalski	215.8	50.2	31.6	30.1	47.5	35.8	Horse	87.24%	3.26%	9.50%
C012	Przewalski	220	51	33	32.9	46.3	31.2	Donkey	5.43%	49.64%	44.93%
C013	Przewalski	212.2	49.7	33	30.2	47.2	32.6	Horse	73.77%	11.88%	14.35%
C014	Przewalski	217.9	49.7	31.9	31.2	47	34.7	Horse	63.45%	8.35%	28.20%
C015	Przewalski	212.8	46.7	33	31.4	46.2	34.8	Horse	70.76%	1.42%	27.82%
C016	Przewalski	223.8	49.6	34.4	31.7	46.3	35.3	Mule	19.75%	6.36%	73.89%
C017	Przewalski	215.7	49.5	35.2	33.9	51	34.5	Horse	95.07%	0.16%	4.77%
C018	Pony	156.8	36.2	24.6	25.8	38.3	25.4	Horse	96.45%	3.00%	0.55%
C019	Pony	177.7	40.9	27.4	30.4	41	29.3	Horse	81.09%	5.92%	12.99%
C020	Pony	217	51.7	35.4	33.6	48.8	36	Horse	53.58%	1.99%	44.44%
C021	Pony	200.4	45.1	29.3	29	43.8	32.8	Horse	84.08%	5.50%	10.43%
C022	Pony	210	50	33.8	32.6	47.8	34.9	Horse	73.89%	2.11%	24.00%
C023	Pony	208.5	45.1	29.5	31.2	45.3	32.6	Horse	79.71%	4.00%	16.29%
C024	Pony	216.8	45.6	32	31.7	41.7	34.9	Mule	0.02011	0.04021	0.93968
C025	Pony	214.5	45.5	31.7	29.7	46.1	35.3	Horse	0.90501	0.00636	0.08863

Measurements for Modern Control Data (Metacarpal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C026	Pony	217.2	50.4	32.8	32.8	46.3	35.7	Mule	23.86%	6.80%	69.34%
C027	Pony	190	41.8	26.4	28.1	38.8	30.6	Donkey	23.71%	44.32%	31.96%
C028	Pony	230	51.9	33.8	31.7	48	36.5	Mule	34.75%	8.67%	56.58%
C030	Pony	203.2	45.5	29.7	28.7	44.3	34.5	Horse	90.44%	2.03%	7.52%
C031	Pony	194	44.4	26.1	26.2	41.1	32.1	Horse	65.18%	28.42%	6.40%
C032	Pony	189.5	42.6	28.9	31.2	42.9	31.5	Horse	81.65%	2.46%	15.89%
C033	Arab	263	56.5	38.8	35.3	55.4	42.4	Horse	55.96%	0.15%	43.89%
C034	Arab	247.6	51.6	31.4	32.6	53.2	39.1	Horse	97.63%	0.13%	2.23%
C035	Arab	262.7	56.3	34.1	35.4	53.8	39	Mule	32.99%	4.67%	62.34%
C036	Arab	238.5	51.9	35.2	32.3	51.2	36.7	Horse	79.40%	1.40%	19.20%
C037	Arab	249	54.3	35.9	35.7	54	39	Horse	70.25%	0.42%	29.33%
C038	Norvège	246	52	32	34.5	51	38	Horse	52.60%	2.25%	45.15%
C039	(Horse)	268	62	39	43	64	47	Horse	97.11%	0.00%	2.89%
C040	Tonkin	196	41	26.5	29	41	31	Horse	67.80%	11.66%	20.54%
C041	Tarpan	203	44.5	30.1	32.5	46.7	33	Horse	94.73%	0.35%	4.92%
C042	Islande	160	35	24	25	36	27	Horse	90.18%	7.14%	2.68%
C043	Tarpan	207.5	45.5	28	31	44	35	Horse	68.93%	4.14%	26.93%
C044	Shetland	180	37	26	25	38	29.2	Horse	88.31%	6.63%	5.06%
C045	(Horse)	277	61	37.5	40	55	44	Mule	0.70%	0.29%	99.01%
C046	(Horse)	258	54	33	37	54	40	Horse	54.14%	0.57%	45.29%
C047	Boulonnais	279	69	41	47	70	50	Horse	98.84%	0.00%	1.16%
C048	Shetland	187	41	25	30	43	29	Horse	94.82%	3.06%	2.12%
C049	Grand	253	59	37	42	61	44	Horse	96.67%	0.00%	3.33%
C050	Poney	130	34	22	22	32.1	24	Horse	69.15%	30.03%	0.82%
C051	Islande	194	46	29	31	46	34	Horse	97.64%	0.38%	1.99%

Measurements for Modern Control Data (Metacarpal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C052	Arabe	262	54	36	35.5	55	40	Horse	71.72%	0.25%	28.03%
C053	Shetland	160	34.5	20.5	23.5	35	24.5	Horse	57.08%	41.90%	1.02%
C054	Poney	160	34	22	23	37	25.5	Horse	97.20%	2.62%	0.18%
C055	Welsh	167	38	24	28	38	28.5	Horse	84.85%	8.87%	6.28%
C056	Poney	138	34.5	20.1	23	35	24	Horse	92.06%	7.81%	0.14%
C057	Poney	188	40	24.5	28	40	29.7	Horse	74.36%	16.62%	9.02%
C058	Grand	240	55	34	37	54.5	41	Horse	88.64%	0.08%	11.28%
C059	(Horse)	248	52	33.5	36.5	53	40	Horse	69.24%	0.16%	30.60%
C060	Shetland	148	35.2	22.2	25	37	26.6	Horse	98.61%	1.17%	0.22%
C061	Shetland	159	37	23.1	27	39	29	Horse	99.14%	0.48%	0.38%
C062	Shetland	165	40.5	25	25.2	39	28.1	Horse	88.20%	10.75%	1.05%
C063	Shetland	158	36	24	26	37	27.6	Horse	94.90%	3.37%	1.73%
C064	Islande	215	45.5	30	30.2	46	35	Horse	89.73%	1.08%	9.19%
C065	Islande	210	47.7	28	28.5	45	34	Horse	80.74%	12.09%	7.18%
C066	Islande	209	48	30.8	32.3	46.2	34	Horse	67.62%	4.83%	27.56%
C067	Hannover	269	62.5	40.2	42	64.3	49	Horse	98.33%	0.00%	1.67%
C068	Hannover	257	64	38	43	64	46	Horse	98.48%	0.00%	1.52%
C069	Konik	209	48	29.7	32	47.6	35	Horse	94.19%	0.82%	4.99%
C070	Exmoor	203	44	27	29.7	45.3	33.3	Horse	97.43%	0.74%	1.83%
C071	Shetland	151	34	20.5	23	34.2	24.2	Horse	65.75%	33.47%	0.77%
C072	Islande	200	46	29	29	43.8	32	Horse	74.07%	14.40%	11.54%
C073	Welsh	182	41.7	28	28.1	41.4	29.3	Horse	86.87%	7.53%	5.60%
C074	Welsh	213	48	30	32	48.2	34	Horse	94.11%	1.19%	4.70%
C075	Islande	215	50.2	30	34.1	48	36	Horse	71.46%	2.72%	25.82%
C076	Arabe	243	50	32	32.3	51	37	Horse	88.58%	0.86%	10.56%

Measurements for Modern Control Data (Metacarpal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C077	Poney	201	43	30	30.7	43.1	32	Horse	63.09%	4.50%	32.41%
C078	Mongol	220	48.5	30.5	31.8	47.5	35	Horse	79.33%	3.33%	17.34%
C079	Mongol	215	46	30.3	29.5	46	35.3	Horse	91.27%	1.13%	7.60%
C080	Mongol	223	48	30	33	46.5	36	Mule	44.97%	3.75%	51.29%
C081	Tarpan	220	46	29	32.3	46	35	Horse	65.38%	2.91%	31.71%
C082	Arabe	250	55.5	35	33.5	53.7	38	Horse	79.28%	2.26%	18.46%
C083	Corse	259.5	58	36	34	56	42	Horse	89.56%	0.30%	10.14%
C084	(Horse)	217	44.5	29.5	30	44	34.1	Horse	55.51%	6.24%	38.25%
C085	(Horse)	225	48.5	28.1	34	47	34.8	Mule	41.59%	9.83%	48.58%
C086	(Horse)	261	61	38	42	63	47	Horse	98.56%	0.00%	1.44%
C087	Camargue	224	49	31	35	49	35	Horse	64.95%	1.95%	33.10%
C093	Exmoor Left	194.9	48.18	29.31	31.61	44.42	34.98	Horse	73.29%	4.71%	22.00%
C094	Welsh cob	228.13	52.41	32.09	37.39	51.36	37.77	Horse	62.32%	0.63%	37.05%
C095	Pony 3158	177.88	38.85	24.72	29.69	41.06	29.69	Horse	95.94%	1.33%	2.73%
C096	Race Horse 123 Left	273.63	60.89	37.05	37.32	59.34	45.68	Horse	86.04%	0.05%	13.92%
C097	NF Pony 137 left	224.64	47.4	31.46	30.34	47.93	36.78	Horse	92.67%	0.47%	6.86%
C098	Shetland 604 left	150.47	34.32	20.66	23.19	33.28	24.51	Donkey	41.43%	57.07%	1.50%
C100	Imm horse 636 right	262.29	52.58	34.3	32.55	53.76	40.28	Horse	88.75%	0.26%	10.98%
C103	Unknown Horse right	220.55	47.14	29.49	23.73	42.52	31.1	Donkey	7.86%	88.85%	3.29%
D001	Donkey	181.5	40.6	27.3	25.1	36.5	26.2	Donkey	2.85%	91.92%	5.23%
D002	Donkey	186.5	36.8	24.9	24	33.8	24.3	Donkey	0.43%	96.71%	2.86%
D003	Donkey	166.5	37.4	24.9	24.4	35	26.1	Donkey	19.72%	74.04%	6.24%
D004	Donkey	165.2	36.7	25.3	21.7	32.2	24.2	Donkey	1.18%	97.21%	1.61%
D005	Donkey	165.2	35.7	23.4	20.7	29.4	23.7	Donkey	0.09%	99.22%	0.69%
D006	Donkey	191.7	43.1	28.4	25.2	37.4	29.9	Donkey	3.89%	82.14%	13.97%

Measurements for Modern Control Data (Metacarpal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
D007	Donkey	180.2	42	28.7	25.6	37.6	28.3	Donkey	11.98%	74.81%	13.22%
D008	Donkey	173	35.5	25.2	25.1	32.7	24.1	Donkey	0.99%	91.01%	8.00%
D009	Donkey	175.9	37.2	28.5	22.7	34.8	26.3	Donkey	12.68%	76.34%	10.98%
D010	Donkey	211.6	48.5	31.1	29.4	40.1	31.3	Donkey	0.23%	72.96%	26.80%
D011	Donkey	170.5	36.4	24.6	23.9	34	25.7	Donkey	8.34%	85.38%	6.28%
D012	Donkey	179.1	35.8	24.9	21.9	34	25.4	Donkey	6.22%	90.41%	3.37%
D013	Donkey	192.6	44.3	31.2	24.6	40	29.7	Donkey	23.47%	64.60%	11.93%
D014	Donkey	189.5	43.4	29.2	25.5	38.8	29	Donkey	10.11%	78.46%	11.43%
D015	Olduvai	179.4	37.1	23.5	24.3	34.1	26.1	Donkey	2.61%	92.69%	4.70%
D016	Syrie	203	40	26	26	37	27	Donkey	0.91%	91.54%	7.55%
D017	(Donkey)	160.5	37.5	21.5	24	34.5	24	Donkey	6.22%	92.96%	0.83%
D018	Afrique	180	40	26.5	26	36.5	26.5	Donkey	4.74%	86.96%	8.30%
D021	Crête	194	41	26	26	36.5	27.5	Donkey	0.96%	92.02%	7.02%
D022	(Donkey)	200.5	40	25.5	26	38	27.5	Donkey	4.44%	87.27%	8.29%
D023	Nubie	199.5	42	26	25	36.5	28	Donkey	0.44%	95.63%	3.94%
D024	(Donkey)	182.5	36	23.5	25	33.3	25	Donkey	0.77%	93.80%	5.42%
D025	Zoo	194	42	25.5	27	36	28	Donkey	0.31%	92.24%	7.45%
D026	(Donkey)	179	37.5	25	24	33	25	Donkey	0.38%	96.29%	3.33%
D027	(Donkey)	167	34	22	21.7	33	24.2	Donkey	11.10%	87.31%	1.59%
D028	(Donkey)	171	33	20	20	29	21	Donkey	0.04%	99.83%	0.14%
D029	Ane Blanc	215	46	27.5	29.5	43	31.5	Donkey	15.63%	60.37%	24.00%
D030	Ane Blanc	212	48	29	29	40	31.5	Donkey	0.34%	81.63%	18.04%
D031	(Donkey)	157	31	20.2	20	29	22.5	Donkey	1.65%	97.55%	0.80%
D032	(Donkey)	180	35.3	24.5	24.7	33	24.5	Donkey	0.97%	92.14%	6.89%
D033	(Donkey)	155	33.5	21.2	20.7	30	23	Donkey	1.37%	97.95%	0.68%

Measurements for Modern Control Data (Metacarpal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
D034	anglais	180	37	24	23	34.7	25.8	Donkey	5.31%	91.74%	2.96%
D035	Argentine	225	51.5	31	30	43	32	Donkey	0.25%	85.40%	14.35%
D036	S Peru	185	40	25.7	25.7	36	27	Donkey	2.25%	90.54%	7.21%
D037	S Peru	188	39	26	25	35	27.7	Donkey	1.85%	86.43%	11.72%
D038	(Donkey)	205	45.5	29	27	40	32	Donkey	6.43%	67.01%	26.57%
D039	Turquie	173	35	21.5	21	31.5	23	Donkey	0.34%	99.28%	0.39%
D040	Turquie	180	38	24.7	22.7	34.5	26.5	Donkey	3.64%	93.26%	3.10%
D041	(Donkey)	171	35.1	22	22.1	32	23.1	Donkey	0.61%	98.67%	0.72%
D042	(Donkey)	167	36.3	22.1	21.7	32	23.5	Donkey	0.56%	98.95%	0.49%
D043	(Donkey)	148	29	18.5	19	27	19.1	Donkey	0.28%	99.58%	0.15%
D044	(Donkey)	173	38	25	26	36	28	Donkey	32.24%	51.72%	16.04%
D045	(Donkey)	193.5	42	26.5	26	37.5	30	Donkey	5.98%	77.71%	16.31%
D046	(Donkey)	163	38	25	28.2	38	29	Horse	89.60%	4.34%	6.06%
D047	(Donkey)	178	36	24	24	35	26	Donkey	15.02%	78.55%	6.43%
D048	(Donkey)	185	42	27	25	37	29	Donkey	6.35%	84.41%	9.24%
D049	(Donkey)	188	42	27	25.5	37	29	Donkey	4.23%	84.84%	10.93%
D050	(Donkey)	188	37	25	24	35.5	25.7	Donkey	4.40%	90.40%	5.20%
D051	(Donkey)	183	41	25	28	38.5	29	Donkey	28.14%	55.19%	16.67%
D052	Amérique du Sud	161	31	20	18.5	29	22	Donkey	1.01%	98.67%	0.32%
D053	(Donkey)	189	39	25	24	35	26	Donkey	0.73%	96.52%	2.75%
D054	Lesbos	216.3	48.1	30	30.9	44.2	33	Mule	15.88%	36.07%	48.06%
D055	(Donkey)	161	33	21	22	29	21	Donkey	0.08%	99.47%	0.45%
D056	(Donkey)	196	45	27	28.5	38	31	Donkey	1.18%	75.88%	22.94%
D058	(Donkey)	182	36	25	25	36.5	26	Donkey	32.71%	57.86%	9.43%
D059	(Donkey)	177	35	22.3	23	31.9	24	Donkey	0.46%	97.85%	1.70%

Measurements for Modern Control Data (Metacarpal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
D061	Donkey 3349 Right	166.52	34.9	21.4	24.78	32.74	24.28	Donkey	3.05%	93.60%	3.35%
D062	Donkey 546 left	189.27	41.39	24.74	25.98	36.29	26.94	Donkey	0.67%	96.02%	3.31%
D063	Donkey 131 left	175.64	34.69	21.52	22.37	31.35	23.25	Donkey	0.25%	98.93%	0.83%
D064	Donkey 132 left	183.55	42.36	25.96	27.2	38.48	27.89	Donkey	9.30%	82.69%	8.01%
M001	Mule	217.1	48.2	31.2	30.4	44.5	33	Mule	19.48%	31.90%	48.62%
M002	Mule	213.8	43.5	29.5	28.4	44.4	33.5	Horse	87.97%	2.48%	9.55%
M003	Mule	230.5	50.8	33	31.9	43.9	34.7	Mule	0.69%	23.42%	75.89%
M004	Mule	228.1	48.6	31.4	34.1	47.1	34.8	Mule	20.92%	5.52%	73.56%
M005	Mule	213	46.7	30.7	31.2	47.6	35.6	Horse	95.70%	0.30%	4.00%
M006	Mule	265.8	63.1	46.9	39.9	57.2	42.8	Mule	1.09%	0.06%	98.85%
M007	Mule	222.2	50.1	32.4	32.2	45.7	34.6	Mule	11.85%	16.43%	71.72%
M008	Mule	233.3	54.8	36.7	34.5	49.2	36.4	Mule	6.20%	6.46%	87.34%
M009	Mule	266	57.8	39.4	34.1	52.8	40.1	Mule	5.00%	2.52%	92.48%
M012	NY 204211	259	55.5	34	37	52	39.5	Mule	5.75%	2.13%	92.12%
M013	NY 14116	235	55	33	35	49	38	Mule	8.66%	8.03%	83.31%
M014	AA 1534	270	60.5	39	40.5	55.4	46	Mule	1.59%	0.04%	98.37%
M015	AA 98766	260	53.5	35	33	50	37	Mule	5.46%	10.74%	83.79%
M016	UNSM 5084	272	67	40	47.5	64	47.7	Mule	27.55%	0.01%	72.44%
M017	A 543	254	54.5	35.5	39	54	40	Mule	21.29%	0.24%	78.47%
M018	MU 1970-5	216.3	48.1	30	30.9	44.2	33	Mule	15.88%	36.07%	48.06%
M019	MCZ 1655	215	45	28.5	30.5	43	32	Mule	19.89%	31.31%	48.79%
M020	MCZ 1656	251	51.5	34	31	47	39.5	Mule	5.32%	4.17%	90.51%
M022	Gen 753/69	241	52	33	33.5	48	38	Mule	9.20%	4.67%	86.14%
M023	HL mlt 5	207	46	29	31	42	32.5	Mule	9.90%	30.00%	60.10%
M024	LY 95156	210	45	29	29	42	32	Mule	19.37%	39.34%	41.29%

Appendix I.IV – Measurements of Modern Control Data (Femur)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	DC	Bp	SD	Bd	Determination	Horse	Donkey	Mule
C001	Przewalski	356	52.4	108.8	35.1	85.2	Horse	49.15%	19.39%	31.46%
C002	Przewalski	340	49.4	100.1	32.9	81.6	Horse	42.66%	42.11%	15.24%
C003	Przewalski	355	51.3	106.5	34.6	83.1	Horse	45.66%	24.79%	29.55%
C004	Przewalski	350	48.9	95	38.7	83.3	Horse	58.30%	31.89%	9.81%
C005	Przewalski	359	56.5	110.2	38.4	91.2	Horse	66.70%	7.31%	25.99%
C006	Przewalski	368	54.7	119	38.4	92.9	Horse	54.10%	7.91%	37.99%
C007	Przewalski	341	52	99	40.1	82	Horse	74.67%	9.47%	15.86%
C008	Przewalski	353	52.3	101.9	31.7	84.7	Donkey	38.98%	41.86%	19.16%
C009	Przewalski	360	55	103.9	40.8	84.1	Horse	67.27%	5.75%	26.97%
C010	Przewalski	366	55.6	103.8	39.7	90.4	Horse	69.95%	10.92%	19.13%
C011	Przewalski	355	56.5	107.1	35	84.5	Horse	53.22%	9.28%	37.51%
C012	Przewalski	368	53.7	106.3	39.8	86.3	Horse	60.89%	10.58%	28.53%
C013	Przewalski	341	50.4	98.5	36	86.6	Horse	57.61%	32.84%	9.56%
C014	Przewalski	363	54.6	105.4	41.1	86.6	Horse	68.52%	6.82%	24.66%
C015	Przewalski	357	53.8	104.3	38.8	84.5	Horse	63.77%	10.10%	26.13%
C016	Przewalski	362	52.1	112.3	37.8	82.8	Horse	46.21%	9.40%	44.39%
C017	Przewalski	382	59.9	117.2	43	92.2	Horse	54.94%	1.49%	43.57%
C018	Pony	289	40.2	82	29.8	67.8	Donkey	19.58%	78.35%	2.07%
C019	Pony	353	45	99.3	31	79	Donkey	15.41%	75.97%	8.62%
C020	Pony	394	53.4	114.4	41.5	96.2	Horse	56.15%	16.09%	27.76%
C021	Pony	351	54.1	111.2	40.9	85.5	Horse	65.74%	3.93%	30.32%
C022	Pony	381	57.7	118.2	42.8	93	Horse	56.84%	2.47%	40.69%
C023	Pony	355	50.4	100.3	40.8	81.9	Horse	66.94%	13.91%	19.15%
C024	Pony	384	59	116.1	40.1	93.3	Horse	52.75%	3.89%	43.36%
C025	Pony	372	55.8	109.6	36.5	88.4	Horse	50.52%	12.50%	36.98%

Measurements for Modern Control Data (Femur, cont'd)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	DC	Bp	SD	Bd	Determination	Horse	Donkey	Mule
C026	Pony	393	58.1	118.3	42.1	94.4	Horse	51.33%	3.56%	45.11%
C027	Pony	358	50.7	102.2	33.3	81.4	Donkey	37.70%	37.96%	24.34%
C028	Pony	396	60.3	115.3	39.6	95.5	Horse	50.12%	5.06%	44.82%
C029	Pony	399	57.9	119	39	95.7	Mule	42.85%	7.51%	49.64%
C030	Pony	359	51.3	102.4	30.3	84.7	Donkey	27.02%	56.23%	16.75%
C031	Pony	331	49.7	101	31.8	78.7	Horse	45.00%	34.59%	20.42%
C032	Pony	344	48.5	99.2	33.2	77.5	Donkey	38.87%	41.11%	20.02%
C033	Arab	433	61.4	126.9	41.8	101.5	Mule	29.33%	3.07%	67.61%
C034	Arab	423	60	120.3	39.3	97.2	Mule	31.27%	6.44%	62.29%
C035	Arab	441	64.6	131.6	42.9	105.4	Mule	26.24%	1.33%	72.43%
C036	Arab	406	55.4	114.6	38.2	91.9	Mule	35.57%	15.54%	48.89%
C037	Arab	424	60.5	126.4	38.8	101	Mule	28.64%	5.52%	65.84%
C041	Tarpan	375	52	107	36.5	85	Horse	42.62%	24.23%	33.15%
C044	Shetland	312	46	89	31.5	72	Donkey	39.06%	52.57%	8.37%
C045	(Horse)	481	69	140	47	112	Mule	14.94%	0.33%	84.72%
C046	(Horse)	433	67	127	49.5	102	Mule	38.79%	0.23%	60.98%
C048	Shetland	332	55	103	31.5	79	Horse	52.25%	13.44%	34.32%
C049	Grand	444	70	146	54	115	Mule	36.03%	0.04%	63.93%
C050	Poney	230	40	68	25.2	63	Donkey	21.78%	77.72%	0.51%
C054	Poney	285	38.5	83	25	63	Donkey	8.03%	90.20%	1.77%
C055	Welsh	310	44	95	29	72	Donkey	25.69%	65.36%	8.95%
C056	Poney	235	37	74	25	67	Donkey	11.94%	87.77%	0.29%
C057	Poney	330	48	92	31	78	Donkey	31.86%	60.25%	7.90%
C058	Grand	472	70	144	51	108	Mule	12.39%	0.05%	87.57%
C059	(Horse)	426	62	124	42	101	Mule	35.94%	2.93%	61.13%

Measurements for Modern Control Data (Femur, cont'd)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	DC	Bp	SD	Bd	Determination	Horse	Donkey	Mule
C067	Hannover	472	74	153	56	123	Mule	28.32%	0.02%	71.66%
C068	Hannover	463	70	138	53	111.5	Mule	30.12%	0.09%	69.79%
C076	Arabe	410	56	116	37	95	Mule	33.49%	20.54%	45.98%
C077	Poney	352	48	99	35	83	Donkey	38.43%	49.86%	11.71%
C078	Mongol	383	55	118	40	90	Mule	45.02%	5.91%	49.06%
C079	Mongol	363	56.5	109	36.5	87	Horse	54.43%	8.74%	36.84%
C080	Mongol	403	60	121	42	92	Mule	34.77%	1.70%	63.53%
C081	Tarpan	401	58	113	40	91	Mule	43.15%	6.59%	50.26%
C082	Arabe	411	60	122	43	97	Mule	41.71%	2.48%	55.81%
C084	(Horse)	390	60	119	45	94	Horse	55.41%	1.18%	43.41%
C086	(Horse)	498	73	149	55	118	Mule	14.90%	0.03%	85.07%
C089	Exmoor	362	51	108.7	35	88	Horse	44.21%	32.52%	23.27%
C090	Islande	317	48	98.5	35	79	Horse	61.79%	25.89%	12.32%
C091	Fjord	415	62	121	49	96	Mule	48.59%	0.55%	50.86%
C092	Islande	403	61	119	44	92	Mule	40.79%	1.14%	58.08%
C093	Exmoor right	359	51.51	108.96	39.36	82.5	Horse	55.31%	9.56%	35.13%
C094	Welsh cob Left	402	59.42	128.26	48.76	103.95	Horse	63.63%	0.97%	35.40%
C095	Pony 3158 right	339	44.05	98.01	31.28	77.05	Donkey	19.43%	72.29%	8.28%
C096	Race Horse 123 left	454	66.83	138.26	48.52	110.88	Mule	28.37%	0.35%	71.28%
C097	NF Pony 137 left	382	54.83	118	38.86	91.19	Mule	45.33%	8.22%	46.46%
C098	Shetland 604 left	278.28	38.24	80.95	26.88	65.85	Donkey	10.70%	88.16%	1.14%
D001	Donkey	302	43.1	89.6	27.9	70.7	Donkey	19.76%	75.58%	4.66%
D002	Donkey	319	42	89.6	26.3	71.2	Donkey	7.95%	89.24%	2.80%
D003	Donkey	300	40.1	86.9	27.4	69.1	Donkey	10.91%	86.91%	2.18%
D005	Donkey	275.3	37.4	79.5	26.3	67.4	Donkey	7.69%	91.71%	0.60%

Measurements for Modern Control Data (Femur, cont'd)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	DC	Bp	SD	Bd	Determination	Horse	Donkey	Mule
D006	Donkey	321	42.8	90.1	30.9	78.7	Donkey	16.06%	81.76%	2.18%
D007	Donkey	308	42.7	92	29.9	74.6	Donkey	21.83%	74.12%	4.05%
D008	Donkey	281	37.9	81.2	30	63.9	Donkey	18.63%	79.33%	2.04%
D009	Donkey	300	41.5	84.8	30.2	72	Donkey	19.33%	78.51%	2.16%
D010	Donkey	361	49.3	104.1	32.7	85.5	Donkey	29.41%	55.19%	15.40%
D011	Donkey	287	39.1	81.1	25.1	64.2	Donkey	7.66%	90.96%	1.39%
D012	Donkey	329	45.3	94.5	29.2	80.2	Donkey	16.57%	79.46%	3.97%
D013	Donkey	325	45.3	94.2	31.2	80.5	Donkey	24.93%	70.59%	4.48%
D015	Olduvai	289	42.4	84.7	28.7	69	Donkey	24.11%	72.65%	3.25%
D016	Syrie	324	40	87	28.5	68.5	Donkey	7.60%	89.87%	2.54%
D017	(Donkey)	268	40	80	26.5	65.5	Donkey	16.92%	81.55%	1.54%
D019	Ethiopia	298	41	86	27	68	Donkey	12.56%	84.77%	2.68%
D020	(Donkey)	333	45	97	30.1	73	Donkey	22.36%	64.60%	13.04%
D021	Nubie	346	45	98	27	74	Donkey	9.80%	80.86%	9.34%
D025	(Donkey)	325	44	95	31	74	Donkey	24.67%	66.81%	8.52%
D026	(Donkey)	305	61	89	26	70	Horse	56.91%	8.47%	34.62%
D029	Ane Blanc	364.5	50	103	33	83	Donkey	31.03%	48.14%	20.84%
D030	Ane Blanc	355	50	103	32.5	83	Donkey	34.45%	46.12%	19.43%
D031	(Donkey)	266	35	75	22	60	Donkey	2.83%	96.84%	0.34%
D032	(Donkey)	293	36.9	79	25	65	Donkey	3.67%	95.77%	0.56%
D045	(Donkey)	326	43	90	31	77	Donkey	16.05%	81.10%	2.85%
D056	(Donkey)	330	44.5	91.5	32	76.5	Donkey	23.73%	70.97%	5.31%
D058	sans crâne	301	42	83	27	70	Donkey	11.46%	86.74%	1.81%
D059	sans crâne	303	37	86	25	66	Donkey	3.76%	95.16%	1.08%
D060	sans crâne	272	37	78	24.5	61	Donkey	6.68%	92.41%	0.91%

Measurements for Modern Control Data (Femur, cont'd)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	DC	Bp	SD	Bd	Determination	Horse	Donkey	Mule
D061	Donkey 3349 Right	300	36.14	81.36	28.21	66.24	Donkey	5.46%	93.76%	0.78%
D062	Donkey 546 left	316	42.68	89.15	28	72.54	Donkey	12.57%	84.23%	3.20%
D063	Donkey 131 left	294.88	36.17	77.54	23.74	63.62	Donkey	2.30%	97.31%	0.40%
D064	Donkey 132 left	320.5	44.27	92	31.5	76.66	Donkey	25.94%	69.14%	4.92%
M001	Mule	391	51.4	112.3	37.2	82.8	Mule	28.95%	17.20%	53.85%
M002	Mule	376	52.8	102.6	33.2	84.4	Donkey	32.83%	40.55%	26.62%
M003	Mule	389	54.1	110.9	40.5	89.9	Horse	51.60%	12.02%	36.38%
M004	Mule	386	53.2	120.3	39.5	87.4	Mule	34.61%	6.33%	59.06%
M005	Mule	379	54.3	113.6	40.2	87.9	Horse	49.96%	7.23%	42.80%
M006	Mule	467	70.2	139.5	52.8	109.7	Mule	22.53%	0.07%	77.40%
M007	Mule	397	53.9	106.7	37.2	87.7	Horse	37.47%	25.89%	36.65%
M008	Mule	412	60.7	133.3	41.6	98.5	Mule	24.64%	1.12%	74.25%
M009	Mule	437	67	131.6	55	117.3	Horse	73.43%	0.25%	26.32%
M012	NY 204211	464	65	136	45	103	Mule	12.55%	0.49%	86.96%
M013	NY 14116	410	63	129	44	99	Mule	34.75%	0.68%	64.57%
M014	AA 1534	472	75	149	54	119	Mule	22.79%	0.02%	77.19%
M015	AA 98766	433	66.5	126	39.5	96	Mule	15.59%	0.74%	83.67%
M016	UNSM 5084	450	72	135	46	109	Mule	23.55%	0.17%	76.29%
M019	MCZ 1655	370	54	110	35	83	Mule	38.10%	13.64%	48.26%
M020	MCZ 1656	409	64	115	39	97	Mule	43.35%	3.60%	53.06%
M021	(Mule)	410	62	124	43	101	Mule	46.53%	1.96%	51.51%
M022	GE 753-69	387	59	119	42	96	Horse	56.35%	2.94%	40.71%
M023	HL mlt 5	358	50	114	37	88	Horse	50.32%	20.35%	29.33%

Appendix I.V – Measurements of Modern Control Data (Tibia)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	SD	Bp	Bd	Dd	Determination	Horse	Donkey	Mule
C001	Przewalski	328	36.4	93	70.4	47.2	Horse	76.63%	4.70%	18.67%
C002	Przewalski	318	36.5	85.5	64.6	41.3	Horse	72.59%	7.05%	20.36%
C003	Przewalski	316	38.1	87.4	67.2	42.8	Horse	82.43%	4.18%	13.39%
C004	Przewalski	309	39.2	85.2	66.7	42.4	Horse	68.60%	12.70%	18.71%
C005	Przewalski	332	42.5	94	75.4	46.2	Horse	92.83%	0.56%	6.62%
C006	Przewalski	332	40	94.3	71.1	45.4	Horse	93.89%	0.24%	5.87%
C007	Przewalski	305	41.4	85.6	65	39.4	Horse	96.99%	0.24%	2.76%
C008	Przewalski	320	39.8	88.8	69.1	44.1	Horse	75.69%	5.52%	18.79%
C009	Przewalski	330	43.5	90	74.1	45.1	Horse	65.52%	7.75%	26.73%
C010	Przewalski	326	41.4	90.1	70.5	43.7	Horse	85.91%	1.52%	12.57%
C011	Przewalski	330	38.5	92.1	69	45	Horse	83.69%	1.40%	14.91%
C012	Przewalski	328	40.1	92.6	72.4	46.5	Horse	81.40%	2.91%	15.69%
C013	Przewalski	307	40.2	92	70.3	44.6	Horse	98.82%	0.10%	1.09%
C014	Przewalski	325	42.3	94.5	71.9	46.4	Horse	93.38%	0.33%	6.29%
C015	Przewalski	324	43.1	88.8	70.3	42.3	Horse	88.77%	1.00%	10.24%
C016	Przewalski	334	40.5	89.7	69	43.8	Horse	59.56%	4.95%	35.49%
C017	Przewalski	337	46.5	97.9	77	47.1	Horse	96.91%	0.04%	3.05%
C018	Pony	252.2	30	72.9	53.6	33.7	Horse	97.38%	2.10%	0.53%
C019	Pony	296	32.1	85.5	60.4	39.7	Horse	98.76%	0.19%	1.05%
C020	Pony	359	43.6	95.3	74.2	52.1	Mule	0.65%	34.45%	64.90%
C021	Pony	313	39	90.2	66.6	40.1	Horse	99.63%	0.01%	0.36%
C022	Pony	314	33.5	84.6	62	39.2	Horse	92.11%	1.35%	6.54%
C023	Pony	345	40	97.2	73.6	49.9	Horse	51.58%	4.49%	43.93%
C024	Pony	340	38.9	97.2	72.5	44.1	Horse	99.42%	0.00%	0.58%
C025	Pony	321	40.7	84.3	65.1	41.5	Mule	30.44%	22.28%	47.28%

Measurements for Modern Control Data (Tibia, cont'd)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	SD	Bp	Bd	Dd	Determination	Horse	Donkey	Mule
C026	Pony	338	40.5	93.7	72	44.3	Horse	93.99%	0.19%	5.82%
C027	Pony	336	38.1	93.4	71	43.4	Horse	97.41%	0.07%	2.52%
C028	Pony	338	42.1	99.4	71.9	48	Horse	94.99%	0.05%	4.97%
C029	Pony	357	41	95.7	76	45.3	Horse	88.20%	0.29%	11.51%
C030	Pony	337	33.2	88	67.3	40.8	Horse	89.47%	1.23%	9.30%
C031	Pony	293	30.2	86	62.9	38.6	Horse	99.89%	0.01%	0.10%
C032	Pony	308	35.2	83.7	63.2	41.9	Horse	47.44%	28.43%	24.13%
C033	Arab	398	43.5	104.4	80.4	52.8	Mule	7.80%	1.15%	91.05%
C034	Arab	387	40.1	100	75.8	48.2	Mule	29.64%	0.78%	69.57%
C035	Arab	394	43.4	105.3	83.2	52	Mule	45.70%	0.41%	53.89%
C036	Arab	369	39.7	98.4	77.2	48.7	Horse	52.94%	1.90%	45.16%
C037	Arab	357	39.6	100	79.9	49.8	Horse	89.68%	0.45%	9.87%
C041	Tarpan	342	38.5	87.5	69	42	Horse	47.53%	8.99%	43.49%
C044	Shetland	276	33	77	61	38	Horse	75.36%	21.05%	3.59%
C045	(Horse)	427	48	115	89	56	Mule	39.06%	0.03%	60.91%
C046	(Horse)	391	45	105	81	52.5	Mule	22.99%	0.59%	76.42%
C048	Shetland	302	34	84	64	38	Horse	99.16%	0.14%	0.71%
C049	Grand	404	53	122	90	59	Horse	96.29%	0.00%	3.72%
C050	Poney	204	26	66	51	31	Horse	98.95%	1.03%	0.02%
C054	Poney	255	27	70	52	31	Horse	97.30%	2.27%	0.44%
C055	Welsh	283	32	75	56.5	36	Horse	52.93%	37.72%	9.35%
C056	Poney	211	25	65	53	33	Horse	63.43%	36.44%	0.13%
C057	Poney	293	35	82	64	39	Horse	96.10%	1.74%	2.16%
C058	Grand	422	49.5	119	91	59	Horse	58.59%	0.01%	41.40%
C059	(Horse)	375	43	101	79	51	Mule	29.69%	2.00%	68.31%

Measurements for Modern Control Data (Tibia, cont'd)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	SD	Bp	Bd	Dd	Determination	Horse	Donkey	Mule
C067	Hannover	435	54	127	99	63	Horse	85.57%	0.00%	14.43%
C068	Hannover	415	53	117	89	57	Horse	61.31%	0.01%	38.69%
C076	Arabe	373	39	98	77	48	Horse	51.64%	1.76%	46.60%
C077	Poney	323	35.5	84	63	39	Horse	77.21%	4.10%	18.69%
C078	Mongol	348	39	97	74	47	Horse	90.19%	0.30%	9.51%
C079	Mongol	333	38	93	71	43	Horse	98.27%	0.05%	1.68%
C080	Mongol	350	43	100	76	49	Horse	88.93%	0.16%	10.90%
C081	Tarpan	369	40	95	70	44	Horse	50.49%	0.53%	48.99%
C082	Arabe	363	40	101	78.5	50	Horse	82.63%	0.42%	16.95%
C084	(Horse)	360	42	96	76	47	Horse	58.83%	1.76%	39.42%
C086	(Horse)	438	53	123	94	60	Horse	59.53%	0.00%	40.47%
C093	Exmoor left	304.5	38.27	88.35	66.94	42.78	Horse	96.64%	0.55%	2.81%
C094	Welsh cob	365	44.06	105.71	78.62	50.28	Horse	96.48%	0.01%	3.51%
C095	Pony 3158 right	293.48	31.86	82.05	59.46	38.61	Horse	95.29%	1.68%	3.03%
C096	Race Horse 123 left	417.5	48.99	118.67	91.48	57.09	Horse	91.17%	0.00%	8.83%
C097	NF Pony 137 left	340	35.68	95.87	72.71	47.16	Horse	92.02%	0.57%	7.42%
C098	Shetland 605 left	247.56	27.36	67.39	51.81	31.57	Horse	70.63%	28.23%	1.15%
C101	Horse DC57 left	310.5	35.49	88.82	66.38	43.2	Horse	94.91%	0.95%	4.15%
D001	Donkey	285	33.4	72.7	56.6	37.6	Donkey	1.10%	94.96%	3.95%
D002	Donkey	297	28.6	70.4	55.8	36.2	Donkey	0.19%	98.02%	1.80%
D003	Donkey	276.3	30.9	69.8	56.3	35.6	Donkey	1.62%	96.48%	1.90%
D004	Donkey	252	31.2	71.1	53.9	35.6	Donkey	36.00%	61.27%	2.74%
D005	Donkey	265.8	27.8	67.3	52.1	33.1	Donkey	4.74%	93.35%	1.91%
D006	Donkey	298	32.3	77.1	61.8	42.5	Donkey	0.16%	97.97%	1.88%
D007	Donkey	282.3	31.5	77.2	60.1	42.6	Donkey	0.63%	97.46%	1.92%

Measurements for Modern Control Data (Tibia, cont'd)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	SD	Bp	Bd	Dd	Determination	Horse	Donkey	Mule
D008	Donkey	273.5	30.5	65.8	52.9	35.4	Donkey	0.02%	99.58%	0.40%
D009	Donkey	290	31	72.5	56.3	37.7	Donkey	0.52%	96.62%	2.86%
D010	Donkey	257	27	62.2	49.6	31.8	Donkey	0.19%	99.47%	0.34%
D011	Donkey	331	35.3	83.6	68.2	43.9	Donkey	1.82%	81.56%	16.61%
D012	Donkey	276.5	28.7	67.3	51	34.2	Donkey	0.34%	98.14%	1.53%
D013	Donkey	306	33	82	64.5	42.1	Donkey	21.60%	63.89%	14.51%
D014	Donkey	312	34	82	65.3	44	Donkey	1.56%	89.93%	8.51%
D015	Olduvai	271	30	70.6	55.7	39.2	Donkey	0.07%	99.45%	0.48%
D016	Syrie	314	34.5	71.5	59.5	36	Donkey	0.16%	95.37%	4.47%
D017	(Donkey)	249	31	67	55.5	37	Donkey	0.20%	99.57%	0.24%
D018	Afrique	286	33	73	57	38	Donkey	0.90%	95.59%	3.52%
D019	Ethiopia	282	31	71	54	35	Donkey	4.75%	89.56%	5.70%
D022	(Donkey)	309	34	77	60.5	39	Donkey	2.55%	85.24%	12.21%
D023	Nubie	325	33	78	61	40.5	Donkey	0.26%	90.22%	9.52%
D025	(Donkey)	313	36	76	62	39	Donkey	0.67%	90.90%	8.42%
D026	(Donkey)	288	30	70	54	34	Donkey	3.31%	91.38%	5.32%
D029	Ane Blanc	348	38	83.5	65	45	Donkey	0.04%	81.45%	18.52%
D030	Ane Blanc	328	35.3	83.5	67.5	43.5	Donkey	3.19%	77.48%	19.34%
D031	(Donkey)	249	26	61	47	31	Donkey	0.23%	99.45%	0.32%
D032	(Donkey)	285	31	67.5	52.5	34	Donkey	0.24%	97.68%	2.08%
D045	(Donkey)	300	32.5	77.5	62	43	Donkey	0.11%	98.08%	1.82%
D056	(Donkey)	312	35	80	64	44.5	Donkey	0.08%	96.57%	3.35%
D058	sans crâne	285	31	73	57.2	37	Donkey	3.89%	91.75%	4.36%
D059	sans crâne	285	27.5	66	51.5	33	Donkey	0.18%	98.57%	1.25%
D060	sans crâne	252	28.5	64	50	32.5	Donkey	0.88%	98.48%	0.65%

Measurements for Modern Control Data (Tibia, cont'd)

		Measurement					DFA	Probabilities		
ID	Sp./Breed	GL	SD	Bp	Bd	Dd	Determination	Horse	Donkey	Mule
D061	Donkey 3349	281.09	29.88	67.47	50.54	33.87	Donkey	0.33%	97.33%	2.34%
D062	Donkey 546 left	298.33	32.78	73.4	58.14	37.07	Donkey	1.47%	92.53%	6.00%
D063	Donkey 131 right	279.82	27.34	67.24	50.15	32.08	Donkey	2.98%	93.21%	3.81%
D064	Donkey 132 left	292.22	33.98	78.85	60.92	41.16	Donkey	7.16%	83.51%	9.33%
M001	Mule	368	37	86.9	66.2	47.4	Donkey	0.01%	74.58%	25.41%
M002	Mule	356	34	85.7	67.2	42	Mule	6.27%	35.97%	57.76%
M003	Mule	364	39.4	92.4	72	51.8	Donkey	0.05%	69.91%	30.04%
M004	Mule	368	41.3	94	71.2	46.8	Mule	6.80%	5.99%	87.22%
M005	Mule	341	37.5	91	70.8	44.4	Horse	69.47%	4.09%	26.45%
M006	Mule	415	49.4	115.7	88.6	59.3	Mule	16.12%	0.10%	83.78%
M007	Mule	361	38.2	91.5	72.3	45.3	Mule	18.15%	12.75%	69.10%
M008	Mule	392	45.3	104.4	75.6	49.4	Mule	35.27%	0.08%	64.65%
M009	Mule	417	45	110.1	82.5	54	Mule	14.02%	0.11%	85.87%
M010	Mule	418	51.1	119.8	97.7	63.6	Mule	27.66%	0.20%	72.14%
M011	Mule	403.1	45.5	103.6	82.7	50.8	Mule	16.03%	0.61%	83.36%
M012	NY 204211	424	48	110	83	55	Mule	2.29%	0.16%	97.55%
M013	NY 14116	372	48	102	78	49	Horse	65.03%	0.13%	34.84%
M014	AA 1534	419	51	124.5	96	63	Horse	85.31%	0.00%	14.69%
M015	AA 98766	393	44	98	80	51	Mule	1.04%	10.70%	88.26%
M019	MCZ 1655	339	41	87	67	42	Mule	28.52%	10.34%	61.14%
M020	MCZ 1656	386	41	97	78	50	Mule	2.54%	11.97%	85.49%
M022	GE 753-69	359	46	97	78	49	Mule	34.10%	3.67%	62.23%
M023	HL mlt 5	344	43	93	70	50.5	Mule	1.13%	35.75%	63.12%

Appendix I.VI – Measurements of Modern Control Data (Metatarsal)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C002	Przewalski	252	47.2	40.9	27.6	45.4	33.9	Horse	81.31%	1.65%	17.04%
C003	Przewalski	255.9	47.2	42.9	30.2	43.9	35.3	Mule	12.87%	9.33%	77.79%
C004	Przewalski	253.8	47	42.1	29.7	44.3	34.4	Mule	31.39%	6.60%	62.01%
C005	Przewalski	262.6	51.3	43.9	32	48.3	38.5	Horse	54.79%	1.69%	43.52%
C006	Przewalski	263.6	49.1	45.1	30.9	47.5	37.5	Mule	38.34%	0.81%	60.84%
C007	Przewalski	236.2	46.7	40	31.3	43.4	32.2	Horse	67.32%	6.28%	26.40%
C008	Przewalski	256.3	49	41.9	30.5	44.1	35.1	Mule	16.82%	24.03%	59.16%
C009	Przewalski	261.2	50.7	43.1	32.8	45.4	34.4	Mule	20.41%	14.73%	64.87%
C011	Przewalski	259.1	51.9	47.2	26.7	47.8	36.8	Horse	88.58%	0.32%	11.10%
C012	Przewalski	263	50.2	45.2	31.1	45.8	36.2	Mule	18.88%	5.52%	75.60%
C013	Przewalski	253.2	52.9	42.2	28.4	46.6	33.7	Horse	92.78%	2.61%	4.61%
C014	Przewalski	262.7	50	44.3	29.8	47.1	34.6	Horse	68.32%	1.15%	30.54%
C015	Przewalski	256.3	49.7	42.9	30.9	45.3	35.2	Mule	36.05%	9.25%	54.70%
C016	Przewalski	267.6	49.9	43.4	29.7	46.2	35.5	Mule	32.05%	6.61%	61.35%
C017	Przewalski	260.5	50.1	45.5	32	49.3	35.1	Horse	87.06%	0.06%	12.89%
C020	Pony	255.9	47.1	44.7	31.5	47.7	37.3	Horse	54.36%	0.17%	45.46%
C021	Pony	242.2	46.8	37.8	27.9	44.6	35.1	Horse	83.17%	4.88%	11.96%
C023	Pony	249.1	43.8	41.2	30.2	44.8	34.3	Mule	43.70%	0.88%	55.41%
C024	Pony	258	47.2	42.5	30.5	49	35.6	Horse	90.68%	0.04%	9.28%
C025	Pony	259.5	48.6	44.9	30	46.4	36.7	Mule	38.12%	1.41%	60.47%
C026	Pony	256.7	50.3	45.6	31.4	46.4	38.4	Mule	27.02%	2.99%	70.00%
C027	Pony	226	42.2	37.2	26	40.6	32.1	Horse	67.61%	11.42%	20.97%
C028	Pony	276	52	47.7	30.6	47.7	38	Mule	15.43%	2.20%	82.37%
C031	Pony	232	44.4	38.4	24	42.6	33.4	Horse	91.46%	2.35%	6.19%
C032	Pony	231	41.8	37.7	28.1	42.9	32.1	Horse	84.42%	0.94%	14.64%

Measurements for Modern Control Data (Metatarsal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C034	Arab	296	49.6	51.9	32.7	51.7	39.7	Mule	6.08%	0.01%	93.91%
C035	Arab	316	59	53.3	34.6	55.8	41.6	Mule	21.13%	0.06%	78.81%
C036	Arab	285	55.5	42.6	31.2	52	39.2	Horse	85.71%	0.97%	13.32%
C037	Arab	286	55.2	47.5	28.8	53.6	40.4	Horse	94.14%	0.02%	5.84%
C038	Norvège	292	53	41	34.5	52	40	Mule	38.13%	1.80%	60.07%
C039	(Horse)	306	62	49	41.5	63	48	Horse	95.35%	0.00%	4.65%
C040	Tonkin	241	42	33	25.5	42	32.5	Horse	63.72%	19.82%	16.47%
C041	Tarpan	253	47.5	39	29.5	45.5	35	Horse	67.36%	5.56%	27.08%
C042	Islande	200	34	32	22.5	37.5	29	Horse	93.90%	1.41%	4.69%
C043	Tarpan	247.5	47	38	29	45	35.5	Horse	71.43%	6.94%	21.63%
C044	Shetland	221	40.3	33	23	40	31	Horse	87.33%	7.88%	4.80%
C045	(Horse)	319	61	49	42	57	44.5	Mule	4.83%	0.32%	94.85%
C046	(Horse)	305	57	48	34.5	54	42	Mule	22.66%	0.46%	76.88%
C047	Boulonnais	322	71	53	46	70	52	Horse	99.57%	0.00%	0.43%
C048	Shetland	230	43.5	32.5	28	44	30.3	Horse	98.33%	0.57%	1.10%
C049	Grand	295	62	49	40	63	47	Horse	99.38%	0.00%	0.62%
C050	Poney	161	31.5	28	21	32.7	25	Horse	96.37%	3.09%	0.55%
C051	Islande	239	51	40	28	47	36	Horse	98.47%	0.37%	1.16%
C052	Arabe	310	57	44	33	54.5	41	Horse	51.31%	1.07%	47.62%
C054	Poney	200	34.5	27.5	20.5	36	27	Horse	84.16%	13.85%	1.98%
C055	Welsh	205	38.5	30	25	38	30	Horse	72.23%	23.27%	4.50%
C056	Poney	173	34	27	21	34.5	25	Horse	96.93%	2.81%	0.26%
C057	Poney	231	41	33	26.5	41	31	Horse	70.04%	15.34%	14.62%
C058	Grand	318	60	49	38	60	47	Horse	54.71%	0.02%	45.27%
C059	(Horse)	292	54	44	36	52	40.1	Mule	21.27%	1.14%	77.59%

Measurements for Modern Control Data (Metatarsal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C060	Shetland	182	35	30.5	23	37.5	27	Horse	99.55%	0.18%	0.28%
C061	Shetland	192	37	31	25	38.5	30	Horse	97.48%	1.18%	1.34%
C062	Shetland	201	40	31.5	25	39	29	Horse	95.44%	3.40%	1.15%
C063	Shetland	190	37	33	24	37.8	29	Horse	97.63%	0.96%	1.42%
C064	Islande	256	45	37	29.2	46.3	36	Horse	71.08%	1.90%	27.02%
C065	Islande	255	49	38	28	46	35	Horse	82.96%	6.15%	10.89%
C066	Islande	252	45.5	40	30.5	47.8	36	Horse	86.96%	0.11%	12.93%
C067	Hannover	310	62	56	39.3	63	50	Horse	83.45%	0.00%	16.55%
C068	Hannover	306	60	50	40	62.2	46.8	Horse	93.72%	0.00%	6.28%
C069	Konik	254	47	39	31.7	49.2	39	Horse	87.96%	0.14%	11.91%
C070	Exmoor	245	45	37	27.3	45	34.2	Horse	89.27%	1.49%	9.24%
C071	Shetland	184	33	28	22.3	35	26.9	Horse	90.83%	7.13%	2.04%
C072	Islande	237	45	35	28	43	32.6	Horse	77.45%	11.97%	10.58%
C073	Welsh	218	40.5	33.6	28	41.2	31.2	Horse	89.46%	3.05%	7.49%
C074	Welsh	254	49	39	30	48.2	35.5	Horse	95.32%	0.30%	4.38%
C075	Islande	265	50	40	32	48.5	38.2	Horse	63.22%	2.58%	34.20%
C076	Arabe	290	53	43	30	51	38.5	Horse	62.79%	1.30%	35.92%
C077	Poney	245	42.5	35	27	42.5	33.3	Horse	48.75%	17.15%	34.10%
C078	Mongol	265	49	39	30	47	36	Horse	61.13%	6.35%	32.52%
C079	Mongol	261	47	37.5	29.3	46	26.8	Horse	95.10%	0.65%	4.25%
C080	Mongol	260	50	40	32	46.3	38.5	Mule	24.67%	19.11%	56.22%
C081	Tarpan	267	47.5	39	31.2	47.5	37	Mule	45.75%	2.99%	51.26%
C082	Arabe	294	52	42	31	54	40	Horse	87.19%	0.05%	12.76%
C084	(Horse)	265	50	41	31	48	36	Horse	72.10%	1.86%	26.04%
C085	(Horse)	264	50	37.2	32	50	36.9	Horse	94.23%	0.38%	5.39%

Measurements for Modern Control Data (Metatarsal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C086	(Horse)	315	62	49	40.5	64	49	Horse	94.82%	0.00%	5.18%
C087	Camargue	265	50	38.3	31	51	37.5	Horse	97.29%	0.07%	2.64%
C088	Turquie	290	53.86	45.88	30.36	52.07	41.44	Horse	54.31%	0.45%	45.24%
C089	Exmoor	245	45	40.5	28.3	45	34.8	Horse	76.24%	0.90%	22.86%
C091	Fjord	280	55	43	35	54	40	Horse	92.40%	0.06%	7.54%
C092	Islande 1	273	50	40	33	47.5	37	Mule	21.61%	10.29%	68.11%
C093	Exmoor pony left	235.81	50.04	37.21	29.66	45.25	36.65	Horse	86.07%	8.72%	5.21%
C094	Welsh cob	272.68	52.8	39.7	34.82	53.92	40.83	Horse	96.18%	0.03%	3.79%
C096	Race Horse 123 Left	309.5	60.97	47.5	35.66	60.29	47.03	Horse	93.00%	0.01%	7.00%
C097	NF Pony 137 left	264.29	47.52	38.5	28.69	49.03	38.47	Horse	87.96%	0.35%	11.69%
C098	Shetland 604 left	185.62	33.71	25.78	21.34	32.97	25.67	Donkey	26.72%	71.94%	1.34%
C100	Imm Horse 636 left	310	54.98	44.44	30.48	55.35	42.1	Horse	71.72%	0.12%	28.16%
D001	Donkey	214.7	38.8	36.5	24.5	35.2	27.9	Donkey	7.36%	73.83%	18.82%
D002	Donkey	227.5	38.5	31.2	22.4	33.2	26.2	Donkey	0.08%	99.21%	0.71%
D003	Donkey	199.7	35.5	30	21.8	33.1	27.4	Donkey	4.45%	92.76%	2.78%
D004	Donkey	200.4	35.7	31.7	20.7	32.2	25.2	Donkey	3.85%	93.58%	2.57%
D005	Donkey	201.6	34	28.8	20	28.2	24.5	Donkey	0.01%	99.86%	0.13%
D006	Donkey	228.2	42.4	37.7	24.5	36.2	31.1	Donkey	0.84%	91.90%	7.26%
D007	Donkey	216.9	42.1	38.5	24.3	36	30.1	Donkey	4.81%	83.94%	11.25%
D008	Donkey	204.6	36.1	29.9	22.7	31.1	23.9	Donkey	0.22%	99.20%	0.58%
D010	Donkey	247.5	43.5	38.6	28.7	40.2	32.2	Mule	3.73%	47.29%	48.98%
D011	Donkey	205.7	35.9	31.6	22.2	32.6	25.8	Donkey	1.86%	95.12%	3.03%
D012	Donkey	215.1	35.3	30.4	20.7	32.5	25.6	Donkey	0.74%	97.28%	1.99%
D013	Donkey	225.7	42.1	39.7	23.3	39.6	30.7	Horse	70.68%	9.22%	20.10%
D014	Donkey	224.6	41.4	39.1	25	38.1	30.3	Mule	25.42%	36.60%	37.99%

Measurements for Modern Control Data (Metatarsal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
D015	Olduvai	215	39.5	32	23.1	34.7	27.1	Donkey	2.13%	95.98%	1.89%
D016	Syrie	238	38.5	32	23.5	35	27.5	Donkey	0.21%	96.81%	2.98%
D017	(Donkey)	190	36.5	31	21	33	25	Donkey	24.98%	72.95%	2.08%
D018	Afrique	214	39.5	33	24	35.2	27.5	Donkey	4.43%	91.53%	4.04%
D020	(Donkey)	207	35	29	22	32	26	Donkey	0.48%	98.34%	1.18%
D021	Crête	231.5	40	31	22.5	36	29	Donkey	0.81%	97.48%	1.71%
D022	(Donkey)	233	40	33	24	36.5	29	Donkey	1.50%	92.96%	5.54%
D023	Nubie	239	40	33	23	36	30	Donkey	0.30%	96.43%	3.27%
D025	(Donkey)	227.5	41.5	33.2	26	33	28	Donkey	0.01%	99.69%	0.31%
D026	(Donkey)	215.5	36	30	23	33.5	26	Donkey	1.12%	96.18%	2.70%
D027	(Donkey)	206.5	32.5	26	20	31.1	25	Donkey	0.39%	98.89%	0.71%
D028	(Donkey)	204	32	27.5	19	29.5	23	Donkey	0.19%	99.24%	0.57%
D029	Ane Blanc	255	44	37	28	44	33	Horse	50.90%	7.99%	41.11%
D030	Ane Blanc	246	45	38	27	39.5	32	Donkey	2.09%	81.86%	16.05%
D031	(Donkey)	189	31	24	19	28	24	Donkey	0.06%	99.84%	0.11%
D032	(Donkey)	216	34.5	30	23	33.7	25.5	Donkey	2.88%	90.28%	6.85%
D033	(Donkey)	188	31	25	19	29.9	24.2	Donkey	1.53%	97.88%	0.59%
D034	anglais	215	36.3	28.7	23	34.8	27	Donkey	4.18%	92.60%	3.23%
D035	Argentine	265	49	38	28	42.5	33.5	Donkey	2.12%	86.11%	11.77%
D036	S Peru	222	39	28.7	24	35.3	28.5	Donkey	0.64%	98.37%	0.99%
D037	S Peru	223	37.7	31	23.5	34	28	Donkey	0.27%	97.82%	1.91%
D038	sans crâne	248	43	33.5	24.5	39	32	Donkey	1.24%	93.29%	5.47%
D039	Turquie	206	33	25	20	31.3	24.6	Donkey	0.43%	99.13%	0.43%
D040	Turquie	217	36.5	30	21.8	33.3	27.1	Donkey	0.53%	97.94%	1.53%
D041	(Donkey)	205	32	26.5	22	32	24	Donkey	2.18%	95.21%	2.60%

Measurements for Modern Control Data (Metatarsal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
D042	(Donkey)	202	34	28	21	32	25	Donkey	1.94%	96.63%	1.43%
D043	(Donkey)	183	27	23	17	26.1	20.7	Donkey	0.12%	99.69%	0.19%
D044	(Donkey)	209	37.5	32	24	35	29	Donkey	6.03%	87.06%	6.91%
D045	(Donkey)	230	41	32	24	36	30.8	Donkey	0.31%	98.16%	1.54%
D047	(Donkey)	207	38	27.5	23	35	28	Donkey	4.51%	94.49%	0.99%
D048	(Donkey)	220	42	35	23.5	37	30	Donkey	9.40%	84.89%	5.71%
D049	(Donkey)	223	39	33	23	35	27	Donkey	1.96%	94.09%	3.96%
D053	(Donkey)	228	37	30	22.1	34.5	27.1	Donkey	0.64%	97.01%	2.35%
D055	(Donkey)	193	32	25.5	22.7	29	22	Donkey	0.12%	99.58%	0.30%
D056	(Donkey)	237	41	34	28	36	32.1	Donkey	0.04%	96.17%	3.79%
D058	sans crâne	218	38	30	22	34.3	28	Donkey	0.87%	97.83%	1.30%
D059	sans crâne	211	33.5	28	22	31.8	25.9	Donkey	0.31%	98.17%	1.52%
D061	Donkey 3349	201.02	31.63	25.51	23.7	31.55	24.76	Donkey	0.83%	97.28%	1.89%
D062	Donkey 546 left	224.65	40.75	30.41	23.52	33.84	28.09	Donkey	0.05%	99.71%	0.25%
D063	Donkey 131 right	212.73	32.26	25.94	22.46	30.36	24.58	Donkey	0.04%	99.43%	0.53%
D064	Donkey 132 left	218.64	41.15	31.58	25.18	37.15	29.78	Donkey	6.64%	89.99%	3.38%
M001	Mule	260.1	44.4	42	26.5	44.1	33.4	Mule	34.37%	2.54%	63.10%
M002	Mule	256.9	44.3	39.8	26.4	44.1	35.7	Mule	34.04%	5.75%	60.22%
M004	Mule	269.7	47.3	40.6	30.1	46.3	36.4	Mule	21.94%	5.29%	72.78%
M005	Mule	260	48.8	39	29.5	45.4	35.1	Horse	45.08%	18.43%	36.49%
M006	Mule	311	58.6	55.4	36.2	51.3	43	Mule	0.24%	0.56%	99.20%
M007	Mule	259.8	48.1	44.5	28.9	45.5	35.7	Mule	33.86%	2.59%	63.55%
M008	Mule	274	53	50.5	32.6	50.1	38.7	Mule	37.43%	0.15%	62.41%
M009	Mule	316	56.1	53.3	34.3	54.2	41.3	Mule	4.74%	0.04%	95.22%
M010	Mule	314	59.7	59.4	35.7	56.4	45.4	Mule	5.17%	0.01%	94.83%

Measurements for Modern Control Data (Metatarsal, cont'd)

		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
M012	NY 204211	299	56	46	36	51.8	40	Mule	9.59%	2.30%	88.11%
M013	NY 14116	275	51	40	34	49	38	Mule	34.83%	5.41%	59.76%
M014	AA 1534	311	59	48.5	39	56.5	45	Mule	13.09%	0.19%	86.72%
M015	AA 98766	301	52	43	31.5	50	38	Mule	10.61%	3.69%	85.71%
M016	UNSM 5084	313	68	54	47	64	49	Horse	75.97%	0.00%	24.03%
M017	A 543	300	54	43	36	53	41	Mule	18.85%	0.99%	80.15%
M018	MU 1970-5	262.2	45	38	26.5	44.2	33.4	Mule	43.48%	11.43%	45.08%
M019	MCZ 1655	255	43	39.5	28.5	41	33	Mule	3.16%	24.75%	72.09%
M020	MCZ 1656	300	53	49	29	48	41	Mule	1.01%	3.98%	95.01%
M021	(Mule)	285	53.2	46	33.1	51	39.7	Mule	32.68%	0.65%	66.67%
M023	HL mlt 5	242	45	35	30	42	33.7	Donkey	16.41%	57.71%	25.89%
M024	LY 95159	246	45.3	35	27	40.5	33	Donkey	3.44%	87.70%	8.86%

Appendix I.VII – Measurements of Modern Control Data (Anterior PH1)

Anterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C001	Przewalski	85.2	50.7	32.9	36.8	42.9	25.3	Mule	13.93%	1.63%	84.44%
C002	Przewalski	77	50.1	30.4	38.2	37.3	22.2	Mule	38.73%	2.02%	59.25%
C004	Przewalski	81.4	49.4	27.7	35.3	39	23.2	Mule	11.78%	13.84%	74.38%
C005	Przewalski	72.8	50.6	30.3	34.7	37.8	22.6	Horse	82.72%	0.30%	16.98%
C006	Przewalski	75.5	49.9	30.4	33.3	39.6	22.1	Horse	77.94%	0.73%	21.33%
C007	Przewalski	79.6	50.1	33	35.8	43.7	24.4	Horse	66.67%	0.15%	33.18%
C008	Przewalski	74.2	49.2	33.7	32.2	39.6	22.7	Horse	83.17%	0.42%	16.40%
C009	Przewalski	78.7	52.2	34.7	34	41.4	24	Horse	75.76%	0.20%	24.05%
C010	Przewalski	78.9	50.9	31.1	33.1	41.8	23.8	Horse	67.55%	0.64%	31.81%
C011	Przewalski	74.9	53.2	32.5	36.4	40.1	24	Horse	88.96%	0.02%	11.01%
C012	Przewalski	82	51.4	32.2	32.2	41.3	22.7	Horse	48.63%	3.64%	47.73%
C013	Przewalski	73.4	51.7	33.5	34.6	40.4	23.3	Horse	93.42%	0.02%	6.56%
C014	Przewalski	79.8	51.9	32.3	35.2	42.4	23.5	Horse	72.27%	0.21%	27.52%
C015	Przewalski	75.5	49.9	31.8	36.4	37.8	22.1	Horse	61.01%	1.04%	37.95%
C016	Przewalski	77.8	50.8	30.4	37.1	38	23.4	Mule	37.00%	1.79%	61.21%
C017	Przewalski	82.1	53.9	34.9	36.4	43.8	23.8	Horse	77.54%	0.05%	22.41%
C019	Pony	70.1	46	30.2	31.9	40.5	20.8	Horse	94.39%	0.15%	5.47%
C020	Pony	85.7	52.4	33.7	38.7	42.7	25.2	Mule	16.85%	0.67%	82.47%
C021	Pony	74.3	49.2	31.1	33.3	40.6	23.1	Horse	83.56%	0.24%	16.20%
C022	Pony	79.1	54.9	34.7	34.9	47.9	24.6	Horse	98.31%	0.00%	1.69%
C023	Pony	73.2	48.7	32.4	34.8	38.2	22.1	Horse	77.00%	0.55%	22.45%
C024	Pony	82.9	57.1	35	35.2	43.3	23.8	Horse	86.44%	0.03%	13.53%
C025	Pony	81.3	52	31.6	35.7	41.4	24.1	Mule	45.32%	0.83%	53.85%
C026	Pony	82.4	55.8	37.2	37.1	43.7	25.2	Horse	79.52%	0.02%	20.47%
C027	Pony	66.1	45.3	28.5	33.8	36.1	20.7	Horse	90.04%	0.46%	9.49%

Measurements for Modern Control Data (Anterior PH1, cont'd)

Anterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C028	Pony	87.8	53.6	33.7	37	44.6	24.9	Mule	25.56%	0.59%	73.86%
C030	Pony	80.3	47.7	29.9	34.4	41.5	23.5	Mule	26.63%	4.87%	68.50%
C031	Pony	68.8	47.1	27.9	35.5	38.1	22.5	Horse	87.00%	0.17%	12.83%
C033	Arab	100.1	60.4	37.6	43	50	26.7	Mule	10.59%	0.03%	89.38%
C034	Arab	90.5	57.3	32.4	41.6	44.8	25.1	Mule	22.19%	0.13%	77.68%
C035	Arab	93.4	62	36.2	43	47.4	26.4	Mule	46.60%	0.01%	53.39%
C036	Arab	92	54.5	34.6	37	47.1	23.4	Mule	28.74%	0.58%	70.69%
C037	Arab	91.5	58.7	35	38.3	47.6	25.4	Horse	53.70%	0.04%	46.26%
C041	Tarpan	75.2	51.9	33.1	33	41.7	24	Horse	91.94%	0.03%	8.03%
C048	Shetland	73	48	30	30.3	38	21.5	Horse	77.31%	3.08%	19.61%
C050	Poney	48	37	25	23.3	30	16.1	Horse	99.07%	0.64%	0.29%
C055	Welsh	64	44	28.5	28	35.5	20	Horse	93.86%	1.40%	4.74%
C056	Poney	52	40	24	23.8	32	17.5	Horse	99.27%	0.36%	0.37%
C057	Poney	69	46.2	30	29	37	22	Horse	84.38%	2.25%	13.37%
C059	(Horse)	95.1	57.7	40	37	45	26.9	Mule	7.17%	0.65%	92.18%
C060	Shetland	55	42	27.5	27	34.2	20	Horse	99.39%	0.05%	0.56%
C061	Shetland	61.9	45.2	28.5	27.5	35.1	20.1	Horse	97.91%	0.28%	1.81%
C062	Shetland	63.5	44	30	27	35.1	20	Horse	94.60%	1.41%	4.00%
C063	Shetland	61.9	41	28.5	27	35	19	Horse	91.90%	3.44%	4.66%
C064	Islande	80	54	33.2	33	42	24	Horse	80.97%	0.16%	18.88%
C065	Islande	75.5	52	33	33	41	23.1	Horse	91.23%	0.06%	8.71%
C066	Islande	79	54	35	34.5	43	25	Horse	86.97%	0.02%	13.01%
C067	Hannover	105	74	49	45.2	56	32	Horse	81.93%	0.00%	18.07%
C068	Hannover	98	67.8	43.5	44.5	53	29	Horse	83.62%	0.00%	16.38%
C069	Konik	86	54	34	32	44	24.5	Mule	48.78%	1.18%	50.04%

Measurements for Modern Control Data (Anterior PH1, cont'd)

Anterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C070	Exmoor	75.1	50.8	32.6	32	42	23	Horse	92.86%	0.06%	7.09%
C071	Shetland	54.7	38	24.5	23	30	17	Horse	70.06%	27.70%	2.24%
C072	Islande	76	51	32.5	30.9	41.2	24	Horse	85.46%	0.24%	14.30%
C073	Welsh	67.8	44	31.6	31.5	38	21.7	Horse	87.01%	0.76%	12.24%
C074	Welsh	80	53	35.3	35	42.3	24	Horse	77.18%	0.10%	22.72%
C075	Islande	85.1	55	37.1	33.5	43.5	27	Mule	44.04%	0.30%	55.66%
C076	Arabe	92.5	54.5	36.5	34.5	47	23.1	Mule	31.35%	1.20%	67.45%
C077	Poney	75	48.5	32.3	30	40	22	Horse	81.22%	1.41%	17.37%
C078	Mongol	87	55	35	32.5	44	23.2	Horse	57.18%	0.97%	41.85%
C079	Mongol	81	51	34	32.6	41.5	24	Horse	49.76%	1.71%	48.53%
C080	Mongol	82	55.5	36	36.5	43.6	25	Horse	80.36%	0.02%	19.62%
C081	Tarpan	86.5	53.5	34	33	42.5	24	Mule	28.78%	3.42%	67.80%
C082	Arabe	92	60.5	39.5	36.5	47	27	Horse	54.93%	0.03%	45.05%
C085	(Horse)	83	54	35	35.5	45	25	Horse	75.31%	0.05%	24.65%
C086	(Horse)	105	70	44	44	57	33	Horse	54.29%	0.00%	45.71%
C089	Exmoor	76	50.5	33	33	42.7	23	Horse	91.35%	0.05%	8.60%
C090	Islande	68	49	32	30	38	21.8	Horse	97.17%	0.06%	2.77%
C091	Fjord	89	59	39	38	46	26.5	Horse	61.41%	0.02%	38.58%
C092	Islande	84	54	37.8	37	44	26	Horse	53.06%	0.08%	46.86%
C093	Exmoor Left	73.8	49.58	33.22	33.85	43.44	24.71	Horse	93.21%	0.01%	6.78%
C094	Welsh cob 3868 Left	85.29	58.59	38.8	40.05	47.57	25.98	Horse	90.77%	0.00%	9.23%
C095	Pony 3158 right	69.97	46.17	31.22	30.3	36.75	20.25	Horse	84.18%	2.69%	13.14%
C096	Modern Race Horse	107.71	63.46	46.96	38.18	52.56	24.77	Mule	16.29%	0.08%	83.63%
C098	Modern Shetland Pon	55.27	39.2	25.08	24.01	31.05	15.33	Horse	92.44%	6.48%	1.08%
C102	Modern Pony	83.33	53.48	34.6	34.33	44.65	17.84	Horse	94.30%	0.07%	5.63%

Measurements for Modern Control Data (Anterior PH1, cont'd)

Anterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
D001	Donkey	69.8	38.8	23.2	27.2	34.1	19.1	Donkey	0.79%	96.42%	2.79%
D002	Donkey	69.6	36.2	22.3	25.5	30.9	17	Donkey	0.01%	99.85%	0.14%
D003	Donkey	59.4	37.5	27.8	27.4	28.9	18	Donkey	10.52%	84.38%	5.10%
D005	Donkey	58.7	32.2	19.4	24.1	27.6	16	Donkey	0.05%	99.84%	0.11%
D006	Donkey	66	40.3	23.1	30	34.1	19.7	Donkey	24.34%	56.44%	19.23%
D007	Donkey	67.6	35.5	20.9	26.1	30.5	17	Donkey	0.02%	99.80%	0.18%
D008	Donkey	66.3	37.7	22.8	27.5	33	18.4	Donkey	1.84%	94.90%	3.26%
D009	Donkey	82.3	41.4	25.8	33.1	36.5	21.7	Donkey	0.03%	95.58%	4.39%
D010	Donkey	62	35.5	21.8	25.9	31.2	18.8	Donkey	1.14%	97.12%	1.74%
D011	Donkey	66.6	34.8	20.2	26.1	31.4	16.6	Donkey	0.05%	99.70%	0.26%
D012	Donkey	69.8	43.5	23.7	32.7	34.3	20.1	Donkey	23.15%	44.10%	32.75%
D013	Donkey	73.7	43.6	23.7	34	34	20.2	Donkey	3.15%	74.06%	22.79%
D029	Ane Blanc	77	42	29	26	36.8	21	Donkey	0.59%	94.86%	4.56%
D031	(Donkey)	59	30.2	23	18	27.3	16.8	Donkey	0.00%	99.98%	0.01%
D032	(Donkey)	69.1	35.1	26	22	31.7	17	Donkey	0.01%	99.90%	0.09%
D033	(Donkey)	61.5	31.5	23.7	19	27.7	16	Donkey	0.00%	99.98%	0.01%
D034	anglais	68	35.9	26.8	21	34	18	Donkey	0.22%	99.38%	0.41%
D035	Argentine	85.3	47.2	35	28.5	40	22.7	Donkey	1.94%	71.74%	26.32%
D036	S Peru	72	40	29.1	24	33	19.3	Donkey	0.18%	98.88%	0.94%
D037	S Peru	73	39	29	24.3	33	19	Donkey	0.06%	99.41%	0.54%
D038	sans crâne	83	42.8	33.2	25.6	36.9	20.4	Donkey	0.04%	98.70%	1.27%
D039	Turquie	66.1	32.8	24.1	20	29	16	Donkey	0.00%	99.99%	0.01%
D040	Turquie	69	35.1	27	21.3	30.6	19	Donkey	0.00%	99.93%	0.07%
D041	(Donkey)	67	35.5	26.9	21.1	30	17	Donkey	0.02%	99.91%	0.07%
D042	(Donkey)	64	35.1	24.5	20.9	30	17	Donkey	0.06%	99.83%	0.12%

Measurements for Modern Control Data (Anterior PH1, cont'd)

Anterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
D043	(Donkey)	54	29.7	20.8	18	25.3	13.9	Donkey	0.02%	99.97%	0.01%
D044	(Donkey)	68	37	28.1	24	33	18.2	Donkey	0.42%	98.59%	0.99%
D055	(Donkey)	64	31	23.1	21	28.2	15.1	Donkey	0.00%	99.99%	0.01%
D056	(Donkey)	76	43	31	25	36.8	20.5	Donkey	2.32%	91.07%	6.62%
D057	(Donkey)	67	38.5	27.5	24.3	33	19	Donkey	1.74%	95.93%	2.33%
D058	sans crâne	70	38	27	23	33	18	Donkey	0.14%	99.38%	0.48%
D059	sans crâne	70	34	25	21.1	29.6	18	Donkey	0.00%	99.98%	0.02%
D061	Donkey 3349 Right	66.04	34.92	25.47	22.48	30.06	17.45	Donkey	0.02%	99.86%	0.12%
D062	Donkey 546 left	75.3	36.94	27.56	23.28	33.58	19.6	Donkey	0.00%	99.86%	0.14%
D064	Donkey 132	70.2	40.79	29.52	24.75	35.85	15.83	Donkey	15.95%	79.74%	4.31%
M001	Mule	79.3	48.4	29.7	35.6	38.6	22.6	Mule	19.65%	9.35%	71.00%
M002	Mule	76.3	51.8	31.5	34.6	38.2	22.2	Horse	72.75%	0.76%	26.49%
M003	Mule	80.9	50.8	31.4	37.6	38	23.1	Mule	16.83%	4.78%	78.39%
M004	Mule	82	50.6	31	37.8	41.4	24.6	Mule	23.08%	1.15%	75.78%
M005	Mule	82.4	52	31.1	35	42	23.7	Mule	44.18%	1.22%	54.61%
M006	Mule	101.8	62.7	38.7	44.6	51.6	29.2	Mule	9.94%	0.01%	90.05%
M008	Mule	94.6	54.6	34.6	38.3	45.8	25.6	Mule	4.53%	1.40%	94.07%
M009	Mule	97	59.6	34.6	41.3	49	27.2	Mule	14.15%	0.05%	85.81%
M010	Mule	102.3	59.8	41.8	47.9	52.6	29.5	Mule	4.40%	0.00%	95.60%
M011	Mule	98.3	58.2	36.5	38.4	49	26.7	Mule	9.26%	0.23%	90.51%
M016	UNSM 5084	108	72	49	44.8	58.5	34.2	Horse	52.98%	0.00%	47.02%
M019	MCZ 1655	89	47.5	35	30	38	22	Donkey	0.08%	93.01%	6.92%
M020	MCZ 1656	96	51	37.5	31	44.5	25	Mule	0.72%	43.58%	55.70%
M022	Gen 753/69	93	52.5	37	32.5	45.5	25	Mule	6.83%	7.69%	85.48%
M023	HL mlt 5	81.7	50.3	35	31	42	24	Mule	45.96%	3.11%	50.93%

Appendix I.VIII – Measurements of Modern Control Data (Posterior PH1)

Posterior PH1	Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C001	Przewalski	80.3	52.7	32.2	40.4	40.8	25.1	Mule	40.24%	0.15%	59.61%
C002	Przewalski	79.4	47.8	31.4	34.1	38.4	22	Mule	19.00%	16.40%	64.60%
C004	Przewalski	85.5	50	28.6	32.7	41.6	23.4	Mule	9.25%	21.61%	69.13%
C005	Przewalski	76.9	50	32.6	34	38.8	22.9	Horse	57.55%	1.72%	40.73%
C006	Przewalski	71.3	50.2	29.9	35.7	37.3	21.7	Horse	87.81%	0.17%	12.02%
C007	Przewalski	76.1	51	32.4	39.1	42.4	23.6	Horse	85.14%	0.02%	14.84%
C008	Przewalski	71.5	48	31.4	33.4	37.7	22.4	Horse	79.78%	0.69%	19.53%
C009	Przewalski	75.8	51.5	35	36.8	40.2	24.2	Horse	78.59%	0.06%	21.35%
C010	Przewalski	76.5	52.3	31.4	35	40.5	24.2	Horse	79.37%	0.13%	20.51%
C011	Przewalski	79.6	52.8	33.7	35.3	42.7	24.2	Horse	78.49%	0.08%	21.43%
C012	Przewalski	76	50.1	31.1	34.4	38.8	23.5	Horse	59.93%	1.14%	38.93%
C013	Przewalski	69	50.8	32	35.2	38.8	22.3	Horse	97.21%	0.01%	2.78%
C014	Przewalski	77.4	51.7	32.3	37	40.9	23.3	Horse	75.89%	0.11%	24.00%
C015	Przewalski	78.8	49.5	32.6	33.2	39.4	22.3	Mule	46.45%	4.47%	49.08%
C016	Przewalski	83.7	50.5	32.1	36.5	40.1	23.7	Mule	11.95%	5.75%	82.30%
C017	Przewalski	80.2	54.1	34.2	38.9	42.4	24.2	Horse	75.94%	0.03%	24.03%
C019	Pony	67.5	45.8	27.8	33.1	38.3	20.3	Horse	94.36%	0.18%	5.46%
C020	Pony	81.8	52.4	33.1	38.1	40.1	24.3	Mule	29.34%	0.83%	69.83%
C021	Pony	72.9	49.9	31.7	36	39.1	23.6	Horse	81.81%	0.11%	18.08%
C022	Pony	77.5	55.5	34.4	37.7	46.4	25.2	Horse	98.01%	0.00%	2.00%
C023	Pony	76.2	49	32.4	32.4	39.3	22.3	Horse	66.51%	2.04%	31.45%
C024	Pony	78.2	55.1	33.7	37.2	41.8	24.1	Horse	89.02%	0.01%	10.97%
C025	Pony	75.7	51.6	31.4	38	39.6	24.2	Horse	70.61%	0.11%	29.28%
C026	Pony	81	54.3	35.3	39	41.6	24.5	Horse	64.10%	0.06%	35.84%
C027	Pony	68	44.3	29.5	30.9	37.1	20.5	Horse	85.52%	1.99%	12.50%

Measurements for Modern Control Data (Posterior PH1, cont'd)

Posterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C028	Pony	83.6	55.1	33.1	39.7	42.8	24.3	Horse	55.66%	0.08%	44.26%
C030	Pony	79.7	49.4	28	37.6	39.9	23.4	Mule	24.66%	2.63%	72.71%
C031	Pony	73.2	47.5	28.3	30.6	39	21.9	Horse	76.46%	2.62%	20.92%
C032	Pony	67.6	47.6	30.7	34.7	39.9	23.5	Horse	95.68%	0.01%	4.31%
C033	Arab	95.5	58.9	35.6	41.8	47	26.2	Mule	12.75%	0.09%	87.17%
C034	Arab	94.7	57.1	33.6	41.4	46.4	25.9	Mule	8.23%	0.22%	91.55%
C035	Arab	95	60	36.5	38.9	48.1	26.6	Mule	29.97%	0.05%	69.97%
C037	Arab	89.5	58.4	33.5	41.7	45.9	24.9	Mule	49.51%	0.02%	50.47%
C041	Tarpan	71.5	53	35.7	34	41	24	Horse	98.09%	0.00%	1.91%
C048	Shetland	71	48	33.1	29.7	36.8	22	Horse	83.13%	1.81%	15.06%
C050	Poney	46	39	25	24	29.5	16	Horse	99.84%	0.07%	0.09%
C054	Poney	55.5	40	27.5	24	32	19.5	Horse	95.45%	2.61%	1.94%
C055	Welsh	61	42.5	32	26	33.5	30	Horse	54.82%	4.69%	40.49%
C056	Poney	50	40	26	24	31	17.3	Horse	99.63%	0.15%	0.23%
C057	Poney	66	49	32.5	29	35	22	Horse	95.85%	0.23%	3.92%
C059	(Horse)	92.1	56.5	42.5	37	44	26.1	Mule	13.51%	0.49%	86.01%
C060	Shetland	54	43	28.7	27	33	19.5	Horse	99.61%	0.03%	0.36%
C061	Shetland	60	45	30.1	26.9	33.5	20.5	Horse	97.95%	0.31%	1.74%
C062	Shetland	63	44.1	31.5	26.5	34	30	Horse	52.73%	4.16%	43.12%
C063	Shetland	59	42	31	26.9	34	19	Horse	97.94%	0.47%	1.60%
C064	Islande	77	54	37	33	40.5	24.3	Horse	89.03%	0.05%	10.93%
C065	Islande	73	53	36.7	32.2	40	24	Horse	96.03%	0.01%	3.96%
C066	Islande	77	55.1	38	33	41.5	25.7	Horse	92.18%	0.01%	7.81%
C067	Hannover	100	74	50	44	53.8	31	Horse	94.97%	0.00%	5.03%
C068	Hannover	98	69	47	42	51	30	Horse	78.87%	0.00%	21.13%

Measurements for Modern Control Data (Posterior PH1, cont'd)

Posterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C069	Konik	84	55.2	38	32	42.5	25	Horse	63.84%	0.40%	35.76%
C070	Exmoor	73	52	35	32	40	23	Horse	95.62%	0.03%	4.36%
C071	Shetland	54	38.5	28	23	29	17	Horse	78.44%	19.53%	2.02%
C072	Islande	72	50.1	35	29.1	39	24	Horse	91.46%	0.20%	8.35%
C073	Welsh	66.1	45.1	34	29	37	21.9	Horse	93.86%	0.38%	5.76%
C074	Welsh	77	54	39	33.7	41.1	24	Horse	92.13%	0.02%	7.85%
C075	Islande	84	55	40	32.2	43	27	Horse	55.29%	0.24%	44.48%
C076	Arabe	88.1	55.2	39	34	40	22.8	Mule	19.73%	6.29%	73.98%
C077	Poney	73	48	35.2	29.3	38	22	Horse	81.01%	1.98%	17.01%
C078	Mongol	82.5	54	38	30.5	42	23	Horse	77.13%	0.60%	22.27%
C079	Mongol	78.6	51.5	37.3	31	40	24	Horse	67.75%	1.04%	31.21%
C080	Mongol	82	54.1	38.5	35.2	42	24.5	Horse	67.31%	0.14%	32.55%
C081	Tarpan	84.5	54	38.5	33	41	24.5	Mule	38.36%	1.67%	59.97%
C082	Arabe	88.5	60	42	34	46	27	Horse	77.68%	0.01%	22.31%
C085	(Horse)	80	55.3	37.8	35	43	24.5	Horse	89.95%	0.01%	10.04%
C086	(Horse)	106	72	49	42	55	32.5	Horse	55.38%	0.00%	44.62%
C089	Exmoor	75	51.3	36.3	31	41	23	Horse	93.32%	0.07%	6.62%
C090	Islande	66	50	33	29	36	21	Horse	98.48%	0.05%	1.48%
C091	Fjord	83.1	60	41.1	37.5	44.2	26	Horse	92.76%	0.00%	7.24%
C092	Islande	82	55	39	35	42	25.5	Horse	68.11%	0.09%	31.80%
C093	Exmoor Left	71.95	50.74	35.3	33.18	42.28	24.3	Horse	97.06%	0.00%	2.94%
C094	Welsh cob	82.91	60.83	42.53	40.38	47.23	26.56	Horse	97.67%	0.00%	2.33%
C096	Modern Race Horse 1	103.64	64.55	49.11	38.49	50.97	23.73	Mule	49.68%	0.02%	50.30%
C097	NF Pony 137	80.58	54.21	38.6	33.4	42.64	17.3	Horse	97.61%	0.03%	2.36%
C099	Modern Shetland Pony	53.53	39.2	26.26	23.42	29.56	14.07	Horse	93.63%	5.73%	0.64%

Measurements for Modern Control Data (Posterior PH1, cont'd)

Posterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
C102	Modern Pony	79.88	53.59	37.7	30.73	41.86	19.3	Horse	95.39%	0.12%	4.50%
D001	Donkey	65.6	39.3	22.9	28	31.1	18.7	Donkey	1.75%	94.91%	3.34%
D002	Donkey	65.4	36.5	20.7	26.1	28.4	17.4	Donkey	0.02%	99.79%	0.19%
D003	Donkey	63.2	37	23.3	27.2	31.2	18.5	Donkey	2.14%	94.92%	2.95%
D004	Donkey	58.7	36.6	21.5	27	28.9	17.2	Donkey	4.29%	93.43%	2.28%
D005	Donkey	53.4	31.6	19.1	24.1	24.7	15.3	Donkey	0.11%	99.78%	0.11%
D006	Donkey	62.4	42	23	29.9	32	18.9	Horse	61.86%	24.77%	13.37%
D007	Donkey	62	35.5	20.5	26.6	27.7	16.4	Donkey	0.09%	99.64%	0.27%
D008	Donkey	61.7	37.8	23.8	28.4	30	18.6	Donkey	4.62%	90.50%	4.88%
D009	Donkey	77	43.3	25.5	32.9	35	20.7	Donkey	0.75%	85.95%	13.31%
D010	Donkey	57.7	36.6	20.8	26.2	29.6	17.2	Donkey	10.44%	86.67%	2.89%
D011	Donkey	60.4	35.2	19.5	26.2	28.8	15.9	Donkey	0.43%	99.08%	0.49%
D012	Donkey	72.4	42.4	24	32.7	37.1	20.8	Mule	18.70%	40.59%	40.71%
D013	Donkey	74.6	42.5	24.2	32.5	36.6	21	Donkey	4.81%	66.81%	28.38%
D026	(Donkey)	87	55.5	40.7	32	41.5	26.5	Mule	24.58%	1.76%	73.67%
D030	Ane Blanc	57	31	24	18	24.2	15.7	Donkey	0.00%	99.99%	0.01%
D032	(Donkey)	67.1	36	27	21	30	16.8	Donkey	0.02%	99.90%	0.08%
D033	(Donkey)	58	32	24.5	19	26	15.5	Donkey	0.01%	99.96%	0.02%
D034	anglais	66	37	28	21.5	31.2	18	Donkey	0.21%	99.41%	0.38%
D035	Argentine	79	48	35	27.7	37	22.9	Donkey	10.85%	54.01%	35.15%
D036	S Peru	68	41	30	22.5	30	19	Donkey	0.34%	98.93%	0.73%
D037	S Peru	69	40	29	23	30.2	18.5	Donkey	0.12%	99.45%	0.43%
D038	sans crâne	77	42.3	32.2	24.8	33.9	20	Donkey	0.09%	98.75%	1.16%
D039	Turquie	62	33.6	24.2	19	27	15	Donkey	0.01%	99.98%	0.02%
D040	Turquie	65	36.8	26.4	21	29	19	Donkey	0.04%	99.81%	0.16%

Measurements for Modern Control Data (Posterior PH1, cont'd)

Posterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
D041	(Donkey)	63	35.5	26	20	27	17	Donkey	0.01%	99.95%	0.04%
D042	(Donkey)	60	36	26	20	27.8	16.9	Donkey	0.24%	99.60%	0.17%
D043	(Donkey)	49.5	30	21	18	23.5	13.3	Donkey	0.10%	99.89%	0.02%
D044	(Donkey)	64	37	27.9	23	30.2	17.9	Donkey	0.49%	98.86%	0.65%
D055	(Donkey)	59	32	24	21	26.8	15	Donkey	0.02%	99.94%	0.04%
D056	(Donkey)	72	42.5	30.5	25	33	20	Donkey	1.11%	95.70%	3.19%
D057	(Donkey)	64	39.7	28.6	24	30	18.5	Donkey	2.60%	95.42%	1.98%
D058	sans crâne	66	37	28	22.5	30.1	17.8	Donkey	0.11%	99.59%	0.30%
D059	sans crâne	64.5	35	25.5	21	27	17.8	Donkey	0.00%	99.96%	0.03%
D061	Donkey 3349 Right	61.83	35.1	25.17	21.63	27.61	17.01	Donkey	0.04%	99.86%	0.10%
D062	Donkey 546 left	70.96	38.24	28.03	22.08	31.61	18.65	Donkey	0.02%	99.78%	0.19%
D064	Donkey 132	66.66	41.52	30.46	24.67	32.53	15.75	Donkey	18.81%	77.62%	3.57%
M001	Mule	85.2	48.1	31.6	34.8	41.8	23.4	Mule	7.01%	14.46%	78.54%
M002	Mule	78.7	49.9	30.8	33.3	38.9	22.5	Mule	41.55%	5.82%	52.63%
M003	Mule	85	51.5	35.1	34.3	40.7	23.2	Mule	18.18%	6.76%	75.06%
M004	Mule	86.9	50.5	33.2	36.2	44.1	25.2	Mule	12.19%	2.00%	85.80%
M005	Mule	75.6	52	30	37.1	40.4	23.7	Horse	81.39%	0.07%	18.54%
M006	Mule	98.2	64.6	37.3	46.1	48.4	28	Mule	21.08%	0.00%	78.92%
M008	Mule	91.4	56.3	32.2	42	45.1	26.2	Mule	10.52%	0.17%	89.31%
M009	Mule	93.2	61.5	33.5	43.7	46.3	27	Mule	27.05%	0.02%	72.94%
M010	Mule	95.9	61.5	39.6	48	48.9	28.9	Mule	17.70%	0.00%	82.30%
M016	UNSM 5084	105.5	70.5	51.3	44	55	35	Mule	30.73%	0.00%	69.27%
M019	MCZ 1655	83	47	35	28	35.5	21.2	Donkey	0.28%	93.86%	5.86%
M020	MCZ 1656	92	54	40	31	43	25	Mule	7.47%	12.24%	80.29%
M021	sans n°	90	60	40.7	34	46	26	Horse	71.45%	0.04%	28.51%

Measurements for Modern Control Data (Posterior PH1, cont'd)

Posterior PH1		Measurement						DFA	Probabilities		
ID	Sp./Breed	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule
M022	Gen 753/69	88	55	39	33.1	44	25	Mule	39.55%	0.79%	59.66%
M023	HL mlt 5	79.5	52	36.7	30.1	39	24	Horse	54.47%	3.43%	42.11%

Appendix I.IX – Measurements of Modern Control Data (the Davis Method)

Posterior PH1 are highlighted in grey, and the misclassifications are indicated with red text.

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C001	Przewalski	85.2	42.9	50.35	36.8	0.94058	3.53666	0.69493	M
C001	Przewalski	80.3	40.8	50.81	40.4	1.48909	4.52042	0.77270	M
C002	Przewalski	77	37.3	48.44	38.2	1.53292	3.96047	0.44151	M
C002	Przewalski	79.4	38.4	48.36	34.1	1.63926	2.77397	0.56400	M
C003	Przewalski	82.4	45	54.61	34.7	0.71046	3.96309	2.98316	H
C003	Przewalski	78.8	43.7	55.46	37.3	1.49551	4.59054	3.00014	H
C004	Przewalski	81.4	39	47.91	35.3	1.70625	3.15375	0.40300	M
C004	Przewalski	85.5	41.6	48.65	32.7	1.69602	2.37410	0.92948	M
C005	Przewalski	72.8	37.8	51.92	34.7	0.38288	3.24092	1.75681	H
C005	Przewalski	76.9	38.8	50.46	34	0.90216	2.83971	1.24924	H
C006	Przewalski	75.5	39.6	52.45	33.3	0.26775	3.11027	2.24442	H
C006	Przewalski	71.3	37.3	52.31	35.7	0.46442	3.52452	1.76848	H
C007	Przewalski	79.6	43.7	54.90	35.8	1.01443	4.20314	2.94806	H
C007	Przewalski	76.1	42.4	55.72	39.1	1.96076	4.95495	2.90892	H
C008	Przewalski	74.2	39.6	53.37	32.2	0.30598	3.24756	2.85345	H
C008	Przewalski	71.5	37.7	52.73	33.4	0.15560	3.20384	2.34881	H
C009	Przewalski	78.7	41.4	52.60	34	0.15740	3.26854	2.18648	H
C009	Przewalski	75.8	40.2	53.03	36.8	0.77770	3.89487	1.94054	H
C010	Przewalski	78.9	41.8	52.98	33.1	0.14070	3.23341	2.51499	H
C010	Przewalski	76.5	40.5	52.94	35	0.32604	3.52946	2.16862	H

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C011	Przewalski	74.9	40.1	53.54	36.4	0.77424	3.92947	2.23012	H
C011	Przewalski	79.6	42.7	53.64	35.3	0.53870	3.76370	2.44307	H
C012	Przewalski	82	41.3	50.37	32.2	1.16746	2.41764	1.59382	H
C012	Przewalski	76	38.8	51.05	34.4	0.66406	3.01819	1.42501	H
C013	Przewalski	73.4	40.4	55.04	34.6	0.83975	4.09195	3.19634	H
C013	Przewalski	69	38.8	56.23	35.2	1.34923	4.56974	3.65377	H
C014	Przewalski	79.8	42.4	53.13	35.2	0.40250	3.61300	2.22414	H
C014	Przewalski	77.4	40.9	52.84	37	0.79938	3.89793	1.82450	H
C015	Przewalski	75.5	37.8	50.07	36.4	0.98712	3.41667	0.62454	M
C015	Przewalski	78.8	39.4	50.00	33.2	1.15160	2.59190	1.23767	H
C016	Przewalski	77.8	38	48.84	37.1	1.36834	3.61488	0.05032	M
C016	Przewalski	83.7	40.1	47.91	36.5	1.66009	3.50795	0.41278	M
C017	Przewalski	82.1	43.8	53.35	36.4	0.73521	3.88526	2.14267	H
C017	Przewalski	80.2	42.4	52.87	38.9	1.26597	4.31929	1.62480	H
C018	Pony	60.7	33.8	55.68	26.2	0.79085	4.08294	3.64630	H
C018	Pony	55.9	34.5	61.72	26	1.57011	4.88783	4.35009	H
C019	Pony	70.1	40.5	57.77	31.9	1.97111	4.87460	1.34404	M
C019	Pony	67.5	38.3	56.74	33.1	1.86842	4.97224	1.07774	M
C020	Pony	85.7	42.7	49.82	38.7	1.11099	3.57064	0.38211	M
C020	Pony	81.8	40.1	49.02	38.1	1.40770	4.44415	0.98894	M

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C021	Pony	74.3	40.6	54.64	33.3	0.70476	3.39176	1.13619	H
C021	Pony	72.9	39.1	53.64	36	1.84668	3.72680	0.74219	M
C022	Pony	79.1	47.9	60.56	34.9	1.69881	3.67024	0.53052	M
C022	Pony	77.5	46.4	59.87	37.7	0.30367	3.07671	2.32205	H
C023	Pony	73.2	38.2	52.19	34.8	0.27238	3.10491	2.36488	H
C023	Pony	76.2	39.3	51.57	32.4	0.39107	3.66037	3.12670	H
C024	Pony	82.9	43.3	52.23	35.2	0.54748	3.77039	3.48760	H
C024	Pony	78.2	41.8	53.45	37.2	0.61394	3.87885	2.93191	H
C025	Pony	81.3	41.4	50.92	35.7	0.25717	3.51827	2.94289	H
C025	Pony	75.7	39.6	52.31	38	2.88007	5.91615	1.82703	M
C026	Pony	82.4	43.7	53.03	37.1	2.67062	5.65356	1.88510	M
C026	Pony	81	41.6	51.36	39	2.84631	5.80656	1.99767	M
C027	Pony	66.1	36.1	54.61	33.8	1.91784	4.99919	1.23163	M
C027	Pony	68	37.1	54.56	30.9	0.93100	2.55059	1.95113	H
C028	Pony	87.8	44.6	50.80	37	1.12219	2.42085	1.72529	H
C028	Pony	83.6	42.8	51.20	39.7	0.59428	3.45579	3.46588	H
C030	Pony	80.3	41.5	51.68	34.4	0.98378	3.37697	3.79296	H
C030	Pony	79.7	39.9	50.06	37.6	0.71622	2.83343	1.62707	H
C031	Pony	68.8	38.1	55.38	35.5	0.88562	2.59356	1.92105	H
C031	Pony	73.2	39	53.28	30.6	1.04700	2.52012	1.61051	H

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C032	Pony	71.1	39	54.85	32.5	1.30701	2.23373	2.16946	H
C032	Pony	67.6	39.9	59.02	34.7	0.80200	2.67839	1.85735	H
C033	Arab	100.1	50	49.95	43	1.21126	2.30749	2.05452	H
C033	Arab	95.5	47	49.21	41.8	0.72661	3.86424	2.04550	H
C034	Arab	90.5	44.8	49.50	41.6	0.60537	3.22573	1.35253	H
C034	Arab	94.7	46.4	49.00	41.4	1.48637	2.46917	0.98561	M
C035	Arab	93.4	47.4	50.75	43	1.70479	2.45747	0.83286	M
C035	Arab	95	48.1	50.63	38.9	0.74322	3.95619	2.67694	H
C036	Arab	92	47.1	51.20	37	0.49940	3.74499	2.53951	H
C037	Arab	91.5	47.6	52.02	38.3	2.76583	5.70873	2.05198	M
C037	Arab	89.5	45.9	51.28	41.7	1.90272	4.99059	1.18699	M
C041	Tarpan	75.2	41.7	55.45	33	0.98750	4.13502	4.36958	H
C041	Tarpan	71.5	41	57.34	34	0.99962	3.54265	3.97475	H
C044	Shetland	66	35	53.03	29	0.96418	3.95191	1.16973	H
C044	Shetland	64	34	53.13	29	0.97404	4.06941	1.92161	H
C045	(Horse)	107	51	47.66	41	0.75585	3.81480	1.61009	H
C045	(Horse)	103	53	51.46	42	0.59977	3.17996	1.38803	H
C046	(Horse)	95.5	47.5	49.74	37	2.18885	5.13773	2.84208	H
C048	Shetland	73	38	52.05	30.3	2.60028	5.50320	3.35412	H
C048	Shetland	71	36.8	51.83	29.7	1.43784	3.92949	0.30655	M

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C049	Grand	99	51	51.52	40	1.37287	3.99944	0.29062	M
C049	Grand	96	49	51.04	36	0.83743	2.75321	2.72306	H
C050	Poney	48	30	62.50	23.3	0.36842	3.51241	3.18142	H
C050	Poney	46	29.5	64.13	24	1.07738	2.49579	2.52977	H
C054	Poney	58	33	56.90	24	1.10752	2.56333	2.76572	H
C054	Poney	55.5	32	57.66	24	0.55231	2.96448	2.69411	H
C055	Welsh	64	35.5	55.47	28	0.79893	3.60608	3.83266	H
C055	Welsh	61	33.5	54.92	26	0.73621	3.93694	3.87137	H
C056	Poney	52	32	61.54	23.8	0.63263	3.43196	3.48947	H
C056	Poney	50	31	62.00	24	0.64015	2.96868	2.86022	H
C057	Poney	69	37	53.62	29	0.69075	2.94646	2.89517	H
C057	Poney	66	35	53.03	29	0.34301	3.61002	3.06221	H
C059	(Horse)	95.1	45	47.32	37	0.59710	3.84180	3.54467	H
C059	(Horse)	92.1	44	47.77	37	0.16299	3.40431	2.79095	H
C060	Shetland	55	34.2	62.18	27	0.73039	2.84602	2.74632	H
C060	Shetland	54	33	61.11	27	1.63481	2.20647	1.21032	M
C061	Shetland	61.9	35.1	56.70	27.5	1.13330	2.40350	2.34650	H
C061	Shetland	60	33.5	55.83	26.9	0.40352	3.04556	2.58994	H
C062	Shetland	63.5	35.1	55.28	27	0.51844	3.01997	2.76341	H
C062	Shetland	63	34	53.97	26.5	1.20102	2.32581	2.20803	H

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C063	Shetland	61.9	35	56.54	27	1.16778	2.35882	2.25106	H
C063	Shetland	59	34	57.63	26.9	1.18057	2.38641	1.65944	H
C064	Islande	80	42	52.50	33	1.23454	2.34467	1.64023	H
C064	Islande	77	40.5	52.60	33	1.12143	2.58285	1.30522	H
C065	Islande	75.5	41	54.30	33	0.97176	2.54243	1.77672	H
C065	Islande	73	40	54.79	32.2	2.12168	1.84675	1.28369	M
C066	Islande	79	43	54.43	34.5	2.12319	1.84666	1.28286	M
C066	Islande	77	41.5	53.90	33	0.72744	2.72034	2.03156	H
C067	Hannover	105	56	53.33	45.2	1.18868	2.40661	1.57049	H
C067	Hannover	100	53.8	53.80	44	2.05671	5.26139	1.17661	M
C068	Hannover	98	53	54.08	44.5	1.85666	4.95526	1.03408	M
C068	Hannover	98	51	52.04	42	1.79474	4.87974	0.93196	M
C069	Konik	86	44	51.16	32	1.80951	4.85409	0.99401	M
C069	Konik	84	42.5	50.60	32	2.06461	5.23971	1.13545	M
C070	Exmoor	75.1	42	55.93	32	1.19712	4.10890	0.65287	M
C070	Exmoor	73	40	54.79	32	0.80462	3.65381	1.05932	H
C071	Shetland	54.7	30	54.84	23	1.03860	4.06344	1.29450	H
C071	Shetland	54	29	53.70	23	1.78859	4.88586	1.00881	M
C072	Islande	76	41.2	54.21	30.9	0.74267	3.00506	1.30087	H
C072	Islande	72	39	54.17	29.1	2.70718	3.19331	1.35967	M

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C073	Welsh	67.8	38	56.05	31.5	0.74978	3.51902	1.07925	H
C073	Welsh	66.1	37	55.98	29	0.36436	3.11468	1.90647	H
C074	Welsh	80	42.3	52.88	35	1.61441	4.17410	5.01044	H
C074	Welsh	77	41.1	53.38	33.7	2.79353	7.05647	7.69176	H
C075	Islande	85.1	43.5	51.12	33.5	1.53502	4.98142	4.88787	H
C075	Islande	84	43	51.19	32.2	1.25721	4.59462	4.21745	H
C076	Arabe	92.5	47	50.81	34.5	1.27009	4.04305	0.37647	M
C076	Arabe	88.1	40	45.40	34	1.37498	3.89434	0.22841	M
C077	Poney	75	40	53.33	30	0.52781	3.81130	3.22819	H
C077	Poney	73	38	52.05	29.3	0.70072	3.88111	2.33301	H
C078	Mongol	87	44	50.57	32.5	2.83142	6.24368	5.70080	H
C078	Mongol	82.5	42	50.91	30.5	3.01709	6.13304	4.99947	H
C079	Mongol	81	41.5	51.23	32.6	0.32677	3.31612	1.85810	H
C079	Mongol	78.6	40	50.89	31	0.72082	2.72545	2.03987	H
C080	Mongol	82	43.6	53.17	36.5	0.37615	3.40566	1.81147	H
C080	Mongol	82	42	51.22	35.2	0.94980	4.06303	2.08193	H
C081	Tarpan	86.5	42.5	49.13	33	0.71300	3.30519	1.13177	H
C081	Tarpan	84.5	41	48.52	33	0.98620	4.03061	1.45774	H
C082	Arabe	92	47	51.09	36.5	0.85097	3.95612	1.90037	H
C082	Arabe	88.5	46	51.98	34	1.18245	4.17416	0.94830	M

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C085	(Horse)	83	45	54.22	35.5	0.57092	3.85470	3.13073	H
C085	(Horse)	80	43	53.75	35	0.62835	3.59663	3.61888	H
C086	(Horse)	105	57	54.29	44	0.86821	3.61801	0.87421	H
C086	(Horse)	106	55	51.89	42	1.33494	4.34688	0.86764	M
C089	Exmoor	76	42.7	56.18	33	0.45147	3.13077	1.70206	H
C089	Exmoor	75	41	54.67	31	1.08617	3.74048	0.46722	M
C090	Islande	68	38	55.88	30	1.11148	4.31369	3.21389	H
C090	Islande	66	36	54.55	29	0.70114	3.06890	3.11946	H
C091	Fjord	89	46	51.69	38	0.56267	3.81557	3.46078	H
C091	Fjord	83.1	44.2	53.19	37.5	2.25945	5.60187	5.02019	H
C092	Islande	84	44	52.38	37	1.12996	2.88663	3.33461	H
C092	Islande	82	42	51.22	35	1.11455	2.92670	3.37387	H
C093	Exmoor Left	73.8	43.44	58.86	33.85	1.02450	2.58547	2.66654	H
C093	Exmoor Left	71.95	42.28	58.76	33.18	1.22061	2.44776	2.70122	H
C094	Welsh cob 3868 Left	85.29	47.57	55.77	40.05	3.16557	7.71878	8.52936	H
C094	Welsh cob 3868 Left	82.91	47.23	56.97	40.38	3.57030	8.41470	9.12848	H
C095	Pony 3158 right	69.97	36.75	52.52	30.3	2.11256	4.96198	5.96076	H
C096	Racehorse 123	107.71	52.56	48.80	38.18	2.16876	5.32525	6.28459	H
C096	Racehorse 123	103.64	50.97	49.18	38.49	1.24022	3.97635	4.56605	H
C097	NF Pony 137	80.58	42.64	52.92	33.4	1.66402	3.82676	4.72824	H

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C098	Modern Shetland Pony	55.27	31.05	56.18	24.01	2.88717	7.20059	8.01216	H
C099	Modern Shetland Pony	53.53	29.56	55.22	23.42	2.98575	7.39784	8.17952	H
C102	Modern Pony	83.33	44.65	53.58	34.33	1.04793	3.13982	3.58224	H
C102	Modern Pony	79.88	41.86	52.40	30.73	1.12996	2.88663	3.33461	H
C104	Davis Horse	73	39.5	54.11	32.2	2.90704	7.19065	7.72359	H
C105	Davis Horse	76.3	39.5	51.77	30.4	2.58080	6.68290	7.24226	H
C106	Davis Horse	71.6	37.3	52.09	29.9	1.46553	4.57170	5.19765	H
C107	Davis Horse	76.6	40.4	52.74	31.6	1.47805	4.19779	4.93655	H
C108	Davis Horse	70.8	38.7	54.66	30	1.43694	3.93073	4.67891	H
C109	Davis Horse	75	41.5	55.33	31.4	1.61396	3.34663	4.23318	H
C110	Davis Horse	71.8	38.9	54.18	30.7	1.52358	4.52493	5.22285	H
C111	Davis Horse	74.1	39.2	52.90	31.1	1.70611	5.04221	5.71416	H
C112	Davis Horse	70.9	37.5	52.89	30.9	0.90787	4.20733	4.03178	H
C113	Davis Horse	80.5	43.6	54.16	33	0.55522	3.75597	3.52315	H
C114	Davis Horse	76.6	42.1	54.96	32.3	2.37066	4.10757	5.31558	H
C115	Davis Horse	74.5	39.9	53.56	33	2.49540	3.56497	4.86316	H
C116	Davis Horse	71.5	37.6	52.59	31	0.94454	4.23684	4.17381	H
C117	Davis Horse	79	38.8	49.11	32	1.12997	4.18233	4.59623	H
C118	Davis Horse	74.1	38.1	51.42	30.6	0.31939	3.51311	2.13835	H
C119	Davis Horse	81.3	42.9	52.77	32.2	0.11786	3.44015	2.58634	H

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
C120	Davis Horse	75.8	40.1	52.90	31.6	0.83998	3.05348	3.26076	H
C121	Davis Horse	75.9	38.8	51.12	30.7	1.25829	2.50244	2.87483	H
C122	Davis Horse	73.2	37.5	51.23	30.7	1.05030	4.36708	3.97967	H
C123	Davis Horse	82.5	41.6	50.42	32	0.62850	3.64547	3.64791	H
C124	Davis Horse	79.1	39.8	50.32	31.9	2.09541	5.49782	5.07375	H
C125	Davis Horse	83	41.6	50.12	33.1	1.98732	5.43392	5.13260	H
C126	Davis Horse	79	40.2	50.89	32.3	0.91229	2.75715	2.85958	H
C127	Davis Horse	86.6	41.8	48.27	30.8	2.08877	4.61823	5.65662	H
C128	Davis Horse	83.5	40.3	48.26	30.8	2.24562	4.23246	5.38109	H
C129	Davis Horse	83.6	43.1	51.56	32.4	0.09177	3.25860	2.43301	H
C130	Davis Horse	82.1	41.3	50.30	32.2	0.30535	3.59376	2.57200	H
D001	Donkey	69.8	34.1	48.85	27.2	2.62059	1.13772	2.24711	D
D001	Donkey	65.6	31.1	47.41	28	2.91571	1.06634	1.77280	D
D002	Donkey	69.6	30.9	44.40	25.5	4.37390	1.23040	2.25161	D
D002	Donkey	65.4	28.4	43.43	26.1	4.58472	1.78713	2.34168	D
D003	Donkey	59.4	28.9	48.65	27.4	2.64033	1.10672	2.14969	D
D003	Donkey	63.2	31.2	49.37	27.2	2.46691	1.31468	2.38987	D
D004	Donkey	58.7	28.9	49.23	27	2.54923	1.24738	2.39730	D
D005	Donkey	58.7	27.6	47.02	24.1	3.82607	0.23647	2.57721	D
D005	Donkey	53.4	24.7	46.25	24.1	4.05880	0.13029	2.48622	D

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
D006	Donkey	66	34.1	51.67	30	1.19551	2.41682	2.57248	H
D006	Donkey	62.4	32	51.28	29.9	1.32476	2.27241	2.44250	H
D007	Donkey	67.6	30.5	45.12	26.1	4.02421	1.04505	2.08772	D
D007	Donkey	62	27.7	44.68	26.6	4.07628	1.34537	2.05550	D
D008	Donkey	66.3	33	49.77	27.5	2.28300	1.49175	2.44465	D
D008	Donkey	61.7	30	48.62	28.4	2.44745	1.28636	1.91154	D
D009	Donkey	82.3	36.5	44.35	33.1	3.18344	3.22101	1.76709	M
D009	Donkey	77	35	45.45	32.9	2.81236	2.85490	1.31847	M
D010	Donkey	62	31.2	50.32	25.9	2.48719	1.68102	2.98676	D
D010	Donkey	57.7	29.6	51.30	26.2	2.17036	2.11997	3.25835	D
D011	Donkey	66.6	31.4	47.15	26.1	3.37341	0.54255	2.15433	D
D011	Donkey	60.4	28.8	47.68	26.2	3.18663	0.64801	2.21613	D
D012	Donkey	69.8	34.3	49.14	32.7	1.52353	2.39025	1.05686	M
D012	Donkey	72.4	37.1	51.24	32.7	0.78280	2.69936	1.84062	H
D013	Donkey	73.7	34	46.13	34	2.44608	3.02822	1.06105	M
D013	Donkey	74.6	36.6	49.06	32.5	1.57930	2.33324	1.08004	M
D015	Olduvai	66.4	32	48.19	24.1	3.48002	0.79633	2.80022	D
D015	Olduvai	62.1	30	48.31	23.2	3.64511	0.99005	3.03426	D
D016	Syrie	75.5	33.5	44.37	24.5	4.57365	1.07707	2.40921	D
D016	Syrie	70	30.5	43.57	23	5.12328	1.32641	2.72306	D

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
D017	(Donkey)	64	32	50.00	22	3.47332	1.98829	3.77555	D
D017	(Donkey)	61	29	47.54	22	4.12712	0.93976	3.14180	D
D018	Afrique	70	34	48.57	23	3.61682	1.14734	3.14422	D
D018	Afrique	66	31.7	48.03	22.3	3.92317	1.05718	3.17691	D
D021	Crête	72.5	35	48.28	23.5	3.58808	0.92206	2.95737	D
D021	Crête	68	32	47.06	22	4.26487	0.77733	3.05246	D
D022	(Donkey)	76	35	46.05	25	3.93864	0.40041	2.28553	D
D022	(Donkey)	70	31.5	45.00	24	4.47095	0.71809	2.46202	D
D023	Nubie	76	34.5	45.39	24	4.34657	0.53021	2.46152	D
D023	Nubie	72	32	44.44	23	4.84640	0.92800	2.65868	D
D024	(Donkey)	74	32	43.24	22	5.42563	1.46052	2.91184	D
D024	(Donkey)	68	31	45.59	25	4.08563	0.59517	2.27129	D
D025	Zoo	73	34.1	46.71	26	3.53034	0.52477	2.12617	D
D025	Zoo	62	29	46.77	22	4.34736	0.69952	3.00632	D
D026	(Donkey)	65	31	47.69	23.1	3.84238	0.73244	2.92160	D
D026	(Donkey)	87	41.5	47.70	32	2.13171	2.20316	0.95178	M
D029	Ane Blanc	77	36.8	47.79	26	3.19404	0.64280	2.28174	D
D029	Ane Blanc	76	35	46.05	25.6	3.81915	0.56046	2.16480	D
D030	Ane Blanc	82	36.2	44.15	25.8	4.39998	1.40197	2.24287	D
D030	Ane Blanc	57	24.2	42.46	18	6.48618	2.12635	3.62773	D

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
D031	(Donkey)	59	27.3	46.27	18	5.37124	1.80585	3.81831	D
D032	(Donkey)	69.1	31.7	45.88	22	4.61286	0.60726	2.89567	D
D032	(Donkey)	67.1	30	44.71	21	5.17486	1.02199	3.03196	D
D033	(Donkey)	61.5	27.7	45.04	19	5.50178	1.44357	3.45529	D
D033	(Donkey)	58	26	44.83	19	5.56417	1.45662	3.43999	D
D034	anglais	68	34	50.00	21	3.70832	2.19191	4.00514	D
D034	anglais	66	31.2	47.27	21.5	4.31340	0.98575	3.20354	D
D035	Argentine	85.3	40	46.89	28.5	2.99153	1.24669	1.61950	D
D035	Argentine	79	37	46.84	27.7	3.15970	1.01564	1.77993	D
D036	S Peru	72	33	45.83	24	4.20963	0.32219	2.47694	D
D036	S Peru	68	30	44.12	22.5	5.04968	1.07437	2.76123	D
D037	S Peru	73	33	45.21	24.3	4.34612	0.65327	2.40368	D
D037	S Peru	69	30.2	43.77	23	5.06054	1.23559	2.70338	D
D038	sans crâne	83	36.9	44.46	25.6	4.33495	1.22203	2.22944	D
D038	sans crâne	77	33.9	44.03	24.8	4.62778	1.28354	2.40037	D
D039	Turquie	66.1	29	43.87	20	5.63791	1.41120	3.21803	D
D039	Turquie	62	27	43.55	19	5.94554	1.66852	3.40766	D
D040	Turquie	69	30.6	44.35	21.3	5.22290	1.07738	2.97111	D
D040	Turquie	65	29	44.62	21	5.20341	1.04546	3.02991	D

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
D041	(Donkey)	67	30	44.78	21.1	5.13370	0.98757	3.01409	D
D041	(Donkey)	63	27	42.86	20	5.95026	1.73413	3.26586	D
D042	(Donkey)	64	30	46.88	20.9	4.55849	1.05035	3.26816	D
D042	(Donkey)	60	27.8	46.33	20	4.91063	1.21648	3.38394	D
D043	(Donkey)	54	25.3	46.85	18	5.21200	1.91071	3.91747	D
D043	(Donkey)	49.5	23.5	47.47	18	5.04511	2.05904	4.04120	D
D044	(Donkey)	68	33	48.53	24	3.40597	0.96915	2.90314	D
D044	(Donkey)	64	30.2	47.19	23	4.01058	0.54669	2.84986	D
D055	(Donkey)	64	28.2	44.06	21	5.37253	1.20822	3.03063	D
D055	(Donkey)	59	26.8	45.42	21	4.95999	0.89854	3.06783	D
D056	(Donkey)	76	36.8	48.42	25	3.21822	0.83667	2.64637	D
D056	(Donkey)	72	33	45.83	25	4.00787	0.48953	2.27627	D
D057	(Donkey)	67	33	49.25	24.3	3.13763	1.28058	3.02581	D
D057	(Donkey)	64	30	46.88	24	3.89044	0.18431	2.57858	D
D058	sans crâne	70	33	47.14	23	4.02365	0.52970	2.84227	D
D058	sans crâne	66	30.1	45.61	22.5	4.58910	0.53097	2.77022	D
D059	sans crâne	70	29.6	42.29	21.1	5.90822	1.88975	3.16288	D
D059	sans crâne	64.5	27	41.86	21	6.06338	2.07432	3.24218	D
D061	Donkey 3349 Right	66.04	30.06	45.52	22.48	4.62012	0.55617	2.76896	D
D061	Donkey 3349 Right	61.83	27.61	44.65	21.63	5.06048	0.93609	2.90888	D

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
D062	Donkey 546 left	75.3	33.58	44.59	23.28	4.74282	0.86493	2.60329	D
D062	Donkey 546 left	70.96	31.61	44.55	22.08	5.00127	0.92284	2.82378	D
D064	Donkey 132	70.2	35.85	51.07	24.75	2.56798	2.10189	3.49984	D
D064	Donkey 132	66.66	32.53	48.80	24.67	3.18154	1.03138	2.81710	D
D065	Davis Donkey	62.9	27.4	43.56	17.8	6.19538	1.90676	3.63324	D
D066	Davis Donkey	58	25.5	43.97	17.6	6.11856	1.89151	3.68046	D
D067	Davis Donkey	77.2	36.7	47.54	25.9	3.29251	0.55836	2.25858	D
D068	Davis Donkey	73.7	36	48.85	28.4	2.37653	1.33307	1.96819	D
D069	Davis Donkey	82.1	36.4	44.34	25.6	4.37486	1.27706	2.24437	D
D070	Davis Donkey	77.4	34.9	45.09	25.2	4.20584	0.85784	2.24341	D
D071	Davis Donkey	70.3	34.2	48.65	23.2	3.55072	1.14684	3.11754	D
D072	Davis Donkey	66.2	31.7	47.89	22.4	3.94157	0.97352	3.12198	D
D073	Davis Donkey	82.9	37.3	44.99	27.1	3.87950	1.34385	1.94226	D
D074	Davis Donkey	77.5	34.4	44.39	27	4.10045	1.55996	2.04716	D
D075	Davis Donkey	67.8	32.2	47.49	23.1	3.90005	0.64645	2.88242	D
D076	Davis Donkey	63.2	31.1	49.21	22.3	3.60443	1.57166	3.47470	D
D077	Davis Donkey	63.1	31.1	49.29	21.7	3.72240	1.72995	3.63496	D
D078	Davis Donkey	59	29	49.15	20.9	3.94185	1.85209	3.78222	D
M001	Mule	79.3	38.6	48.68	35.6	1.42755	3.19130	0.27586	M
M001	Mule	85.2	41.8	49.06	34.8	1.33501	2.95771	0.55015	M

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
M002	Mule	76.3	38.2	50.07	34.6	0.99593	2.94654	0.96581	M
M002	Mule	78.7	38.9	49.43	33.3	1.34361	2.56472	1.01048	M
M003	Mule	80.9	38	46.97	37.6	1.95504	3.95752	0.98930	M
M003	Mule	85	40.7	47.88	34.3	1.79209	2.86233	0.52623	M
M004	Mule	82	41.4	50.49	37.8	1.03208	3.80847	0.64235	M
M004	Mule	86.9	44.1	50.75	36.2	0.79319	3.41079	0.96927	H
M005	Mule	82.4	42	50.97	35	0.67754	3.14406	1.27728	H
M005	Mule	75.6	40.4	53.44	37.1	0.92285	4.04041	2.08863	H
M006	Mule	101.8	51.6	50.69	44.6	2.42993	5.69248	1.44825	M
M006	Mule	98.2	48.4	49.29	46.1	2.73130	6.20905	2.00631	M
M008	Mule	94.6	45.8	48.41	38.3	1.54638	3.99203	0.47343	M
M008	Mule	91.4	45.1	49.34	42	1.88270	5.00498	1.05229	M
M009	Mule	97	49	50.52	41.3	1.68552	4.76582	0.83084	M
M009	Mule	93.2	46.3	49.68	43.7	2.21019	5.47791	1.37394	M
M010	Mule	102.3	52.6	51.42	47.9	3.27379	6.61030	2.07991	M
M010	Mule	95.9	48.9	50.99	48	3.25531	6.65253	2.13726	M
M011	Mule	98.3	49	49.85	38.4	1.22562	3.95913	0.36176	M
M011	Mule	91.8	46.4	50.54	41.8	1.79311	4.90532	0.91508	M
M012	NY 204211	106.5	49.5	46.48	38	2.11245	4.16110	1.27870	M
M012	NY 204211	99	46.2	46.67	36.2	2.09045	3.58786	0.95148	M

Measurements for Modern Control Data (Davis Method, cont'd)

		Measurement				M-Dist			
ID	Sp./Breed	GL	BFd	BFd/GLx100	SD	Horse	Donkey	Mule	Determination
M013	NY 14116	93	45	48.39	35	1.55846	3.03201	0.37977	M
M013	NY 14116	87	42	48.28	34	1.67994	2.74914	0.57714	M
M014	AA 1534	110	53	48.18	40	1.75014	4.51533	0.93058	M
M014	AA 1534	102	49.5	48.53	39	1.57162	4.18792	0.58297	M
M015	AA 98766	103	45	43.69	32	3.55617	3.12578	2.00432	M
M015	AA 98766	96	42	43.75	31.1	3.65718	2.85937	1.96717	M
M016	UNSM 5084	108	58.5	54.17	44.8	2.93590	5.88941	2.03819	M
M016	UNSM 5084	105.5	55	52.13	44	2.41148	5.53431	1.43991	M
M019	MCZ 1655	89	38	42.70	30	4.18865	2.97223	2.36846	M
M019	MCZ 1655	83	35.5	42.77	28	4.47771	2.47178	2.38108	M
M020	MCZ 1656	96	44.5	46.35	31	2.75410	2.08492	1.20297	M
M020	MCZ 1656	92	43	46.74	31	2.61939	2.01637	1.15649	M
M021	sans n°	90	46	51.11	34	0.66902	2.93939	1.52698	H
M022	Gen 753/69	93	45.5	48.92	32.5	1.62777	2.32667	1.04216	M
M022	Gen 753/69	88	44	50.00	33.1	1.16436	2.56776	1.25946	H
M023	HL mlt 5	81.7	42	51.41	31	1.05097	2.45584	2.25860	H
M023	HL mlt 5	79.5	39	49.06	30.1	1.97946	1.73464	1.63229	M

Appendix II.I – Measurements and Species Determination using DFA (Radius)

The same individuals are indicated by * (Individual 1) and ** (Individual 2)

		Measurement							DFA	Probabilities			Squared
ID	Site	GL	Bp	BFp	SD	Bd	BFd	DFd	Determination	Horse	Donkey	Mule	M-Dist
Z001	Winchester*	348	86.73	73.74	39.71	80.6	65.83	36.43	D*	17.02%	**75.95%**	7.03%	3.579402213
Z002	Winchester*	341	86.15	76.57	39.16	80.19	66.36	36.85	H*	**65.09%**	4.36%	30.55%	2.946877994
Z003	Ribchester	323.5	78.32	70.33	35.54	70.79	60.59	35.12	H	**80.94%**	5.19%	13.87%	3.615427002
Z004	Healam Bridge**	347.6	87.67	79.27	38.88	79.82	66.96	36.77	H*	**66.58%**	0.43%	32.99%	2.263710874
Z005	Healam Bridge	296.14	71.52	64.32	33.36	66.19	56.06	33.45	H*	**68.29%**	23.77%	7.95%	7.926392104
Z006	Healam Bridge	367	87.89	79.18	41.24	79.05	68.04	36.13	M	18.68%	0.16%	**81.16%**	3.503125986
Z007	Healam Bridge	292.88	71.89	65.87	32.47	67.38	56.79	31.79	H*	**66.97%**	9.09%	23.93%	0.962526575
Z008	Healam Bridge	292.03	72.85	66.55	32.06	66.17	56.43	33.93	H	**93.38%**	3.74%	2.88%	3.579402213
Z009	Healam Bridge	329.9	79.7	71.93	34.03	72.51	62.17	35.63	H	**81.59%**	4.01%	14.40%	2.946877994
Z010	Healam Bridge	306.82	73.33	67.54	32.13	66.46	56.94	29.95	M*	43.03%	2.89%	**54.08%**	3.615427002

Appendix II.II – Measurements and Species Determination using DFA (Metacarpal)

Determinations from Johnstone (2014) are highlighted in grey.

		Measurement						DFA		Probabilities			Squared
ID	Site	GL	Bp	Dp	SD	BFd	Dd	Determination		Horse	Donkey	Mule	M-Dist
Z011	Chichester Cattlemarket	242	53.1	34	37.2	52.2	39.2	M*	H*	41.00%	0.44%	**58.56%**	2.298632
Z012	Thorpe Thewles	203	46.6	32	29	46.4	34.6	H	H	**97.20%**	0.40%	2.40%	8.508147
Z013	Thorpe Thewles	182	42.3	28	25.8	41.3	30	H	H*	**92.00%**	6.00%	2.01%	7.635908
Z014	Coldharbour Farm	215	47.2	31.1	29.9	48.3	34.8	H	H	**98.08%**	0.32%	1.60%	9.833069
Z015	Coldharbour Farm	207.9	46.8	30.9	32.1	47.3	32.6	H	H	**90.47%**	1.70%	7.84%	5.024408
Z016	Coldharbour Farm	217.7	49.1	32.8	33.4	49.9	34.8	H	H*	**92.97%**	0.44%	6.60%	5.735471
Z017	Beddington Sewage Farm	190.5	43.1	30.5	27.5	42.3	30.5	H	H?	**84.70%**	6.92%	8.38%	5.119526
Z018	Beddington Sewage Farm	190.5	43	30.5	27.8	43.2	30.1	H	H?	**92.24%**	3.56%	4.21%	6.968409
Z019	Beddington Sewage Farm	213.3	42.9	28.8	27.7	42.4	31.5	H?	M?	**49.95%**	24.09%	25.96%	2.473416
Z020	Beddington Sewage Farm	198.4	42.4	30	29.1	42.9	33.2	H	H	**85.81%**	1.39%	12.81%	3.838909
Z021	East Lond RB Cemetary	216.5	48.2	32	32.2	47	32.6	H*	H?	**57.47%**	9.62%	32.91%	1.70923
Z022	Danebury	193	43.2	27.7	28	43.2	31.8	H	H*	**94.88%**	2.42%	2.71%	8.2801
Z023	Danebury	182	41.2	27.8	24.4	39.8	29.8	H	D*	**85.15%**	11.86%	3.00%	6.01879
Z024	Danebury	193	42.5	30	29.7	44	31.8	H	H	**94.95%**	0.72%	4.34%	6.684276
Z025	Danebury	197	44.4	30.6	26.9	43.5	31.2	H	H?	**89.52%**	5.89%	4.59%	6.400726
Z026	Danebury	230	40.2	33.3	25	41.6	32.5	M*	D*	32.56%	9.20%	**58.23%**	1.657041
Z027	Danebury	207	46.1	32.6	31.2	45	33.6	H*	H	**59.71%**	3.17%	37.12%	1.431386
Z028	Danebury	207	45.4	30.8	30.7	45.3	33.8	H	H	**83.54%**	1.79%	14.67%	3.4888
Z029	Danebury	221	51.4	33.9	31.8	51.5	36.2	H	H	**98.27%**	0.18%	1.55%	10.08819
Z030	Danebury	200	42.7	28.7	29.2	44.7	32.4	H	H	**97.14%**	0.59%	2.28%	8.622549
Z031	Elms Farm	205.2	44.3	31	30.8	45.9	33.9	H	H	**93.75%**	0.38%	5.87%	6.077839
Z032	Elms Farm	230	53.9	36.2	33.5	52	39.1	H	H*	**86.65%**	0.27%	13.08%	4.543127
Z033	Longthorpe II	232	52	35	37	49	37	M	M?	5.43%	1.02%	**93.55%**	6.306606
Z034	Scole-Dickleburgh	205.4	43.9	30.8	27.8	42.3	34.1	H*	H?	**64.80%**	5.43%	29.77%	1.871572

Measurements and Species Determination using DFA (Metacarpal, cont'd)

The same individuals are indicated by * (Individual 1) and ** (Individual 2); Determinations from Johnstone (2014) are highlighted in grey.

		Measurement						DFA		Probabilities			Squared
ID	Site	GL	Bp	Dp	SD	BFd	Dd	Determination		Horse	Donkey	Mule	M-Dist
Z035	Orton Hall Farm	247	54	38	39	55	41	H*	H?	**51.94%**	0.03%	48.03%	5.447434
Z036	Orton Hall Farm	210	51	37	33	46	34	M	M	9.49%	5.79%	**84.72%**	4.453132
Z037	Orton Hall Farm	238	50	36	35	52	36	H*	M*	**74.30%**	0.32%	25.38%	3.24826
Z038	Orton Hall Farm	226	50	33	35	52	39	H	H*	**96.53%**	0.02%	3.45%	9.806983
Z039	Southwark	180	40.4	24.9	26.8	42.2	30.9	H	H*	**99.27%**	0.43%	0.29%	15.71109
Z040	Wroxeter Baths basilica	216	48.7	33.6	33.9	47.5	34	M*	H?	43.87%	2.94%	**53.20%**	1.122988
Z041	Wroxeter Baths basilica	216.5	53.4	32.6	32.1	47.4	35.8	M?	H	35.73%	19.64%	**44.63%**	1.608243
Z042	Castleford	194.2	42.4	29.8	29.8	44	32.6	H	H	**95.14%**	0.48%	4.38%	6.74136
Z043	Castleford	232	45.4	34.2	34.6	51.9	35.4	H	H?	**96.93%**	0.02%	3.05%	10.60056
Z044	Castleford	216	50.9	31.8	31.5	48.3	34.4	H	H	**81.22%**	6.22%	12.56%	3.966251
Z045	Fairford	186.08	40.55	26.54	27.78	41.66	30.41	H		**95.11%**	2.30%	2.59%	8.413301
Z046	Fairford	199.13	44.07	28.26	29.42	42.62	32.25	H*		**68.61%**	10.95%	20.44%	2.866369
Z047	Winchester*	230.18	52.93	31.9	33.83	53.24	38.38	H		**98.53%**	0.09%	1.38%	10.78628
Z048	Winchester*	231.27	52.72	32.74	34.26	52.53	38.25	H		**95.08%**	0.20%	4.72%	6.942082
Z049	Winchester	217.03	47.48	28.68	29.63	44.64	34.27	H*		**51.83%**	20.82%	27.35%	2.311252
Z050	Winchester	208.09	45.75	28.89	29.79	44.69	33.66	H		**81.96%**	5.16%	12.88%	3.856591
Z051	Winchester	200.07	42.75	28.76	28.63	44.14	33.17	H		**96.52%**	0.64%	2.84%	7.92667
Z052	Healam Bridge**	233.23	54.06	31.86	33.22	49.35	35.7	M?		29.24%	25.72%	**45.04%**	2.067563
Z053	Healam Bridge	211.45	48.72	29.96	32.15	46.22	34.39	H*		**63.82%**	7.80%	28.38%	2.013501
Z054	Healam Bridge	237.65	51.39	35.08	31.77	49.76	36.51	H*		**58.38%**	3.24%	38.38%	1.360985
Z055	Healam Bridge	210.5	45.79	28.28	31.78	46.12	34.11	H		**88.59%**	1.75%	9.67%	4.4872
Z056	Healam Bridge	205.6	43.87	27.84	30.18	43.77	32.76	H		**78.56%**	5.44%	16.00%	3.316486
Z057	Alcester	201	41.62	28.93	27.62	41.19	30.51	H*		**56.40%**	19.29%	24.32%	0.901294

Appendix II.III – Measurements and Species Determination using DFA (Femur)

The same individuals are indicated by † (Individual 3); Determinations from Johnstone (2014) are highlighted in grey.

		Measurement					DFA		Probabilities			Squared
ID	Site	GL	DC	Bp	SD	Bd	Determination		Horse	Donkey	Mule	M-Dist
Z058	Thorpe Thewles	320.9	45.2	96.5	32.1	79.3	D*	D	33.46%	**59.76%**	6.78%	0.78062
Z059	East Lond RB Cemetary	396	57.3	124.7	44.6	94.5	M*	M	45.03%	1.70%	**53.27%**	0.394755
Z060	Winchester	400	55.7	111	40.1	94	H*		**50.81%**	15.26%	33.93%	0.140468
Z061	Hayton Fort	400	59	132	44	97	M*	M*	34.08%	0.92%	**65.00%**	0.199009
Z062	Healam Bridge†	372.17	52.95	112.28	37.98	87.59	H?		**48.91%**	13.42%	37.67%	0.222165
Z063	Healam Bridge	331	47.5	96.68	33.26	81.37	D*		40.90%	**50.45%**	8.65%	1.207072

Appendix II.IV – Measurements and Species Determination using DFA (Tibia)

The same individuals are indicated by ** (Individual 2), † (Individual 3), and †† (Individual 4), Determinations from Johnstone (2014) are highlighted in grey.

		Measurement					DFA		Probabilities			Squared
ID	Site	GL	SD	Bp	Bd	Dd	Determination		Horse	Donkey	Mule	M-Dist
Z064	Ilchester, Church St	351	45	99.5	77	46	H	H*	**98.17%**	0.01%	1.82%	2.17185
Z065	Chichester Cattlemarket	361.2	44.6	97	79.9	49.1	M*	H*	42.22%	4.59%	**53.20%**	0.923641
Z066	Chichester Cattlemarket	364.2	44.5	96	80.1	47.6	H*	H*	**50.84%**	3.21%	45.95%	1.000256
Z067	Thorpe Thewles	299.9	33.6	79.9	59.2	36.7	H		**90.46%**	3.22%	6.33%	0.641643
Z068	East Lond RB Cemetary	346	42.5	95.5	68.8	45.5	H*	H*	**71.59%**	0.37%	28.04%	0.623055
Z069	East Lond RB Cemetary	359	40.4	98.5	78.3	48.4	H	H*	**83.95%**	0.59%	15.47%	0.078019
Z070	Longthorpe II	332	46	86	65	41	M*		23.82%	6.06%	**70.13%**	0.365813
Z071	Orton Hall Farm	360	46	91	65	47	M		0.25%	10.18%	**89.57%**	3.752391
Z072	Orton Hall Farm	356	50	89	70	46	M		0.45%	17.87%	**81.69%**	3.066351
Z073	Orton Hall Farm	332	44	88	67	43	M*		31.17%	7.75%	**61.08%**	0.698885
Z074	Orton Hall Farm	354	46	89	67	44	M		2.57%	8.18%	**89.25%**	0.704388
Z075	Orton Hall Farm	347	45	93	69	42	H		**85.38%**	0.10%	14.53%	0.750526
Z076	Fairford	287.02	32.1	73.65	58.29	34.19	H*		**68.42%**	25.09%	6.49%	2.442324
Z077	Winchester	325.5	36.67	88.72	67.76	42.48	H		**88.40%**	1.62%	9.98%	0.125063
Z078	Winchester	324	34.87	90.81	66.21	42.18	H		**97.47%**	0.12%	2.41%	0.599483
Z079	Ribchester††	354.5	39.46	95.04	75.22	47.98	M?		43.24%	7.06%	**49.69%**	1.140511
Z080	Healam Bridge**	369.74	41.27	102.26	82.22	52.6	H*		**55.53%**	2.45%	42.03%	0.819023
Z081	Healam Bridge†	330.81	38.51	94.19	70.2	52.46	D*		2.75%	**56.54%**	40.72%	1.622006
Z082	Healam Bridge	327.87	41.28	92.86	72.64	45.85	H		**89.06%**	1.07%	9.87%	0.039514
Z083	Chaucer House	346	35	87	67	43	M*		14.57%	28.07%	**57.36%**	1.144031
Z084	Alcester	317	34.65	81.16	61.76	38.12	H*		**61.15%**	14.33%	24.52%	1.210323

Appendix II.V – Measurements and Species Determination using DFA (Metatarsal)

Determinations from Johnstone (2014) are highlighted in grey.

		Measurement						DFA		Probabilities			Squared
ID	Site	GL	Bp	Dp	SD	BFd	Dd	Determination		Horse	Donkey	Mule	M-Dist
Z085	Lutton/Huntingdon	286	52	45.4	35.3	54.1	40.9	H*	H?	**66.10%**	0.02%	33.88%	2.734818
Z086	Lutton/Huntingdon	272	49	44	30.9	50	37.6	H*	H?	**70.72%**	0.11%	29.17%	1.005038
Z087	Lutton/Huntingdon	254	47	41.7	28.3	47.1	35.7	H	H	**86.57%**	0.27%	13.16%	0.186334
Z088	Ilchester, Church St	256.5	43.2	42.2	34.1	52.2	27.8	H	H*	**99.68%**	0.00%	0.32%	16.12192
Z089	Chichester Cattlemarket	281.9	52	46	34.3	52.7	40.4	H*	H*	**57.63%**	0.06%	42.32%	2.087851
Z090	Chichester Cattlemarket	282.1	52.8	48.4	34.3	52.8	40.4	H*	H*	**53.25%**	0.04%	46.71%	2.763082
Z091	Thorpe Thewles	242	46.4	42.8	27.2	47.2	36.6	H	H*	**95.94%**	0.03%	4.03%	1.545844
Z092	Thorpe Thewles	242	42.1	38.9	25.4	43.3	35.3	H*	M*	**64.70%**	2.00%	33.30%	0.260551
Z093	Beddington Sewage Farm	245	44.6	40	27.6	43.1	35.3	M*	H?	37.72%	8.59%	**53.70%**	0.786046
Z094	East Lond RB Cemetary	270.9	50.8	43.8	30.7	51.2	39.7	H	H*	**86.06%**	0.07%	13.87%	0.818727
Z095	Danebury	242	45.7	36.7	28.2	44.2	35.2	H*	H	**75.16%**	7.59%	17.25%	0.654011
Z096	Danebury	229	42	34.5	24.8	41.6	31.6	H	H	**88.87%**	4.81%	6.32%	1.249431
Z097	Danebury	251	47.8	40.8	28.5	45.1	35.2	H*	H	**66.37%**	4.89%	28.74%	0.41046
Z098	Danebury	251.5	46.4	39.8	31.1	45.7	35.8	H*	H	**52.70%**	2.83%	44.48%	0.639977
Z099	Elms Farm	269	53.4	45.3	30.9	52.3	40	H	H*	**95.41%**	0.03%	4.57%	1.683107
Z100	Elms Farm	256	44.9	40.5	31.1	45.8	33.8	M?	H	49.15%	0.95%	**49.90%**	0.80975
Z101	Longthorpe II	224	40	31	27	40	30	H*	H	**64.70%**	24.28%	11.03%	1.943238
Z102	Longthorpe II	223	40	32	26	40	30	H*	H*	**75.26%**	15.20%	9.54%	1.635859
Z103	Longthorpe II	251	50	41	29	46	35	H	H	**83.30%**	3.54%	13.16%	0.385191
Z104	Scole-Dickleburgh	267.9	48.1	41.2	30.2	45.3	36.7	M*	M	10.76%	13.57%	**75.67%**	0.623907
Z105	Orton Hall Farm	236	42	39	27	44	32	H	H	**91.30%**	0.20%	8.51%	0.370603
Z106	Orton Hall Farm	258	46	39	27	43	34	M?	M	19.05%	32.07%	**48.89%**	1.447461
Z107	Orton Hall Farm	252	45	37	28	44	34	H*	H*	**53.23%**	11.86%	34.91%	1.036234

Measurements and Species Determination using DFA (Metatarsal, cont'd)

The same individuals are indicated by ** (Individual 2), † (Individual 3), and †† (Individual 4), and ‡ (Individual 5).

		Measurement						DFA		Probabilities			Squared
ID	Site	GL	Bp	Dp	SD	BFd	Dd	Determination		Horse	Donkey	Mule	M-Dist
Z108	Orton Hall Farm	276	50	46	32	50	38	M*	H?	44.74%	0.16%	**55.10%**	1.43086
Z109	Orton Hall Farm	215	47	31	30	47	35	H		**99.91%**	0.04%	0.05%	12.06057
Z110	Wroxeter Baths basilica	265	50.1	49.3	30.4	49.4	37.2	H*	H	**69.05%**	0.04%	30.91%	1.955357
Z111	Wroxeter Baths basilica	250.4	45.9	43.3	30.1	45.3	33.1	H*	H	**61.01%**	0.60%	38.40%	0.503229
Z112	Castleford	252	44.9	39.1	27.3	43.2	34.6	M*	M*	30.90%	14.83%	**54.26%**	0.939111
Z113	Fairford	266.15	48.99	41.65	31.01	46.71	35.52	M*		39.14%	4.44%	**56.42%**	0.5407
Z114	Winchester	232.34	44.54	35.98	27.09	42.94	34.29	H		**82.12%**	7.23%	10.66%	0.939121
Z115	Winchester	265	49.2	42.7	28	46.37	36.59	H?		**48.58%**	4.59%	46.83%	0.859308
Z116	Winchester	241	42.8	37.3	26.22	43.64	34.36	H*		**79.19%**	2.14%	18.68%	0.095547
Z117	Winchester‡	251.51	45.06	39.98	27.85	43.94	37.09	M*		26.32%	8.71%	**64.97%**	0.438364
Z118	Ribchester	238.63	43.9	38.5	25.21	43.29	32.46	H		**89.69%**	1.44%	8.87%	0.336066
Z119	Ribchester††	260.55	47.9	42.96	31.02	45.65	33.71	M*		36.74%	2.81%	**60.45%**	0.363578
Z120	Ribchester††	263.14	48.15	43.44	32.27	45.29	35.07	M		11.65%	4.81%	**83.54%**	0.171234
Z121	Ribchester	231.43	41.48	37.78	23.7	41.81	31.67	H		**89.64%**	1.40%	8.96%	0.32023
Z122	Healam Bridge**	275.95	51.66	42.64	32.5	47.6	37.57	M*		15.86%	10.47%	**73.67%**	0.39826
Z123	Healam Bridge**	276.79	52.34	42.93	32.33	49.17	37.64	M*		44.52%	3.27%	**52.21%**	0.657546
Z124	Healam Bridge	238.26	43.28	37.76	24.89	42.63	32.74	H		**83.09%**	3.42%	13.49%	0.355601
Z125	Healam Bridge	242.96	46.9	37.67	27.71	45.92	33.13	H		**97.18%**	0.40%	2.42%	1.602662
Z126	Healam Bridge†	267.66	54.6	44.99	27.58	49.03	38.07	H		**89.62%**	1.29%	9.10%	0.288491

Appendix II.VI – Measurements and Species Determination using DFA (PH1)

		Measurement						DFA	Probabilities			Squared
ID	Site	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule	M-Dist
Z127	Thorpe Thewles	76.1	47	31.1	31.8	39.5	21.8	H*	**55.25%**	5.85%	38.90%	1.273212
Z128	Thorpe Thewles	79.1	53	31.8	35.6	41.6	23.4	H*	**77.50%**	0.14%	22.36%	0.025
Z129	Thorpe Thewles	68.3	47.1	28.2	31.8	37.8	21.5	H	**92.42%**	0.31%	7.27%	0.632184
Z130	Elms Farm	86	58.7	40.1	33	47.2	25.5	H	**93.16%**	0.00%	6.84%	1.377536
Z131	Elms Farm	87.8	56.5	37.3	36.2	47	26.1	H*	**65.65%**	0.03%	34.33%	0.721158
Z132	Elms Farm	87.1	57.3	36.7	35.1	47.8	26.5	H	**80.03%**	0.01%	19.96%	0.795843
Z133	Elms Farm	83.2	56.1	39.8	34.3	45.9	25.6	H	**89.99%**	0.01%	10.00%	0.992092
Z134	Elms Farm	83	56.8	39.4	33.9	46.1	25.8	H	**92.52%**	0.00%	7.47%	1.353244
Z135	Elms Farm	72	49.9	31.6	32.4	45.5	22.6	H	**99.17%**	0.00%	0.83%	4.615456
Z136	Elms Farm	76.9	49.9	32.8	31.6	37.9	21.7	H*	**58.72%**	5.52%	35.76%	1.176786
Z137	Elms Farm	85	57.8	37.7	35.7	45.8	24.5	H	**89.54%**	0.01%	10.46%	0.924466
Z138	Elms Farm	75.1	47.9	30	33.3	41.7	20.5	H	**88.25%**	0.33%	11.43%	0.249094
Z139	Elms Farm	70.9	48.3	32.2	29.2	40.4	21.9	H	**96.03%**	0.11%	3.86%	1.188014
Z140	Elms Farm	69.3	48.7	33.2	28.9	38	20.8	H	**96.64%**	0.17%	3.20%	1.597192
Z141	Tort Hill West	77.5	50.5	35.3	31.4	39	22.1	H*	**69.70%**	2.08%	28.21%	0.567604
Z142	Tort Hill West	68.9	47.3	33.6	29.4	37.3	20.8	H	**94.06%**	0.43%	5.51%	1.092902
Z143	Norman Cross	75.4	49.8	34.9	31.3	39.8	22.2	H	**84.28%**	0.54%	15.18%	0.208404
Z144	Scole-Dickleburgh	87.5	52.8	36.5	33.4	46.3	24.3	H?	**49.76%**	0.50%	49.74%	0.724332
Z145	Scole-Dickleburgh	83.4	53.2	39.2	33.7	43.4	24.9	H*	**61.66%**	0.24%	38.10%	0.322773
Z146	Scole-Dickleburgh	80.7	53.7	36	33.4	44.7	24.1	H	**90.07%**	0.02%	9.90%	0.421758
Z147	Scole-Dickleburgh	78.2	49.2	32.7	32.4	43.3	21.8	H	**84.88%**	0.29%	14.83%	0.089646
Z148	Scole-Dickleburgh	76.8	52.1	36.4	31.6	42.3	24.2	H	**91.22%**	0.05%	8.73%	0.3319
Z149	Fairford	70.8	45.95	32.41	26.4	35.58	19.55	H*	**66.32%**	19.93%	13.75%	2.567935
Z150	Winchester	70.76	46.85	34.91	28.86	37.87	22.16	H	**86.36%**	1.24%	12.40%	0.644401

Measurements and Species Determination using DFA (PH1, cont'd)

The same individuals are indicated by †† (Individual 4), and ‡ (Individual 5).

		Measurement						DFA	Probabilities			Squared
ID	Site	GL	Bp	Dp	SD	BFd	Dd	Determination	Horse	Donkey	Mule	M-Dist
Z151	Winchester	70.81	48.28	35.22	29.12	38.12	22.67	H	**90.63%**	0.45%	8.92%	0.534278
Z152	Winchester	69.77	43	29.22	28.39	36.66	20.56	H*	**53.61%**	23.27%	23.12%	2.407479
Z153	Winchester	69.98	47.33	33.93	29.3	37.93	22.22	H	**90.39%**	0.58%	9.03%	0.615678
Z154	Winchester	68.49	50.56	34.88	30.98	38.66	22.96	H	**97.93%**	0.01%	2.06%	2.104484
Z155	Ribchester††	78.54	56.43	37.89	32.93	40.71	24.1	H	**92.28%**	0.02%	7.70%	0.525812
Z156	Ribchester††	78.86	57.09	37.58	32.82	39.96	24.19	H	**90.50%**	0.04%	9.46%	0.313238
Z157	Winchester	76.83	49.3	32.81	30.27	40.56	22.55	H*	**75.32%**	1.61%	23.07%	0.45483
Z158	Winchester	82.71	53.99	37.14	32.48	41.14	24.71	H*	**53.66%**	0.90%	45.44%	0.647928
Z159	Winchester	78.96	51.81	33.03	33.89	42.83	24.27	H*	**78.71%**	0.13%	21.16%	0.019064
Z160	Winchester	81.78	48.69	33.07	31.23	44.24	23.11	H*	**57.47%**	1.93%	40.60%	0.732727
Z161	Winchester	90.72	59.93	41.6	35.56	45.34	27.25	M*	49.04%	0.05%	**50.91%**	1.066275
Z162	Winchester	85.5	58.19	39.07	37.76	47.22	26.67	H	**87.27%**	0.00%	12.73%	2.001927
Z163	Winchester	93.99	55.44	39.02	35.51	45.73	23.89	M	15.66%	1.59%	**82.75%**	0.143628
Z164	Winchester	81.14	51.35	34.08	34.13	42.35	22.74	H*	**65.63%**	0.60%	33.77%	0.265548
Z165	Ribchester	81.51	53.52	33.5	32.94	39.76	22.59	H*	**56.99%**	2.11%	40.90%	0.774442
Z166	Winchester	78.4	51.23	33.16	32.9	40.36	22.69	H*	**71.19%**	0.87%	27.95%	0.255009
Z167	Winchester	78.31	53.48	36.46	32.46	41.42	25	H	**83.25%**	0.09%	16.66%	0.035037
Z168	Winchester‡	79.15	51.22	36.67	29.38	40	22.92	H*	**68.85%**	2.47%	28.68%	0.649459
Z169	Winchester	80.63	53.56	35.1	34.78	41.32	22.74	H*	**76.07%**	0.23%	23.71%	0.025953

Appendix II.VII – Measurements and Species Determination by the Davis Method (PH1)

Entries highlighted in grey are also determined by DFA (See outcomes in Appendix II.VI).

		Measurement				Species	M-Dist. to Species Centroid		
ID	Site	GL	BFd	BFd/GL x 100	SD	Determination	Horse	Donkey	Mule
Z127	Thorpe Thewles	76.1	39.5	51.91	31.8	H*	**0.731553**	2.631333	2.157505
Z128	Thorpe Thewles	79.1	41.6	52.59	35.6	H	**0.442348**	3.918805	1.828156
Z129	Thorpe Thewles	68.3	37.8	55.34	31.8	H*	**0.722001**	3.987863	3.249362
Z130	Elms Farm	86	47.2	54.88	33	H	**0.590415**	4.048865	2.978248
Z131	Elms Farm	87.8	47	53.53	36.2	H*	**0.72364**	4.231654	2.121314
Z132	Elms Farm	87.1	47.8	54.88	35.1	H*	**0.870781**	4.366058	2.736257
Z133	Elms Farm	83.2	45.9	55.17	34.3	H*	**0.835614**	4.313488	2.919486
Z134	Elms Farm	83	46.1	55.54	33.9	H*	**0.912699**	4.343574	3.078643
Z135	Elms Farm	72	45.5	63.19	32.4	H?	**3.38822**	5.844258	4.744332
Z136	Elms Farm	76.9	37.9	49.28	31.6	M	1.627559	2.359391	**1.32245**
Z137	Elms Farm	85	45.8	53.88	35.7	H*	**0.692229**	4.230476	2.314613
Z138	Elms Farm	75.1	41.7	55.53	33.3	H*	**0.840787**	4.25224	3.138096
Z139	Elms Farm	70.9	40.4	56.98	29.2	H*	**1.313197**	4.069148	3.90471
Z140	Elms Farm	69.3	38	54.83	28.9	H*	**1.024132**	3.431371	3.438069
Z141	Tort Hill West	77.5	39	50.32	31.4	H*	**1.31433**	2.582395	1.687083
Z142	Tort Hill West	68.9	37.3	54.14	29.4	H*	**0.914374**	3.303146	3.196777
Z143	Norman Cross	75.4	39.8	52.79	31.3	H	**0.614392**	3.227164	2.533091
Z144	Scole-Dickleburgh	87.5	46.3	52.91	33.4	H	**0.092441**	3.618663	2.266294
Z145	Scole-Dickleburgh	83.4	43.4	52.04	33.7	H	**0.364762**	3.453292	1.894884
Z146	Scole-Dickleburgh	80.7	44.7	55.39	33.4	H*	**0.802211**	4.233722	3.086963
Z147	Scole-Dickleburgh	78.2	43.3	55.37	32.4	H*	**0.731209**	4.082259	3.190908
Z148	Scole-Dickleburgh	76.8	42.3	55.08	31.6	H*	**0.654502**	3.889286	3.196902
Z149	Fairford	70.8	35.58	50.25	26.4	D*	2.356756	**1.628109**	2.593225

Measurements and Species Determination by the Davis Method (PH1, cont'd)

The same individuals are indicated by ** (Individual 2), † (Individual 3), †† (Individual 4), and ‡ (Individual 5); Entries highlighted in grey are also determined by DFA (See outcomes in Appendix II.VI).

		Measurement				Species	M-Dist. to Species Centroid		
ID	Site	GL	BFd	BFd/GL x 100	SD	Determination	Horse	Donkey	Mule
Z150	Winchester	70.76	37.87	53.52	28.86	H*	**1.090273**	3.041803	3.097046
Z151	Winchester	70.81	38.12	53.83	29.12	H*	**0.996642**	3.173702	3.149646
Z152	Winchester	69.77	36.66	52.54	28.39	H*	**1.361941**	2.676432	2.891352
Z153	Winchester	69.98	37.93	54.20	29.3	H*	**0.934905**	3.306911	3.2266
Z154	Winchester	68.49	38.66	56.45	30.98	H*	**1.072369**	4.15866	3.621174
Z155	Ribchester††	78.54	40.71	51.83	32.93	H	**0.540754**	3.263024	1.943757
Z156	Ribchester††	78.86	39.96	50.67	32.82	H*	**0.962025**	2.950014	1.533382
Z157	Winchester	76.83	40.56	52.79	30.27	H*	**0.861487**	3.055971	2.688232
Z158	Winchester	82.71	41.14	49.74	32.48	M	1.336374	2.652996	**1.274811**
Z159	Winchester	78.96	42.83	54.24	33.89	H	**0.450684**	4.027889	2.664727
Z160	Winchester	81.78	44.24	54.10	31.23	H	**0.522315**	3.571862	2.954801
Z161	Winchester	90.72	45.34	49.98	35.56	M	0.992311	3.326952	**0.731671**
Z162	Winchester	85.5	47.22	55.23	37.76	H*	**1.517894**	4.83708	2.582221
Z163	Winchester	93.99	45.73	48.65	35.51	M	1.430823	3.043742	**0.292437**
Z164	Winchester	81.14	42.35	52.19	34.13	H	**0.287052**	3.568014	1.886763
Z165	Ribchester	81.51	39.76	48.78	32.94	M	1.609165	2.526189	**0.894037**
Z166	Winchester	78.4	40.36	51.48	32.9	H*	**0.668077**	3.167857	1.817737
Z167	Winchester	78.31	41.42	52.89	32.46	H	**0.312775**	3.452867	2.396607
Z168	Winchester‡	79.15	40	50.54	29.38	H*	**1.642869**	2.249362	2.139363
Z169	Winchester	80.63	41.32	51.25	34.78	H	**0.588992**	3.461304	1.402936
Z170	Healam Bridge**	90.7	42.97	47.38	32.32	M	2.174546	2.099375	**0.882473**
Z171	Healam Bridge**	91.2	42.95	47.09	31.26	M	2.417317	1.803436	**1.073944**

Measurements and Species Determination by the Davis Method (PH1, cont'd)

The same individuals are indicated by † (Individual 3).

		Measurement				Species	M-Dist. to Species Centroid		
ID	Site	GL	BFd	BFd/GL x 100	SD	Determination	Horse	Donkey	Mule
Z172	Healam Bridge†	80.01	41.74	52.17	32.44	H	**0.519444**	3.261026	2.145511
Z173	Healam Bridge†	81.12	42.41	52.28	32.78	H	**0.416912**	3.350262	2.131487
Z174	Healam Bridge	73.47	39.55	53.83	30.69	H	**0.632438**	3.414962	2.945509
Z175	Healam Bridge	76.13	40.33	52.98	33.34	H	**0.086291**	3.62373	2.296917
Z176	Healam Bridge	72.61	40.74	56.11	31.73	H*	**0.961688**	4.174185	3.462774
Z177	Winchester	86.35	47.06	54.50	38.75	H*	**1.547077**	4.83409	2.228519
Z178	Winchester	86.43	46.91	54.28	38.67	H*	**1.475317**	4.777073	2.15075
Z179	Winchester	86.64	45.56	52.59	35.71	H	**0.467223**	3.936296	1.810559
Z180	Healam Bridge	94.31	45.08	47.80	33.46	M	1.889626	2.436105	**0.668588**
Z181	Healam Bridge	84.48	41.23	48.80	32.63	M	1.640701	2.465365	**0.969148**
Z182	Healam Bridge	83.64	42.92	51.32	35.31	H	**0.583058**	3.575437	1.344206
Z183	Healam Bridge	78.58	40.83	51.96	31.08	H*	**0.870862**	2.963122	2.294787
Z184	Healam Bridge	77.21	41.36	53.57	31.78	H	**0.393828**	3.517765	2.718211
Z185	Healam Bridge	80.71	42.29	52.40	33.36	H	**0.277109**	3.482171	2.083389
Z186	Healam Bridge	82.04	44.41	54.13	37.91	H*	**1.264895**	4.631908	2.16626
Z187	Healam Bridge	82.05	42.82	52.19	35.67	H	**0.464908**	3.838841	1.653834
Z188	Healam Bridge	80.53	46.12	57.27	35.37	H*	**1.723516**	4.941717	3.43295
Z189	Healam Bridge	79.1	39.46	49.89	29.88	H*	**1.738508**	2.162459	1.85151
Z190	Hayton Fort	72	42.5	59.03	30	H*	**1.880242**	4.689778	4.241689
Z191	Hayton Fort	71	41.5	58.45	30	H*	**1.698806**	4.546887	4.135357
Z192	Haddon	76.4	41.2	53.93	32.1	H	**0.350302**	3.663948	2.78985
Z193	Haddon	88.7	46.8	52.76	37.5	H*	**0.908806**	4.278356	1.661435
Z194	Haddon	83.7	41.3	49.34	34.7	M	1.23763	3.017908	**0.661879**

Measurements and Species Determination by the Davis Method (PH1, cont'd)

		Measurement				Species	M-Dist. to Species Centroid		
ID	Site	GL	BFd	BFd/GL x 100	SD	Determination	Horse	Donkey	Mule
Z195	Haddon	75.3	42.1	55.91	31.4	H*	**0.901564**	4.077275	3.444598
Z196	Haddon	74.1	39.6	53.44	30.5	H*	**0.704756**	3.276359	2.854002
Z197	Wroxeter Baths basilica	80.3	46	57.29	35.5	H*	**1.748494**	4.961901	3.42584
Z198	Newstead fort	70	40.9	58.43	30.6	H*	**1.696895**	4.611865	4.086898
Z199	Thorley	84.26	43.88	52.08	36.34	H	**0.604203**	3.931708	1.514651
Z200	Chichester Cattlemarket	93.4	48.2	51.61	37.7	H*	**0.900039**	4.07046	1.145015
Z201	Chichester Cattlemarket	93.4	47.8	51.18	38.3	M	1.039667	4.089777	**0.902794**
Z202	Chichester Cattlemarket	90.6	47.2	52.10	35.3	H	**0.41013**	3.75281	1.670385
Z203	La Sagesse	80.3	45.3	56.41	32.9	H*	**1.119817**	4.412024	3.427857
Z204	Winchester Palace	73	43.2	59.18	30.3	H?	**1.933239**	4.760101	4.248255
Z205	E London RB cemetery	81.2	45.1	55.54	34.3	H*	**0.966439**	4.401797	3.036017
Z206	E London RB cemetery	81	46.3	57.16	34.6	H*	**1.573759**	4.816086	3.469997
Z207	E London RB cemetery	85.5	47	54.97	35.2	H*	**0.919195**	4.402186	2.755691
Z208	E London RB cemetery	85.3	46.7	54.75	35.3	H*	**0.865674**	4.366141	2.669355
Z209	Elms Farm	81.5	48.7	59.75	35.4	H?	**2.569655**	5.466596	4.021734
Z210	Elms Farm	84.1	42.8	50.89	32.7	H	**0.903267**	2.981813	1.636506
Z211	Elms Farm	77	40	51.95	31.2	H	**0.847708**	2.98129	2.27116
Z212	Tort Hill West	82.6	42.3	51.21	30.1	H	**1.295877**	2.576695	2.217328
Z213	Scole-Dickleburgh	90.9	48.6	53.47	36.6	H	**0.805658**	4.28208	2.048328
Z214	Scole-Dickleburgh	77.5	42.7	55.10	32	H	**0.642798**	3.953282	3.15678
Z215	Market Deeping	74.4	38.9	52.28	30.5	H	**0.91823**	2.95179	2.493934
Z216	Market Deeping	75	39.3	52.40	29.6	H	**1.1036**	2.831449	2.668954

Appendix III.I – Species Determinations by Site Types (Urban)

Entries highlighted in grey are specimens from element with low accuracy (i.e. femur), contain possible error, low probability (i.e. "possible" identifications), or from other time period (i.e. Iron Age) and thus not included in interpretation. Entries are sorted by site name.

Bone ID	Site	Context	Element	Det.	Note
Z017	Beddington Sewage Farm		MC	H	
Z018	Beddington Sewage Farm		MC	H	
Z019	Beddington Sewage Farm		MC	H?	
Z020	Beddington Sewage Farm		MC	H	
Z093	Beddington Sewage Farm		MT	M*	
Z011	Chichester Cattlemarket		MC	M*	
Z065	Chichester Cattlemarket		Tibia	M*	
Z066	Chichester Cattlemarket		Tibia	H*	
Z089	Chichester Cattlemarket		MT	H*	
Z090	Chichester Cattlemarket		MT	H*	
Z200	Chichester Cattlemarket		PH1	H*	
Z201	Chichester Cattlemarket		PH1	M	
Z202	Chichester Cattlemarket		PH1	H	
Z064	Ilchester, Church St		Tibia	H	
Z088	Ilchester, Church St		MT	H	SD-Dd error?
Z001	Winchester	GR594 Sk. 682	Radius	D*	Individual 1
Z002	Winchester	GR594 Sk. 682	Radius	H*	Individual 1
Z047	Winchester	GR594 Sk. 682	MC	H	Individual 1
Z048	Winchester	GR594 Sk. 682	MC	H	Individual 1
Z049	Winchester	SXS79- 879	MC	H*	
Z050	Winchester	VR77-XII-2586	MC	H	
Z051	Winchester	HA72-II-21	MC	H	
Z060	Winchester	Victoria Road	Femur	H*	
Z077	Winchester	VR79 Ph. 152	Tibia	H	
Z078	Winchester	NR75 Ph. 24-II	Tibia	H	
Z114	Winchester	VR78-XIV-3838	MT	H	
Z115	Winchester	HA74- XI-257	MT	H?	
Z116	Winchester	HA74- XI-373	MT	H*	
Z117	Winchester	NR75-II-561	MT	M*	Individual 5
Z150	Winchester	VR77 Ph. 73	PH1	H	
Z151	Winchester	VR78 Ph. 51	PH1	H	
Z152	Winchester	VR75 Ph. 276	PH1	H*	
Z153	Winchester	VR75 Ph. 276	PH1	H	
Z154	Winchester	HA74 Ph. 65	PH1	H	
Z157	Winchester	VR78 Ph. 51-X	PH1	H*	
Z158	Winchester	VR77 Ph. 913	PH1	H?	
Z159	Winchester	VR77 Ph. 202	PH1	H*	

Species Determinations by Site Types (Urban, cont'd)

Bone ID	Site	Context	Element	Det.	Note
Z160	Winchester	VR77 Ph. 206	PH1	H*	
Z161	Winchester	VR77 Ph. 206	PH1	M*	
Z162	Winchester	HA72 Ph. 7 TR I	PH1	H	
Z163	Winchester	HA72 Ph. 2 TR I	PH1	M	
Z164	Winchester	HA74 Ph. 76	PH1	H*	
Z166	Winchester	NR75-477	PH1	H*	
Z167	Winchester	VR74-449	PH1	H	
Z168	Winchester	NR75-561	PH1	H*	Individual 5
Z169	Winchester	HA74-401	PH1	H*	
Z177	Winchester	GR594 Sk. 682	PH1	H*	Individual 1
Z178	Winchester	GR594 Sk. 682	PH1	H*	Individual 1
Z179	Winchester	VR72 Ph. 6-II-79	PH1	H	
Z040	Wroxeter Baths basilica		MC	M*	
Z041	Wroxeter Baths basilica		MC	M?	
Z110	Wroxeter Baths basilica		MT	H*	
Z111	Wroxeter Baths basilica		MT	H*	
Z197	Wroxeter Baths basilica		PH1	H*	

Appendix III.II – Species Determinations by Site Types (Military)

Entries highlighted in grey are specimens from element with low accuracy (i.e. femur), contain possible error, low probability (i.e. "possible" identifications), or from other time period (i.e. Iron Age) and thus not included in interpretation. Entries are sorted by site name.

Bone ID	Site	Context	Element	Det.	Note
Z042	Castleford		MC	H	
Z043	Castleford		MC	H	
Z044	Castleford		MC	H	
Z112	Castleford		MT	M*	
Z061	Hayton Fort		Femur	M*	
Z190	Hayton Fort		PH1	H*	
Z191	Hayton Fort		PH1	H*	
Z033	Longthorpe II		MC	M	
Z070	Longthorpe II		Tibia	M*	
Z101	Longthorpe II		MT	H*	
Z102	Longthorpe II		MT	H*	
Z103	Longthorpe II		MT	H	
Z198	Newstead fort		PH1	H*	
Z003	Ribchester	RB89 209 B22	Radius	H	
Z079	Ribchester	RB89 733-3663	Tibia	M?	Individual 4
Z118	Ribchester	RB 100-1249	MT	H	
Z119	Ribchester	RB89 733-3663	MT	M*	Individual 4
Z120	Ribchester	RB89 733-3663	MT	M	Individual 4
Z121	Ribchester	RB89 124-7370	MT	H	
Z155	Ribchester	RB89 3663-733	PH1	H	Individual 4
Z156	Ribchester	RB89 3663-733	PH1	H	Individual 4
Z165	Ribchester	RB89 782 B13	PH1	M	

Appendix III. III – Species Determinations by Site Types (Rural)

Entries highlighted in grey are specimens from element with low accuracy (i.e. femur), contain possible error, low probability (i.e. "possible" identifications), or from other time period (i.e. Iron Age) and thus not included in interpretation. Entries are sorted by site name.

Bone ID	Site	Context	Element	Det.	Note
Z045	Fairford	FTF89 3019/4/3	MC	H	
Z046	Fairford	FTF86 201/C	MC	H*	
Z076	Fairford	FTF88 2396/c	Tibia	H*	
Z113	Fairford	FTF88 2391/A	MT	M*	
Z149	Fairford	FTF88 703/A	PH1	D*	
Z004	Healam Bridge	7613	Radius	H*	Individual 2
Z005	Healam Bridge	5069	Radius	H*	
Z006	Healam Bridge	5069	Radius	M	
Z007	Healam Bridge	2461	Radius	H*	
Z008	Healam Bridge	7306	Radius	H	
Z009	Healam Bridge	5239	Radius	H	
Z010	Healam Bridge	5028	Radius	M*	
Z052	Healam Bridge	7613	MC	M?	Individual 2
Z053	Healam Bridge	5069	MC	H*	
Z054	Healam Bridge	5069	MC	H*	
Z055	Healam Bridge	7130	MC	H	
Z056	Healam Bridge	5561	MC	H	
Z062	Healam Bridge	7294	Femur	H?	Individual 3
Z063	Healam Bridge	6973	Femur	D*	
Z080	Healam Bridge	7613	Tibia	H*	Individual 2
Z081	Healam Bridge	7294	Tibia	D*	Individual 3
Z082	Healam Bridge	5045	Tibia	H	
Z122	Healam Bridge	7613	MT	M*	Individual 2
Z123	Healam Bridge	7613	MT	M*	Individual 2
Z124	Healam Bridge	5069	MT	H	
Z125	Healam Bridge	5027	MT	H	
Z126	Healam Bridge	7924	MT	H	Individual 3
Z170	Healam Bridge	7613	PH1	M	Individual 2
Z171	Healam Bridge	7613	PH1	M	Individual 2
Z172	Healam Bridge	7294	PH1	H	Individual 3
Z173	Healam Bridge	7294	PH1	H	Individual 3
Z174	Healam Bridge	2850	PH1	H	
Z175	Healam Bridge	2837	PH1	H	
Z176	Healam Bridge	5042	PH1	H*	
Z180	Healam Bridge	7613	PH1	M	Individual 2
Z181	Healam Bridge	5002	PH1	M	
Z182	Healam Bridge	6813	PH1	H	

Species Determinations by Site Types (Rural, cont'd)

Bone ID	Site	Context	Element	Det.	Note
Z183	Healam Bridge	5031	PH1	H*	
Z184	Healam Bridge	5042	PH1	H	
Z185	Healam Bridge	5045	PH1	H	
Z186	Healam Bridge	5251	PH1	H*	
Z187	Healam Bridge	5028	PH1	H	
Z188	Healam Bridge	5028	PH1	H*	
Z189	Healam Bridge	5561	PH1	H*	
Z085	Lutton/Huntingdon		MT	H*	
Z086	Lutton/Huntingdon		MT	H*	
Z087	Lutton/Huntingdon		MT	H	
Z143	Norman Cross		PH1	H	
Z199	Thorley		PH1	H	
Z012	Thorpe Thewles		MC	H	
Z013	Thorpe Thewles		MC	H	
Z091	Thorpe Thewles		MT	H	
Z127	Thorpe Thewles		PH1	H*	
Z128	Thorpe Thewles		PH1	H*	
Z141	Tort Hill West		PH1	H*	
Z142	Tort Hill West		PH1	H	
Z212	Tort Hill West		PH1	H	

Appendix III.IV – Species Determinations by Site Types (Small Town)

Entries highlighted in grey are specimens from element with low accuracy (i.e. femur), contain possible error, low probability (i.e. "possible" identifications), or from other time period (i.e. Iron Age) and thus not included in interpretation. Entries are sorted by site name.

Bone ID	Site	Context	Element	Det.	Note
Z057	Alcester	ALC-7048	MC	H*	
Z084	Alcester	ALC01176	Tibia	H*	
Z083	Chaucer House	ABMAP10840	Tibia	M*	
Z031	Elms Farm		MC	H	
Z032	Elms Farm		MC	H	
Z099	Elms Farm		MT	H	
Z100	Elms Farm		MT	M?	
Z130	Elms Farm		PH1	H	
Z131	Elms Farm		PH1	H*	
Z132	Elms Farm		PH1	H	
Z133	Elms Farm		PH1	H	
Z134	Elms Farm		PH1	H	
Z135	Elms Farm		PH1	H	
Z136	Elms Farm		PH1	H?	
Z137	Elms Farm		PH1	H	
Z138	Elms Farm		PH1	H	
Z139	Elms Farm		PH1	H	
Z140	Elms Farm		PH1	H	
Z209	Elms Farm		PH1	H	
Z210	Elms Farm		PH1	H	
Z211	Elms Farm		PH1	H	
Z034	Scole-Dickleburgh		MC	H*	
Z104	Scole-Dickleburgh		MT	M*	
Z144	Scole-Dickleburgh		PH1	H?	
Z145	Scole-Dickleburgh		PH1	H*	
Z146	Scole-Dickleburgh		PH1	H	
Z147	Scole-Dickleburgh		PH1	H	
Z148	Scole-Dickleburgh		PH1	H	
Z213	Scole-Dickleburgh		PH1	H	
Z214	Scole-Dickleburgh		PH1	H	
Z039	Southwark		MC	H	Bendrey, 1999

Appendix III.V – Species Determinations by Site Types (Others)

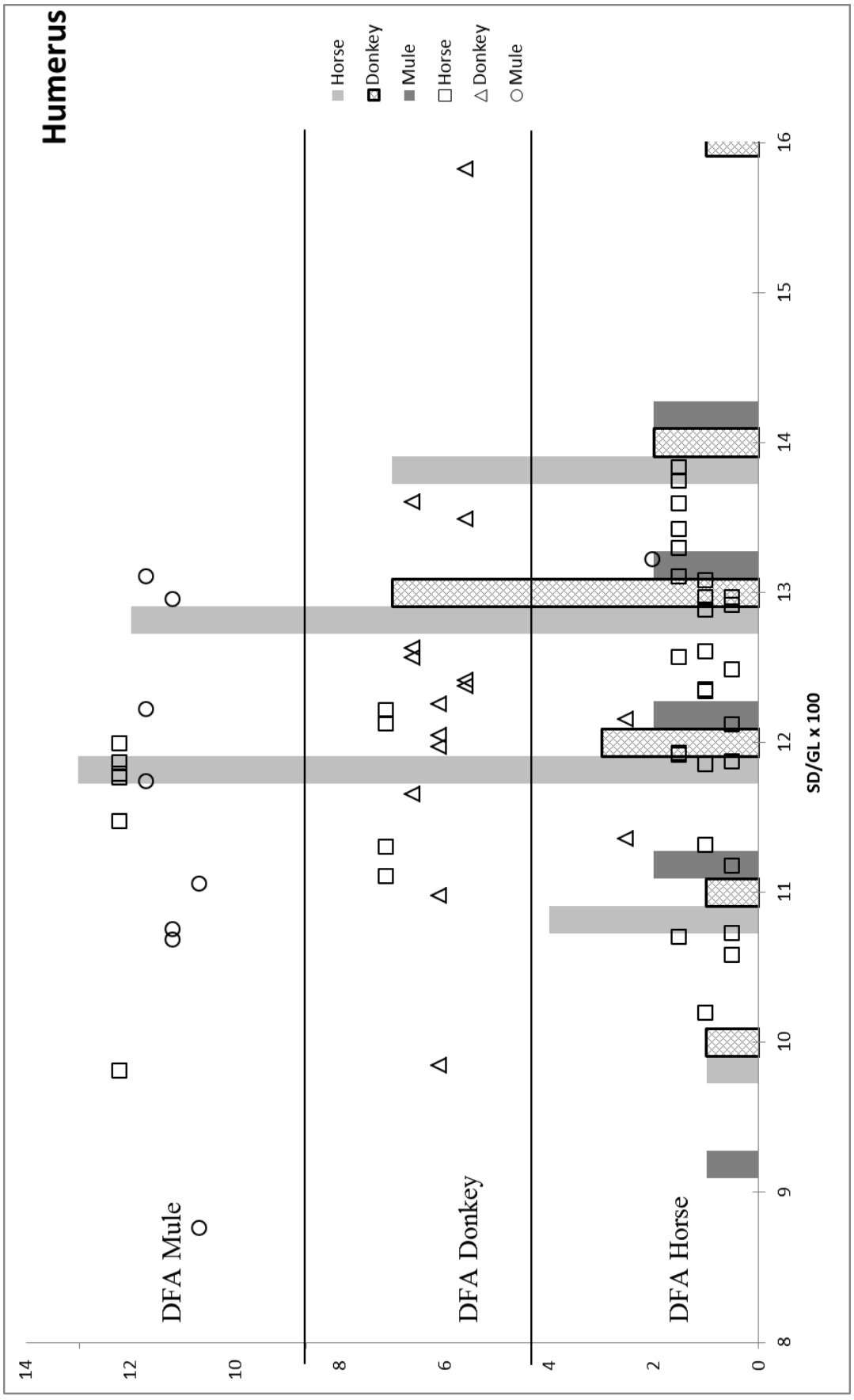
Entries highlighted in grey are specimens from element with low accuracy (i.e. femur), contain possible error, low probability (i.e. "possible" identifications), or from other time period (i.e. Iron Age) and thus not included in interpretation. Entries are sorted by site name.

Bone ID	Site	Context	Element	Det.	Note
Z021	E London RB cemetery		MC	H*	Cemetary
Z059	E London RB cemetery		Femur	M*	Cemetary
Z068	E London RB cemetery		Tibia	H*	Cemetary
Z069	E London RB cemetery		Tibia	H	Cemetary
Z094	E London RB cemetery		MT	H	Cemetary
Z205	E London RB cemetery		PH1	H*	Cemetary
Z206	E London RB cemetery		PH1	H*	Cemetary
Z207	E London RB cemetery		PH1	H*	Cemetary
Z208	E London RB cemetery		PH1	H*	Cemetary
Z192	Haddon		PH1	H	Other
Z193	Haddon		PH1	H*	Other
Z194	Haddon		PH1	M	Other
Z204	Winchester Palace		PH1	H	Other
Z035	Orton Hall Farm		MC	H*	Villa
Z036	Orton Hall Farm		MC	M	Villa
Z037	Orton Hall Farm		MC	H*	Villa
Z038	Orton Hall Farm		MC	H	Villa
Z071	Orton Hall Farm		Tibia	M	Villa
Z072	Orton Hall Farm		Tibia	M	Villa
Z073	Orton Hall Farm		Tibia	M*	Villa
Z074	Orton Hall Farm		Tibia	M	Villa
Z075	Orton Hall Farm		Tibia	H	Villa
Z105	Orton Hall Farm		MT	H	Villa
Z106	Orton Hall Farm		MT	M?	Villa
Z107	Orton Hall Farm		MT	H*	Villa
Z108	Orton Hall Farm		MT	M*	Villa
Z109	Orton Hall Farm		MT	H	Villa, GL error?
Z014	Coldharbour Farm		MC	H	Iron Age
Z015	Coldharbour Farm		MC	H	Iron Age
Z016	Coldharbour Farm		MC	H	Iron Age
Z022	Danebury		MC	H	Iron Age
Z023	Danebury		MC	H	Iron Age
Z024	Danebury		MC	H	Iron Age
Z025	Danebury		MC	H	Iron Age
Z026	Danebury		MC	M*	Iron Age; MT?
Z027	Danebury		MC	H*	Iron Age
Z028	Danebury		MC	H	Iron Age

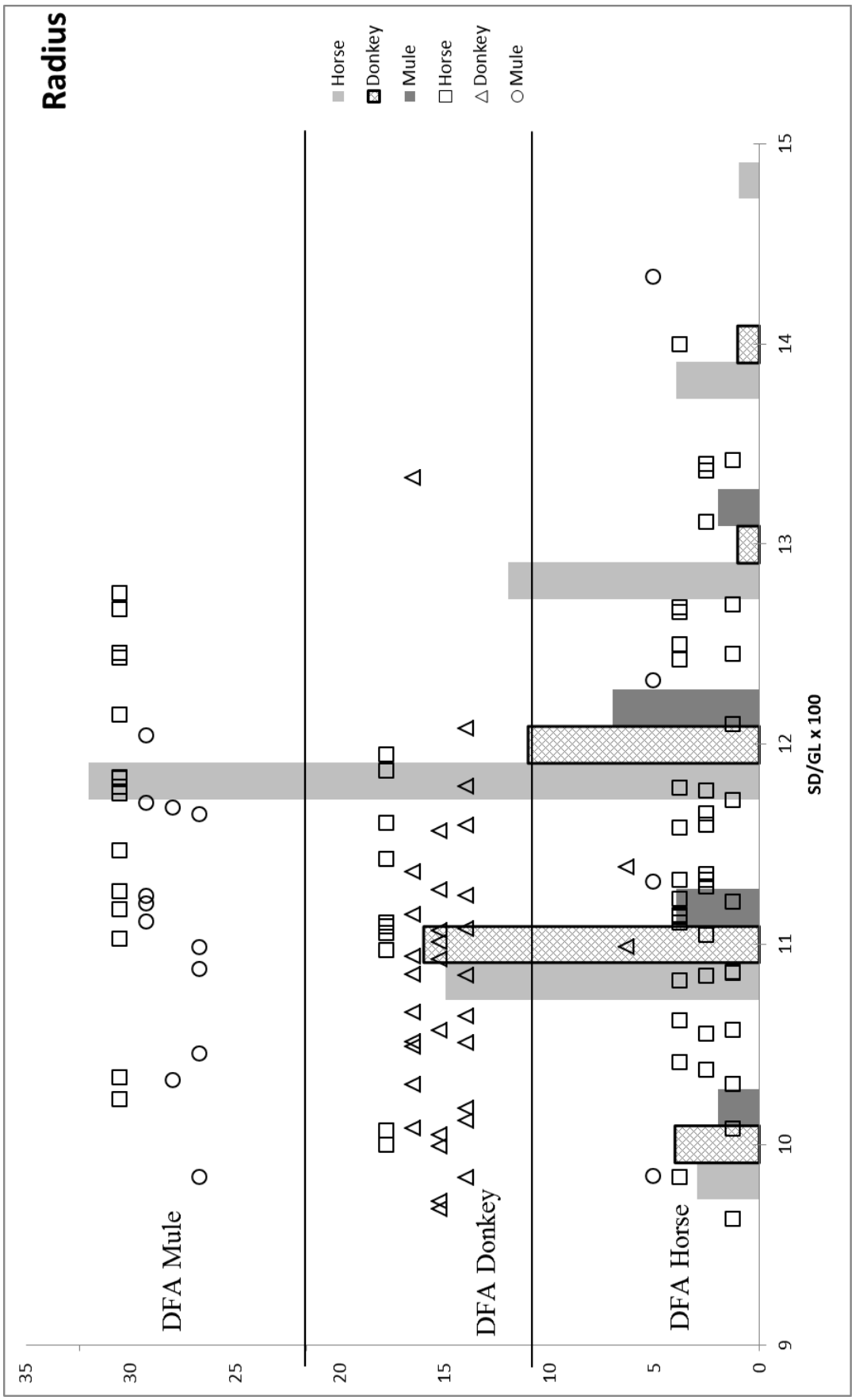
Species Determinations by Site Types (Others, cont'd)

Bone ID	Site	Context	Element	Det.	Note
Z029	Danebury		MC	H	Iron Age
Z030	Danebury		MC	H	Iron Age
Z095	Danebury		MT	H*	Iron Age
Z096	Danebury		MT	H	Iron Age
Z097	Danebury		MT	H*	Iron Age
Z098	Danebury		MT	H*	Iron Age
Z195	Haddon		PH1	H*	Iron Age
Z196	Haddon		PH1	H*	Iron Age
Z203	La Sagesse		PH1	H*	Iron Age
Z215	Market Deeping		PH1	H	Iron Age
Z216	Market Deeping		PH1	H	Iron Age
Z058	Thorpe Thewles		Femur	D*	Iron Age
Z067	Thorpe Thewles		Tibia	H	Iron Age
Z092	Thorpe Thewles		MT	H*	Iron Age
Z129	Thorpe Thewles		PH1	H	Iron Age

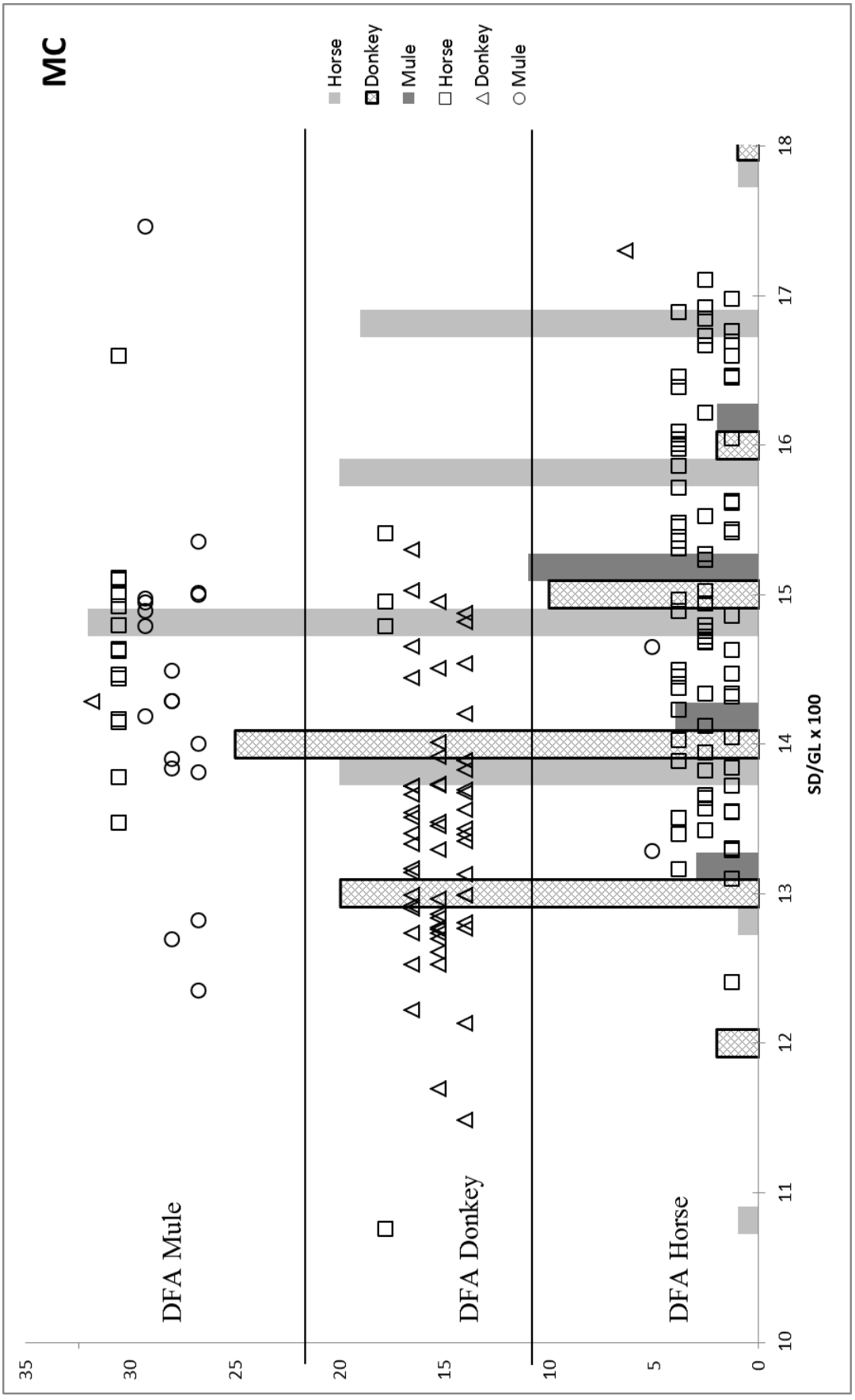
Appendix IV.I – SD-GL Shape Indices (Modern Control Data – Humerus)



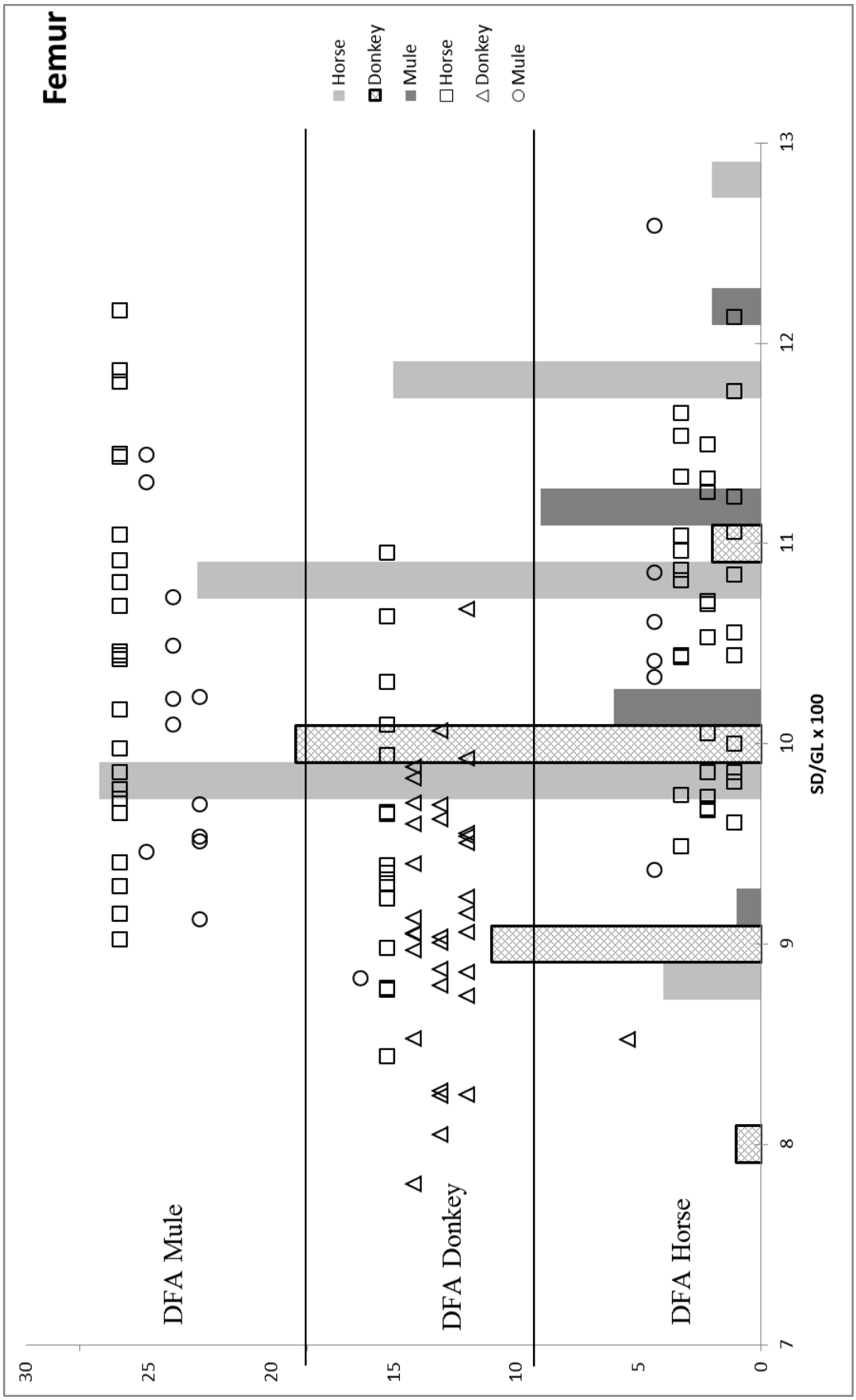
Appendix IV.II – SD-GL Shape Indices (Modern Control Data – Radius)



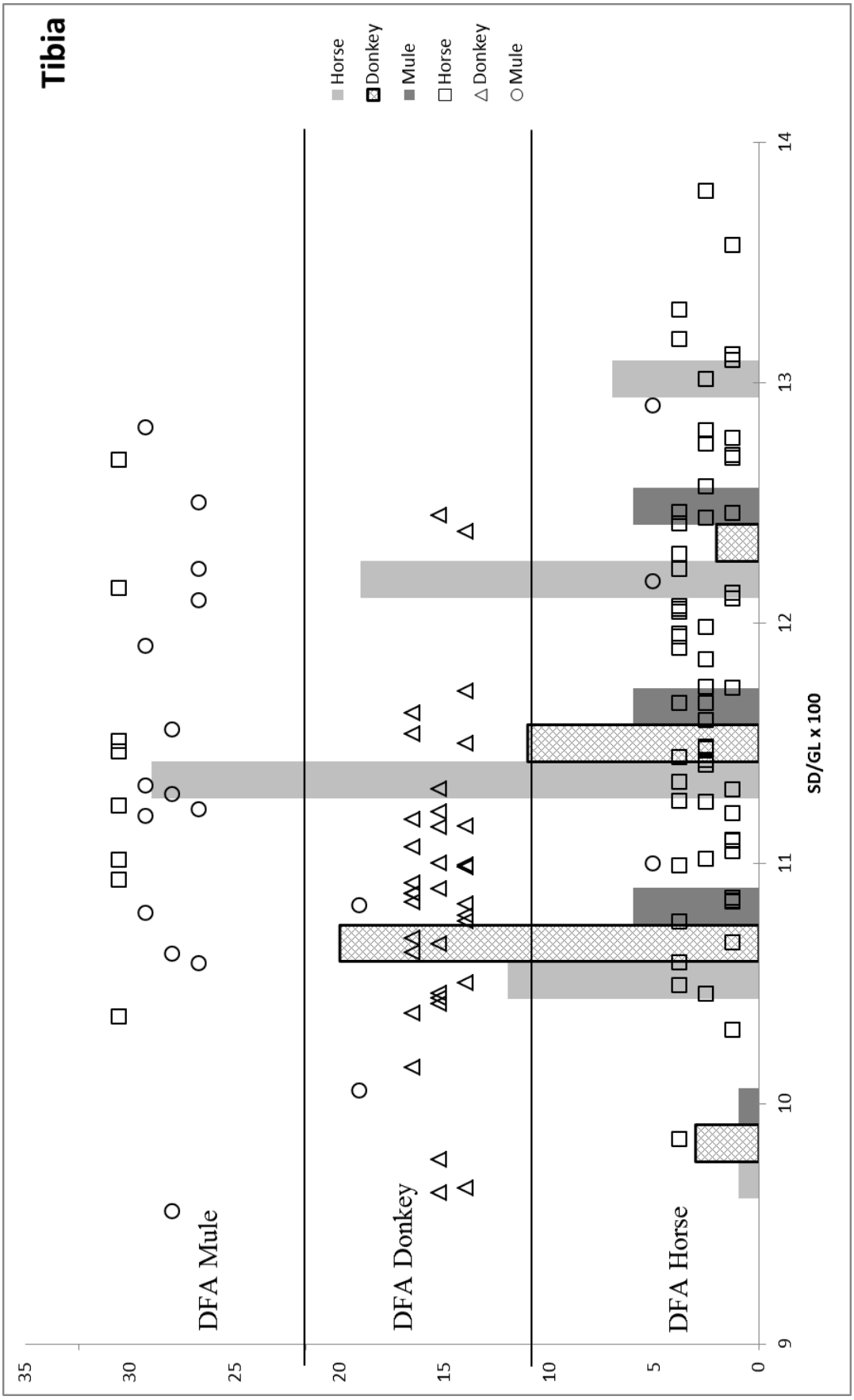
Appendix IV.III – SD-GL Shape Indices (Modern Control Data – MC)



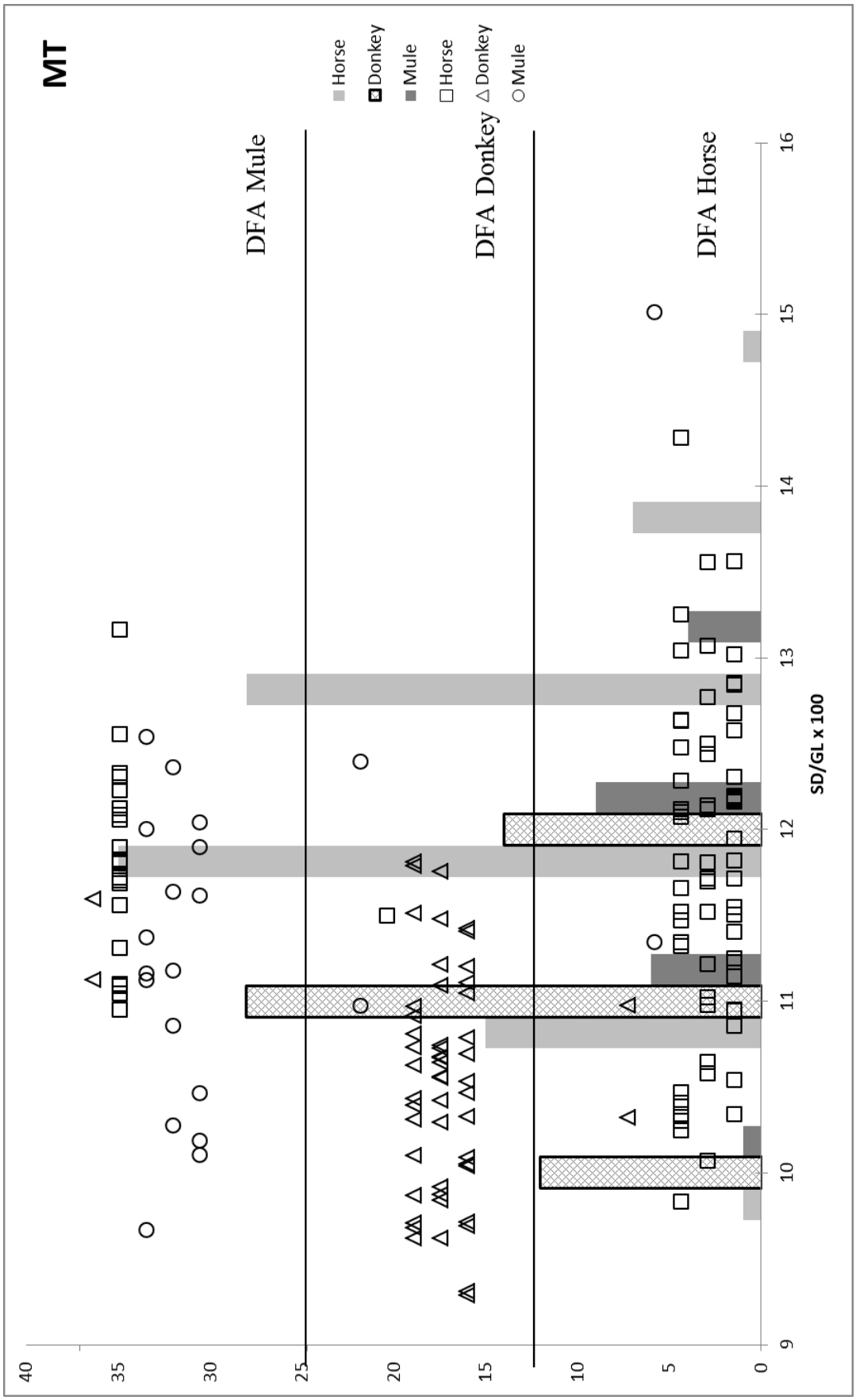
Appendix IV.IV – SD-GL Shape Indices (Modern Control Data – Femur)



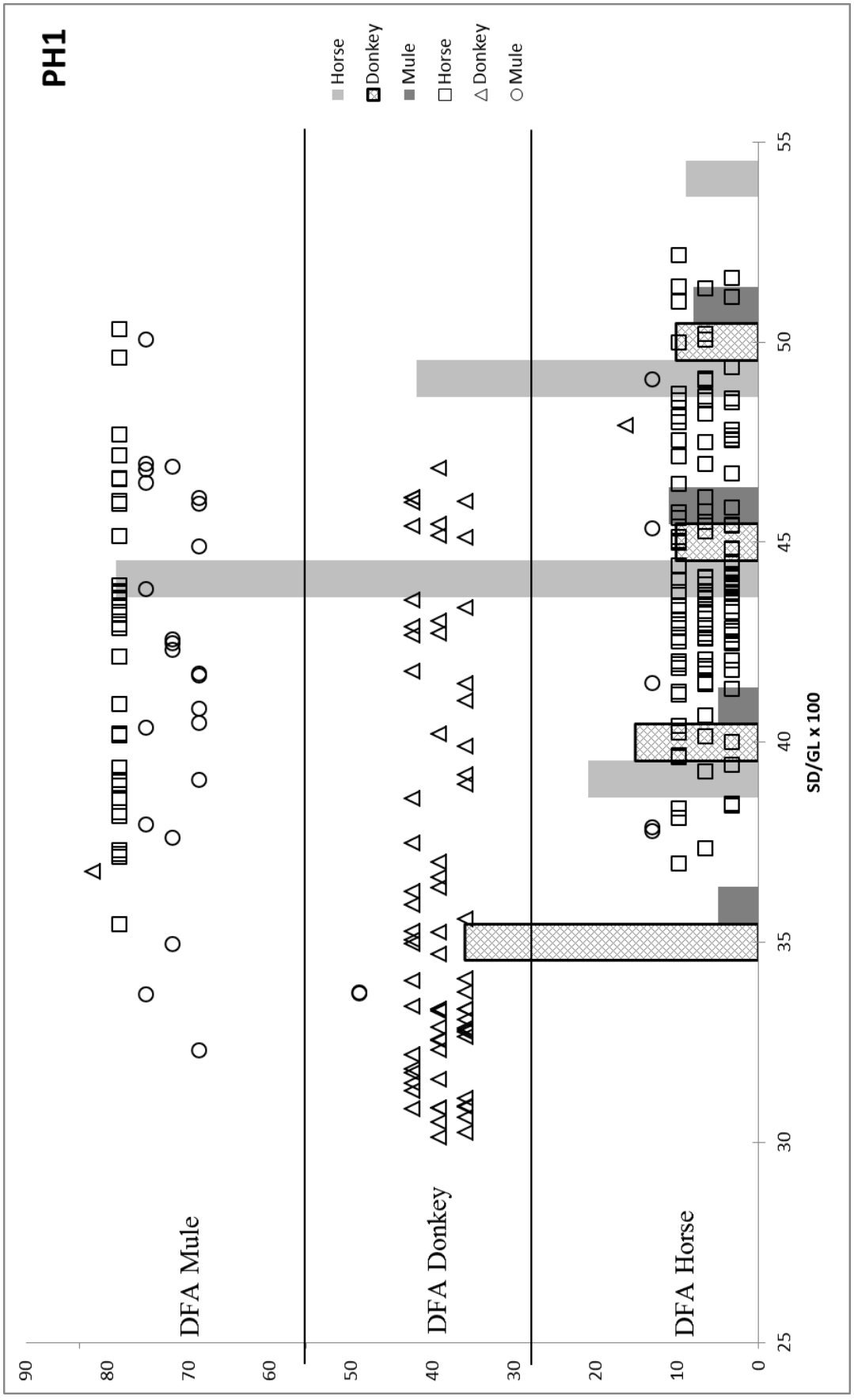
Appendix IV.V – SD-GL Shape Indices (Modern Control Data – Tibia)



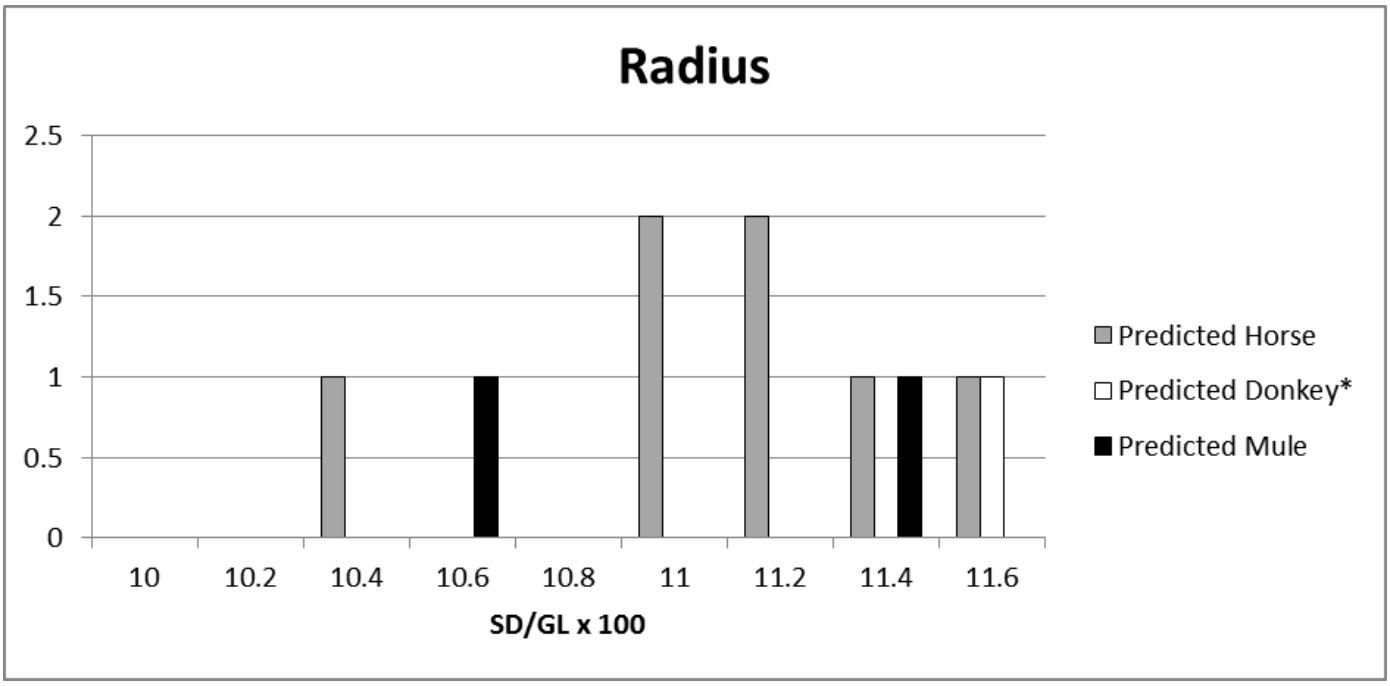
Appendix IV.VI – SD-GL Shape Indices (Modern Control Data – MT)



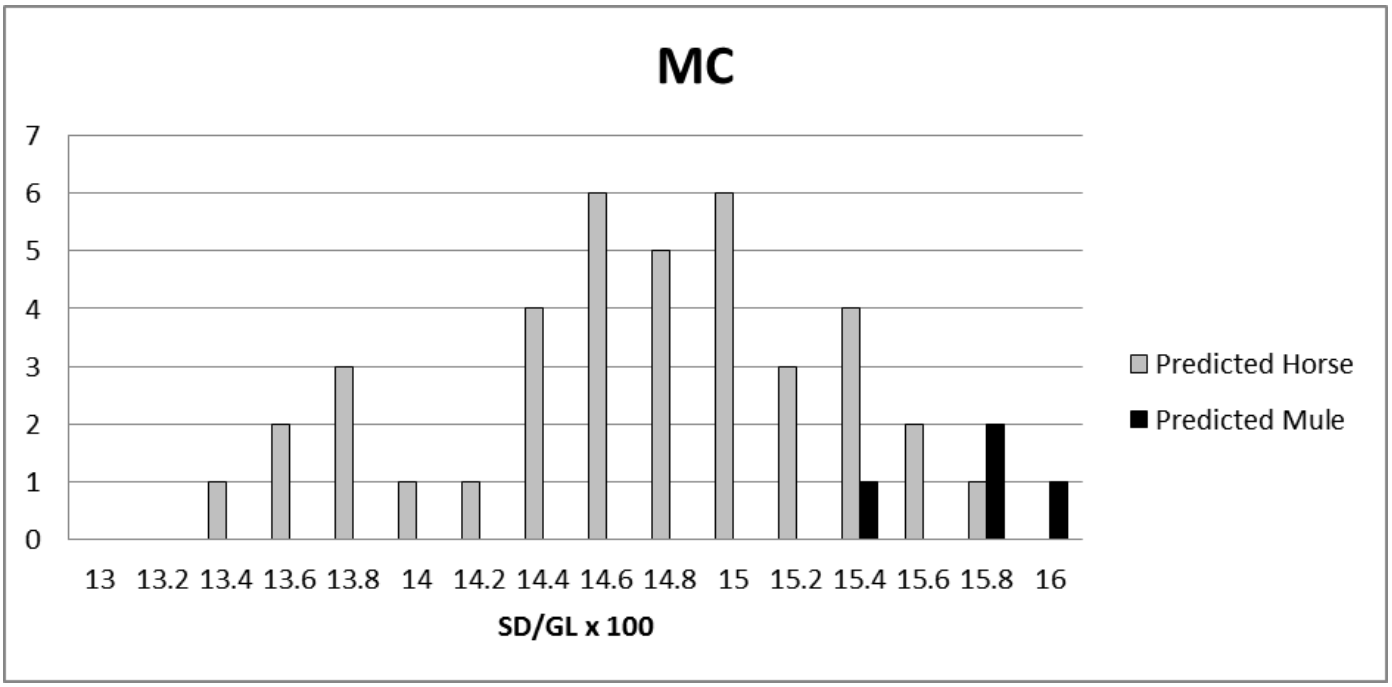
Appendix IV.VII – SD-GL Shape Indices (Modern Control Data – PH1-All)



Appendix IV.VIII – SD-GL Shape Indices (Archaeological Specimens)

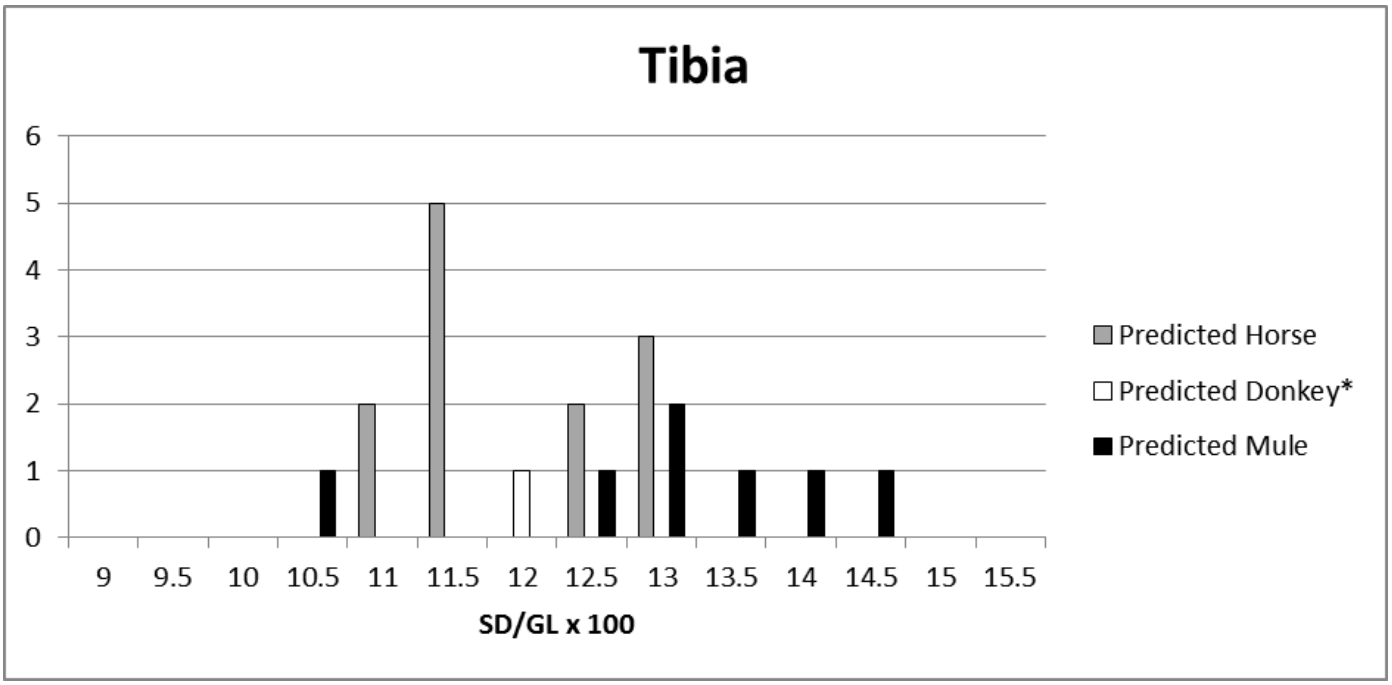


* - This predicted donkey is from a near complete skeleton (Winchester SK-682) which is determined as a horse basede on other elements. Note the other radius of this individual has similar SD-GL shape index.

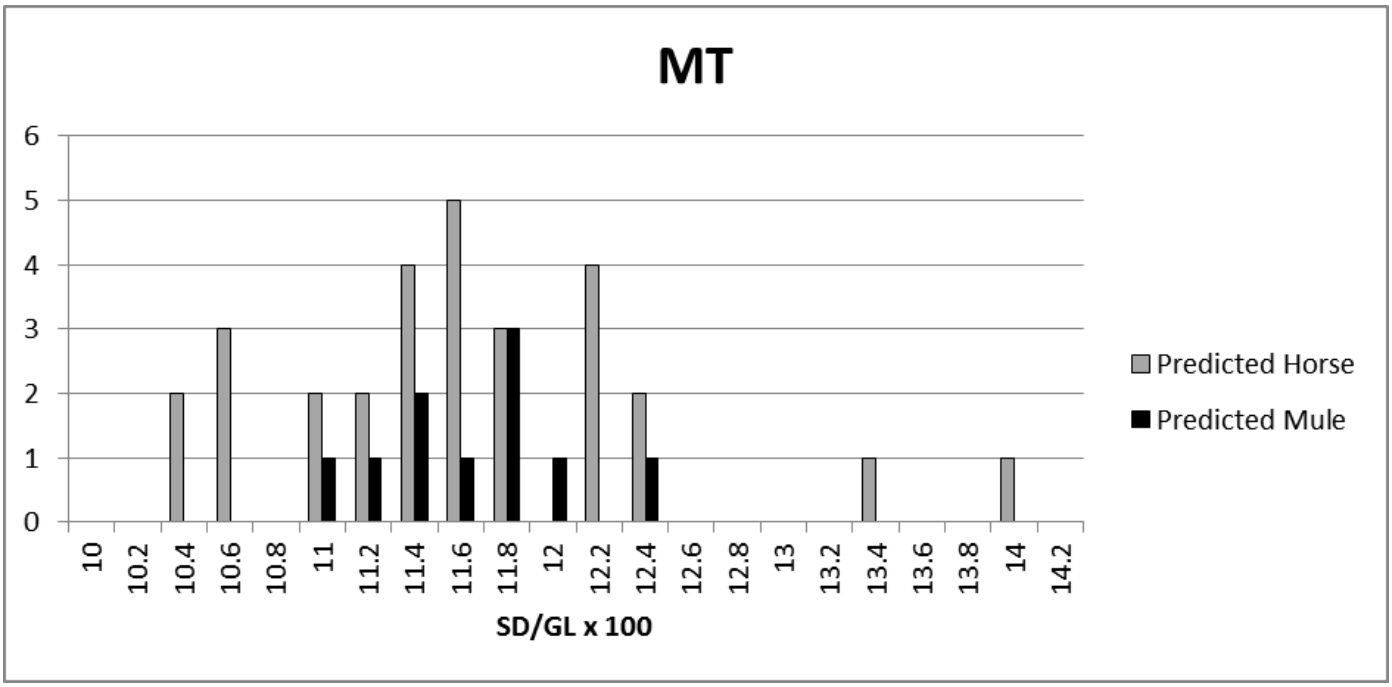


The predicted mules turns out to be more robust than most predicted horses in MC.

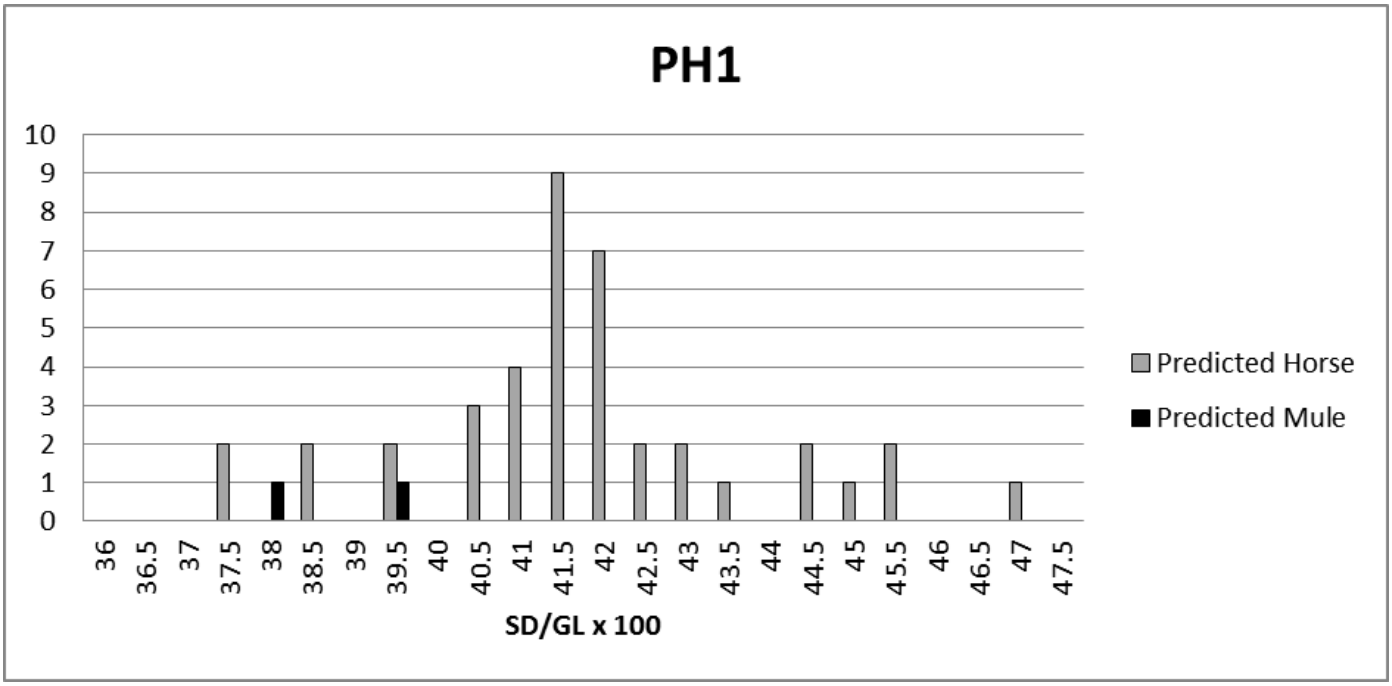
Appendix IV.VIII – SD-GL Shape Indices (Archaeological Specimens. cont'd)



* - This predicted donkey is from a partial skeleton (HB 7294) and is determined as horse based on its MT.



Appendix IV.VIII – SD-GL Shape Indices (Archaeological Specimens. cont'd)



Appendix V – Isotopic Outcomes

Site	Context	Tooth	Sp.	$^{18}O_{SMOW}$ (‰)	$^{13}C_{VPDB}$ (‰)	$^{87}Sr/^{86}Sr$	$^{18}O_{DW}$* (‰)
Winchester	VR-3136	P_2	H	26.13	-12.95	0.709777	-6.34156
	VR-440	P_2	H	25.18	-13.78	0.711864	-7.60363
	HA-75	P_4	H	25.63	-14.27	0.708448	-7.01193
	NR-495	P2	H	25.78	-12.48	0.708609	-6.81314
	VR-410	$M_{1/2}$	H	25.41	-13.90	0.708296	-7.29906
	VR-2608	$P_{3/4}$	H	25.36	-12.66	0.709629	-7.36623
	VR-1594	$M_{1/2}$	H	24.33	-12.89	0.708485	-8.74609
	VR-1280	M_1	H	25.17	-12.88	-	-7.62534
	HA-99	$M_{1/2}$	H	25.70	-13.60	0.709304	-6.92435
	HA-13	$M_{1/2}$	H	25.87	-12.80	-	-6.68812
	NR-113	M_1	H	25.49	-13.15	0.709389	-7.19556
	NR-557	$M_{1/2}$	H	25.81	-12.49	-	-6.77301
	CT-225	$M_{1/2}$	H	24.94	-13.00	0.709986	-7.92491
	VR-481	P_2	PM	25.55	-13.58	0.715700	-7.1169
	VR-405	$M_{1/2}$	PM	25.14	-13.72	0.708550	-7.66036
Alcester	ALC-5175	$P_{3/4}$	H	25.35	-14.73	-	-7.38897
	ALC-1020	P_2	H	25.21	-14.02	0.710272	-7.57094
	ALC-1147	P_2	H	25.05	-14.18	0.710947	-7.78048
	ALC-3002	$M_{1/2}$	PM	26.38	-14.05	0.711513	-6.0192
Ribchester	RB-259	P_2	H	24.73	-13.91	-	-8.2037
	RB-743	P_2	H	25.20	-13.35	-	-7.57798
	RB-989	$M_{1/2}$	H	25.22	-13.17	-	-7.55871
	RB-254	P_3	H	25.38	-14.32	-	-7.35103
	RB-9069	M_2	H	25.55	-14.38	-	-7.11465
	RB-8078	P_2	H	25.67	-13.17	-	-6.96288
	RB-5053	$P_{3/4}$	H	24.65	-12.59	-	-8.30936
	RB-728	P_2	PM	25.10	-13.19	-	-7.72029
Fairford	FTF-2052	P_3	H	25.23	-13.54	-	-7.54754
	FTF-369	P_2	H	25.03	-13.62	-	-7.80768
	FTF-14	$M_{1/2}$	H	24.66	-13.89	-	-8.30361
	FTF-857	$M_{1/2}$	H	25.38	-13.82	-	-7.34143
	FTF1039	$M_{1/2}$	H	25.05	-13.65	-	-7.78731
	FTF-2229	M_1	H	26.31	-13.68	-	-6.10671
	FTF-250	$M_{1/2}$	H	25.18	-13.26	-	-7.60571
	FTF-3124	$M_{1/2}$	H	24.70	-13.61	-	-8.24632
	FTF-2459	$M_{1/2}$	PD	23.98	-13.97	0.710207	-9.20126
Serbia	SERB-01	P_2	H	21.91	-11.18	-	-11.9601
	SERB-03	P_3	PD	23.60	-12.49	-	-9.7149
	SERB-02	M_2	PM	25.39	-12.70	-	-7.3246
	SERB-04	P_4	PM	25.05	-11.08	-	-7.78568

* - $^{18}O_{DW}$ value is estimated first from converting $^{18}O_{SMOW}$ into $^{18}O_{PO4}$ and then into $^{18}O_{DW}$. Detail of the conversions is explained in Section 7.4

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