Leveraging paleoproteomics (ZooMS) to enrich zooarchaeological data and investigate the ancient animal economies of Inner Asia

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Abbreviations

µg:	microgram
µl:	microliter
AC:	acid
ACN:	acetonitrile
aDNA:	ancient deoxyribonucleic acid
AmBic:	ammonium bicarbonate
Amel-X:	amelogenin x-linked
Amel-Y:	amelogenin y-linked
AMS:	accelerator mass spectrometry
AMUL:	archaeological multiplex user labs
BCE:	before common era
C18:	octyldecylsilane
CE:	common era
CHCA:	α-cyano-4-hydroxycinnamic acid
COL1:	type I collagen
COL1α1:	alpha 1 chain of type I collagen
COL1α2:	alpha 2 chain of type I collagen
Da:	daltons
DE:	Germany
DHB:	dihydrobenzoic acid
DOI:	digital object identifier
EBA:	early bronze age
ESI:	electrospray ionization
EXT:	extract
Fig.	figure
FT-MS:	fourier transform ion cyclotron
HCl:	hydrogen chloride
HILIC:	hydrophilic interaction liquid chromatography
HPLC:	high-performance liquid chromatography
Int:	mass intensity
IT:	ion trap
kDA:	thousand daltons
LBA:	late bronze age
LC-MS/MS:	liquid chromatography with tandem mass spectrometry
LFQ:	label-free quantification
LSC:	liquid scintillation counting
M:	molar
M1:	whole mass
M2:	fragmentation mass
mM:	millimolar
MALDI:	matrix-assisted laser desorption ionization
MALDI-TOF:	matrix-assisted laser desorption ionization time-of-flight
MALDI-TOF-MS:	matrix-assisted laser desorption ionization time-of-flight mass spectrometry
MALDI-TOF-PMF:	matrix-assisted laser desorption ionization time-of-flight peptide mass fingerprinting

MAU:	minimal animal unit
MBA:	middle bronze age
mg:	milligrams
MNE:	minimum number of elements
MNI:	minimum number of individuals
MS:	mass spectrometry
mtDNA:	mitochondrial deoxyribonucleic acid
mRNA:	messenger ribonucleic acid
m/z:	mass-to-charge ratio
NaOH:	sodium hydroxide
NISP:	number of identified specimens
NZS:	Nizhnyaya Sooru
PMF:	peptide mass fingerprinting
proα1:	proalpha1
proα2:	proalpha2
PTM:	post-translational modification
Q:	quadrupole
RNA:	ribonucleic acid
RP:	reversed phase
rpm:	rotations per minute
s/n:	signal-to-noise ratio
SCX:	strong-cation exchange
SE:	secondary extract
SEC:	size exclusion
sp.:	species
TFA:	trifluoroacetic acid
TOF:	time-of-flight
TBK:	Tashbulak
Tbl.	table
v/v:	volume percent
ZK513-1:	trench ZK513-1
ZooMS:	zooarchaeology by mass spectrometry

ZooMS Markers (Brown et al. 2021a)

α2 292:	COL1α2 292-309
α2 454:	COL1α2 454-483
α2 484:	COL1α2 484-498
α2 502:	COL1α2 502-519
α1 508:	COL1α1 508-519
α1 586:	COL1α1 586-618
α2 757:	COL1α2 757-789
α2 793:	COL1α2 793-816
α2 978:	COL1α2 978-990

Summary

Inner Asia has been a critical region for the dispersal of domesticated species across Eurasia since early prehistory. And yet, the ancient animal economies of Inner Asia have been understudied in comparison to those of West and East Asia. Although innovative research in this area has resulted in a number of important studies and publications, there remain many gaps in our understanding. For my own PhD project I have used ZooMS to enrich the faunal data available from three Inner Asian archaeological sites—Nizhnyaya Sooru, ZK513, and Tashbulak— in order to better understand the human-animal relationships which characterized them. My main research goals were to clarify patterns of sheep versus goat exploitation in different archaeological contexts and to identify potential early domesticates, such as horses, for subsequent radiocarbon and aDNA analysis.

At Nizhnyaya Sooru in the Central Altai, my ZooMS analysis clarified the taxonomic identifications of a selection of faunal data recovered from the Eneolithic to Iron Age layers, revealing a persistent reliance on sheep, a possible emergence of goat husbandry during the Iron Age, and the seeming absence of equids until the Middle Bronze Age. At ZK513 in Outer Mongolia, I used ZooMS to identify sheep, goats, cattle, and equids in the earliest layers, supporting Afanasievo-introduced pastoralism but not horse domestication, as the Eneolithic equids were subsequently genomically identified as *Equus ovodovi*. ZooMS data from the later layers hints at increased hunting activities, though data resolution remains limited. At Tashbulak, my ZooMS analysis secured for the first time a preference for goats over sheep in a Medieval Transoxian settlement. Notably, I also identified camels, which are virtually absent from the zooarchaeological record of Central Asia despite their use in long-distance trade and diplomacy. Their presence as Tashbulak might suggest agropastoralist adaptations to climate change under Qarakhanid rule.

Looking forward, the continued development of collagen peptide markers for Inner Asian fauna (e.g. antilopines, cervids, candids) alongside the targeted integration of ZooMS, AMS radiocarbon dating, and aDNA analysis into faunal analysis, promises to transform our understanding of ancient human-animal relationships. Future research would benefit from applying these techniques to underrepresented taxa such as birds and reptiles and expanding Equus-specific analyses (e.g. ZooMS with chymotrypsin) to trace the earliest appearance of domesticated horses in Inner Asia. The combination of ZooMS and zooarchaeology, especially alongside other lines of biomolecular and biogeochemical evidence, has the potential to revolutionize our understanding of ancient animal economies. I am optimistic about the potential that such integrated approaches will have on Inner Asian archaeological research in the near future.

Zusammenfassung

Innerasien war seit der frühen Vorgeschichte eine Schlüsselregion für die Verbreitung domestizierter Tierarten in Eurasien. Dennoch wurden die tierwirtschaftlichen Systeme des alten Innerasiens im Vergleich zu denen West- und Ostasiens weniger intensiv untersucht. Obwohl innovative Forschungen in diesem Bereich zu wichtigen Studien und Veröffentlichungen geführt haben, bestehen nach wie vor viele Wissenslücken. In meinem Promotionsprojekt habe ich ZooMS (Zooarchaeology by Mass Spectrometry) eingesetzt, um die faunalen Daten von drei innerasiatischen Fundorten – Nizhnyaya Sooru, ZK513 und Tashbulak – zu erweitern und die Mensch-Tier-Beziehungen, die diese Orte prägten, besser zu verstehen.

Meine Hauptziele waren, die Nutzungsmuster von Schafen im Vergleich zu Ziegen in unterschiedlichen archäologischen Kontexten zu klären und potenzielle frühe domestizierte Tiere wie Pferde zu identifizieren, um diese anschließend mittels Radiokarbon- und aDNA-Analysen genauer zu untersuchen. In Nizhnyaya Sooru im zentralen Altai konnte meine ZooMS-Analyse die taxonomische Zuordnung von Tierknochen aus Schichten vom Äneolithikum bis zur Eisenzeit präzisieren. Dabei zeigte sich eine anhaltende Abhängigkeit von Schafen, ein mögliches Aufkommen der Ziegenhaltung in der Eisenzeit und das scheinbare Fehlen von Equiden bis zur mittleren Bronzezeit. In ZK513 in der äußeren Mongolei identifizierte ZooMS Schafe, Ziegen, Rinder und Equiden in den frühesten Schichten, was die Einführung von Pastoralismus durch die Afanasievo-Kultur unterstützt, aber keine Domestikation von Pferden nachweist. Die Equiden aus dem Äneolithikum wurden genomisch als *Equus ovodovi* bestimmt. ZooMS-Daten aus späteren Schichten deuten auf eine Zunahme von Jagd-Aktivitäten hin, wobei die Datenauflösung begrenzt bleibt.

In Tashbulak konnte meine ZooMS-Analyse erstmals eine Präferenz für Ziegen gegenüber Schafen in einer mittelalterlichen transoxanischen Siedlung nachweisen. Bemerkenswerterweise identifizierte ich auch Kamele, die in der zooarchäologischen Überlieferung Zentralasiens nahezu fehlen, obwohl sie im Fernhandel und in der Diplomatie eine wichtige Rolle spielten. Ihr Vorkommen in Tashbulak könnte auf agropastorale Anpassungen an den Klimawandel unter der Herrschaft der Karachaniden hinweisen.

Zukünftig verspricht die Weiterentwicklung von Kollagenpeptid-Markern für innerasiatische Fauna (z. B. Antilopen, Hirsche, Caniden) in Kombination mit der gezielten Integration von ZooMS, AMS-Radiokarbon-Datierung und aDNA-Analysen, unser Verständnis der alten Mensch-Tier-Beziehungen grundlegend zu verändern. Zukünftige Forschung sollte diese Methoden auf unterrepräsentierte Taxa wie Vögel und Reptilien anwenden und Equus-spezifische Analysen (z. B. ZooMS mit Chymotrypsin) ausweiten, um das früheste Auftreten domestizierter Pferde in Innerasien nachzuverfolgen. Die Kombination von ZooMS und Zooarchäologie, insbesondere in Verbindung mit weiteren biomolekularen und biogeochemischen Ansätzen, hat das Potenzial, unser Verständnis der alten Tierwirtschaften zu revolutionieren. Ich bin optimistisch, dass solche integrierten Ansätze die archäologische Forschung in Innerasien in naher Zukunft entscheidend voranbringen werden.

List of Publications

First Author Publication (Appendix 01)

Manuscript A - Hill, E., & Albarella, U. (2024). An international, open-access dataset of dental wear patterns and associated broad age classes in archaeological cattle mandibles. Scientific Data, 11(1), 713.

https://www.nature.com/articles/s41597-024-03377-y

Middle Author Publication (Appendix 02)

Manuscript B - Pan, J., Liu, X., Baca, M., Calvière-Tonasso, L., Schiavinato, S., Chauvey, L., Tressières, T., Perdereau, A., Aury, J., Oliveira, P.H., Wincker, P., Abdykanova, A., Arsuaga, J.L., Bayarsaikhan, J., Belinskiy, A.B., Carbonell, E., Davoudi, H., Garrido, J.L., Gilbert, A.S., Hermes, T., Warinner, C., Kalmykov, A.A., Lordkipanidze, D., Mackiewicz, P., Mohaseb, A., Richter, R., Sayfullaev, N., Shapiro, B., Shnaider, S., Southon, J., Stefaniak, K., Summers, G.D., van Asperen, E.N., Vanishvili, N., Hill, E., Kuznetsov, P., Reingold, S., Hansen, S., Mashkour, M., Berthon, R., Taylor, W.T.T., Houle, J., Hekkala, E., Popović, D., & Orlando, L. (2024). Genome-wide population affinities and signatures of adaptation in hydruntines, sussemiones and Asian wild asses. Molecular Ecology, e17527.

https://onlinelibrary.wiley.com/doi/pdf/10.1111/mec.17527

1. Introduction

The ancient animal economies of Inner Asia have been understudied in comparison to those of West and East Asia. A wealth of scholarship and scientific research has been dedicated to investigating the relationships between human migration and the domestication of both plants and animals, yet the role of Inner Asia in this story is poorly understood. This is in spite of the fact that Inner Asia has been a critical region for the dispersal of domesticated species across Eurasia as well as an epicenter of multi-cultural contact, coexistence, and exchange. The Altai Mountains have functioned as a crossroads of Eurasia since the time of Neanderthals and Denisovans, and Central Asia was the crux of diplomacy and exchange in Eurasia during the Silk Road period.

The growing realization of the importance of this region combined with recent scientific advances has led to a renaissance of Inner Asian archaeology in the past decade. Innovative research in this area has resulted in a number of important studies and publications, yet there remain many gaps in our understanding. My own contribution to this body of knowledge consists of my application of paleoproteomics to taxonomically identify animal bone fragments recovered from three archaeological settlement sites from across Inner Asia (Fig.1). I have additionally sampled from comparative specimens to screen and predict the collagen peptide markers of goitered gazelle (*Gazella subgutturosa*) and sika deer (*Cervus nippon*) as measured by MALDI-TOF. Finally, I have also reviewed and compiled the faunal data available from the settlement site contexts of Bronze Age Siberia, Bronze Age Outer Mongolia, and Medieval Transoxiana.

Fig.1 Map of archaeological sites with faunal assemblages analyzed in this dissertation.

1.1. Archaeological Sites

1.1.1. Nizhnyaya Sooru

Nizhnyaya Sooru is a stratified settlement site in the Central Altai Republic of Southern Siberia (Larin et al. 1988). The site is noteworthy for the exceptional preservation of *in situ* faunal remains attributed to multiple cultures and time periods (Tishkin et al. 2021). Nizhnyaya Sooru has been AMS radiocarbon dated to the Eneolithic period, with domesticated sheep remains from the site yielding dates of ca. 3300–2900 cal BC (Hermes et al. 2020b). Remarkably, the complex includes an Afanasievo settlement that does not present evidence of subsequent occupation or intrusive burials (Hermes et al. 2020b). The few hundred animal bone fragments that were recovered from early excavations at Nizhnyaya Sooru have already been analyzed (Kosintsev 2005). Renewed excavation has uncovered thousands more animal bone fragments which are currently undergoing analysis, a portion of which (n=171) were also selected for ZooMS analysis. Access to this site was facilitated by Alexey Tishkin of Altai State University.

1.1.2. ZK513

ZK513 is a stratified settlement site in the Zuunkhangai region of Outer Mongolia (Houle et al. 2022). ZK513 is one of only three archaeological habitation sites in Outer Mongolia that have been AMS radiocarbon dated to the Eneolithic and Early Bronze Age (ca. 2030–1880 BCE) (Houle et al. 2022). This unique site has presented archaeologists with the rare opportunity to study a pastoralist habitation that was occupied from Bronze Age to the Medieval Turk-Uyghur periods (Houle et al. 2022). The discovery and excavation of prehistoric settlement sites and the robust analysis of recovered faunal remains, including biomolecular approaches where possible, is necessary to clarify the virtually unknown Eneolithic and Bronze Age animal management practices of Outer Mongolia. The faunal remains (n= 2,735) from the highly stratified ZK513-1 Trench have already been analyzed by a zooarchaeologist (Houle et al. 2022). One hundred and forty-three were selected for ZooMS analysis. Access to this site was facilitated by Jean-Luc of Houle of Western Kentucky University.

1.1.3. Tashbulak

The Qarakhanid era settlement site of Tashbulak in the Jizzakh Region of Uzbekistan is unique in that it is both a highland complex and an urban complex from which thousands of animal bone fragments have been recovered. This has provided researchers with a rare opportunity to perform a robust zooarchaeological analysis of a large assemblage of archaeological fauna from a Medieval Transoxian site. Archaeological data from Tashbulak have the potential to provide valuable insight into Medieval modes of pastoralism and subsistence practices under Turko-Islamic rule in highland urban contexts. Faunal analysis of the thousands of bone fragments that were uncovered from Tashbulak is ongoing, 340 of which were also selected for ZooMS. Access to this site was provided by Fahrod Maksudov of the National Center of Archaeology at the Uzbekistan Academy of Sciences and Michael Frachetti of Washington University in St. Louis.

1.2. Research Questions

1.2.1. Bronze Age Animal Economies

The attribution of taxonomic identities to archaeological fauna, such as domesticated sheep, goat, cattle, and horse, is critical to the reconstruction of ancient animal economies. In Southern Siberia and Outer Mongolia, challenges in profiling prehistoric faunal assemblages include morphologically distinguishing sheep from goat, discerning domesticated taxa from wild, and the general difficulty of identifying fauna from fragmented animal bone assemblages. Archaeologists investigating the emergence of pastoralism in the Eneolithic and Early Bronze Age Southern Siberian and Outer Mongolian contexts are also rarely able to recover faunal remains from settlement sites (Alekhine et al. 1995; Honeychurch 2015; Houle 2014; Houle et al. 2022; Tishkin et al. 2021; Wright 2021). Some faunal data from prehistoric burial and ritual sites are available (e.g. Erdenebaatar & Kovalev 2007; Eregzen 2016; Kovalev & Erdenebaatar 2009) and evidence for evolving human-animal relationships can been found in rock art and funerary monuments (Jacobson-Tepfer 2012; Jacobson-Tepfer et al. 2006; Wright et al. 2021).

The exact timing and pathways of domesticated mammal dispersals into Inner Asia are thus currently unknown, but were likely driven by Afansievo migrations from the Western Eurasian Steppe through Southern Siberia and into Mongolia around the Early Bronze Age (Honeychurch et al. 2021; Taylor et al. 2019; Wright et al. 2021). Researchers have speculated that domesticated sheep (*Ovis aries*), goats (*Capra hircus*), and taurine cattle (*Bos taurus*) disseminated into Inner Asia as part of a complex process of human migration, trade, and cultural exchange ca. 8,000 years ago (e.g. Frachetti 2012). Here I investigated what animal economies looked like in the Bronze Age periods of Southern Siberia and Outer Mongolia, including hunting prevalence, and whether or not Eneolithic pastoralism can be inferred from the archaeological record–with an eye for Afanasievo contexts.

1.2.2. Prehistoric Horse Domestication

Horses were originally domesticated from wild horses (*Equus ferus*) ca. 5500 years ago in the Botai archaeological cultural sphere of Central Asia (Gaunitz et al. 2018; Librado et al. 2021; Rosengren et al. 2021; Warmuth et al. 2012). Although Botai horses were the ancestors of Przewalski's horses (*Equus ferus przewalskii*), they were not not the ancestors of modern domesticated horses (Gaunitz et al. 2018; Librado et al. 2021; Rosengren et al. 2021). Modern domesticated horses were recently discovered to have instead been domesticated from wild horses in the Western Eurasian Steppe, probably in the Volga-Don region, ca. 4000 years ago (Librado et al. 2021). The timing of domesticated horse (*Equus caballus*) arrival in the Eastern Eurasian Steppe is a subject of contention (Outram 2023; Outram et al. 2021;Taylor & Barrón-Ortiz 2021), though it is clear that the practice was widespread by the Late Bronze Age (Taylor 2017; Taylor et al. 2017, 2020b). Bone morphology and dental metrics are generally unfit tools for distinguishing wild from domesticated archaeological equid remains (Geigl & Grange 2012; Twiss et al. 2017). Here I investigated whether or not equids have been recovered from

Afanasievo settlement sites, as well as the earliest appearance of domesticated horses in Southern Siberia and Outer Mongolia.

1.2.3. Medieval Animal Economies

A lack of faunal remains and robust zooarchaeological reporting has complicated the reconstruction of Medieval Transoxian animal economies. The questions surrounding Qarakhanid era subsistence practices in particular are not related to the onset of animal domestication, but to the modes of pastoralism practiced and how these modes varied by landscape, elevation, degree of urbanization, and identity. While caprine dominance in the herds of Central Asia has long been established, the difficulties involved with discriminating between sheep and goat bones has obscured patterns of sheep : goat ratios in different spatial, temporal, and cultural contexts. Medieval Transoxian sheep and goat exploitation is thus poorly understood, especially in relation to culling profiles and secondary product specialization. The impact of Arab Expansion and Islamification on pig rearing and consumption in Medieval Transoxiana is equally unclear. Finally, the underrepresentation of camel remains recovered from Medieval Central Asian archaeological contexts more broadly is not yet understood. Here I investigated the modes of pastoralism and animal exploitation that could be inferred from the archaeological record of Medieval Transoxiana, with an emphasis on caprine, camel, and suid pastoralism.

1.2.4. Medieval Wooling Economies

Arab historiographers such as Mukaddasi have written that within Transoxiana, the region of Ustrushna was renowned for the production of woolen textiles. The logistics of wool production are virtually unknown. There are many gaps in our current understanding, ranging from which animal wools were used, where the wooling animals were raised, how artisans acquired raw wool or yarn from these animals, on what scale they were producing woolen textiles, and how scales of production changed under Qarakhanid rule in response to shifting religious identities and intensified Silk Road trade. A lack of both surviving woolen textiles and relevant written records greatly hinders our ability to reconstruct Medieval wooling economies in Ustrushna and Transoxiana. Perhaps our best window into these wool production economies is zooarchaeology and material culture finds. It seems unlikely that camel wool was commonly worked, as very few camel bones have been recovered from the Medieval urban, mixed, or rural archaeological contexts of Transoxiana. At the same time, the comparative abundance of sheep and goat bones that have been recovered from these contexts so far have provided little clarification. Here I investigated whether or not there is evidence of wooling economies in Medieval Transoxian contexts.

1.2.5. Medieval Camel Exploitation

Camels were the preferred load-bearing animals of the Silk Road period, with Dromedary camels (*Camelus dromedarius*) being utilized west of Transoxiana and Bactrian camels (*Camelus bactrianus*) being exploited to the east (Whitfield & Sims-Williams 2004). It is known

that merchants and envoys traveling from Transoxiana to China generally did so on camelback, and that camels were often offered (and expected) as tribute (Kim 2011). Although camels are incredibly resilient and well-adapted to arid environments they still need to stop for rest and water after ca. 30 km of burdened travel, emphasizing the important role of oases along Trans-Eurasian exchange routes (Dong et al. 2021). Camels crossing the Gobi desert between China and Central Asia were often pushed to their limit (Dong et al. 2021), and it is likely that many perished along the way. If camels were more likely to perish in trans-desert journeys than while stationary, this might partially explain why their remains are not commonly recovered from Silk Road period Central Asian faunal assemblages. The low representation of camel remains could also suggest that they were not being managed locally for wool production. At the same time, camels had to be managed and bred somewhere, and surely utilized for more than transportation. Here I investigated whether or not there is evidence for intensified camel management in different Transoxian contexts.

1.2.6. Inner Asian Caprine Husbandry

It is currently unclear how fixed sheep to goat ratios were throughout different regions and archaeological periods of ancient Inner Asia. Sheep dairying has been identified as a hallmark of Western Eurasian Steppe pastoralism during the Eneolithic period (Scott et al. 2022), though less is known about prehistoric caprine management strategies in the Eastern Eurasian Steppe (see Wilkin et al. 2020) or other regions of Central Asia (Taylor et al. 2021a). Modern and historical herd composition data collected from census records provide insight into regional variations, but cannot be viewed as fully reliable analogs for prehistoric practices. Here I investigated whether or not there is evidence for shifting ratios of sheep and goat in the faunal assemblages recovered from Bronze Age and Medieval settlement site contexts of Inner Asia, or if a consistent prevalence of either can be inferred from the archaeological record.

1.3. Objectives

1.3.1. Faunal Data Enrichment

The attribution of taxa to archaeological fauna is critical to the reconstruction of ancient subsistence strategies and animal economies. In the context of Inner Asia, challenges in profiling faunal assemblages include morphologically distinguishing closely related species (especially discerning domesticated taxa from wild) and the general difficulty of identifying bone fragments. Researchers are increasingly incorporating ZooMS into their faunal analyses in an effort to address some of these challenges (see Brown et al. 2021a; Korzow-Richter et al. 2022). The intersection of ZooMS and zooarchaeology has been an ongoing conversation since ZooMS was developed (see Albarella 2018; Bouchard et al. 2020; Brown et al. 2021b; Ruebens et al. 2023, 2024; Sierra et al. 2023; Silvestrini et al. 2022; Sinet-Mathiot et al. 2019; Torres-Iglesias et al. 2024; Wang et al. 2024). Concerns have been raised about the destructive nature of ZooMS (see Pálsdóttir et al. 2018), the biasing effects of ZooMS on NISP counts (see

Discamps et al. 2024), and the application of ZooMS to analyze as many samples from a faunal assemblage as possible without proper context (Albarella 2018).

These concerns are valid, yet ZooMS can be used in a targeted and mindful way by selecting samples that are morphologically unidentifiable to a taxon or whose taxonomic attributions are tentative, ambiguous, or limited to size-based groups. I have used ZooMS to taxonomically identify a selection of fragmented animal bones from three faunal assemblages. My intention was to enrich each faunal report, allowing for more in depth analyses such as the reconstruction of herd compositions and hunting activities. My goal was to verify morphological identifications, identify and correct any misidentifications, and to refine the morphological taxonomic attributions of fragments that were limited to tentative attributions (e.g. “Ovis?”), ambiguous attributions (e.g. “Ovis/Capra/Gazella”), size-based mammal classes (e.g. “Medium Mammal”), or were otherwise indeterminate. The samples that I collagen peptide fingerprinted were selected specifically to facilitate the secure identification of equids, caprines, camelids, antilopines, and cervids. My objective was not to identify as many animal bone fragments as possible, but to identify samples of interest with the potential to address relevant research questions.

Equids

A major challenge that researchers face when trying to disentangle the narratives of horse domestication in Inner Asia is that equid remains are not easily distinguished by morphology alone. Morphometric criteria do exist, but they are not entirely reliable and assigning species level identification to fragmented equid remains with accuracy is not easily accomplished (Chuang & Bonhomme 2019; Geigl & Grange 2012; Payne 1991; Taylor et al. 2020b,c; Twiss et al. 2017). This has led to the publication of conflicting reports of the same archaeological equids from the Afanasievo sites of Kara-Tenesh and Balykhutul being morphologically identified as both domesticated horses (Frachetti 2012) and possibly wild horses (Honeychurch et al. 2021). Here I used ZooMS to see if equids could be identified in the Eneolithic and Early Bronze Age layers of either site, and if so, to submit these specimens for radiocarbon dating and genomic analyses. The identification of DOM2 lineage horses in these early layers would provide valuable insight into history and routes of horse domestication into Inner Asia. The identification of wild horses would indicate the need to be cautious when attributing species-level attributions to equid remains recovered from Eneolithic and Early Bronze Age sites in Southern Siberia or Outer Mongolia.

Camelids

Camelids are not particularly difficult to identify morphologically, yet their remains are rarely recorded in reports of Medieval Central Asian faunal assemblages. This is despite the fact that camels were essential for Silk Road period trade and diplomacy. We do not know where the most important camel breeding centers of Central Asia were during the reign of Qarakhanid Khanate, or if any of these centers were in Transoxiana. It seems unlikely that camels would have been managed extensively in highland regions, though they may have been managed at oases or in the outskirts of cities. Travelers and merchants in need of camels surely would have

preferred to do so at sites along the routes they were already traversing. There are records of Chinese merchants trading bolts of silk for camels in Samarkand (see Hansen 2005), but it is unclear if camels were being reared in or near Samarkand, or if they were exported there. The seeming lack of camel remains from Termez (Portero et al. 2022) does not suggest that camels were being managed in cities. The comparison of camel representation in faunal assemblages from different Medieval Transoxian contexts (e.g. highland versus lowland) could help to clarify some of these aspects of camel husbandry under the Qarakhanid Khanate. Here I used ZooMS to see if camel remains could be securely identified in the Medieval assemblage from Tashbulak.

Caprines

The morphological attribution of wild or domesticated status to caprine remains is a significant challenge (Clutton-Brock et al. 1990; Halstead et al. 2002; Helmer 2000), and there are wild species of both sheep (i.e. argali, or *Ovis ammon*) and goat (i.e. Siberian ibex, or *Capra siberica*) endemic to Inner Asia. Argali are generally larger than domesticated sheep (Houle et al. 2022), but juvenile and subadult argali remains could cause confusion. The remains of these species are not easily sorted from one another (Hermes et al. 2021), though criteria have been developed for sorting wild from domesticated goats (Zeder 2006b), Siberian ibex from domestic goat (Meadow 1989), and recently argali (*Ovis ammon*) from domestic sheep (Wang et al. 2020). This has resulted as caprine remains frequently being recorded as “sheep/goat” or “ovicaprid” (e.g. the “ovicaprid/roe-deer” sample SS ASU MD 1 from Maily Dugan; Svyatko et al. 2017), hindering research into the ancient animal management and exploitation practices of Inner Asia.

Here I used ZooMS to clarify ambiguous morphological attributions of caprines by discerning sheep (*Ovis* sp.) fragments from goat (*Capra* sp.) fragments. My reasoning here was two-fold. By clarifying whether significantly more sheep or more goat remains were present, I could infer reliance on sheep versus goat for each context and seek to identify patterns in herd composition throughout all three archaeological sites. A thorough analysis would require the full zooarchaeological analysis of each assemblage, however. My refinement of certain taxonomic attributions would contribute to this analysis. My use of ZooMS here was also intended to identify specimens which would be ideal candidates for subsequent aDNA analysis aiming to identify domesticated sheep and goats. By reconstructing the maternal ancestry of any specimens identified as domesticated, and radiocarbon dating them, the timing and routes of dispersal of these species from West Asia into Inner Asia could possibly be reconstructed.

Antilopines & Cervids

Eneolithic and Bronze Age reliance on hunting and herding are poorly understood throughout Southern Siberia and Outer Mongolia. The role of hunting in Medieval highland communities observing Islamic burial traditions in Transoxiana is also unknown. Here I used ZooMS to examine all three faunal assemblages for *Cervus* sp., *Capreolus* sp., *Gazelle* sp. and adjacent medium bovid specimens, and possibly identify fragments from these species that had not been

recorded by zooarchaeologists. Securely identifying deer or antelope bone fragments would allow the inference that hunting was taking place, at least during specific periods of occupation.

1.3.2. Collagen Peptide Marker Screening (MALDI-TOF)

There are currently no published collagen peptide markers for a number of the antelope and deer common to Inner Asia, including Prezewalskii's gazelle (*Procapra prezewalskii*), goitered gazelle (*Gazella subgutturosa*), Mongolian gazelle (*Procapra gutturosa*), Siberian roe deer (*Capreolus pygarus*), Siberian musk deer (*Moschus moschiferus*), Altai wapiti (*Cervus canadensis*), Bactrian wapiti (*Cervus elaphus bactrianus*), and sika deer (*Cervus nippon*). In order to determine if the MALDI spectra of goitered gazelle and sika deer differed either from one another or from their close antelope and deer relatives with published markers, and would thus be good candidate species for subsequent LC-MS/MS-based marker development, I subsampled reference specimens from a comparative collection and screened them using MALDI.

1.4. Structure

The faunal assemblages that I analyzed with collagen peptide mass fingerprinting were recovered from the archaeological settlements of Nizhnaya Sooru, ZK513, and Tashbulak. These three sites vary widely in spatial and temporal context, from prehistoric Southern Siberia and Outer Mongolia to Medieval Uzbekistan. I have structured this dissertation as a discussion of the archaeological cultures, settlement sites, faunal data, and animal economies associated with these regions and time periods of Inner Asia. I emphasize the archaeological methods, theories, and practices which have impacted the reconstruction of animal economies from these separate but connected archaeological records. Due to the extensive number of topics that needed to be addressed and the multiple bodies of archaeological data that needed to be provided I have not written one background chapter, but eighteen.

My background chapters begin with a broad overview of subsistence archaeology in relation to Inner Asia. I detail the methods available to archaeologists to reconstruct the archaeological subsistence practices, with an emphasis on zooarchaeology, biogeochemical zooarchaeology, and biomolecular zooarchaeology. I discuss the methods and criteria available for the analysis of key Inner Asian mammals, as well as how they have been applied to reconstruct domestication events and human-animal relationships. I then explore how these methods can be used to investigate ancient animal management strategies, including an overview of the ecological niches of key domesticated mammals of Inner Asia, and how these may be reflected in historical herd compositions. I also discuss the archaeological markers of pastoralism and the theories addressing pastoralist emergence in Inner Asia.

My overview of the historical events and theoretical paradigms which have underpinned the collection and reporting of the (zoo)archaeological data covers a wide array of subjects. These subjects include Marxism, Marrism, ethnogenesis, nomadology, craniometry, and material

culture typology as they relate to archaeological practice during the Soviet era. I further overview their legacy and impact upon Inner Asian archaeology after the collapse of the Soviet Union. I also discuss the history and practice of zooarchaeology specifically in the countries in which each context that I overview is situated, i.e. Russia and Mongolia. This review grounds my discussion of the archaeological cultures, settlement site archaeology, faunal data, and animal economies associated with Bronze Age Southern Siberia, Bronze Age Outer Mongolia, as well as the research questions attached to them.

My discussion of the archaeology and animal economies of Medieval Transoxiana is preceded by a necessary review of the prehistory of Central Eurasia that is largely centered around ancient Trans-Eurasian exchange networks. Trans-Eurasian exchange networks were critical to the dispersal of domesticated animals into (and out of, in the case of camels) Inner Asia. By endeavoring to reconstruct the history and logistics of their emergence, the role of human and animal migrations in the formation and evolution of ancient animal economies can be better understood. The innovations which facilitated these networks and thus connect the three faunal assemblages I analyzed from Inner Asia range from the prehistoric inventions of agriculture, wheels, and chariots, to the infrastructure, roadworks, and commerce invested in by the empires of Antiquity, to the rise of the so-called Silk Roads and the Arab conquest. My overview of these phenomena is necessary to contextualize the wide variety of settlement sites and animal bone assemblages that have been recovered from the archaeological record of Inner Asia, including those specific to my own study.

After providing a thorough background of the archaeological contexts associated with the faunal assemblages, I overview which samples were selected from each assemblage (and why). I then detail the subsampling methods, sample pretreatment protocols, instrumentation, and method of data analysis that I adhered to throughout the course of my research. Finally, I present my results. I overview the quality control, sample collagen preservation, and proteomics-based taxonomic identifications of mammals as well as a limited number of birds and reptiles. I compare and contrast my results with the respective zooarchaeological data, including of tentative, ambiguous, incorrect, and size-based morphological identifications, and overview the stratigraphic distribution of my proteomics-based identifications. I overview how my proteomics-based identifications have contributed to the overall body of NISP data available for key taxa from specific regional / temporal contexts. My “Materials & Methods” and “Results” chapters also include overviews of my MALDI screening of collagen peptide mass values for known markers of reference collection specimens.

In my “Discussion” chapter I draw upon the results of my analysis and filter them through the contextual prisms provided in my background chapters to provide my interpretation of the animal economies of Nizhnyaya Sooru, ZK513, and Tashbulak. For each site I examine animal management practices during different archaeological periods as well as human-animal relationships with specific taxa through time. These taxa necessarily vary somewhat by site, though I address the management of cattle (*Bos* sp.), equids (*Equus* sp.), caprines (*Ovis* sp. / *Capra* sp.), antelopes (*Gaezlle* sp., etc.), and deer (*Cervus* sp. / *Capreolus* sp.) at each. Camels and chickens are addressed less uniformly, as their remains were only identified at Tashbulak. I

conclude my “Discussion” chapter with suggested tryptic masses of common collagen peptide markers for goitered gazelle (*Gazella subgutturosa*) and sika deer (*Cervus nippon*), as well as their relation to published markers for other antiopines and cervids and suggestions for future research.

My Conclusion chapter is a mirror of this Introduction chapter. First I overview what my study has contributed to our understanding of Nizhnyaya Sooru, ZK513, and Tashbulak as well as Bronze Age animal economies, prehistoric horse domestication, Medieval animal economies, Medieval wooling economies, Medieval camel exploitation, and Inner Asian caprine husbandry. I then summarize how my ZooMS-based identifications have enriched the NISP data available for Inner Asian equids, camels, and caprines, and how my MALDI screening of antilopine and cervid collagen might aid future researchers. Finally, I discuss future directions in the analysis of Inner Asian archaeological fauna. It is my sincere hope that my work here will be of use to current and future researchers of this fascinating yet poorly understood area of archaeology.

2. Subsistence Archaeology

2.1. Introduction

“Food resources from animals and plants provided the necessities of life for any population, whatever period in history or geographical position.” (Vretemark et al. 2010)

In this chapter, I will explore the archaeology of the human subsistence strategies which have developed throughout Inner Asia. I will first very briefly overview human subsistence strategies and the archaeological methods of their reconstruction through the analysis of human remains, botanical remains, material culture remains, structural remains, and soil composition. I will then explore the analysis of archaeological fauna, also known as zooarchaeology. My overview will include taphonomy, paleopathology, taxonomic identification, specimen quantification, sex attribution, sex ratio determination, and age-at-death estimation through a zooarchaeological lens. I will also explore the ways zooarchaeologists can model these faunal data to reconstruct archaeological animal communities and human lifeways.

2.2. Human Subsistence Strategies

“The domestication of the major food mammals is one of the most crucial developments in the history of humankind.” (Rowley-Conwy et al. 2012)

Environmental conditions, resource availability, physical geography, human technology, social complexity, and cultural frameworks have all drastically influenced the trajectory and fluidity of human survival strategies (Thurston & Fischer 2007; Vretemark et al. 2010). Classifications of these strategies, i.e. subsistence strategies, can be viewed as points along a spectrum of dependence on wild versus domesticated food sources (Rietz & Wing 2008). One of the earliest forms of hominid subsistence was hunting and gathering, or the hunting of wild animals and gathering of wild plants (Marlowe 2005). Agriculture and pastoralism are subsistence strategies which emerged after hunting and gathering, at different times in different areas, in a series of poorly understood and non-linear events across the world. Agriculture involves the intentional management and domestication of animals and / or plants (Rindos 2013) and remains a major subsistence strategy to this day. A simple definition of pastoralism is the mobile management of domesticated animal herds (Dong 2016). I will discuss the many definitions and expressions, as well as the archaeological markers, of pastoralism in-depth in the next chapter of this dissertation (“Animal Economies in the Archaeological Record”). First, I will detail the methods that archaeologists use to reconstruct the diverse and mixed subsistence strategies which past humans developed and adapted in response to their unique environments and conditions.

2.3. Reconstructing Subsistence Strategies

"By comparing the results of archaeozoological and macrobotanical case study analysis from settlements…we can propose general tendencies for agrarian economy, and subsistence patterns can be suggested." (Vretemark et al. 2010)

Archaeologists endeavor to reconstruct the subsistence strategies of past populations using evidence has been left in the archaeological record. These lines of evidence include human remains, faunal remains, botanical remains, material culture remains, structural remains, and soil composition (Butzer 1982; Isakkson 2010; Rietz & Wing 2008). The analysis of human skeletal morphology, dental wear patterns, musculoskeletal stress markers, and paleopathological lesions can provide a window into human activity and subsistence strategies (Hawkey 1998; Larsen 1987; Molnar 2011; Nagy & Hawkey 1993; White & Folkens 2005). Human paleofeces and fecal steroids can provide direct and contextual data about an individual's diet (Fry 1985; Sobolik et al. 1996). Human stable isotope analysis and protein tandem mass spectrometry of human dental calculus are used in paleodietary reconstruction (Ambrose 1993; Hendy 2021, 2023; Hendy et al. 2018a,b; Warinner et al. 2014).

Turning to material cultural remains, the utility and portability of tools, containers, and artifacts offer insight into the practices and mobility (or lack thereof) of an archaeological population. Lithic analysis has long provided insight into subsistence activities, prey and resource selection, and mobility (Odell 2006). Ceramic assemblage and compositional analysis can aid in identifying traditions and techniques of manufacture, which can provide insight into cultural interactions, trade networks, lifeways, and mobility (Hunt 2017). Organic residue analysis and shotgun proteomic analysis of containers and sherds can reveal the former contents of recovered vessels (Chowdhurry et al. 2021; Hendy 2018, 2021, 2023; Oudemans 2007; Outram & Bogaard 2019; Paskulin et al. 2024; Rosiak et al. 2020; Tanasi et al. 2021; Solazzo et al. 2008). Recent developments in archaeological science which can now confirm the presence of certain organic substances with objects of material culture have been invaluable in reconstructing human lifeways and subsistence practices (Outram & Bogaard 2019).

Archaeologists are sometimes fortunate enough to directly recover plant remains, including visible *macrobotanicals* such as seeds, cereals, sedges, skins, pulps, fibers, roots, tubers, and charred wood, and microscopic *microbotanicals* such as phytoliths, pollens, spores, and starch grains (García-Granero et al. 2015). The collection of archaeobotanicals (or rather the lack thereof) from the archaeological sites of Inner Asia will be revisited throughout this dissertation (see Chapters 03-05). Botanical remains provide a very straight-forward insight into paleodiets, as well as the social contexts (Palmer & Van der Veen 2002) and environmental conditions (Mercuri et al. 2010; Reitz & Shackley 2012) which influence them. Neglecting robust recovery of botanicals from archaeological contexts can lead to a bias in subsistence interpretation, placing an inaccurate emphasis on the role of animal exploitation (Struever 1986). The analysis of plant DNA recovered from archaeological contexts can provide equally valuable insights into ancient economies, subsistence activities, and human population mobility (Schlumbaum et al. 2008).

Archaeologists (and other researchers, such as paleoecologists) can also infer subsistence pathways, economic activities, resource exploitation, and land use from the analysis of the soils and sediments that archaeological botanicals are sometimes recovered from (Hassan 1978; Hill & Rapp 2020). The analysis of sedimentary DNA (sedDNA) has been used to reconstruct livestock farming history, for example (see Giguet-Covex et al. 2014). A more straightforward method of animal management reconstruction is faunal analysis, or zooarchaeology, which is the most relevant of the aforementioned methods to this dissertation. I will explore zooarchaeological methodology and practice in-depth in the subsequent section, with an emphasis on the analysis (and related issues) of faunal remains from the archaeological sites of Inner Asia,.

2.4. Zooarchaeology

"One important aspect of being human is the range of interactions that we have with other animals…of all of the aspects of past human lives that archaeologists can set out to investigate, our involvement with other animals is one of the few that can be explored across all cultures, and throughout the history and prehistory of our species." (O'Connor 2008)

Zooarchaeology is the study of faunal remains (such as bones, teeth, hide, and feces) recovered from archaeological contexts (Grayson 1984). Zooarchaeologists analyze the morphology of fossilized animal tissues in pursuit of taxonomic and sexual attribution, as well as the estimation of physiological age-at-death (O'Connor 2008; Reitz & Wing 2008). Zooarchaeologists also examine faunal remains for modifications (butchering, gnawing, and weathering) and pathologies (O'Connor 2008; Lyman 1987; Reitz & Wing 2008; Rixson 1989). Where possible, zooarchaeologists endeavor to reconstruct detailed profiles from faunal assemblages by estimating composition and age-at-death data (O'Connor 2008; Reitz & Wing 2008). The distributions of these data are then modeled and interpreted to infer patterns of culling, management, and seasonality (O'Connor 2008; Reitz & Wing 2008; see also Payne 1973). Additionally, the taphonomic histories of animal remains can reveal significant information about methods and processes of animal exploitation (Lyman 2010; Orton 2012), while pathological bone lesions can reveal human care or neglect (Bartosiewicz & Gal 2013, 2018). Although the analysis of archaeological fauna is a complex and multifaceted process, zooarchaeology is critical to investigating ancient subsistence strategies. The following sections will introduce and explore the ways in which zooarchaeologists analyze and interpret archaeological animal assemblages.

2.4.1. Faunal Taphonomy

"One could say that archaeologists were preadapted to thinking taphonomically (from the perspective of a biased and incomplete archaeological record) given their interests in culture and human behavior, things that only exist among living people." (Lyman 2010)

Any in-depth discussion about the analysis of faunal remains would be incomplete without an in-depth discussion about taphonomy. Taphonomy has been assigned numerous definitions since its conception by the Soviet Russian paleontologist Ivan Antonovich Efremov (see

Efremov 1940) and subsequent adaptation by archaeologists around the world (see Lyman 2010). For the purposes of this dissertation, I define taphonomy as the activities and processes befalling any once-living organism at death and afterwards. Organic remains are subject to the physical and chemical characteristics of their surrounding environment as well as the biological realities of their own bodies, a fact that is incredibly important to any zooarchaeological study due to the resulting information modification (often loss) and potential bias introduction that comes from analyzing an incomplete representation of an organism after its death (Bartosiewicz 2013; Lyman 1987, 2010).

The paradigm of taphonomic activity is complex and can be sliced and diced many ways. Forensic scientists have divided taphonomy into progressive stages of *necrological* (immediate death), *biostratinomical* (pre-burial), and *diagenetic* (post-burial) (Pokines & Symes 2014). Archaeologists have created major categories of taphonomic damage such as disarticulation (i.e. anatomical dissociation), scattering or dispersal, fossilization, and mechanical modification (Lyman 1987). All of these groupings are relevant to the analysis of faunal remains, whose taphonomic histories are written at every stage relevant to the forensic scientist and susceptible to every type of damage perceived by the archaeologist.

Amongst these taphonomic damages, disarticulation and re-deposition are notorious for obstructing faunal analysis. Zooarchaeologists are forced to contend with the reality that the majority of the faunal remains they recover were deposited in fragments away from the spatial contexts in which they were killed and processed, and possibly further disturbed by scavengers or their environment (Bartosiewicz 2013; Lyman 1987). This directly influences the measurements that zooarchaeologists use to quantify the taxonomic and skeletal element abundances which are essential to their interpretations of animal interactions with humans and their environment, and who have attempted to cope with this issue by labeling, modeling, and observing controlled taphonomic phenomena (Lyman 1987).

There is an abundance of other diagenetic phenomena which zooarchaeologists must take into account. Weathering can fragment in-situ bone, alter bone morphology and density, and distort (or mimic) bone modifications (Behrensmeyer 1978). Erosion, or general bone loss, can equally impact the collection of biometric data (Pokines & Symes 2014). Microorganisms such as fungi, algae, and bacteria can demineralize bone and hinder preservation (Jans 2004). Bone fissuring can be caused by pressure, temperature, and a host of chemical processes, and may be misinterpreted (Pokines & Symes). Burning hastens bone mineralization by destroying organic matter (Efford 2016). Bone is also subject to alteration via excavation, transportation, storage conditions, and commercial preparation (Karr & Outram 2015; Lyman 1987). These processes are but a sample of the physical, chemical, and biological activities that faunal remains can be subjected to.

It is worth noting that taphonomic damage may also be mistaken for evidence of pathology, i.e. *pseudopathology*, or even etchings of human script (Bartosiewicz 2013). On a macroscopic level, taphonomy can create illusions of disease, predation, or cultural behavior, compromise taxonomic identification, interfere with patterns of distribution, obscure spatial contexts, distort

biometric data, and corrupt quantitative measurements. On a microscopic level, taphonomic damage can hinder magnetic resonance imaging and biomolecular analyses such as radiocarbon dating, peptide mass fingerprinting (PMF), stable isotope analysis, genetic analysis, and genomic analysis (Bartosiewicz 2013; Fellows-Yates 2013).

Zooarchaeologists are obliged to take taphonomy and its many challenges into account when analyzing faunal remains (e.g. Faith & Thompson 2018). As of yet, taphonomical information *loss* is an issue that no statistical method or advance in biomolecular archaeology has been able to resolve. Fortunately, the problem is not so great that zooarchaeologists have had to forgo faunal analysis altogether. Frameworks have been created to aid in the contextualization of data that taphonomy can *add* to a faunal assemblage, such as identifying refuse disposal, body part selection, and food preparation and butchery practices (e.g. Orton 2012; see also Rainsford & O'Connor 2018). Taphonomical histories, combined with paleopathological histories, when properly approached can provide archaeologists with a great deal of information about animal economies and their human exploitation. The next section of this dissertation will explore the ways in which the identification of paleopathological legions may (and have) contributed to the analysis of faunal remains.

2.4.2. Faunal Paleopathology

"...developing osteological techniques for understanding human-animal interactions has proven to be the linchpin of emerging knowledge of domestic animals in East and Central Asia." (Taylor et al. 2020c)

Similar to taphonomy, faunal paleopathology as the study of diseases and trauma detectable in archaeological animals originated within paleontology (e.g. Marsigli 1726; Esper 1774). Traditional techniques in human (paleo)pathology are not readily applicable to fossil fauna, owing to the impressive diversity of the animal kingdom and the complexity of its evolutionary interplay with disease (Bartosiewicz & Gal 2013). Developing unique criteria for faunal paleopathology has proven challenging, considering the extremely low representation of pathological archaeofauna in faunal assemblages, a lack of reference collections, training, and proficiency, and the resultant high margin of pathological misidentification (Bartosiewicz & Gal 2013).

Despite these complications the observation and analysis of faunal paleopathology can provide unique insights into ancient economies, exploitation strategies, and human-animal relationships (Bendrey 2014; O'Connor 2008; Sick & Kohut 2024). In the context of Inner Asian archaeology, faunal paleopathology has been used to infer horse traction and transport, horseback riding, and pastoralism. Differential distributions of spinal lesions have been associated with horse traction (e.g. cart pulling) versus riding, and have been used to argue for different modes of horse exploitation (Taylor 2024). Occlusal surface damage to the second mandibular premolar teeth of horses has been connected with bit chewing and presented as evidence of horseback riding at the Eneolithic sites of Botai and Kozhai 1 in northern Kazakhstan (Brown & Anthony 1998; Anthony & Brown 2011), though these findings have since been disputed (Taylor 2024; Taylor & Barrón-Ortiz 2021) .

Bit wear analysis has proven to be an insightful but complicated method with many factors that must be taken into consideration. Firstly, individual premolars should be compared to their counterparts when seeking to identify sources of anthropogenic occlusion, which may also result from ancient equine dentistry practices (Taylor & Barrón-Ortiz 2021). Bit wear may also result from cart traction involving a bridle and bit, and should subsequently be interpreted as evidence of horseback riding with caution and ideally alongside other lines of skeletal evidence (Taylor & Barrón-Ortiz 2021). Significantly *malocclusion*, or natural dental misalignment, has both been noted for its potential to be mistaken for bit wear *and* suggested as a potential marker of horse domestication (Anthony & Brown 2011), highlighting the complexity and subjectivity of paleopathological dental analyses.

The absence of occlusal surface damage on mandibular horse premolars paired with maxillary premolar occlusal surface damage and other dental pathologies observed in archaeological horse remains has been used to argue for domesticated horse management involving the use of shallow rein angles and fast gaits in Late Bronze Age Mongolia (Taylor et al. 2015). Beyond dentition, analyses of cranial pathologies such as asymmetry, premaxillary remodeling, and left nasal bone deformity have also been integrated into arguments for horse bridling,riding, transport, and mobile pastoralism in Late Bronze Age Mongolia, and even incorporated into reconstructions of bridles from this context (Taylor et al. 2014; Taylor et al. 2015; Taylor 2017; Taylor & Tuvshinjargal 2018).

Combined dental and cranial pathologies observed in radiocarbon dated archaeological horses from the Novoil'inovskiy 2 Cemetery have been interpreted as evidence of horse exploitation involving bridle and cheek pieces in Late Bronze Age Northern Kazakhstan (Chechuskov et al. 2020). Uniquely, paleopathology also offers a theoretical method of identifying female horse remains by virtue of their pathological nature, the assumption being that female horses exhibit more chronic laming and poorer dental care (Cross 2018). By and large, the application of faunal paleopathological analyses in early Central Eurasian contexts has been in a quest to establish when the earliest forms of domesticated horse management and utilization developed, and to understand what these practices looked like.

2.4.3. Identifying Faunal Remains

"The identification of animal remains will only be as good as the skill-level of the analyst and the completeness of the modern comparative osteological collections." (Peres 2010).

Having discussed some of the many ways in which animal bones and teeth may be modified and reorganized before (and during, and after) recovery by archaeologists, this section will focus on what zooarchaeologists actually do with faunal remains. Taxonomic determination is essential to zooarchaeological assemblage interpretation and is one of the primary goals of faunal analysis (Albarella 2018; Boessneck & von den Driesch 1978; Driver et al. 2011; Rietz & Wing 2008). Zooarchaeological methods rely on skeletal morphology and measurements to assign taxonomic categories to faunal remains, a process which might be more appropriately called *attribution* than identification (O'Connor 2008). While biomolecular methods such as aDNA analysis and peptide mass fingerprinting can heighten the accuracy and resolution of

taxonomic identifications (see Chapters 04–06), here I will focus on the former before discussing the latter.

Archaeological assemblages from Inner Asia may contain remains from a wide array of wild and domesticated fauna including herbivores such as aurochsen (*Bos primigenius (†)*), domesticated cow (*Bos taurus*), wild yak *(Bos mutus),* domesticated yak *(Bos grunniens),* domesticated horse (*Equus caballus*), wild horse (*Equus ferus*) Prezwalski's horse (*Equus ferus przewalskii*), onager (*Equus hemionus*), khulan (*Equus hemionus hemionus*), Bactrian camel (*Camelus bactrianus*), markhor (*Capra falconeri*), Siberian ibex (*Capra siberica*), domesticated goat (*Capra hircus*), domesticated sheep (*Ovis aries*), mouflon (*Ovis orientalis*), urial (*Ovis vignei*), argali (*Ovis ammon*), saiga antelope (*Saiga tatarica*), Mongolian gazelle (*Procapra gutturosa*), goitered gazelle *(Gazella subgutturosa),* Siberian roe deer (*Capreolus pygarus*), sika deer (*Cervus nippon*), wapiti (*Cervus canadensis*), elk/moose (*Alces alces*), Bactrian wapiti (*Cervus elaphus bactrianus*), domesticated pig (*Sus scrofa domesticus*), and wild boar (*Sus scrofa*). Possible carnivores include brown bear (*Ursus arctos*), snow leopard (*Panthera unicia*), Asiatic cheetah (*Acinonyx jubatus venaticus*), Asiatic wildcat (*Felis lybica ornata*), wild cat (*Felis silvestris*), sand cat (*Felis margarita*), reed cat (*Felis chaus*), caracal (*Caracal caracal*), Eurasian lynx (*Lynx lynx*), Pallas's cat (*Otocolobus manul*), domesticated cat (*Felis catus*), wolf (*Canis lupus*), dog (*Canis familiaris*), golden jackal (*Canis aureus*), corsac fox (*Vulpes corsac*), and red fox (*Vulpes vulpes*). Smaller game animals include a wide array of badgers, hares, weasels, martens, stoats, and polecats. Domesticated chickens (*Gallus domesticus*) and hundreds of other birds, as well as dozens of reptiles, are also prevalent in certain regions of Inner Asia.

While taphonomy can greatly hinder taxonomic identification, there are additional issues that zooarchaeologists must contend with (see LeFebvre & Sharpe 2018). In Chapter 03, I will explore some of these challenges as they apply to the individual taxonomic groups of greatest interest to this dissertation– i.e. cattle (*Bos* sp.), equids (*Equus* sp.), camelids (*Camelus* sp.), caprines (*Ovis* sp.; *Capra* sp.), antelopines (*Gazella* sp., *Procapra* sp.; *Saiga* sp.), cervids (*Cervus* sp.; *Capreolus* sp.), and suids (*Sus* sp.). Although I review the availability of published osteological atlases and morphometric criteria for each taxon, it is important to note that many zooarchaeologists work with comparative collections. Having access to quality reference specimens and hands-on experience is more valuable than having access to published illustrations and morphometric criteria (Albarella 2018; LeFebvre & Sharpe 2018; Peres 2010).

2.4.4. Quantifying Faunal Remains

"The history of zooarchaeology…has involved a shift from producing estimates of taxonomic abundances to measuring various taphonomic processes and effects within taxa. As a result, many new quantitative units and terms have been proposed…we must strive for clarity in our discussions of quantitative data." (Lyman 1994a)

Determining the presence and absence of taxa in faunal assemblages is of great interest to zooarchaeologists, but so is measuring their representation, i.e. *relative abundance* (Grayson 1984; Lyman 1994a). In the context of subsistence strategy studies, quantifying faunal remains aids zooarchaeologists in understanding which animals were exploited at what times and with

what level of importance (Grayson 1984; Reitz & Wing 2008). The importance of quantification cannot be underestimated because the measurement of relative abundance directly affects subsequent zooarchaeological analyses. During taxonomic attribution zooarchaeologists (generally) quantify the total number of bones and teeth recovered from an archaeological context, or the *number of identified specimens* (NISP) (Grayson 1984).

Stand-alone NISP counts once formed the core of faunal analysis but have since been criticized for being easily biased by factors including excavation methods, differential preservation, butchery patterns, differential diagnostic morphology of different elements that vary by taxa (which do not all have the same number of teeth and bones), differential susceptibility to taphonomic damage, and the potential representation of one or more taxa in fragments while the remaining taxa are represented by whole elements (Grayson 1984; Klein & Cruz-Uribe 1984). Frequencies of skeletal parts (secondary data) are now often used in conjunction with NISP (a primary data specimen count), namely *Minimum Number of Individuals* (MNI) and *Minimum Number of Elements* (MNE) (Grayson & Frey 2004).

MNI counts were originally introduced to help calculate the amounts of meat provided by different animals (White 1953). MNI evades the NISP problems of interdependence and skeletal variability by focusing on the smallest possible number of individual animals that could be represented in an assemblage based upon the elements recovered (Grayson 1984; Reitz & Wing 2008). MNI is instead dependent upon aggregation (e.g. layer, phase, whole site), which is up to the zooarchaeologists discretion, and caution must be observed when comparing MNI counts from different sites. Additionally, MNI counts (along with MNE counts) have not always maintained a consistent definition and disclosure of what is meant by MNI / MNE has not always been provided in faunal reports (Reitz & Wing 2008). I consider MNE to be the smallest possible number of elements represented in an archaeological assemblage (Lyman 1994a).

Following this definition, a hypothetical assemblage consisting of 5 left tibia, 2 right tibia, and 12 unknown fragments would have an MNI of 5 (the smallest possible number of animals), an MNE of 7 (the smallest possible number of elements), and an NISP of 19 (the total number of specimens). Notably, a “ZooMS e-NISP” count has also recently been suggested for assemblages that will also undergo ZooMS analysis, to be calculated by “dividing the total ZooMS mass of identified bones (g) by the mean mass of morphologically identified bones for that taxon (g/NISP)”, per taxon (Discamps et al. 2024). An exhaustive list of the many other quantitative units that have been used by zooarchaeologists is beyond the scope of this dissertation (the curious reader is directed to Lyman 1994a), which will focus instead on the analyses that NISP, MNI, and MNE counts can be incorporated into to investigate the emergence of pastoralism in Eneolithic and Early Bronze Age Inner Asia.

2.4.5. Sexing Faunal Remains

“The ability to differentiate between male and female animals in the faunal assemblage from an archaeological site provides invaluable information on strategies of animal exploitation as practised by past human populations.” (Horwitz et al. 1990)

Having determined which taxa are represented in a faunal assemblage and in what quantities, zooarchaeologists interested in subsistence strategies will endeavor to reconstruct an assemblage profile that includes sex and age-at-death distribution data (Klein & Cruz-Uribe 1984; Reitz & Wing 2008). The determination of the sex of archaeological animal remains is a complicated endeavor. Differential primary and secondary characteristics arise from sexual dimorphism, mostly limited to pelvis and canine morphology, horns, and antlers. Zooarchaeologists typically examine skeletal elements which are sexually dimorphic (e.g. pelvises), primary sex characteristics (e.g. baculae), and secondary sex characteristics (e.g. antlers) to try and establish the sex of individual animal remains (Klein & Cruz-Uribe 1984; Meadow 1983; Reitz & Wing 2008; Ruscillo 2003). Criteria have not been developed for all of the key Inner Asian species that I emphasize throughout this chapter; I provide a thorough review of these in Chapter 03. Even in species where published criteria are available, processes such as castration and hybridization which affect an animal's physiological development can impact sex determination and skew the results of faunal analyses. Taphonomic damage and fragmentation can also obscure analyses, especially in cases where sexually immature specimens need to be isolated.

2.4.6. Sex Ratios

"In order to understand exploitation strategies...it is necessary to be able to identify and separate between male and female animals represented in the deposits...biased sex ratios in an assemblage may have important implications as regards patterns of human as well as animal activity…" (Horwitz et al. 1990)

Having established the methods available to zooarchaeologists to assign sex to faunal remains (see section "2.4.5."), I will now explore how these data can be modeled, analyzed, and interpreted for inference into ancient animal economies and subsistence strategies. It is important to be mindful of the same difficulties involved with accurately sexing ancient animal remains, and maintain awareness that these remains constitute incomplete, taphonomically damaged assemblages which do not wholly represent their once-living communities. That being said sex data, or more specifically *sex ratios*, can provide valuable insight into herd demographics, hunting behavior, seasonality, and secondary product specialization (Klein & Cruze-Uribe 1984). Sex ratios are thus an indispensable tool in the investigation and reconstruction of ancient pastoralist practices.

Despite the frequent incorporation of sex ratios in faunal analyses, they are generally not given much explanation in zooarchaeological publications. Sex ratio interpretations are largely contextual; fundamental baselines, templates, and introductory literature are lacking (for a strong but old exception, see Klein & Cruze-Uribe 1984). This is in stark contrast to mortality profiles, where attempts to assign animal management and product production strategies from reconstructed age-at-death patterns have been published for decades (e.g. Payne 1973; Redding 1981, 1984; Greenfield 1988, 2005; Vigne & Helmer 2007)– despite the fact that mortality data must be handled with the same level of caution as sex data. I will explore mortality profiles in-depth in the subsequent section ("I.IV.VIII.").

A key study looking at the sex ratios of archaeological mountain gazelle remains (*Gazella gazella*) outlined key avenues of interpretation: seasonal occupation, culling methods, and product specialization (Horwitz et al. 1990). Uneven sex ratios are generally interpreted as indicating sexually selective subadult culling practices (Isaakidou 2020), which may in turn be interpreted multiple ways. Another important study investigating animal exploitation in Old Kingdom Egypt deemed a predominantly female caprine assemblage an archaeological rarity that may have resulted from the relocation of juvenile males for consumption (Redding 1992). A predominance of females in an archaeological cattle assemblage from Bronze Age Kazakhstan was subsequently interpreted as having likely been managed for secondary product production (Outram et al. 2011).

Sex ratio data can also provide valuable insights on its own; archaeologists have recognized that male to female ratios in horse remains recovered from ritual and non-ritual assemblages from Eurasia were even from the Upper Paleolithic to the Early Bronze Age (Fages et al. 2020). The over-representation of male horses observed after the conception of the Bronze Age has been attributed to a gendering of horses that supposedly followed an alleged emergence of gender inequality in Eurasian societies (Fages et al. 2020). Sex ratio interpretation is, however, generally interdependent upon the archaeological context as a whole, and ideally combined with age-at-death data when investigating herd management and product specialization strategies.

2.4.7. Aging Faunal Remains

“The estimation of age at death has generated a great deal of research, principally into better ways of attributing age at death to archaeological specimens.” (O’Connor 2008)

Zooarchaeologists estimate the relative age-at-death of faunal remains the same way they generally attribute sex– by the examination of bones and teeth. Each element presents its own series of challenges during analysis. Complications involved with aging animal bones arise from sexual dimorphism, breed variation, and imprecise fusion stages (Davis 2012; Greenfield & Arnold 2008; Klein & Cruz-Uribe 1984; O'Connor 2008; Reitz & Wing 2008). Teeth preserve better in the archaeological record than bone (Hollund et al. 2013, 2014; Scott 2008) and can provide age-related data beyond sexual maturation or concluded epiphyseal fusion (Reitz & Wing 2008), but cannot directly reveal the absolute age of an individual. Dental analysis is often combined with osteological analysis to estimate the relative age-at-death in faunal remains (Jones & Sadler 2012).

The distal and proximal ends of long bones, or *epiphyses*, fuse at different ages in different species (Chaplin 1971; Davis 1987; Hesse & Wapnish 2008; Klein & Cruz-Uribe 1984; Lesbre 1898; O'Connor 2008; Schmid 1972; Silver 1969; Uerpmann 1973). As an individual animal matures, its long bone epiphyses gradually join with its long bone shafts, or *diaphyses*. By examining the presence or absence of epiphyseal fusion, zooarchaeologists can make educated estimates about the age range of the animal at their time of death. Zooarchaeologists frequently use (but do not always define) early, middle, and late fusion stages which are then subjectively assigned to age ranges such as *infant*, *juvenile*, *subadult*, and *adult* (Marciniak

2014; Moran & O'Connor 1994). This lack of clarity about how fusion stages are defined leads to unclear data and problems with dataset comparability.

The age of epiphyseal fusion varies not just between species but also between individuals within the same species, further compromising age-at-death estimates (Hatting 1948; Klein & Cruz-Uribe 1984; Marciniak 2014; O'Connor 2008; Tchirvinsky 1909; Todd & Todd 1938; Wallace 1948). Fusion ages are not known for all wild species, though we do know that they tend to be strongly inconsistent with absolute age (Greenfield & Arnold 2008). This same variation is also found in different domesticated animal breeds, though to a lesser extent (Greenfield & Arnold 2008; O'Connor 2008). Even if accurate physiological ages could be determined, epiphyseal fusion concludes when an animal matures and so is not useful for distinguishing age classes beyond "adulthood" (Crabtree 1982; Klein & Cruz-Uribe 1984; Greenfield & Arnold 2008; Payne 1973).

Additionally, taphonomic biases can arise not only from disarticulated assemblages but also because immature bones are less likely to endure in the archaeological record (O'Connor 2008). This differential preservation can bias subsequent data modeling, such as mortality profile construction (Greenfield & Arnold 1986, 1989, 1991, 2008: O'Connor 2008). A solid understanding of the issues surrounding age-at-death estimation, epiphyseal fusion, and fusion age ranges is crucial to archaeological investigations into subsistence strategies and pastoralism. Equally important is an understanding of age-at-death estimation methods centered upon dental analysis.

The analysis of dental eruption and wear (sometimes called attrition) is the primary method by which zooarchaeologists estimate relative age-at-death (O'Connor 2008). *Eruption* refers to the projection of teeth upwards through the alveolar bone and into the occlusal plane (Davis 2012; White et al. 2011). Mammals possess a primary set of teeth which are replaced over time by a secondary set in sequences of eruption, the timing of which is generally consistent amongst individual animals (Davis 2012; Hillson 2005; O'Connor 2008; Rietz & Wing 2008). Stages of eruption may be examined and compared to timelines of known dental development in order to assess approximate age (Davis 2012; Hillson 2005; O'Connor 2008; Rietz & Wing 2008).

Wear refers to the exposure of dentine and cementum beneath the enamel of teeth which have erupted into occlusion and experience continual wear through contact with other surfaces (Davis 2012; Hillson 2005). Wear is a life-long process and the resultant patterns of tooth wear may be examined to estimate relative age-at-death (Hillson 2005; O'Connor 2008). Though wear is progressive it does not occur at a fixed rate even amongst members of the same species, due to variations in dental morphology, diet, nutrition, and individual behavior (Davis 2012; Hillson 2005; Legge 1992; O'Connor 2008; Reitz & Wing 2008). By examining dental eruption and wear, zooarchaeologists can assess the relative age class of an archaeological animal's dentition (Davis 2012; Hillson 2005; O'Connor 2008; Reitz & Wing 2008) in accordance with an age class model of their choice (e.g. Higham 1967; Grigson 1982; Halstead 1985; O'Connor 1988; Legge 1992; Jones & Sadler 2012).

The dental age class model selected by zooarchaeologists has a strong influence on their assemblage reconstructions and subsequent subsistence strategy interpretation. The versatility of the many dental age class models developed by zooarchaeologists over the past fifty years is influenced by the span and quantity of the individual age classes. The advantage of having fewer rather than more age classes (e.g. O'Connor 1988; Legge 1992; Halstead 1985) is that the distribution of age-at-death data are less likely to be spread too thin, which is useful when analyzing small assemblages; the disadvantage is that resolution is diminished, and clusters of specific ages may go unnoticed. Conversely, a greater quantity of age classes can be useful as an animal's lifespan may continue years beyond heavy dental wear and broad categories in younger animals can hinder the investigation of herd management strategies (Jones & Saddler 2012).

Some dental age class models have been constructed with inherent biases (e.g. Highams 1967; Grigson 1982; Grant 1975, 1982) and the robusticity of others is dependent on the sample sizes they are applied to (e.g. Halstead 1985, O'Connor 1988, Legge 1992, Jones & Saddler 2012). The nuances and limitations of dental age class models must be kept in mind when producing and comparing mortality data derived from dental analyses, especially when reconstructing herd composition and investigating subsistence strategies. Dental analysis and age class attribution is frequently combined with the examination of epiphyseal fusion to estimate the age-at-death, due to the inherent limitations of each approach.

There is no "one size fits all" age-at-death estimation for archaeological fauna, due to the diversity of both animal physiology and archaeological assemblages / contexts. Assemblage size, taxonomic distribution, sexual and skeletal part representation, and taphonomic history all greatly influence method selection. Methods available to zooarchaeologists include the analysis of epiphyseal fusion, dental eruption, and dental wear–all of which have several limitations that must be taken into account. The resultant ages-at-death are often best viewed as relative as opposed to absolute, although absolute age estimation is not beyond the realm of possibility.

2.4.8. Mortality Profiles

"Moreover, culling profiles are subjected (as all archaeological objects) to a lot of biases…" (Brochier 2013)

Faunal age-at-death distributions were originally conceived for ecological analyses (Deevey 1947) but can also reveal evidence of exploitative human behavior upon archaeological animal populations- especially when evaluated in context with sex ratios (Davis 2012). Graphical reconstructions of age-at-death frequency distributions (mortality profiles) can be analyzed to infer whether a population was stable or unbalanced, i.e. exhibiting augmented or diminished representations of certain age classes (Lyman 1994; O'Connor 2008; Stiner 1990). Age-at-death data derived from wild animal assemblages can in turn be utilized to extrapolate hunting tactics, seasonal killing, and seasonal occupation (Klein 1982; Payne 1973, Reitz & Wing 2008, Stiner 1990). The mortality profiles of domesticated animal assemblages may be interpreted to infer herd specialization and livestock management practices (Arbuckle & Atici 2013; Gillis 2022; Hesse 1982; Jones & Sadler 2012; Payne 1973).

There is no shortage of challenges involved in reconstructing mortality profiles; sample size, diagenesis, sex ratios, theory indetermination, mixed subsistence strategies, statistical methods, and age-class determination all present their own issues (Arbuckle 2008; Bartosiewicz 1999; Brochier 2013; Greenfield 1988, 2010; Levine 1982b; Lyman 1987; Marciniak 2014; Marom & Bar-Oz 2009; Meadow 1989b; Munson 2000; Price et al. 2016; Reitz & Wing 2008; Zeder 2006b). A plethora of mortality profile models and “templates” have been presented throughout the course of several decades, and they do not all agree with one another. For example, an early influential archaeological study associated caprine assemblages dominated by adult females with both meat and dairy production (the former especially with males culled at ages between 2 and 3 years), and an equal distribution of adult males and females (and the presence of castrated males) with wool production (Payne 1973). And yet, wild animal assemblages have been distinguished from domesticated herd assemblages under the assumption that the former should consist of animals in their prime and the latter of adolescent males (Abdi 2015).

Later studies on caprine mortality profiles suggested that 5:1 ratios of sheep to goat could represent either energy or protein offtake, while 1:1 ratio of males culled at ages between 9 months and 2 years reflected herd scrutiny (Redding 1981, 1984). The aforementioned wool production “template” for sheep (Payne 1973) was extended to represent traction in cattle (Greenfield 1988, 2005). Non-sex-specific mortality templates followed correlating meat production strategies with cullings between 6 months and 1 year or 1 year and 2 months, as well as dairy production strategies with cullings between 0 and 3 months or 2 years and 4 years, and wool production with cullings between 4 and 6 years (Vigne & Helmer 2007; see Brochier 2013 for comments and criticisms). Mortality models have also been applied to equids and wild ungulates (e.g. Levine 1982a; Lyman 1987).

These templates often fail to accurately reflect herd management and product specialization strategies (Cribb 1985, 1987; McCormick 1992; Russell 2004). Although mortality profiles have been met with heavy criticism they have proven to be valuable and continue to be incorporated into faunal analyses. Mortality profiles are generally depicted as either histograms conveying dental data, epiphyseal fusion data (or both), or frequencies of fused and unfused bones, or as ternary diagrams depicting three age classes for individual bones (Marciniak 2014). The effectiveness of mortality profiles and sex ratios are ultimately dependent upon taxonomic identification and quantification, sex determination, age-at-death estimation, and archaeological context. When approached with a solid understanding of these concepts and a robust approach to their determination, the resultant mortality profiles can be invaluable tools in the reconstruction of archaeological animal economies.

The incorporation of mortality profiles into the faunal analyses and subsistence studies of Inner Asia is very limited, though examples do exist. An unpublished master's dissertation used bar graphs of fusion age ranges to argue for a sedentary agropastoralist economy (as opposed to nomadic) at the Iron Age site of Taldy-Bulak 2 in Kazakhstan, suggesting that caprines were primarily slaughtered for meat and cattle primarily used for traction (Haruda 2007). Mortality profiles reconstructed from the epiphyseal and dental data of caprines recovered from the Late Bronze Age / Early Iron Age farmhouse site of Chap I (in the Tien Shan Mountain region of

Kyrgyzstan) were used to argue to for a specialized wool economy as opposed to a meat production economy (Ananyevskaya et al. 2021). Moving forward, archaeological investigations into Inner Asian animal economies would ideally endeavor to incorporate mortality profiles into their analyses, along with other lines of supportive evidence

2.4.9. Zooarchaeology: Conclusion

"Unlike potsherds or stone tools, bones have been alive…our collection and interpretation of archaeological data depends…on our understanding of the…underlying zoology…defining our research aims in terms of relations between people and other animals…encourages us to….research…what we actually want to know, rather than…what we think we can find out from a particular data source." (O'Connor 2008)

Faunal analysis can be extremely complex, yet also extremely rewarding. Archaeological animal remains are subject to a wide array of phenomena that can alter their spatial distribution and physical state from death to recovery, and even after. Zooarchaeologists can often use these taphonomic histories to reconstruct elements of human-animal relationships, but must also contend with the taphonomic loss that inevitably biases their analyses. This information is generally most valuable when taxonomic identification is possible, yet the difficulties involved are manifold. Morphology can be plastic and is often influenced by hybridization, region, climate, stress, and sexual dimorphism. Valuable lines of evidence can be found here as well; stress can lead to pathological lesions that the analyst can use to reconstruct past conditions, and sexual dimorphism can facilitate sex attribution. Information about human-animal relationships can also be inferred from pathological lesions observed in animal bones, especially horse domestication and riding in the context of inner Asia.

Variability can also be a great hindrance, and biometric overlap is especially difficult to account for in attempts to distinguish species (and sexes). This is perhaps most impactful in efforts to distinguish the bones of domesticated taxa from wild taxa, not to mention intermediate and feral taxa. The limited osteomorphometric diagnostic criteria that zooarchaeologists have developed can be seriously compromised by biometric variability, as well as sexual differences, physiological maturity, and processes such as castration. Robust osteomorphometric criteria for identifying, sexing, and aging is also not available for all animals, and the traditional emphasis on West Asia in key animal domestication studies has left a gap in criteria for certain Inner Asian taxa. Age-at-death estimation methods involve their own complex issues regarding epiphyseal fusion, dental eruption, and dental wear, and yet is this very complexity that allows zooarchaeologists to estimate their physiological age to begin with.

Zooarchaeologists who are able to attribute taxonomic, sex, and age data to their archaeological assemblage of interest may then also attempt to reconstruct sex ratios and mortality profiles. Mortality profiles may then be used to infer animal management and secondary product specialization strategies in the case of domesticated taxa, as well as patterns of hunting and seasonality in the case of wild taxa. Mortality profiles have been used to argue for the presence of both meat-based and wooling / dairying economies at different archaeological sites in Inner Asia, for example. Mortality profiles can also be contrasted through different regions and time periods to identify overarching trends and developments in animal

husbandry and hunting, which may be examined in tandem with climate change and human historical data.

2.5. Subsistence Archaeology: Conclusion

“The importance of creating this linkage between economy and material culture cannot be underestimated in the way it provides a more holistic and integrated view of human cultural systems and change.” (Outram & Bogaard 2019)

Human subsistence strategies are fluid. They evolve as mixed modes and adaptations of hunting, foraging, herding, and agricultural activities in response to environmental conditions and technological innovation. A number of methods are available to archaeologists investigating ancient subsistence strategies, including the analysis of archaeological human skeletons, botanicals, soils, inorganic materials, residues, and animals. Among these, faunal analysis is crucial to the reconstruction of ancient human subsistence strategies, animal economies, and human-animal relationships more broadly. Zooarchaeological methods are largely borrowed from paleontology and ecology, and are often rooted in morphometric analysis. The morphometrical analysis of faunal remains to attribute taxonomy, determine sex, and estimate age-at-death involves the analysis of bones and teeth, which is complicated by an abundance of factors including taphonomic loss, morphological plasticity, physiological processes, biometric overlap between species, and species hybridization. Advances in archaeological science have led to the incorporation of biogeochemical and biomolecular methods into analyses which can help clarify and enrich zooarchaeological data. I will discuss the applications of these methods in the next chapter.

3. Biogeochemical Zooarchaeology

3.1. Introduction

"...there has been a recent explosion in archaeological research that combines zooarchaeology and…biogeochemistry in order to investigate how human-animal relationships shape and direct…ancient societies." (Makarewicz 2016)

Zooarchaeological methods generally rely upon the taphonomic, morphological, biometrical, and spatial analyses of animal remains to characterize archaeological assemblages. Late twentieth century archaeologists began incorporating chemical approaches into their faunal analyses, using stable isotope analyses to gain more insight into archaeological animal mobility, diets, and environments, as well as radiocarbon dating to more precisely reconstruct chronological contexts. Although both methods are often referred to by archaeologists as biomolecular (e.g. Brown & Brown 2013; Rosengren et al. 2021), I consider the term biogeochemical to be more appropriate. Stable, radiogenic, and radioactive isotopes are not biomolecules, but chemical elements which become incorporated into the tissues of living animals through biochemical processes related to the carbon cycle, photosynthesis, and trophic networks. I have titled this chapter accordingly and here will explore the biogeochemical techniques most commonly utilized by zooarchaeologists and researchers–i.e. stable isotopic analysis and radiocarbon dating.

3.2. Stable Isotope Analysis

"Forty years after its emergence…isotope-based…analysis is a mature discipline, and its methods are widely applied to a variety of archaeological questions and contexts…Nevertheless, many uncertainties and ambiguities remain that complicate straightforward interpretation of isotopic data." (Warinner 2014)

Stable isotopes are the non-decaying atoms of an element with varying atomic masses, and their analyses have long been incorporated into archaeological and paleoecological reconstructions (DeNiro 1987; Gifford-Gonzalez 2018; Malainey 2011; Warinner 2014). This section explores how certain different isotopes (i.e. carbon, nitrogen, strontium, oxygen) become incorporated into the archaeological record and how the analysis of their ratios has been integrated into zooarchaeological studies. Emphasis is placed on investigations into Inner Asian subsistence and animal management strategies. Attention is also drawn to the fact that stable isotope analyses are not as straightforward as often presented (Warinner 2014), and that this is especially true in the context of Central Eurasia. Stable isotopes can provide powerful lines of evidence for zooarchaeologists, but must be interpreted with caution (Britton 2017; Gifford-Gonzalez 2018; Makarewicz 2016; Rosengren et al. 2021; Szpak 2022).

3.2.1. Stable Carbon Isotopes (^{12}C, ^{13}C)

There are two stable carbon isotopes present in earth's atmosphere (^{12}C and ^{13}C) which are absorbed into plants during photosynthesis (Farquhar et al. 1989; Post et al. 1990). Carbon

isotopes are subsequently incorporated into animal tissue through plant consumption and differences in $\delta^{13}C$ values are predominantly the result of distinct photosynthetic pathways of the plants consumed (Ambrose 1990; Cerling & Harris 1999; DeNiro & Epstein 1978; DeNiro 1985; Warinner 2014). Plants which predominate in temperate and boreal forest mid-latitude environments such as wheat, rice, barely, soybean, and rice follow the C_3 pathway. Plants such as sorghum, maize, sugarcane, and foxtail millet which are more commonly found in arid environments follow the C_4 pathway. Different types of plants also exhibit different d13C values and C3 environment plants growing in or under a canopy, with less light and recycling of carbon exhibit depleted d13C values while those in open, arid environments have higher values (Bonafini et al 2013; Drucker et al 2008).

Animal metabolic processes result in isotopic fractionation of 4-5‰ between consumed plants and bone collagen, enabling the estimation of the relative contribution of C3 versus C4 plants to animal diets (Ambrose 1993). There are several challenges that archaeologists must be mindful of involved with interpreting the δ13C values of bone collagen, dentine, and enamel bioapatite to reconstruct plant consumption in animals. Firstly, minor carbon isotopic enrichment occurs at each trophic level in a food chain (Bochrens et al. 2003; Schoeninger 1985; Syvatko 2016) resulting in a 1.1 ± 0.2‰ difference between primary consumers (herbivores) and predators (Bocherens 2015). Isotopic enrichment can also be detected between mothers and suckling infants (Jenkins et al. 2011; Wright and Schwarcz 1998). Secondly, the consumption of marine resources also produce higher δ13C values in consumers, which can complicate distinguishing between the isotopic signatures of very different food sources (Schoeninger & Deniro 1984).

A similar problem is presented by freshwater fish consumption, which can be mistaken for C3 plant consumption (Ambrose 1993). Additionally, non-dietary factors such as the canopy effect in forests, can influence the carbon isotopic ratios (van der Merwe & Medina 1991). Finally, carbon isotope data derived from bone collagen only reflects the last decade of an animal's life due to bone remodeling (Syvatko 2016). Despite these challenges, stable carbon isotope analysis of faunal remains from archaeological sites continues to provide invaluable insights into animal dietary ecology (Finucane et al. 2006; Gifford-Gonzalez 2018; Zangrando et al 2014). $\delta^{13}C$ values are ideally interpreted alongside other forms of evidence (Gifford-Gonzalez 2018), especially combined carbon and nitrogen stable isotope analyses (Syvatko 2016), as will be explored later in this section.

3.2.2. Stable Nitrogen Isotopes (^{14}N, ^{15}N)

Nitrogen has two stable isotopes, ^{14}N and ^{15}N which are absorbed into plants through bacterial degradation in soil (Svyatko 2016; Warinner 2014). Plants typically exhibit $\delta^{15}N$ values ranging from -5 - 18‰, and these stable nitrogen isotope ratios are incorporated into animal skeletal tissues through consumption (Warinner 2014). A ~3-6‰ shift can be observed in the transference of $\delta^{15}N$ collagen values from resource to consumer (Hedges & Reynard 2007; O'Connell et al. 2012). Subsequently, ^{15}N values of animal bone collagen can provide insight into animal diet, ecology, trophic positioning, predator-prey relationships, and possibly environmental topography (Bocherens & Drucker 2003; Bocherens 2003; 2015; Ugan & Coltrain

2011). Weaning patterns and milk production in animals can also be inferred from $\delta^{15}N$ values derived from tooth dentine (Balasse & Tresset 2022).

Importantly, nitrogen data derived from bone collagen can be influenced by bone remodeling (Svyatko 2016). Other factors which can influence δ15N values in bones and teeth include aquatic resource consumption, climate and aridity, and manuring (Bogaard et al. 2007, 2013; Murphy & Bowman 2006; Schoeninger & DeNiro 1984; Syvatko 2016; Warinner 2014). Ideally $\delta^{15}N$ values should be analyzed in tangent with additional lines of evidence including other stable isotopes, faunal remains, botanical remains, and paleoenvironmental data. It is, in my experience, uncommon for archaeological studies exclusively centered upon stable nitrogen isotopic data.

3.2.3. Stable Strontium Isotopes (^{84}Sr, ^{86}Sr, ^{88}Sr; ~ ^{87}Sr)

The three naturally occurring stable strontium isotopes are ^{84}Sr, ^{86}Sr, ^{88}Sr, as well as the radiogenic ^{87}Sr. ^{87}Sr is derived from the radioactive decay of Rubidium 87 that is present in earth's crust (Faure & Powell 2012). Strontium isotopes become incorporated into an animal's mineral tissue (e.g. bone collagen and dental enamel) following the consumption of water and food resources (Bentley et al. 2006; Holt et al. 2021; Slovak & Payton 2011). Bone is susceptible to diagenesis and its incorporation of $^{87}Sr/^{86}Sr$ from the burial environment makes it useful as a proxy for the local bioavailable $^{87}Sr/^{86}Sr$ signature, but not ideal for identifying local versus non-local individuals.

As strontium is primarily incorporated into the environment through soil and underlying geology, strontium ratios exhibit geographical variation (Faure & Powell 2012). Strontium values from dental enamel ($^{87}Sr/^{86}Sr$, $^{88}Sr/^{86}Sr$) can be compared to bioavailable strontium isotope ratios in order to assess provenance and mobility patterns in past animal individuals (Bentley 2006; Ericson 1985; Knudson et al. 2010; Montgomery 2010; Price et al. 2002). The $^{87}Sr/^{86}Sr$ ratios observed in archaeological materials (including faunal remains) can be compared with values expected from the local geology, with inconsistent $^{87}Sr/^{86}Sr$ ratios indicating a non-local origin (Slovak & Payton 2011). Isoscapes may be spatially modeled to provide more precise insight into the origins and migration patterns of the samples analyzed (Bataille & Bowen 2012; Bataille et al. 2018, 2020; Willmes et al 2018). There are a number of challenges involved in strontium mapping and data interpretation, which are reviewed by Holt et al. (2021).

Mobility may also be investigated on sub-annual and seasonal timescales by analyzing the strontium isotope ratios found in tooth enamel, which forms incrementally (Hoppe et al. 1999, 2004). Utilizing this approach, the $^{87}Sr/^{86}Sr$ values of archaeological fauna have been examined alongside estimated age-at-death distributions to investigate long-distance animal trade and seasonal transhumance (Arnold et al. 2013). More recently, researchers investigating monthly animal mobility in the Altai mountains created isotope profiles from dental $^{87}Sr/^{86}Sr$ which allowed them to reconstruct livestock mobility in 45-day windows (Lazzerini et al 2021b). Though there was some (as of yet) inexplicable variability, this study may prove to be very valuable for future isotopic investigations of the Altai Mountains.

3.2.4. Stable Oxygen Isotopes (^{16}O, ^{17}O, ^{18}O)

There are three oxygen stable isotopes (^{16}O, ^{17}O, ^{18}O) which become incorporated into the environment (and thus the archaeological record) through the water cycle and the movement and intake of water (Malainey 2010). In zooarchaeological contexts, $\delta^{16}O$ ratios have been used to infer coastal proximity, drinking sources, and climate (Svyatko 2016). The $\delta^{18}O$ ratios of marine shells have been used to infer site seasonality and environmental conditions (Burchell et al. 2012, 2013; Çakirlar & Şeşen 2013; Deith 1983, 1985, 1986; Mannino et al. 2003, 2007; Milner 2002; Pilaar Birch 2013; Shackleton 1973).

Although single-proxy oxygen stable isotope analyses are not as common in zooarchaeology as the aforementioned isotopes, they can reveal insights into animal husbandry and management practices (Pederzani & Britton 2019). Variations in $\delta^{18}O$ ratios observed in archaeological horse molars have been used to date the seasonality of their slaughter and provide insight into Bronze Age Mongolian horse-slaughtering practices (Lazzerini et al. 2020). Similarly, the sequential oxygen isotope analyses of archaeological caprine teeth has been used to determine their date of slaughter and establish a continuity of Iron Age Mongolian herding practices into modern times (Lazzerini et al. 2021a).

3.2.5. Combined Stable Isotopes

Stable isotope ratios can also be analyzed in zooarchaeological studies in relation to one another. Stable isotope ratios of $\delta^{13}C$ and nitrogen $\delta^{15}N$ reveal C3 versus C4 plant consumption as well as marine versus terrestrial diets (Chrisholm et al. 1982; DeNiro 1987; Schoeninger & DeNiro 1984; Svyatko 2016; van der Merwe 1982; van der Merwe and Vogel 1978; Vogel & van der Merwe 1977; Walker & DeNiro 1986). Variations within $\delta^{13}C$ and nitrogen $\delta^{15}N$ values recorded in animal assemblages have been linked to landscape variability and are commonly used to infer both domestic and wild animal management strategies (Chazin et al. 2019; Hammond & O'Connor 2013; Janzen et al. 2020; Knockaert 2018; Madgwick et al. 2013; Makarewicz 2014; Makarewicz & Tuross 2006; Samei et al. 2023; Stevens et al. 2013).

Recently, researchers have demonstrated that the combined $\delta^{13}C$ and $\delta^{18}O$ analyses of dental enamel and tail hair can provide insight into animal mobility and land use (Lazzerini et al. 2021a; see also Spyrou et al. 2024). Combined $\delta^{15}N$ and $\delta^{18}O$ stable isotope ratios have proven to be unreliable for assessing animal mobility (Lazzerini et al. 2019), but have been used to investigate the impacts of fur trade on exploited animal populations (Szpack et al. 2013) and argue for the systematic grazing and pasturing of horses in Bronze Age Kazakhstan (Ventresca Miller et al. 2019). The multiproxy analysis of $^{87}Sr/^{86}Sr$, $\delta^{18}O$, and $\delta^{34}S$ isotope ratios can enhance the resolution and accuracy of migration reconstructions (Britton et al. 2023). Combined $^{87}Sr/^{86}Sr$, $\delta^{13}C$, and $\delta^{18}O$ ratios have been combined with faunal analysis in an effort to determine the underlying mechanisms of regional resource scarcity (Fisher & Valentine 2013) and reconstruct the diets, ecology and mobility patterns of Pleistocene herbivores (Heddell-Stevens et al. 2024). Investigations into livestock management practices in Neolithic

Europe (Kamjan et al. 2020) and during the Mongol Empire (Fenner et al. 2020) have combined $^{87}Sr/^{86}Sr$, $\delta^{15}N$, $\delta^{13}C$, and $\delta^{18}O$.

This is a simplified and non-exhaustive overview of the many multiproxy approaches available to the stable isotope analysis of archaeological fauna. Both single and multiple stable isotope analyses can be elegantly combined with morphological and biomolecular lines of evidence such as tooth wear stages, taphonomical reconstructions, radiocarbon dating, and peptide fingerprinting. It is the research question and the nature of the assemblage that should determine which approach to use, and which analyses to combine. Sample size and representation are also relevant, as often only a handful of samples will be selected for isotopic analysis out of a faunal assemblage that can consist of thousands of identified specimens. Another major factor which must be considered is the *biome* which characterizes the faunal assemblage in question–especially when that biome is within the Eastern Eurasian Steppe.

3.2.6. Stable Isotopes & The Steppe Biome

"Obviously, even in temperate climatic zones such as the Eurasian Steppe, variation in isotopic values of their inhabitants can be determined not only by diet, but also by environmental factors (e.g. a change in humidity). Failure to take into account such factors may lead to erroneous conclusions on the diet of the populations." (Svyatko 2016)

Approximately forty percent of the Earth's terrestrial surface is covered in grasslands, the largest of which is situated within the Eurasian Steppe (Jiao et al. 2017; Petermann & Buzhdygan 2021). The *Eastern* Eurasian Steppe is a vast region whose exact geographical boundaries shift depending on who is writing about it. For the purposes of this dissertation, the Eastern Steppe spans modern-day Mongolia as well as parts of modern-day Russia and China (Jeong et al. 2020). The Eastern Eurasian Steppe contains wide swatches of semi-arid temperate grasslands that experience annual drought, hot and stormy summers, and freezing winters (Sala 2001; Woodward 2008). The arid and semi-arid conditions arising from this extreme continental climate are thought to have limited the natural resources available to prehistoric inhabitants, making it difficult for them to unanimously sustain sedentary agricultural lifestyles and leading to the emergence of a multitude of subsistence strategies (Frachetti 2012; Zhao et al. 2021, 2022).

The nutrient-rich mollisol soils of the Eastern European Steppe support grassy graminoids and flowering forbs, which are grazed upon by the cervids and antilopines discussed earlier in this dissertation (e.g. *Saiga tatarica*, *Procapra subgutturosa*, and *Capreolus pygarus*) (Woodward 2008). Though dominated by C3 plants, C4 plants are also apart of the overall steppe biome and their numbers have continued to increase with climate change, aridification, and overgrazing (Auswerwald et al. 2009; Pyankov et al. 2000; Wittmer et al. 2010; Yang et al. 2022; Zhang et al. 2009). Unfortunately, mixed C3 and C4 plant landscapes such as the Eastern Eurasian Steppe present a number of challenges for stable isotope analysis.

Differences within the C3 and C4 photosynthetic pathways result in distinct carbon isotopic signatures (O'Leary 1981) and animals which have consumed both C3 and C4 plants will present mixed carbon isotopic signatures that are difficult to correctly interpret. The variable

growth and overlap of C3 and C4 plants can also lead to differential environmental characteristics and patterns of land use, and subsequently inconsistent spatial ranges of $\delta^{13}C$ and nitrogen $\delta^{15}N$ ratios of the soil and plants within the Steppe isoscape (Šantrůčková et al. 2000; Wynn & Bird 2007). The intense seasonal shifts and drought periods within the Eastern Eurasian Steppe add a temporal complication (Paruelo & Lauenroth 1996; von Fischer et al. 2008). It is critical that researchers take regional, seasonal, and environmental factors into account when applying stable isotope analysis to reconstruct the ancient animal economies and human lifeways of the Eastern Eurasian Steppe (Svyatko 2016), as well as Inner Asia more broadly.

3.2.7. Stable Isotope Analysis: Conclusion

"Although bone isotope analysis can reveal…proportions of…animal foods in the diet, it cannot specify the species actually taken and processed…isotopic studies cannot shed much light on the handling of animal bodies prior to their death or after. Only zooarchaeological analysis…can elucidate these topics. Ideally, archaeofaunal data can be read in a dialogue with the bone isotope data..." (Gifford-Gonzalez 2018)

Stable isotope analysis can greatly complement zooarchaeological reconstructions of animal (including human) diets, seasonality, mobility, and management practices. The analysis of carbon isotopes (^{12}C, ^{13}C) can help to distinguish between C3 and C4 plant consumption, while nitrogen isotopes (^{14}N, ^{15}N) can provide information about trophic levels, weaning, and consumption. Strontium isotopes (^{84}Sr, ^{86}Sr, ^{88}Sr, ^{87}Sr) are useful in establishing geographic origin and mobility patterns, and oxygen isotopes (^{16}O, ^{17}O, ^{18}O) can reveal environmental conditions and water sources. Interpreting stable (and radiogenic) isotopic data from archaeological animal tissue is not straightforward, especially for faunal assemblages recovered from biomes characterized by mixed C3/C4 plant landscapes and intense seasonal variation– e.g. the Eastern Eurasian Steppe. Fish (especially freshwater) consumption can be also confused with C3 plant consumption, due to the similar carbon isotopic signatures they produce. Although the interpretation of isotopic signatures requires careful consideration of regional, seasonal, and ecological contexts, isotopic analysis is an extremely valuable tool for the reconstruction of past subsistence and animal management strategies. That being said, isotopic analysis is not a replacement for faunal analysis, and is best combined with zooarchaeological (and sometimes also biomolecular) methods.

3.3. ^{14}C Radiocarbon Dating

"...archaeologists tended to accept the radiocarbon dates uncritically as absolute figures without fully appreciating the errors which were implicit in the method…the scientists in the radiation laboratories did not always appreciate the importance of the past history of the sample, the nature of the site, the possibility of contamination and so on." (Henderson 1970)

The previous section defined and explored the archaeological applications of the analysis of *stable* isotopes such as carbon ^{12}C and ^{13}C. Radiocarbon dating exploits the half-life (5,700 ± 30 years) and decay of the *radioactive* isotope ^{14}C to measure the age of carbon-based materials younger than 55,000 years old (Arnold & Libby 1949; Bronk Ramsey 2008; Hajdase et

al. 2021; Henderson 1970; Malainey 2011; Taylor 2020a; Wood 2015). These carbon-based materials include faunal remains, which may be directly dated or dated by contextual association with archaeological objects and strata. The ability to directly date faunal remains Is valuable because archaeological context is often otherwise unavailable, due to issues such as site disturbance, stratigraphic disarray, and the many difficulties involved with using cultural material finds to associate a period of time with a complex space. The issues have especially impacted archaeological studies in Inner Asia, as I will discuss in-depth in the upcoming chapters of this dissertation.

Radiocarbon dating is not a foolproof method. Many archaeological sites have been inaccurately dated as a result of *the old wood effect*, i.e. the achronological inclusion of older wood into newer deposits. Caution also must be taken when radiocarbon dating faunal remains, as porous animal bones can become contaminated by their burial environments. This has proven to be the case for a number of bones dated from Bronze Age Mongolian sites (Zazzo et al. 2019). Additionally, the use of LSC dating as opposed to AMS dating can also lead to unreliable radiocarbon dates–an unfortunate reality for many prehistoric Southern Siberian dates (e.g. Alekseev et al. 2001; Dolukhanov et al. 1970; Görsdorf et al. 2001; Semenstsov et al. 1998; Semyontsov et al. 1972; see Poliakov & Lazaretov 2020; Poliakov et al. 2019; Svyatko et al. 2009). I will explore LSC and AMS radiocarbon dating below.

3.3.1. Liquid Scintillation Counting (LSC)

“Liquid scintillation counting became possible with the discovery in 1950 that the dilute solutions of some compounds can emit fluorescent light.” (Henderson 1970)

Liquid Scintillation Counting (LSC) can be used to estimate the age of an organic sample suspended in a scintillation liquid by measuring the radioactive decay of its ^{14}C isotopes with a liquid scintillation (LS) spectrometer (Arnold 1954; Henderson 1970; Polach et al. 1974; Pringle et al. 1955). Radioactive decay within the scintillation liquid excites the solvent molecules, and the resultant energy transfer leads to light emission within the LS spectrometer (Arnold 1954; Henderson 1970; Polach et al. 1974; Pringle et al. 1955). The light emission is collected by a photodetector and converted into an electrical signal corresponding with the radioactive decay of the sample’s ^{14}C isotopes (Arnold 1954; Henderson 1970; Polach et al. 1974; Pringle et al. 1955).

The radioactive decay rate is then calibrated to discriminate between sample radiation and background radiation, to account for the interference and absorption of light emission (i.e. *quenching*), and finally to provide an estimated age range for the sample (Arnold 1954; Henderson 1970; Polach et al. 1974; Pringle et al. 1955). Many of the radiocarbon dates for prehistoric Southern Siberian archaeological materials were measured using LSC radiocarbon dating, before the widespread adoption of AMS radiocarbon dating in archaeological science (see Poliakov & Lazaretov 2020; Poliakov et al. 2019; Svyatko et al. 2009). Importantly, LSC radiocarbon dating both requires larger sample sizes and produces less precise age estimates than AMS radiocarbon dating (Gilman et al 1998; Harris 1987; Takahashi et al. 2010).

3.3.2. Accelerator Mass Spectrometry (AMS)

"Radiocarbon dating by accelerator mass spectrometry (AMS) differs fundamentally from conventional 14C dating because it is based on direct determination of the ratio of 14C:12C atoms rather than on counting the radioactivity of 14C. It is therefore possible to measure much lower levels of 14C in a sample much more rapidly than the conventional technique allows." (Harris 1987)

Accelerator Mass Spectrometry (AMS) can be used to estimate the age of an organic sample by accelerating the sample's ionized carbon through an accelerator mass spectrometer (AMS) and measuring the relative abundance of radioactive ^{14}C in relation to stable carbon isotopes (Fedi 2009; Harris 1987; Hedges & Gowlett 1986). The sample is first chemically treated and converted into either carbon dioxide (CO_2) or graphite (Fedi 2009; Hedges & Gowlett 1986). The converted sample is then ionized and accelerated in an AMS which discriminates between the carbon ions based upon mass, essentially measuring the sample's ^{14}C concentration (Fedi 2009; Hedges & Gowlett 1986). This ratio is then used to calculate the sample's age against the half-life of ^{14}C and calibrated to adjust for known variations in atmospheric ^{14}C levels over time (Fedi 2009). The development of AMS radiocarbon dating in the late twentieth century revolutionized archaeological science (Harris 1987; Taylor 1991), and led to the measurement of more reliable dates for archaeological materials and remains from Inner Asian contexts (e.g. Hermes et al. 2020, 2021; Poliakov & Lazaretov 2020; Poliakov & Svyatko 2021; Poliakov et al. 2019; Svyatko et al. 2009; Taylor et al. 2019).

3.3.3. Multiproxy Approaches

The refinement of chronological and taxonomic contextualization that can be achieved by combined radiocarbon and genetic analyses is paving the way for tracing back the dispersal of domesticated animals throughout Inner Asia (Taylor et al. 2020c). Reliable radiocarbon dates directly derived from the dentine of domesticated sheep (Poz-113280 & Poz-113281) from the Eneolithic Afanasievo settlement of Nizhnyaya Sooru possibly represent the oldest known animals originally domesticated in West Asia that have been found in Inner Asia (Hermes et al. 2020b). Radiocarbon dates derived directly from archaeological caprines recovered from Maily Dugan and Perviy Mezhelik-1 (UBA-22989 & UBA-29309, Svyatko et al. 2017) may also represent domesticated sheep or goat found in Afanasievo contexts, but at the time of this dissertation no results from genetic testing on these samples have been published.

Combined radiocarbon and genetic analyses can also help resolve the question of the role of horses in the dispersal of domesticated animals and emergence of pastoralism in Central Eurasia. My own collagen peptide fingerprint analysis of fragmented faunal remains from the highly stratified Mongolian habitation site ZK513-1 (Houle et al. 2022) identified four Early Bronze Age bone samples as *Equus* sp. (discussed further in Chapter 21). These four samples were subsequently selected for aDNA analysis and radiocarbon dating and identified as the now-extinct Sussemione *Equus ovodovi* (Pan et al. 2024). Had these samples instead been identified as *Equus callabus*, they would have represented the oldest evidence of horse domestication in Mongolia and rewritten the narrative of domesticated horse arrival in Inner Asia.

Erroneous radiocarbon dates may have already shaped the narrative of the human-horse relationship in Central Eurasia. The results of Wilkin et al. study (2021) placing horse domestication and milking in the region ca. 4.5-5.3 kya have not been replicable (see Pan et al. 2024), are not supported by more robust contemporary studies (e.g. Scott et al. 2022), and are possibly the result of a radiocarbon dating error. The continued generation of accurate radiocarbon dates derived from prehistoric Inner Asian fauna will help researchers and scientists more accurately place and trace the domestication, exploitation, and dispersal of animals in Central Eurasia. I will revisit this issue in the context of Southern Siberia, Outer Mongolia, and Uzbekistan in subsequent chapters (see Chapters 09–19).

3.4. Biogeochemical Zooarchaeology: Conclusion

"...recent radiocarbon, archaeozoological and stable isotope analyses have led to many new insights..the faunal remains found in settlement layers confirm the trends revealed by bone chemistry, whereas the archaeozoological analyses of faunal remains in graves…show…the importance of…hunting. This illustrates the discrepancy between the symbolic world..and everyday life..." (Eriksson et al. 2003)

Stable, radiogenic, and radioactive isotopes become incorporated into animal tissue in the course of highly complex and interwoven processes that are reflective of local environments and must be taken into account when being analyzed by zooarchaeologists. Freshwater reservoir and old wood effects can be especially detrimental to stable isotopic analysis and radiocarbon carbon dating. When these effects are properly controlled and accounted for, biogeochemical approaches can provide invaluable insight into the diets, mobility, seasonality, exploitation, environments, and chronological contexts of individual archaeological animals as well as archaeological animal economies. These methods are most insightful when combined with zooarchaeological analyses and, in certain cases, the targeted application of biomolecular methods. I will overview some of the biomolecular methods available to zooarchaeologísts, i.e. aDNA analysis and proteomics, in the next chapter.

4. Biomolecular Zooarchaeology

4.1. Introduction

"...biomolecules have been implemented in a broad variety of topics and species, from the extinct Pleistocene megafauna to ancient wild and domestic stocks…their future use has the potential to offer an enhanced understanding of drivers of past faunal diversity on Earth." (Rosengren et al. 2021)

The archaeologists of the late twentieth century began incorporating not only biogeochemical approaches into their faunal analyses, but also biomolecular ones. The emergence of ancient DNA analysis paved the way for genetic research into ancient animal ancestry and domestication lineages. Modern day advancements in archaeological proteomics have also provided revolutionary methods in dietary reconstruction, taxonomic identification, and sex attribution. Although the analysis of other biomolecules such as lipids and carbohydrates have also been incorporated into archaeological research (Brown & Brown 2013), I do not consider their impact and influence to be directly relevant to the topics of my doctoral research or to this dissertation. Instead, I will discuss what I consider to be the most important biomolecules that are analyzed by zooarchaeologists and researchers interested in past animal ecologies and economies– i.e. ancient DNA and ancient proteins. I emphasize paleoproteomics and peptide mass fingerprinting, as is the approach that I have employed in my analysis of Bronze Age and Medieval animal assemblages from Inner Asia

4.2. Ancient DNA

"In the first decade of ancient DNA research, the analysis of zooarchaeological remains followed a clear pattern...The power of PCR allowed researchers to experiment with alternative sources of DNA…Since then, the use of ancient DNA in zooarchaeological studies has expanded considerably." (Barnett 2019)

Stable, radiogenic, and radioactive isotopes are forms of chemical elements whose structures can be called simple in comparison to DNA (deoxyribonucleic acid). DNA is composed of two chains of nucleotides, or phosphate and sugar groups paired with nitrogen bases, which twist around one another in the form of a double helix (Alberts et al. 2002; de Bruyn et al. 2011; Klug 2004; Watson & Crick 1953). DNA essentially provides an organism with instructions for development, survival, and reproduction, and so ancient DNA (aDNA) extracted from organic remains can be used to investigate ancient populations, microbiomes, and pathologies. The analysis of faunal aDNA has provided invaluable insights into the origins and mechanisms of animal evolution and domestication, such as the developments and intersections of agriculture, pastoralism, and zoonotic diseases (Frantz et al. 2020; Higuchi 1984; Irving-Pease et al. 2018; MacHugh et al. 2017; Orlando et al. 2021; Rosengren et al. 2021; Scheu 2018). This section explores the role of faunal aDNA studies in the investigation of the ancient human-animal relationships and subsistence economies of Inner Asia.

Before initiating a discussion about the intersections of aDNA analysis and zooarchaeology, it is necessary to first define key terminology and methodological approaches. *Genetics* refers to the

scientific study of biological heredity, and *molecular genetics* is the study of how genetic information can be encoded in a molecule (Hartl et al. 1998). In zooarchaeological contexts, genetics generally involves the study of specific genes (specific and functional sequences of DNA) and haplotypes (inherited packages of linked genes) to achieve high-resolution taxonomic / sex identifications, as well as to identify genetic markers of domestication (Barnett 2019; Bradley 2006; Geigl 2023; Orlando 2002; Zeder et al. 2006). Mitochondrial DNA (mtDNA), which is only inherited maternally (and without recombination), can be especially useful for identifying the maternal haplotypes, domesticated lineages, evolutionary relationships, and phylogeographies which characterize archaeological animals and their modern descendants (Bradley 2006; Gifford-Gonzalez 2018).

Genomics is the study of whole genomes, or the entirety of an organism's genetic material, as opposed to single genes (Gifford-Gonzalez 2018; Hartl et al. 1998). The whole-genome sequencing of aDNA has allowed researchers to reconstruct animal population dynamics, domestication histories, and biological adaptations on a much broader scale (Barnett 2019; Frantz et al. 2020; Geigl 2023; Gifford-Gonzalez 2018; Irving-Pease et al. 2019; MacHugh et al. 2016). Perhaps the most important archaeological application of animal genomics in the context of Inner Asia has been the reconstruction of domesticated horse lineages, which has confirmed that the ancestors of modern domesticated horses were not managed in ancient Kazakhstan but in the Western Eurasian Steppe (Librado et al. 2021). The importance of this discovery, and the role of horse husbandry in the animal economies of Inner Asia, will be continually revisited through this dissertation (see Chapters 10–19).

Metagenomics is the genomic analysis of microorganisms and microbial communities (Handelsman 2004; Riesenfeld et al. 2004; Wooley et al. 2010). *Ancient metagenomics* is thus the analysis of the non-living microbial genomes recovered from biological materials such as bone, teeth, dental calculus, and paleofeces (Der Sarkissian et al. 2021; Warinner et al. 2017). Ancient metagenomic applications in faunal analysis including screening animal remains for zoonotic bacterial pathogens (Bos et al. 2014; Dimopoulos 2021; Spyrou et al. 2019), investigating environmental adaptations in animals (Liu & Llamas 2020), and reconstructing animal colonization events (Pedersen et al. 2016). To my knowledge, ancient metagenomics have not yet been employed in Inner Asian zooarchaeological contexts.

Genetics and genomics have been the most useful in reconstructing animal domestication events and lineages. I will review what aDNA analyses have elucidated about the evolutionary relationships and migration histories of cattle (*Bos* sp.), equids (*Equus* sp.), camelids (*Camelus* sp.), caprines (*Ovis* sp.; *Capra* sp.), antelopines (*Gazella* sp., *Procapra* sp.; *Saiga* sp.), cervids (*Cervus* sp.; *Capreolus* sp.), and suids (*Sus* sp.) in Chapter 03. While the timing and mechanisms of domesticated animal dispersal across Central Eurasia remains poorly understood, genetic and genomic research has greatly enhanced the body of zooarchaeological knowledge that was once partially limited to morphometrical insights. Ancient DNA analyses can be additionally complemented (and in some cases facilitated by) ancient protein studies, which I will discuss below.

4.3. Ancient Proteins

"The study of ancient proteins is at once a very old and a very young field…the early history of ancient protein research is deeply rooted in the fields of chemistry, anthropology, and geology. However, it was only following the application of soft ionization mass spectrometry…that the study of ancient protein sequences became…the field known as paleoproteomics today." (Warinner et al. 2022)

DNA provides the codes for creating amino acids, which are the building blocks of proteins. Ancient proteins often preserve better than aDNA and are invaluable resources for studying the past, albeit at a lower resolution. Researchers are constantly developing and refining applications of mass spectrometry to analyze proteins recovered from archaeological and historical materials such as faunal and human remains, food remains, ceramics and potsherds, adhesives and binders, textiles, and soil (Buckley 2018; Cleland & Schroeter 2018; Hendy 2021, 2023; Hendy et al. 2018a,b; Korzow-Richter et al. 2022; Warinner et al. 2022). The focus of this subsection will be on the analysis of archaeological proteins recovered from animal remains such as bones, teeth, eggshells, binders, and hides.

Just as it was necessary to clarify the scope and meaning of genetics, genomics, and metagenomics before discussing the intersections of aDNA analysis and zooarchaeology (see section "4.2."), it is necessary to clarify the scope and meaning of proteomics, MS-based proteomics, and peptide mass fingerprinting before discussing the intersections of ancient protein studies and zooarchaeology. *Proteomics* is an all-encompassing term for the identification, quantification, characterization, and functional analysis of proteins (Fields 2001; Guerrera & Kleiner 2005). Methods in proteomics include microscopy, microarray, genetic readouts, de novo assembly, and mass spectrometry (Aebersold & Mann 2003; Cho 2007). Unlike in DNA research, where separate terms have been developed to distinguish the study of individual genes (genetics) from whole genomes (genomics), there is no terminology which distinguishes the study of peptides or individual proteins from whole proteomes (pers.comm. Christina Warinner 2024).

4.4. Paleoproteomics

"In the late 1980s, the advent of soft ionization techniques capable of generating stable gas phase ions from thermally unstable biomolecules, namely…MALDI…and…ESI, laid the way for the development of a set of powerful alternatives…for the…characterization of peptides and proteins." (Cañas et al. 2006)

MS-based proteomics refers to the sequencing of proteins which utilizes mass spectrometry (Aebersold & Mann 2003), the core technology of proteomics (Guerrera & Kleiner 2005) as well as the method most commonly used in archaeology (Buckley 2018; Hendy 2021, 2023; Hendy et al. 2018a,b; Warinner et al. 2022). The terms *paleoproteomics* and *proteomics* are often used interchangeably in the titles of publications detailing the analysis of ancient proteins in archaeological contexts, while terms like "MS-based proteomics" will often only be used in abstracts, methods sections, and other bodies of text. MS-based approaches in paleoproteomics utilize soft-ionization (as opposed to hard-ionization), though they use different

ionization sources. MS-based approaches in paleoproteomics include *shotgun proteomics* and *peptide mass fingerprinting* (PMF).

Differences between shotgun proteomics and PMF are largely related to instrumentation. Shotgun proteomics with LC-MS/MS utilizes *electrospray ionization* (ESI) while MALDI-TOF PMF utilizes *matrix-assisted laser desorption/ionization* (MALDI) (Aebersold & Mann 2003; Sokolowska et al. 2013; Guerrera & Kleiner 2005; Sokolowska et al. 2013). LC-MS/MS and MALDI-TOF also utilize different sample preparation techniques and mass analyzers. LC-MS/MS uses liquid chromatographic separation and tandem mass spectrometry (Sokolowska et al. 2013), while MALDI-TOF uses a crystalizing matrix, steel ground plates, and a single time of flight (TOF) mass spectrometer (Liyanage & Lay 2006) (see also Alehndi 2020; Cañas et al. 2006). There are many applications of non-tandem LC/MS proteomics as well as tandem MALDI-TOF/TOF proteomics outside of archaeology, just as there are inherent differences in the scale and complexity of LC-MS(/MS) and MALDI-TOF(/TOF) proteomics that are not related to tandem versus non-tandem applications. ESI-MS (e.g. LC-MS) is more useful for analyzing complex protein samples, while MALDI-MS (e.g. MALDI-TOF) is better suited for analyzing simple protein samples (Aebersold & Mann 2003; Guerrera & Kleiner 2005).

4.4.1. Shotgun Proteomics

"...bottom-up/shotgun proteomics method has become the easier strategy for protein analysis over the past two decades. However, these advantages also come with some nontrivial challenges in sample preparation, peptide separation, data acquisition, and informatics." (Gao & Yates 2019)

Shotgun proteomics refers to the bottom-up analysis of protein mixtures (Gao & Yates 2019). *Bottom-up* approaches in mass spectrometry begin with protein digestion into peptides, whereas *top-down* methods analyze intact proteins (Gao & Yates 2019; Guerrera & Kleiner 2005; Sokolowska et al. 2013). In LC-MS/MS shotgun proteomics, digested peptides are loaded onto a high performance liquid chromatography (HPLC) column and desalted and purified with either reversed phase (RP), strong-cation exchange (SCX), size exclusion (SEC), hydrophilic interaction liquid chromatography (HILIC), or affinity purification (Gao & Yates 2019). The purified peptides are then ionized (i.e. charged) and converted into a gaseous phase with high-voltage electrical energy, i.e. ESI (Gao & Yates 2019; Guerrera & Kleiner 2005; Sokolowska et al. 2013). The low-flow rate of sample-suspended solution helps to facilitate ionization while also preventing sample fragmentation (Alhendi 2020; Guerrera & Kleiner 2005).

The ionized peptides are then accelerated into a mass spectrometry analyzer, where they are separated by electrical fields (Alhendi 2020; Cañas et al. 2006; Dülcks & Juraschek 1999; Guerrera & Kleiner 2005; Ho et al. 2003). There are currently four main types of mass analyzers that may be coupled with ESI: (i) ion trap (IT), (ii) fourier transform ion cyclotron (FT-MS), (iii) time-of-flight (TOF), and (iv) quadrupole (Q) (Alhendi 2020). Hybrids also exist, such as quadrupole-Orbitrap mass spectrometers (Guerrera & Kleiner 2005; Sokolowska et al. 2013). Some mass analyzers, such as the Orbitrap (which is an ion-trap type mass analyzer), also function as mass detectors. Mass analyzers may also be used with ESI in tandem (Sokolowska et al. 2013), as is the case with LC-MS/MS instruments. The mass analyzers measure the

mass-to-charge ratios (*m/z*) of the ionized peptides, which are then registered and recorded as M1 spectra by mass detectors such as HPLC and UV detectors (Aebersold & Mann 2003; Gao & Yates 2019; Guerrera & Kleiner 2005; Ho et al. 2003; Sokolowska et al. 2013).

Ionized peptides which meet user-defined criteria (i.e. precursor ions) are selected for subsequent fragmentation down their peptide backbones in a second mass analyzer, typically through collision-induced dissociation (CID) or higher-energy collisional dissociation (HCD) (Gao & Yates 2019; Sokolowska et al. 2013). This ion fragmentation results in b-ions (N-terminal fragments) and y-ions (C-terminal fragments), which are measured (m/z ratios) in the second mass analyzer and registered by the second mass detector as M2 spectra (Gao & Yates 2019; Sokolowska et al. 2013). Both M1 (whole mass, MS) and M2 (fragmentation mass, MS/MS) data are then matched against peptide sequences recorded in databases (Gao & Yates 2019). Importantly, while MS/MS data and M2 spectra are used to predict amino acid sequences, only masses are ever recorded by LC-MS/MS. Although LC-MS/MS approaches are sometimes described as LC-MS, without specifying the use of tandem mass spectrometry (e.g. Kotli et al. 2024), it is the additional ion fragmentation step involved in MS-MS which facilitates peptide sequence determination and thus protein identification (Sokolowska et al. 2013).

Shotgun proteomic approaches have a number of archaeological applications, such as the protein characterization of archaeological materials and marker development, and are nearly always conducted utilizing LC-MS/MS (Warinner et al. 2022; see also Guerrera & Kleiner 2005; Sokolowska et al. 2013). LC-MS/MS is perhaps best known in archaeology for the identification of animal proteins in human dental calculus (e.g. Bleasedale et al. 2021; Charlton 2019; Geber et al. 2019; Hendy 2021, 2023; Hendy et al. 2018a,b; Scott et al. 2021, 2022; Tang et al. 2023; Warinner et al. 2014; Wilkin et al. 2020), binders and glues (e.g. Ntasi et al. 2021; Vinciguerra et al. 2016, 2019), textiles (e.g. Scibè et al. 2024; Solazzo 2019; Solazzo & Niepold 2023; Solazzo et al. 2011), and container residues (e.g. Hendy 2021; Siano et al. 2022; Solazzo et al. 2008; Tanasi et al. 2021), but was used very recently to profile bovine dental enamel proteomes for sex determination (Kotli et al. 2024). LC-MS/MS is also used to develop the peptide markers necessary for PMF (e.g. Codlin et al. 2022; Harvey et al. 2018; Janzen et al. 2021; Korzow-Richter et al. 2020; Peters et al. 2021; see also Korzow-Richter et al. 2022), and as an alternative method of taxonomic identification (i.e. SPIN; Rüther et al. 2022).

Amelogenin Peptide-Based Sex Determination

Dental enamel is formed through the extracellular mineralization of carbonated hydroxyapatite crystals within a matrix of secreted enamel proteins. (Bansal et al. 2012; Brookes et al. 1995; Fincham & Simmer 2007). This enamel protein matrix is composed of a principle fraction of amelogenin proteins (~90%) and a minor fraction of enamelin proteins (~10%) (Bansal et al. 2012; Brookes et al. 1995; Fincham & Simmer 2007; Kotli et al. 2024). Amelogenin proteins (Amels) are sex-linked (i.e. sexually dimorphic), with Amel-X being linked to the X-chromosome and Amel-Y being linked to Y-chromosome (Bansal et al. 2012; Brookes et al. 1995; Fincham & Simmer 2007; Kotli et al. 2024). The sequence differences between Amel-X and Amel-Y in

certain taxa (e.g. humans, caprines, cervids, suids, equids, ursids, and a number of large bovids) allows for their sex-determination through biomolecular analyses (Warinner et al. 2022).

Both genetics (PCR amplification) and proteomics (shotgun LC-MS/MS) have been applied to detect sex-specific Amels in human and animal samples (e.g. remains and embryos) for sex determination, predominantly in forensic, ecological, and agricultural contexts (e.g. Grzybowski et al. 2006; Parker et al. 2019; Stewart et al. 2017; Weikard et al. 2006; see also Warinner et al. 2022). MALDI-TOF/TOF approaches have also been used to assign sex to ancient human and hominid remains (e.g. Nielsen-Marsh et al. 2009; Porto et al. 2011). LC-MS/MS was also used in a proteomic investigation into the phylogenetic relationships between Eurasian Pleistocene Rhinocerotids which included the amelogenin peptide-based sex determination of a *Stephanorhinus* sp. fossil specimen (Cappellini et al. 2019).

A very recent study has combined LC-MS/MS with MS ion intensity label-free quantification (LFQ) to quantify the relative abundance of AmelY peptides present in bovine tooth enamel for sex determination (Kotli et al. 2024). LFQ is a post-MS/MS data processing quantification method that is simpler and cheaper than labeled quantification methods such as metabolic isotopic labeling or chemical labeling (Gao & Yates 2019; Guerrera & Kleiner 2005; Sokolowska et al. 2013). MS ion intensity LFQ correlates chromatographic peaks with specific peptides to measure a specific peptide quantity (Sokolowska et al. 2013). Kotli et al. (2024) argue that a relative abundance of AmelY measured in a dental enamel sample is a confident signifier of male sex. The robusticity of this promising approach has yet to be tested. Importantly, AMELY allele deletion can lead to a lack of AmelY peptides in the dental enamel matrix of male human and non-human animal teeth, and can thus bias proteomic sex determinations (Štamfelj 2021).

Peptide Marker Development

LC-MS/MS can be used to develop taxonomically diagnostic peptide markers for PMF (e.g. Codlin et al. 2022; Harvey et al. 2018; Janzen et al. 2021; Korzow-Richter et al. 2020; Peters et al. 2021; Winter et al. 2023; see also Korzow-Richter et al. 2022; McDonald & Yates 2002). Securely identified modern reference specimens selected for LC-MS/MS analysis are first subsampled and screened on a MALDI-TOF to ensure sufficient collagen yield and quality spectra production. High quality specimens are then re-sampled and subjected to LC-MS/MS analysis, and the most intense M1 precursor ions are selected for fragmentation. The resulting fragments are then analyzed with set parameters, and the MS/MS data are uploaded to an MS/MS data repository.

The MS/MS data are then quality-checked using MS/MS protein identification software and compared against a curated protein sequence database (or databases) using specific search parameters. MS/MS data which has passed quality control is then compared against a database constructed from the aligned peptide sequences of related species, outgroup species, and common contaminants. Theoretical peptide mass profiles for the taxa of interest are then predicted based upon the peptide sequences aligned in the comprehensive database, Finally, the predicted masses are matched against peaks observed in MALDI spectra to confirm existing

markers or identify new ones. Peptide marker development is much more complicated, expensive, and time consuming than the PMF it facilitates. I will overview both PMF and MALDI in greater depth below.

4.4.2. Peptide Mass Fingerprinting

"A mass spectrum of the peptide mixture resulting from the digestion of a protein by an enzyme can provide a fingerprint of great specificity–so specific, in fact, that it is often possible to identify the protein from this information alone, without ambiguity." (Cottrell 1994)

PMF is a method of protein identification reliant upon protein digestion and MS to measure peptide mass value "fingerprints" for comparison with MS spectra recorded in a peptide mass value database (Cottrell 1994; Henzell et al. 2003; Ostrom et al. 2000; Thiede et al. 2005). Although both ESI and MALDI mass spectrometry can be used in PMF (Cottrell 1994; Guerrera & Kleiner 2005), archaeological scientists typically use MALDI. MALDI is source of soft-ionization for mass spectrometry which requires the crystallization of molecules (e.g. enzymatically cleaved peptides) in an ultraviolet light absorbing matrix solution (Aebersold & Mann 2003; Alhendi 2020; Cañas et al. 2006; Guerrera & Kleiner 2005; Ostrom et al. 2000; Sokolowska et al. 2013). The most commonly-used matrixes are (i) α-cyano-4-hydroxycinnamic acid (CHCA) and (ii) dihydrobenzoic acid (DHB) (Alhendi 2020). The sample extract(s) and crystallizing matrix are spotted together on a ground steel plate and left to dry.

The ground steel plate is then loaded into the mass spectrometry instrument and the dry, crystalized samples are sublimated by nanosecond laser pulses (Aebersold & Mann 2003; Alhendi 2020; Cañas et al. 2006; Guerrera & Kleiner 2005; Sokolowska et al. 2013). The matrix absorbs the energy from the pulsed laser, which leads to a poorly understood proton-exchange phenomena within the crystallized sample that results in the desorption of protonated (i.e. charged) particles (e.g. ionized peptides) in a gaseous phase (Alhendi 2020; Cañas et al. 2006; Guerrera & Kleiner 2005; Sokolowska et al. 2013). In the case of MALDI-based PMF, the ionized peptides are then accelerated in gaseous phase through a mass analyzer and their *m/z* ratios are quantified by a mass detector (Sokolowska et al. 2013). MALDI is most often coupled with time-of-flight (TOF) mass analyzers, although trap instruments such as ion traps (IT) have also been used (Guerrera & Kleiner 2005; Sokolowska et al. 2013).

TOF mass analyzers consist of an acceleration region, generally composed of a repeller lens and ground aperture which generate an electrical field, and an ion drift tube (Alhendi 2020; Cañas et al. 2006; Guerrera & Kleiner 2005; Liyanage & Lay 2006; Sokolowska et al. 2013). The *m/z* ratios of ionized molecules (e.g. peptides), whose velocities are inversely proportional to their masses, are determined by the time it takes the ions to reach the mass detector after being accelerated through the electrical field (Alhendi 2020; Cañas et al. 2006; Guerrera & Kleiner 2005; Liyanage & Lay 2006; Sokolowska et al. 2013). Lighter ions will arrive at the mass detector faster than heavier ions, resulting in the recording of a TOF spectrum that can be translated into a conventional mass spectrum (Alhendi 2020; Cañas et al. 2006; Liyanage & Lay 2006; Sokolowska et al. 2013).

The popularity of MALDI-TOF-based PMF in archaeology (see Korzow-Richter et al. 2022; Warinner et al. 2022`) is less related to personal preference or method optimization, and more related to accessibility and practicality. The widespread use of both MALDI-TOF and LC-MS/MS in biology has led to their widespread production and maintenance and thus their subsequent adaptation by archaeological scientists, with MALDI- TOF being the considerably cheaper of the two (pers.comm. Christina Warinner 2024). Importantly, just as with LC-MS/MS and shotgun proteomic approaches, MALDI-TOF PMF does not determine the actual sequence of amino acids which characterize a protein. MALDI-TOF PMF instead matches MS spectra peaks of enzymatic masses (most often tryptic masses, but also chymotryptic; see Paladugu et al. 2023) to the peaks of other MS spectra in order to discern taxonomic identity (Korzow-Richter et al. 2022; Warinner et al. 2022). PMF is thus completely dependent upon the quality and quantity of reference spectra available for the identifiable proteins of a wide array of taxa for comparison.

PMF is better suited for the identification of single proteins than complex protein mixtures, though the latter can be done (Sokolowska et al. 2013; Warinner et al. 2022). Although PMF offers lower-resolution data than genetic / genomic or higher-scale proteomic approaches, it remains a cheaper, faster, and more accessible method than the former, and its increasing incorporation into archaeological research has revolutionized zooarchaeology (Korzow-Richter et al. 2022; Warinner et al. 2022). I will dedicate the next chapter of this dissertation to collagen peptide mass fingerprinting, as it is the method I used in my doctoral research. I discuss the peptide mass fingerprinting of archaeological eggshells below, due to their relevance to Inner Asian zooarchaeology.

Eggshell Peptide Mass Fingerprinting

The portability, seasonal availability, nutritional richness, binding properties, and appealing symbolism of bird eggs has led to their longstanding integration into human diet, ritual, and material culture– and thus, of eggshell into the archaeological record (Alcock 2006; Stewart et al. 2013). The mineral binding of eggshell matrices have been demonstrated to provide proteins with greater protection from taphonomic damage than the hydroxyapatite of bone, extending their preservation farther back through time (Demarchi et al. 2016; Warinner et al. 2022). Following this revelation, LC-MS/MS and MALDI-TOF analyses have been used to recover archaeological eggshell proteins (e.g. ovocleidin, ovocalyxin, ovalbumin, struthiocalcin, rheacalcin, ansocalcin, etc.) and develop taxonomically distinct markers for a limited number of avian species (Stewart et al. 2013; Preslee et al. 2017; Warinner et al. 2022).

Notably, the development of chicken eggshell markers by a team of researchers at the Max Planck Institute for Geoanthropology (formerly Science of Human History) allowed them to identify an abundance of archaeological chicken eggshells from several Central Asian archaeological sites (Peters et al. 2024). Their analysis demonstrated the dietary importance of chickens during the Iron Age and Medieval periods (Peters et al. 2024). I will discuss the relevance of their study in the context of subsistence Central Asian archaeology further into this dissertation (see Chapter 19). The continued sequencing and publication of avian genomes will

allow the number of marker peptides and identifiable species of archaeological eggshell to be expanded in the future (Warinner et al. 2022).

4.4.3. Paleoproteomics: Conclusion

"...mass spectrometry has been the workhorse of proteomics and protein-based studies…The mass spectrometry revolution in paleoproteomics has contributed to unprecedented findings over the past two decades…" (Warinner et al. 2020)

Ancient proteins generally preserve better in the archaeological record than aDNA (Buckley et al. 2010), and the advent of soft-ionization mass spectrometry (e.g. ESI and MALDI) has resulted in the application of several MS-based proteomic approaches to faunal analysis which ofter faster, cheaper results at the cost of resolution. LC-MS/MS and MALDI-TOF are the primary MS techniques that have been incorporated into biomolecular zooarchaeology, the first of which is well-suited for the analysis of complex protein mixtures and has been used for peptide-based sex determination methods and to identify of peptide markers. The second, MALDI-TOF, is better suited for single protein identification and is most often used in PMF of collagen (i.e. ZooMS) and eggshell proteins for taxonomic discernment.

Proteomic approaches in zooarchaeology range from relatively new (e.g. ZooMS) to new (e.g. SPIN) to very new (e.g. amelogenin peptide-based sex determination with LFQ). PMF methods in particular will benefit from the continued genome sequencing of a wide array of taxa, which will allow the expansion of sequence databases. The peptide sequences which are available have already facilitated the ZooMS-based discernment of sheep from goat (although not domesticated from wild species), which is extremely valuable in the profiling of archaeological assemblages of Inner Asia. The ability to screen fragmented animal remains to identify specimens of interest for further aDNA and radiocarbon data, especially of equids, to investigate domestication animal lineages and dispersal routes further emphasizes the value of ZooMS in Inner Asian (zoo)archaeology.

4.5. Biomolecular Zooarchaeology: Conclusion

"Zooarchaeologists today explore many exciting arenas." (Reitz & Wing 2008)

As valuable as zooarchaeological data are, not all faunal assemblages are large or well-preserved enough for morphometrical identification, sex attribution, or age-at death estimation. The tactical application of biogeochemical and biomolecular methods has greatly enhanced archaeological research around the world, including in Inner Asia. ZooMS and aDNA analysis have revolutionized taxonomic attribution, although only aDNA analyses are currently capable of distinguishing domesticated taxa from their wild counterparts. LC-MS/MS and LFQ have recently been used to identify and quantify dimorphic dental amelogenin peptides for bovine sex determination. There is currently no biomolecular or biogeochemical method which aids in age-at-death estimation, though radiocarbon dating can determine how old a sample is.

Stable isotopic analysis can provide additional information about animal mobility, diets, and environments.

All of these methods are dependent upon sample preservation, contamination control, and comparative data. Neither biogeochemical nor biomolecular approaches should be viewed as “better than” morphometrical or other zooarchaeological methods, nor should they be considered replacements. Zooarchaeology and archaeology remain necessary to produce primary data as well as to contextualize secondary biogeochemical and biomolecular data. Morphometrical zooarchaeology is also cheaper and more accessible than biogeochemical and biomolecular analysis. Methods should be selected with a solid understanding of their limitations, potential multiproxy applications, and how they can best be used to address research questions. In the next chapter, I will focus specifically on ZooMS as a method of collagen mass fingerprinting archaeological animal bone and tooth fragments.

5. Zooarchaeology by Mass Spectrometry

5.1. Introduction

“Zooarchaeology by Mass Spectrometry (ZooMS) is rapidly becoming a staple in archaeological and cultural heritage science.” (Brown et al. 2021a)

Zooarchaeology by Mass Spectrometry (ZooMS) is essentially PMF applied in archaeological, paleontological, and cultural heritage contexts. ZooMS typically involves the whole digestion of a protein sample for purposes of taxonomic identification, while the PMF analysis of modern samples often involves the mapping of individual proteins for a wide variety of reasons (pers.comm. Samantha Brown 2024). ZooMS was initially developed for the analysis of collagen peptides (Buckley et al. 2009), but has since been expanded to include the analysis of other predominant proteins such as alpha keratins and beta keratins (O'Connor et al. 2015; Solazzo 2017; Solazzo et al. 2013, 2017, 2021, 2023; Serafini et al. 2024) and eggshell proteins (Stewart et al. 2013; Presslee et al. 2017). The most common application of the ZooMS method is still collagen peptide mass fingerprinting, which uses a very small amount of the predominant protein in bone, collagen type I (COL1). COL1 is extracted from faunal remains, digested into peptides, and measured with MALDI-TOF MS (Buckley et al. 2009). Other MS instruments may be used, but MALDI-TOF is by far the most common. I will dedicate this chapter specifically to collagen peptide mass fingerprinting, as it is the method that I have used in my own doctoral research.

5.2. Collagen

“Collagen fibers, by virtue of altering their diameters and modality of packing, provide different tissues with very characteristic features which range from transparency to great tensile strength and from energy storage to heat dissipation…They allow growth to proceed gradually…They protect the body as a whole and organs in particular…” (Nimni 2018)

Collagen molecules consist of three tightly coiled amino acid chains which form a triple helix structure (i.e. fibril) stabilized by hydrogen bonds (Henriksen & Karsdal 2024; Linsenmayer 1991; Nimni 2018; Ramachandran & Kartha 1955; Rich & Crick 1955). Collagen has long been known to be essential for the developmental, physiological, and especially structural functions in vertebrates (Henriksen & Karsdal 2024; Linsenmayer 1991; Nimni 2018). The critical and ubiquitous role of collagen, as well as its intrinsic chemical stability, contributes to its relative survivability in the archaeological record and thus its usefulness for PMF applications in the taxonomic identification of archaeological animal remains (Buckley et al. 2009; Brown et al. 2021a; see also Chapter 06. The most abundant form of mammalian collagen by far is collagen type 1 (COL1).

COL1 is formed from two proalpha1 (proα1) chains encoded by the COL1α1 gene and a proalpha2 (proα2) chain encoded by the COL1α2 gene (Henriksen & Karsdal 2024; Nimni 2018). In a limited number of animals, such as certain species of fish, a duplication of the

COL1α1 gene results in a COL1α3 gene and thus a unique proα3 chain within their COL1 (Brown et al. 2021a). The amino acid sequences of prochains consist of a glycine residue which repeats every third amino acid (i.e. glycine - residue - residue, or G-X-Y), commonly with proline and hydroxyproline residues (i.e. glycine - proline - hydroxyproline, or G-P-O) (Henriksen & Karsdal 2024; Nimni 2018). The taxon-specific variations of amino acid sequences at certain peptide positions within prochains can be detected and measured by mass spectrometry, generally MALDI-TOF or LC-MS/MS (Buckley et al. 2009; Brown et al. 2021a; see also Chapter 04). These positions are largely determined by cell biology, as I will discuss below.

5.2.1. COL1 Gene Transcription, Procollagen Synthesis, & Fibrillogenesis

"In order for the organism to develop an extracellular network of collagen fibers, the cells involved in the biosynthetic process must first synthesize a precursor known as procollagen. This molecule is later enzymatically trimmed of its nonhelical ends, giving rise to a collagen molecule that spontaneously assembles into fibers in the extracellular space." (Nimni 2018)

The COL1α1 and the COL1α2 genes are initially transcribed into messenger RNA (mRNA) in the nucleus of a connective tissue cell, such as a fibroblast or an osteoblast (Nimni 2018). The mRNA is then transported to the cell's cytoplasm within the endoplasmic reticulum (Nimni 2018). The mRNA is subsequently translated into proα1 and proα2 chains (and a proα3 chain, in some fish) which are constructed with temporary *signal peptides* and *propeptides* at the beginning (N-terminal) and end (C-terminal) of their amino acid sequence (Nimni 2018). N- and C-terminal signal peptides and propeptides are crucial, as they facilitate the alignment and assembly of the pro-chains (Nimni 2018). Three prochains are then synthesized into a single helical *procollagen* molecule (with signal peptides and propeptides) in the cell's endoplasmic reticulum (Nimni 2018). The procollagen molecule is subsequently transferred to (and modified within) the cell's Golgi apparatus, and then secreted into the extracellular matrix (Nimni 2018). Finally, during a process called *fibrillogenesis*, procollagen peptidases (i.e. enzymes) cleave the signal peptides and propeptides from the N- and C-terminals, resulting in a stable and mature COL1 triple helix (Nimni 2018).

5.2.2. Collagen Peptide Positions

"Standardizing the nomenclature to the position from the start of the highly conserved, G-X-Y, helical region provides a consistent naming system applicable to all vertebrates and avoids accidental duplication of names by different groups during marker development and publication." (Brown et al. 2021a)

Ultimately, it is the COL1α1 and the COL1α2 genes that largely determine the mammalian COL1 amino acid sequences measured by MALDI (or other forms of mass spectrometry). Collagen peptide positions refer to the locations of a collagen peptide within such a COL1 amino acid sequence. It is important to recognize that the COL1α1 and the COL1α2 amino acid sequences reported in protein sequence databases include signal peptide and propeptide sequences, and that these are not present in mature COL1 molecules (Brown et al. 2021a). Post-translational modifications (PTMs) also impact the tryptic masses of COL1 peptides measured by a MALDI (Brown et al. 2021a; Chowdhurry & Buckley 2022; Korzow-Richter et al. 2022). Fibrillogenesis is also very relevant to both the location of the collagen peptide positions which exhibit

taxonomically diagnostic amino acid sequences as well as the tryptic masses themselves. The stabilization of the COL1 helical structure is partially reliant upon the recurrent, patterned repetition of glycine, proline, and hydroxyproline residues (Nimni 2018), and sequence differences arise from variations in this pattern across different taxa. These variations can be referred to as *amino acid polymorphisms*.

5.2.3. Collagen Peptide Markers

"Peptide peaks that can be seen as specific to a particular taxonomic level are referred to as markers and it is a combination of these markers that allows the refinement of taxonomic identification to family level… genus level..and occasionally to species level" (Harvey et al. 2018)

The locations of taxonomically diagnostic peptide positions themselves can be viewed as the result of fibrillogenesis, as COL1 is highly conservative by result as well as slow to mutate (Brown et al. 2021a). Many tryptic cleavage locations, characterized by arginine and lysine residues, are thus conserved across most vertebrates (Brown et al. 2021a). The alignment of COL1 amino acid sequences to a conserved peptide position at the beginning of the helical region and the subsequent residue numbering of collagen peptide markers has allowed for collagen peptide marker notation standardization (Brown et al. 2021a). I have adapted a table of the 9 collagen peptide markers most commonly used in the taxonomic analysis of mammals from Brown et al. (2021a) and provided it below (Tbl.1). This table does not represent the only collagen peptide markers currently in use, especially for cetaceans and non-mammalian animals such as reptiles and fish.

Tbl.1 Table of common ZooMS marker notation and positions adapted from Brown et al. (2021a).

Shorthand Name	Complete Name	Gene	Prochain	Whole Sequence	Mature Peptide	Helical Region	Tryptic Position
α2 292	COL1α2 292-309	COL1α2	proα2	380	301	292	A2T26
α2 454	COL1α2 454-483	COL1α2	proα2	542	463	454	A2T41/42
α2 484	COL1α2 484-498	COL1α2	proα2	572	493	484	A2T43
α2 502	COL1α2 502-519	COL1α2	proα2	590	511	502	A2T45
α1 508	COL1α1 508-519	COL1α1	proα1	685	524	508	A1T47
α1 586	COL1α1 586-618	COL1α1	proα1	763	602	586	A1T55/56
α2 757	COL1α2 757-789	COL1α2	proα2	845	766	757	A2T67
α2 793	COL1α2 793-816	COL1α2	proα2	881	802	793	A2T69
α2 978	COL1α2 978-990	COL1α2	proα2	1066	987	978	A2T85

**The table in Brown et al. 2021a mislabeled the start of the α1 508 marker as "507" in the helical region and the start of the α1 586 marker as "585", and so differs slightly from the table above.*

In this table, peptide positions are situated within their location along the (numbered) amino acid residue sequence. "Whole Sequence" refers to the position within the amino acid sequence of the procollagen molecule, i.e. the complete genetic sequence. "Mature Peptide" refers to the position within the amino acid sequence of the helical region as well as the non-helical telopeptides which flank it (see Brown et al. 2021a). "Tryptic Position" refers to the position of a

tryptic peptide (i.e. a peptide that has been fragmented after trypsin digestion) within the overall protein sequence. The markers that I have presented here (e.g. α2 502) are recommended by Brown et al. (2021a) due to their location within the helical region, because the length of signal peptides, propeptides, and telopeptides can vary widely between different vertebrates. I will use these markers to display all of my own MALDI-TOF MS data in this chapter as well as my subsequent results chapters.

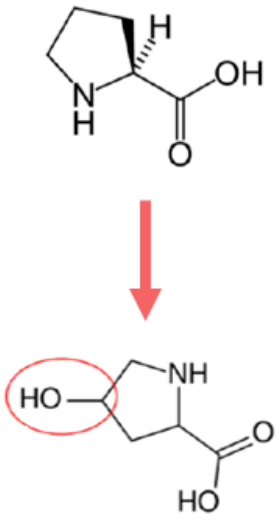
5.2.4. Collagen Peptide Mass Shifts

"...particular PTMs, such as the deamidations of asparagine and glutamine residues, continue to accumulate in proteins that remain into the forensic, archaeological, and palaeontological records." (Chowdhury & Buckley 2022)

Importantly, both biological PTMs and diagenetic (i.e. post-mortem) modifications can affect the tryptic masses of collagen peptides. Proline hydroxylation and oxidation both cause a +16 Da mass shift, while the deamidation of asparagine to aspartic acid or glutamine to glutamic acid causes a +1 Da mass shift (Chowdhury & Buckley 2022; Nimni 2018; Perez Hurtado & O'Connor 2012; Stadtman et al. 2005). Although a variety of other PTMs and diagenetic modifications are known to take place in collagen, these three are among the most common (Creecy et al. 2021; van Doorn et al. 2012) and most visible (pers.comm. Christinna Warinner 2024). Thus, +16 Da mass shifts recorded in MALDI markers must be regarded with caution, as they may represent mass differences between amino acids (e.g. between proline and leucine; see Fig.2) or oxidization. While LC-MS/MS can be used to distinguish between the two, MALDI cannot. It is for this reason that collagen peptide markers should be determined using LC-MS/MS mass sequence data as opposed to MALDI-TOF MS data.

Fig.2 Table of mutation mass shifts and an illustration of proline oxidation.

	G	A	S	P	V	T	C	L/I	N	D	Q/K	E	M	H	F	R	Y	W
	57	71	87	97	99	101	103	113	114	115	128	129	131	137	147	156	163	186
G 57		14	30	40	42	44	46	56	57	58	71	72	74	80	90	99	106	129
A 71	-14		16	26	28	30	32	42	43	44	57	58	60	66	76	85	92	115
S 87	-30	-16		10	12	14	16	26	27	28	41	42	44	50	60	69	76	99
P 97	-40	-26	-10		2	4	6	16	17	18	31	32	34	40	50	59	66	89
V 99	-42	-28	-12	-2		2	4	14	15	16	29	30	32	38	48	57	64	87
T 101	-44	-30	-14	-4	-2		2	12	13	14	27	28	30	36	46	55	62	85
C 103	-46	-32	-16	-6	-4	-2		10	11	12	25	26	28	34	44	53	60	83
L/I 113	-56	-42	-26	-16	-14	-12	-10		1	2	15	16	18	24	34	43	50	73
N 114	-57	-43	-27	-17	-15	-13	-11	-1		1	14	15	17	23	33	42	49	72
D 115	-58	-44	-28	-18	-16	-14	-12	-2	-1		13	14	16	22	32	41	48	71
Q/K 128	-71	-57	-41	-31	-29	-27	-25	-15	-14	-13		1	3	9	19	28	35	58
E 129	-72	-58	-42	-32	-30	-28	-26	-16	-15	-14	-1		2	8	18	27	34	57
M 131	-74	-60	-44	-34	-32	-30	-28	-18	-17	-16	-3	-2		6	16	25	32	55
H 137	-80	-66	-50	-40	-38	-36	-34	-24	-23	-22	-9	-8	-6		10	19	26	49
F 147	-90	-76	-60	-50	-48	-46	-44	-34	-33	-32	-19	-18	-16	-10		9	16	39
R 156	-99	-85	-69	-59	-57	-55	-53	-43	-42	-41	-28	-27	-25	-19	-9		7	30
Y 163	-106	-92	-76	-66	-64	-62	-60	-50	-49	-48	-35	-34	-32	-26	-16	-7		23
W 186	-129	-115	-99	-89	-87	-85	-83	-73	-72	-71	-58	-57	-55	-49	-39	-30	-23	



5.2.5. Archaeological Collagen

"Studies of paleontological and archaeological collagen have revealed that well-preserved, high molecular weight collagen...can still be found even within extremely old bones (>1 Mya)...collagen is nevertheless still susceptible to taphonomy and diagenesis." (Korzow-Richter et al. 2022)

The rising popularity of ZooMS is related not only to the advantages of MALDI-TOF PMF in comparison to other biomolecular methods (see Chapter 04), but also to the ubiquity of collagen within organic archaeological materials. These materials include not only bones and teeth but also ivory (Coutu et al. 2016), antler (Ashby et al. 2015), parchment (Fiddyment et al. 2019), leather (Brandt et al. 2018), and glues (van der Sluis et al. 2023) (see also Korzow-Richter et al. 2022). A number of protocols have been developed for the extraction of COL1 from archaeological samples, including acid soluble, acid insoluble, and non-destructive protocols (Brown et al. 2020; Buckley et al. 2009; Fiddyment et al. 2015; Martisius et al. 2020; Welker et al. 2016; van Doorn 2012; van der Sluis 2014; see also Evans et al. 2023; Wang et al. 2021). The enzyme most frequently used for protein digestion is trypsin, though chymotrypsin may also be used to discern stenoid equids from caballoid equids (Paladugu et al. 2023). The masses of taxa-specific collagen peptides are measured with MALDI-TOF and recorded as unique spectra which serve as taxonomic signatures; these spectra can be compared to reference spectra in order to discriminate the genus and occasionally species of origin (Buckley et al. 2009).

5.3. MALDI Spectra

Collagen peptide markers are located within amino acid sequences that have been numbered for notation purposes, but their distribution as recorded on a MALDI spectrum is non-sequential. MALDI spectra instead display the increasing *m/z* ratios of peptides, not the order of the peptides along an annotated protein sequence. MALDI *m/z* ratios are the product of the mass of a peptide, measured in units called *daltons* (Da), divided by its charge. The charges recorded by a MALDI are only ever +1 (pers.comm. Christinna Warinner 2024). In ZooMS, trypsin is most often used to cleave collagen peptides at known cut sites at arginine and lysine residues (Buckley et al. 2009, but see also Paladugu et al. 2023), resulting in tryptic peptides. The masses of tryptic peptides, i.e. tryptic masses (measured in Da), are used to both establish and identify collagen peptide markers (Buckley et al. 2009). The *m/z* ratios displayed on a MALDI spectrum are identical to tryptic masses that they are calculated from, due to the +1 charge, and so the two terms are used interchangeably when describing ZooMS data. The *m/z* ratios recorded on a MALDI spectrum are compared to published collagen peptide markers for taxonomic identification.

5.4. Applications of ZooMS

"The collagen-peptide method has advantages over other non-morphological methods of sheep/goat distinction because of the long-term survival of collagen over other biomolecules such as ancient DNA." (Buckley et al. 2010)

Species-level identifications are sometimes possible among canids, cervids, fish, amphibians, and rodents, whose collagen is less conservative than the collagen of larger mammals (Brown et al. 2021b; Buckley & Cheylan 2020; Buckley et al. 2016; de Kock et al. 2023; Harvey et al. 2018, 2019; Richter et al. 2011, 2020). One of the most valuable and practical applications of ZooMS in assemblage analysis is the discernment of sheep versus goat remains (Buckley et al. 2010), especially in Inner Asia. Caprines predominate in the animal assemblages recovered from archaeological sites, though ratios of sheep and goat within them are hard to distinguish morphologically and remain poorly understood (see Chapter 06). ZooMS cannot be used to distinguish between most domesticated mammals and their wild counterparts, owing to the largely conservative nature of collagen (and thus COL1 amino acid sequences).

Zooarchaeologists endeavoring to determine whether or not domesticated animal remains are represented in prehistoric assemblages must instead use morphological criteria and / or aDNA analysis. ZooMS can also be helpful in this regard, as the method may be used to identify fragmented faunal remains to a genus level and thus identify specimens of interest that may be selected for subsequent aDNA and biogeochemical analyses. The use of ZooMS as a "screening method" has been especially gaining traction in Eurasian (including Inner Asian) assemblages and has been used to identify Denisovans and other early hominids (Brown et al. 2016), Pleistocene megafauna (Brown et al. 2021b), and possible Bronze Age domesticates (Taylor et al. 2020b) (see also Korzow-Richter et al. 2022). Some of these samples have been subsequently subjected to additional biomolecular and biogeochemical analysis such as mtDNA lineage reconstruction, radiocarbon dating, and stable isotope analyses (e.g. Brown et al. 2016; Pan et al. 2024 [see Appendix 02]; Tarlykov et al. 2021). A number of archaeological samples that I have collagen peptide mass fingerprinted have also been submitted to secondary analyses, as I will detail in the "Results" section of this dissertation (see Chapter 21).

5.5. ZooMS & Zooarchaeology

"The aim of zooarchaeology is not to identify as many fragments as possible from a faunal assemblage. This is useless at the best, and misleading at the worst…I would be very wary to conclude that an "all fragments" approach is better than a selective one. To move towards a system in which any unspecified fragments are recorded would take us back to the "wilderness" of not having any clear control or clarity of what is exactly being recorded." (Albarella 2018)

As ZooMS is essentially a method of taxonomic identification, it can complement zooarchaeological methods by verifying, refining, and at times correcting morphological identifications. For some studies, this may mean submitting a limited number of fragments for analysis (e.g. Silvestrini et al. 2022); for others, this may involve fingerprinting the bulk of an assemblage (e.g. Bouchard et al. 2020). For studies which are not focused on presence / absence data, e.g. to identify early domesticates or a specific taxon, or where the entire assemblage is not highly fragmented, there is little reason to submit every faunal fragment for ZooMS (Albarella 2018). The intersection of ZooMS and zooarchaeology can significantly complicate taxonomic frequency counts, e.g. NISP counts (see Chapter 02), especially by increasing the representation of large animals whose remains are susceptible to being

fragmented by carnivores (e.g. bovines) (Brown et al. 2021b; Rubens et al. 2024; Sinet-Mathiot et al. 2019). ZooMS-based identifications can also decrease the representation of medium-sized animals such as caprines (Sinet-Mathiot et al. 2019) and reindeer (Discamps et al. 2024), although these animals are also susceptible to predation.

The challenges involved with ZooMS, zooarchaeology, and quantification are currently being addressed by a number of researchers (e.g. Discamps et al. 2024). At the same time, the targeted application of ZooMS to certain skeletal elements can help to refine taxonomic counts (Torres-Iglesias et al. 2024), and can be useful for the interpretation of taphonomic data more generally (Bouchard et al. 2020; Discamps et al. 2024; van der Sluis et al. 2014). It has also been suggested that combined ZooMS and fragment weight / length data could be used to investigate taphonomic princesses (Wang et al. 2024). Although ZooMS cannot be used to help assess sex or estimate age, the method can be used to help produce mortality profiles, for example by discriminating between sheep and goat mortality data (e.g. Sierra et al. 2023). ZooMS has also been used by (zoo)archaeologists incorporating other lines of biogeochemical (e.g. isotopic) and biomolecular (e.g. genetic) lines of evidence into their faunal analyses (e.g. Pan et al. 2024 [see Appendix 02]; Pilaar Birch et al. 2019; van der Sluis et al. 2014). Researchers are still learning how to best integrate ZooMS and zooarchaeological data, though recent studies of their combined potential are promising.

5.6. Conclusion

“Within the context of archaeology, the application of ZooMS to faunal assemblages has allowed a wide range of topics to be explored, including domestic herd management, choices relating to secondary product use, exploitation of wild species, and the appearance of commensal species.” (Korzow-Richter et al. 2022)

In this chapter I focused on ZooMS as a method of collagen peptide fingerprinting. I overviewed collagen, COL1, and collagen peptide markers, as well as collagen peptide marker positions and notation. I also discussed how MALDI spectra display peptide mass measurements as *m/z* ratios, alongside some of the PTMs which can cause mass shifts that deviate from the expected peptide masses based upon the COL1 amino acid sequences. I discussed some of the applications and limits of ZooMS, including a need for reference spectra and the limits of taxonomic resolution that the method can provide. Finally, I discussed some of the main challenges and benefits involved with integrating ZooMS analysis with other zooarchaeological methods, including specimen quantification and taphonomic interpretation. In the next chapter, I will discuss the availability of both published zooarchaeological criteria and published collagen peptide markers for the mammals of key importance to the human subsistence strategies and animal economies of Inner Asia.

6. Faunal Analysis of Inner Asian Taxa

6.1. Introduction

“Animal bone assemblages must be retained; like books in a library, they represent archives to which we should regularly return to in order to extract additional information. To claim to have analyzed an assemblage fully comprehensively represents nothing more than a self-delusional chimera.” (Albarella 2018)

Having established the methods by which zooarchaeologists may analyze faunal remains, I will now discuss how these methods have been applied to distinct taxonomic groups. My overview will include key insights provided by aDNA analyses as well as the morphometric and biomolecular approaches available for taxonomic attribution, sex assessment, and age-at-death estimation. I will focus on seven major taxonomic groups–cattle (*Bos* sp.), equids (*Equus* sp.), camelids (*Camelus* sp.), caprines (*Ovis* sp.; *Capra* sp.), antelopines (*Gazella* sp., *Procapra* sp.; *Saiga* sp.), cervids (*Cervus* sp.; *Capreolus* sp.), and suids (*Sus* sp.). I will discuss the various zooarchaeological criteria and collagen peptide markers that have been published for the Inner Asian species of these groups, as well as the issues related to their faunal analysis.

6.2. Cattle

Ancient DNA has played a critical role in the reconstruction of both taurine (*Bos taurus*) and zebu (*Bos indicus*) cattle domestication events (Bollingino et al. 2012; Cai et al. 2014; Caramelli 2006; Chen et al. 2010, 2018, 2023; Edwards et al. 2004; Frantz et al. 2020; Lei et al. 2006; Park et al. 2015; Rosengren et al. 2021; Troy et al. 2001; Zhang et al. 2013). The taurine cattle of Central Eurasia were originally domesticated from *Bos primigenius primigenius* ca. 10,500 years ago in the Euphrates Valley of West Asia and introduced into East Asia ca. 5000 years ago, where they would crossbreed with South Asian zebu cattle domesticated from *Bos primigenius nomadicus* and domesticated yak (*Bos grunniens*) thousands of years later (Cai et al. 2014; Chen et al. 2023; Lei 2006; Rosengren et al. 2021). The dispersal of domesticated taurine cattle from West Asia into East Asia almost certainly involved human-driven herd migration through Inner Asia. It has been suggested that domesticated taurine cattle were introduced into the region ca. 6000 years ago (Frachetti 2012), but this process is as of yet poorly understood.

In China, modern northern cattle breeds are primarily taurine while southern cattle breeds are predominately zebu (Cai et al. 2007a). Ancient zebu cattle hybridized with Mongolian taurine cattle, most likely along the Silk Road ca. 1000 years ago, and while modern Mongolian taurine cattle are closely related to aurochsen, neither share close affinity with modern East Asian cattle breeds (Brunson et al. 2023; Yue et al. 2014). Modern day Russian taurine cattle are also a hybrid of *Bos taurus* and *Bos indicus* (Kantanen et al. 2009; Sermyagn et al. 2018; Solodoneva et al. 2023; Yurchenko et al. 2018). Interestingly, modern taurine cattle breeds in Kazakhstan exhibit a notable absence of zebu ancestry (Yamanaka et al. 2019). Further research is needed

to elucidate the history of prehistoric taurine cattle breeding and migration from West Asia into Inner Asia, and the subsequent admixture of taurine cattle with zebu cattle.

6.2.1. Identifying Cattle

Taurine cattle (*Bos taurus*) and aurochsen (*Bos primigenius*) are both known to have varied greatly in size throughout different regions and time periods (Albarella 1997; Janz et al. 2020; Wright 2013). Aurochsen (*Bos primigenius*) were larger than their domesticated descendants (e.g. *Bos taurus*) but were also strongly sexually dimorphic. Female aurochsen remains can be mistaken even by specialists for the remains of male domesticated cattle, and vice versa. This issue is compounded by the size variation aurochsen have exhibited in different spatial and temporal contexts and which sometimes mirror domesticated cattle (Davis 1987; Schibler & Schlumbaum 2014; Wright 2013), including in the Eastern Eurasian Steppe (Janz et al. 2020). Modern taurine bulls (*Bos taurus*) range on average between 450-1800 kg, females range between 360-1,100 kg, and modern steppe cattle breeds in particular range between 300-800 kg (Abdelmanova et al. 2021).

Collagen peptide peptide markers have been published for multiple Inner Asian bovine species including domesticated taurine cattle (*Bos taurus*), aurochs (*Bos primigenius*), domesticated yak (*Bos grunniens*), and wild yak (*Bos mutus*) (Buckley et al. 2009; Buckley & Collins 2011; Kirby et al. 2013; Welker et al. 2016; Buckley et al. 2017). ZooMS cannot be used to distinguish between these species (Tbl.2). Additionally, there are two 3017 *m/z* tryptic peptides in bovine collagen which can be detected by MALDI (COLIα2 757-789 & COLIα2 89-130) (Buckley et al. 2009). Unfortunately only COLIα2 89-130 is actually diagnostic of bovines, and MALDI cannot be used to make this distinction. Therefore, tryptic masses of 3017 *m/z* must be used with caution when making taxonomic identifications in cattle. Neither ZooMS nor zooarchaeology can distinguish domesticated cattle from wild bovines with complete certainty, though zooarchaeology is the most useful in this aspect.

Tbl.2 Table of published tryptic masses of collagen peptide markers in Inner Asian bovine species.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Bos primigenius	1105.6	1192.6	1208.6	1427.7	1580.8	1648.8	2131.1	2792.4	2853.4	2869.4	3017.4	3033.4
Bos taurus	1105.6	1192.6	1208.6	1427.7	1580.8	1648.8	2131.1	2792.4	2853.4	2869.4	3017.4	3033.4
Bos grunniens	1105.6	1192.6	1208.6	1427.7	1580.8	1648.8	2131.1	2792.4	2853.4	2869.4	3017.4	3033.4
Bos mutus	1105.6	1192.6	1208.6	1427.7	1580.8	1648.8	2131.1	2792.4	2853.4	2869.4	3017.4	3033.4

**Markers were taken from Buckley et al. 2009; Buckley & Collins 2011; Kirby et al. 2013; Welker et al. 2016; Buckley et al. 2017.*

6.2.2. Assessing Cattle Sex

Although cattle (*Bos primigenius*, *Bos taurus*) are strongly sexually dimorphic, it is not easy to quantify what the average weights of males compared to females from the ancient breeds of Inner Asia would have been. The males would have been larger and more angular than the females, who would have had wider hips and more gracile horns. Again, these traits are not

easy to quantify and organize into precise osteometric criteria for the benefit of zooarchaeologists seeking to sex Inner Asian cattle (*Bos primigenius*, *Bos taurus*) remains. Despite this biometric overlap, distinction between the two taxa is largely determined by size and occasionally horn core morphology (Bökönyi & Bartosiewicz 1987; Guintard 2005; Tekkouk & Guintard 2007). These challenges may have led to the inconsistent faunal reports from archaeological sites such as Tamsabulag in Inner Mongolia, where the same Neolithic animal remains have been attributed to “cattle-breeding” in one publication (i.e. Sériadès 2004) and aurochsen in another (i.e. Zhao 2021).

Zooarchaeologists generally endeavor to sex cattle (*Bos primigenius*, *Bos taurus*) remains by analyzing their pelvises (Duerst 1926; Grigson 1982a; Uerpmann 1973), horncores (Armitage 1982; Armitage & Clutton-Brock 1976; Grigson 1976; Sykes & Simmons 2007), and metapodials (Boessneck 1956; Fock 1966; Higham 1969; Howard 1961; Mennerich 1968; Matolcsi 1970; Svensonn et al. 2008; Telldahla et al. 2012; Thomas 1988; Zalkin 1960). The most reliable of these elements is the pelvis, which are unfortunately a rarity (intact at least) in archaeological assemblages (Sykes & Simmons 2007). There is also no guarantee that an archaeological assemblage will contain any of sexually dimorphic elements (though metapodials do have a high recovery rate), or that these elements will retain sexually diagnostic features (Sykes & Simmons 2007; Telldahla et al. 2012). Assemblages can also contain remains from multiple cattle breeds which overlap in size, castrated males with elongated longbone and modified horncore morphology, or draught cattle with enlarged morphology (Albarella 1997; Bartosiewicz et al. 1993; Knecht 1966; Mennerich 1968; Telldahla et al. 2012; Thomas 1988).

6.2.3. Estimating Cattle Age

There are also a number of dental criteria available for aging cattle. O’Connor’s (1988) broad age class system for cattle was followed by a ten-tier system by Legge (1992), adapted from Grant (1875, 1982) and a dental development study of Iron Age sheep (Ewbank et al. 1964). Whereas previous tooth wear systems for aging archaeological cattle were expansions and fusions of pre-existing eruption and wear studies, Legge’s (1992) system included data derived from cementum and crown height studies as well as dental radiography. Legge’s (1992) system was also unique for taking deciduous third premolars into account as well as stages of root development and bovine pillar wear. Legge (1992), O’Connor (1988), and Halstead (1985) all provide only a small quantity of age classes for adult cattle.

The dental age class system subsequently developed for cattle by Jones & Sadler (2012) decades later is incredibly detailed, making observations of the positioning of cement / enamel junctions and root arches of the molars to distinguish main stages. The quality and quantity of both main and subclasses of Jones & Sadlers’ (2012) age class system is advantageous in the analysis of larger assemblages, but would dilute data rendered from smaller assemblages. A limited amount of data can be derived from smaller assemblages and specimens exhibiting incomplete lower molar rows, and in such cases broader age stages are advisable in reconstructing mortality profiles. For example, in Greenfield’s (1988) investigation of herd

composition and secondary product production in the Central Balkans, the number of age classes used was reduced down to three.

Epiphyseal fusion data recorded from cattle remains can be used to complement dental data (Chaplin 1971; Habermehl 1975; Silver 1969; Uerpmann 1973), though the effects of sexual dimorphism should be taken into account. Metacarpi growth concludes earlier in bulls than cows, for example, while humeri growth concludes earlier in cows than bulls (Bartosiewicz 1984). Epiphyseal data can also be used on its own. A recent reconstruction of agropastoralist strategies at a Late Bronze Age / Early Iron Age farmhouse in Kyrgyzstan used epiphyseal fusion data (following Silver 1969) to argue that the majority of the cattle (*Bos taurus*) remains belonged to adults who had likely been kept alive for traction as opposed to slaughtered for meat (Ananyevskaya et al. 2021). Aging archaeological cattle via epiphyseal fusion and dental analysis remains a nuanced endeavor, and zooarchaeologists must adapt their age-at-death estimation methods to suit their unique faunal assemblages and archaeological contexts.

6.3. Equids

The history of the human-horse relationship is as fascinating as it is complex, and aDNA analysis has contributed greatly to our understanding of this relationship (Cieslak et al. 2010; Fages et al. 2019; Frantz et al. 2020; Librado & Orlando 2021; Orlando 2018; Rosengren et al. 2021; Schubert et al. 2014). The morphological plasticity observed in equids has demonstrated that osteomorphometry alone is not suitable for classifying them phylogenetically (Geigl & Grange 2012). Genomic research has proven that modern horses (i.e. DOM2 lineage horses, *Equus caballus*) were domesticated from wild horses (*Equus ferus*) in the Western Eurasian Steppe, probably in the Volga-Don region, ca. 4000 years ago (Librado et al. 2021).

Horses were also domesticated from wild *Equus ferus* ca. 5500 years ago in Eneolithic Central Asia, presumably by the archaeological Botai culture of Kazakhstan (Gaunitz et al. 2018; Librado et al. 2021; Rosengren et al. 2021; Warmuth et al. 2012). Genetic studies have demonstrated that these Botai horses were the ancestors of the Przewalski's horse (*Equus ferus przewalskii*), but not the ancestors of modern domesticated horses (*Equus ferus caballus*) (Gaunitz et al. 2018; Librado et al. 2021; Outram et al. 2021; Rosengren et al. 2021; Taylor & Barrón-Ortiz 2021). To date there is no consensus as to the taxonomy of Prezwalski’s horse (*Equus ferus przewalskii*) and it has been argued both that they are feral descendants of domesticated horses from Botai (Gaunitz et al. 2018) and that they were never domesticated at all (see Taylor & Barrón-Ortiz 2021). What is clear is that they do not descend from the same lineage as modern domesticated horses (Librado et al. 2021).

Importantly, this recent revelation has disproved the long-standing theory that domesticated horses were a part of a cultural “Indo-Iranian package” that spread throughout the Eurasian Steppe ca. 3500 years ago (Anthony 2007; de Barros Damgaard et al. 2018b; Narasimhan et al. 2019). This is only one example of how aDNA can help disentangle and refine our understanding of the human-horse relationship in Inner Asia. Genomic sequencing was also

used to identify equine bone as *Equus ovodovi* as opposed to *Equus callabus*, confirming that the extinct sussemione was still present and being exploited in Bronze Age Western Mongolia (Pan et al. 2024; Appendix 02). This is extremely relevant to horse domestication studies, as *Equus ovodovi* bones are susceptible to being falsely identified as domesticated *Equus callabus*. Archaeological equine bones from Neolithic and Early Bronze Age assemblages actually representing *Equus ovodovi* may also be a possibility in Altai and Inner Mongolian assemblages (Cai et al. 2022; Vilstrip et al. 2023).

The equines of Neolithic and Bronze Age Central Eurasia were not limited to *Equus callabus* and *Equus ovodovi*; the extant Asiatic wild ass (*Equus hermonius*), also known as the hemione or onager, was also present in the region. Onagers (*Equus hemionus*) and khulans (*Equus hemionus hemionus*) are Eurasiatic asses whose stenoid ancestors diverged from the caballoid ancestors of horses ca. 5.5 mya (Bennett et al. 2017). The bones of the Asiatic wild ass can be easily morphologically misidentified as those of a domesticated horse (Taylor et al. 2020b), but fortunately their genes are more distinct. Recent genomic studies have confirmed that Asiatic wild asses are closely related to the donkeys (*Equus africanus*) which dispersed into Eurasia ca. 4000 years ago, but they are not descended from them (Pan et al. 2024; Todd et al. 2021). European wild asses (*Equus hydruntinus*), or hydruntines, and kiangs (*Equus kiang*) on the other hand are likely subspecies of Asiatic wild asses (*Equus hermonius*), with hydruntines dispersing west into the Western Eurasian Steppe and kiangs dispersing east into the Tibetan Plateau (Pan et al. 2024). The dispersals and relationships of asses throughout Central Eurasia can be better understood with further genetic and genomic research (e.g. Vershinina et al. 2021).

6.3.1. Identifying Equids

Although much effort has been put into developing morphometric criteria for distinguishing the equids which populated ancient Europe and Western Asia (see Armitage & Chapman 1979; Baxter 1998; Davis 1980; Grigson 2012; Hanot & Bochaton 2018; Johnstone 2004; Peters 1998; Uerpmann & Uerpmann 1994), distinguishing Inner Asian equids from one another has not been as high of a priority. Fortunately there is significant overlap and morphometric criteria have been developed for distinguishing between wild horses, domesticated horses, and onagers (Cucchi et al. 2017; Davis 1982; Eisenmann 1986; Eisenmann & Bekouche 1986; Eismann & Mashkour 2000). However, the dental criteria have not been found to be reliable and morphological distinction remains overall challenging and subjective (Chuang & Bonhomme 2019; Geigl & Grange 2012; Payne 1991; Twiss et al. 2017).

A lack of robust criteria for distinguishing Inner Asian equids has likely contributed to inconsistencies in faunal reports. Faunal remains from the Afanasievo-associated archaeological sites such as Kara-Tenesh and Balykhutul have been reported as both domesticated (Frachetti 2012) and possibly wild (Honeychurch et al. 2021b), painting an unclear picture about horse domestication and exploitation in the Eneolithic and Bronze Age Altai Mountain region (see Chapter 01). I will discuss the misidentification of archaeological equid remains and issues surrounding the timing of horse dispersal in-depth in subsequent chapters

(see Chapters 09–15). ZooMS can be used to help resolve the morphological misidentifications of equids by distinguishing caballoids from stenoids (Tbls. 3–4), though the enzyme chymotrypsin must be used to cleave at the α1 1016 peptide marker site (Paladugu et al. 2023) (Tbl.3).

Tbl.3 Table of published tryptic & chymotryptic masses of collagen peptide markers in equid species.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)	α1 1016
Equus caballus	1105.6	1182.6	1198.6	1427.7	1550.8	1649.8	2145.1	2792.4	2883.4	2899.4	2983.4	2999.4	2497.1
Equus przewalskii	1105.6	1182.6	1198.6	1427.	1550.8	1649.8	2145.1	2792.4	2883.	2899.4	2983.4	2999.4	2511.1

**Markers were taken from Buckley et al. 2009, 2017; Buckley & Collins 2011; Desmond et al. 2018; Kirby et al. 2013; Paladugu et al. 2023; Welker et al. 2016. Only the masses provided for peptide position α1 1016 are chymotryptic (Paladugu et al. 2023).*

Tbl.4 Table of published tryptic masses of collagen peptide markers in Inner Asian equid species.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Equus caballus	1105.6	1182.6	1198.6	1427.7	1550.8	1649.8	2145.1	2792.4	2883.4	2899.4	2983.4	2999.4
Equus przewalskii	1105.6	1182.6	1198.6	1427.7	1550.8	1649.8	2145.1	2792.4	2883.4	2899.4	2983.4	2999.4
Equus hemionus	1105.6	1182.6	1198.6	1427.7	1550.8	1649.8	2145.1	2792.4	2883.4	2899.4	2983.4	2999.4
Equus hydruntinus	1105.6	1182.6	1198.6	1427.7	1550.8	1649.8	2145.1	2792.4	2883.4	2899.4	2983.4	2999.4

**Markers were taken from Buckley et al. 2009, 2017; Buckley & Collins 2011; Desmond et al. 2018; Kirby et al. 2013; Welker et al. 2016.*

6.3.2. Assessing Equid Sex

Neither the stenoids (*Equus hemionus*, *Equus hemionus hemionus*) nor the caballoids (*Equus caballus*, *Equus ferus*, *Equus ferus przewalskii*) of Inner Asia are strongly sexually dimorphic (see Berger et al. 2001; Van Asperen 2013; Willoughby 1975). Pelvic shape and canine tooth absence and presence are used to attribute sex to archaeological equid remains (Sisson 1914; St. Clair 1975). The reliability of these approaches is influenced by sample preservation and excavation, and thus not suitable for all assemblages. Further complicated arise from the fact that female equids of various age classes have been shown to exhibit canine teeth (Cornevin & Lesbre 1894; Ellenberger 1887; Youatt 1843) and the effects of castration on equid pelvis morphology are poorly understood (Nistelberger et al. 2019). Sexing taphonomically damaged equid remains with limited osteomorphometric criteria is not easily achieved in any geographical context, and one can only admire zooarchaeologists for having made the most out of a difficult situation (e.g. Taylor 2016).

6.3.3. Estimating Equid Age

Equids (*Equus* sp.) were of great interest to the late nineteenth century and early twentieth century zoologists, and multiple techniques were developed for aging live horses (*Equus caballus*) through the examination of their dentition (e.g. Axe 1905; Cornevin & Lesbre 1894; Duerst 1922; Fitzwygram 1901; Galvayne 1912; Goubaux & Barrier; Sisson & Grossman 1953; Tagland & Barone 1950; see also Levine 1979, 1982). Decades later a landmark PhD

dissertation (Levine 1979) provided a method for aging archaeological horses (*Equus caballus*) up to ca. fifteen years by establishing height-wear curves for cheek teeth. While Levines' (1979) method is only applicable to adult horses (*Equus caballus*), horses younger than five years may now be attributed age based upon eruption stages (Evans et al. 2007).

Eruption sequences have not only been used to develop age-at-death estimation methods for domesticates horses (*Equus caballus*), but have also been used to develop estimation methods for Inner Asian equids. The dentition sequences of 440 khulan (*Equus hemonius hemonous*) crania were recorded and a method was developed for aging (i) specimens up to five years of age by analyzing eruption sequences and (ii) specimens over five years by analyzing annual lines in tooth cementum (Lkhagvasuren et al. 2013). Uniquely, equid (*Equus* sp.) incisors are not capped but have a deeply convex infundibulum that wears down in stages and can be reliably aged from five years up to eight years (Axe 1905; Levine 1982b; Evans et al. 2007; Sisson & Grossman 1953). Rates of epiphyseal fusion in equids roughly correspond with dental eruption, and the two may be combined to assign age classes to their remains (see Evans et al. 2007; Reitz & Wing 2008).

There are currently several methods available for the age-at-death estimation in archaeological equids, depending on the assemblage in question. A fairly recent study synthesized Levine's (1979) height wear curves with eruption schedules and incisor wear patterns to estimate the age-at-death of subadult, juvenile, and adult horse (*Equus* sp.) crania from multiple Late Bronze Age Mongolian sites (Taylor 2016). The same study which used epiphyseal fusion to estimate the age-at-death of cattle remains in late prehistoric Kyrgyzstan (i.e. Ananyevskaya et al. 2021) also used epiphyseal fusion to argue that the majority of horses (*Equus* sp.) present in the assemblage had been kept alive past their prime slaughtering age, for traction and possibly dairying. Although horses are not typically as commonly recovered from Inner Asian archaeological contexts as caprines (see Chapters 12–19), there are a number of methods that may be adapted to estimate the age-at-death of those which are recovered.

6.4. Camelids

Both thee ancestor and place of origin of domesticated Bactrian camels (*Camelus bactrianus*) are currently unknown (Chuluunbat et al. 2014; Ganbold et al. 2018; Ji et al. 2009: Ming et al. 2016, 2017, 2020; Silbermayr et al. 2010). The most recent genomic analyses suggest that Bactrian camels were domesticated from an unknown ancestor ca. 4,500 years ago in Central Asia, and later dispersed east into the Mongolian Plateau where they introgressed with wild Bactrian camels (Ming et al. 2020). There is a substantial need for further research to confirm if this is correct, and if so, to identify the ancestor of domesticated Bactrian camels and clarify their relationships with wild Bactrian camels and the Dromedary camels of West Asia (*Camelus dromedarius*). There is also no clear origin center for their domestication, beyond "Central Asia".

6.4.1. Identifying Camelids

Zooarchaeologists have endured to understand and develop osteological criteria for distinguishing the bones of Bactrian camel (*Camelus bactrianus*) from those of dromedary camels (*Camelus dromedarius*) since the onset of the twentieth century (Harris et al. 2010; Köhler-Rollefson 1989; Lesbre 1903; Olsen 1988; Steiger 1990; Wapnish 1984). These morphological criteria have been applied with mixed results, successfully in some studies (Peters & von den Driesch 1997; von den Driesch & Obermaier 2007) and less successfully in others (De Grossi 2006; Grigson 2012; Pigière & Henrotay 2012; Reynaud-Savioz & Morel 2005; Studer & Schneider 2008; Uerpmann 1999). These discrepancies may be the result of using misidentified reference specimens to develop the criteria as well as intraspecific variation and interspecific overlap (Martini et al. 2017).

More material has been published on the anatomy and osteology of single-humped dromedary camels (e.g. Smuts & Bezuidenhout 1987; Walker 1985) than of double-humped Bactrian camels. However, dromedaries are not endemic to Inner Asia and will thus not be discussed further in this chapter. There is an abundance of literature that may be used to identify camelid remains in Inner Asian assemblages, and by context (potentially) attribute them to Bactrian camels. It is worth noting that very few camelid remains have been identified in the faunal assemblages of prehistoric or historic Inner Asia, an issue that I will discuss in-depth further into this dissertation (see Chapters 18–19). Collagen peptide markers have been published for Bactrian camels (Rybczynski et al. 2013; Welker et al. 2016) (Tbl.5).

Tbl.5 Table of published tryptic masses of collagen peptide markers in Inner Asian camelid species.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Camelus bactrianus	1105.6	1221.6	1235.6	1443.7	1550.8	1635.8	2131.1	2820.4	2883.4	2899.4	3975.4	2991.4

**Markers were taken from Rybczynski et al. 2013; Welker et al. 2016.*

6.4.2. Assessing Camelid Sex

There are currently no published guides for assigning sex to Bactrian camel (*Camelus bactrianus*) remains. Researchers have established that Bactrian camels (*Camelus bactrianus*) exhibit limited sexual dimorphism; males are larger in body and canine dentition, and pelvis shape also varies between males and female (Smuts & Bezuidenhout 1987; Steiger 1990; von den Driesch & Obermaier 2007). Unfortunately, the non-pelvic postcranial elements of camels (*Camelus sp.*) do not appear to be sexually dimorphic (Martini et al. 2018). Accurately sexing the archaeological remains of Bactrian camels (*Camelus bactrianus*) based on osteology is challenging. In the context of Inner Asia, there is little opportunity to attempt to do so, as camel remains are rarely recovered in archaeological contexts (see Chapters 18–19).

6.4.3. Estimating Camelid Age

There are currently no published guides for estimating the age-at-death of Bactrian camel (*Camelus bactrianus*) or dromedary camel (*Camelus dromedarius*) remains. The most recent (to my knowledge) comparative osteological and dental study of the two species was not able to identify significant differences between their dentition and progressive dental wear (Martini et al. 2018). Although Martini et al. (2018) did not produce any tooth wear stages or age classes for either species of camel, they did report in-depth about the dental wear that they observed. Simplified, they noted that (in both *Camelus bactrianus* and *Camelus dromedarius*) the first mandibular incisor (i1) narrows, the mandibular and maxillary fourth premolar (p4, P4) and third molar (m3, M3) occlusal surfaces broaden, and the first and second mandibular and maxillary molar (m1, m2, M1, M2) occlusal surfaces both broaden and shorten (Martini et al. 2018).

I have yet to come across a faunal report which has attempted to estimate the age-at-death of Bactrian camel (*Camelus bactrianus*) remains by dental wear analysis. Epiphyseal fusion data associated with cattle (*Bos taurus*) has been used to estimate the age-at-death of dromedary camel (*Camelus dromedarius*) remains (e.g. Prust et al. 2020; von den Driesch & Obermaier 2007); I have also not seen this approach applied to Bactrian camel (*Camelus bactrianus*). The only faunal report I have come across which made some attempt of aging Bactrian camel (*Camelus bactrianus*) remains (from the Medieval Sogdian / Uzbek fortress Kafir Kala; see see Chapter 19) determined that the two specimens recovered belonged to a single adult, based on the size and thickness observed in the bones (Serrone et al. 2017).

6.5. Caprines

Domesticated sheep (*Ovis aries*) and goats (*Capra hircus*) are arguably the most important animals in Central Eurasian pastoralist economies. Rediscovering the history of their domestication in West Asia and subsequent dispersal through Inner Asia and into East Asia is essential to deepen and enrich our understanding of ancient human-animal relationships and subsistence strategies. The analysis of caprine aDNA has been critical to this endeavor, helping to reveal that *Ovis aries* was domesticated from five lineages of wild sheep (*Ovis orientalis*) and *Capra hircus* was domesticated from five or six lineages of wild bezoar ibex (*Capra aegagrus*) ca. 8000-11,000 years ago in the Fertile Crescent region of West Asia (Amillis et al. 2017; Colli et al. 2015; Daly et al. 2018; Frantz et al. 2020; Gerbault et al. 2012; Hiendleder et al. 2002; Luikart et al. 2001; Lv et al. 2015; Meadows et al. 2007; Naderi et al. 2007, 2008; Pedrosa et al. 2005; Rosengren et al. 2021; Sardinia et al. 2006; Sultana et al. 2003; Tapio et al. 2006; Yang et al. 2023b; Yi et al. 2022; Zeder 2017; Zheng et al. 2020). The bezoar ibex (*Capra aegagrus aegagrus*) is not found in Inner Asia, though its close relative the Siberian ibex (*Capra siberica*) is (van der Greer 2008).

Domesticated sheep from West Asia initially dispersed into Central Eurasia and eastward through the Mongolian Plateau into China and India ca. 6500 years ago, and then again ca. 4500 years ago (Ganbold et al. 2019; Lv et al. 2015; Yang et al. 2023b; Zhao et al. 2017). Inner

Asian Argali (*Ovis ammon*) have been excluded as the ancestor of *Ovis aries*, having diverged ca. 1.1 mya (Sanna et al. 2015). The recent genetic analysis of Late Neolithic and Early Bronze Age sheep remains from China, including Xinjiang in the Altai region, and Uzbekistan suggests that the first wave of domesticated sheep were routed through Uzbekistan and Northwest China, while the second wave was routed through the Altai and Inner Mongolia (Yang et al. 2023b). These findings are further supported by the results of genetic analyses of archaeological sheep remains recovered from Neolithic Kyrgyzstan and Bronze Age Kazakhstan, as well as Eneolithic and Bronze Age sites in the Southern Siberian Altai, which confirm the presence of *Ovis aries* (Dymova et al. 2017; Hermes et al. 2019, 2020b; 2022; Taylor et al. 2021a).

Contrary to early theories on the origins of domesticated sheep (Ryder 1984), there is currently no genetic evidence that endemic argali (*Ovis ammon*) were independently domesticated in Inner Asia. While argali admixture has been detected in Tibetan and South Asian domestic sheep (Hu et al. 2018; Zhao et al. 2017), the lack of argali admixture detected in Chinese domestic sheep (Cai et al. 2007b, 2011; Hiendleder et al. 1998, 2002) also refutes theories that East Asian sheep were independently domesticated from argali or other wild sheep (Bo 1986, Xie 1985) and instead suggests that human-driven domestic sheep dispersals from East Asia to South Asia involved argali hybridization (Yang et al. 2023b; Zhao et al. 2017). PCA comparisons of domestic sheep remains from Neolithic Kazakhstan further demonstrate a continuity of domestic sheep lineage transmission from West Asia, to Central Asia, to South and East Asia (Taylor et al. 2021a).

The importance of this clarification cannot be understated as it indicates a remarkably extensive, ancient transmission of domesticated animals across an incredibly vast landmass, likely involving complex trade networks and economies whose roots may have been laid during the Neolithic. Ancient Inner Asia was not only an epicenter for domesticated sheep dispersal, but was also key in the dissemination of domesticated goats from West Asia to East Asia (Amillis et al. 2017). The domestic goats of the Fertile Crescent were herded through Central Asia into Mongolia, and later introgressed with a separate population of goats that may have been domesticated in South Asia (Ganbold et al. 2020; Hermes et al. 2020a). Modern mtDNA analyses have suggested that a unique lineage of domestic goats developed in Southwest China, possibly as the result of a local and independent domestication event, which subsequently dispersed into North China (Peng et al. 2022; Yi et al. 2022). More research is needed to evaluate the authenticity of these claims and reconstruct the complex history of goat (and sheep) domestication and migration in Inner Asia.

6.5.1. Identifying Caprines

Distinguishing domesticated sheep (*Ovis aries*) remains from domesticated goat (*Capra hircus*) remains is both challenging (using morphological methods) and insightful when investigating animal economies and subsistence strategies- especially pastoralism (Bartosiewicz 1999; Boessneck 1969; Halstead et al. 2002; Lloveras et al. 2022; Payne 1973, 1985; Reitz & Wing 2008). Distinguishing between wild (e.g. *Ovis ammon*, *Capra siberica*) and domesticated sheep and goat (*Ovis aries*, *Capra hircus*) has proven equally important and challenging for

zooarchaeologists (Clutton-Brock et al. 1990; Helmer 2000; Halstead et al. 2002). That being said, reliable morphological and geometric morphometric criteria are available (e.g. Boessneck 1970; Boessneck et al. 1964; Haruda 2017; Payne 1985; see also Jeanjean et al. 2023; Zeder & Lapham 2010; Zeder & Pilaar 2010).

Criteria for the morphological and osteometric distinction of argali (*Ovis ammon*) and domestic sheep (*Ovis aries*) have only recently been made available (Wang et al. 2020). Little criteria exist for distinguishing Siberian ibex (*Capra sibirica*) from domesticated goat (*Capra hircus*) (see Hermes et al. 2020b; Meadow 1989b), though general criteria have been developed for sorting wild from domesticated goats (Boessneck 1969; Zeder 2006b). Certain skeletal elements are more difficult to taxonomically discriminate than others, especially when recovered in fragmented and taphonomically damaged assemblages. The resultant “sheep/goat” and “ovicaprid” attributions recorded in faunal reports have hindered research into animal domestication, herd management practices, and the emergence of pastoralism in Inner Asia. ZooMS can be used to discriminate between *Ovis* sp. and *Capra* sp. (Buckley et al. 2010), though no markers have been published for *Ovis ammon* or *Capra siberica* (Tbl.6). ZooMS has so far been used to discern between *Ovis* sp. and *Capra* sp. bone fragments from archaeological sites in Kazakhstan (Tarlykov et al. 2021), Kyrgyzstan (Taylor et al. 2018, 2021a), Mongolia (Taylor et al. 2020a, 2021b), and Siberia (Brown et al. 2021b).

Tbl.6 Table of published tryptic masses of collagen peptide markers in Inner Asian caprine species.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Capra hircus	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3093.4
Ovis aries	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4

**Markers were taken from Buckley et al. 2009, 2010, 2017; Buckley & Collins 2011; Kirby et al. 2013; Welker et al. 2016.*

6.5.2. Assessing Caprine Sex

Siberian ibex (*Capra siberica*) and argali (*Ovis ammon*) both exhibit a high degree of sexual dimorphism (Li et al. 2017; Wang et al. 2020). Osteomorphometrics have been used to attribute sex to Pleistocene argali (*Ovis ammon*) remains from Southern France, using criteria intended for white tailed deer (*Odocoileus virginianus*), domesticated sheep (*Ovis aries*), and domesticated goat (*Capra hircus*) (Rivals 2000; Rivals et al. 2006). There are no criteria for attributing sex to Siberian ibex (*Capra siberica*) remains, though the examination of degrees of ossification in long bones has been used to determine the sex of Iberian ibex (*Capra pyrenaica*) (Serrano et al. 2006), as has mixture analysis applied to the forelimbs of Alpine ibex (*Capra ibex*) (Fernández et al. 2007).

Domesticated sheep (*Ovis aries*) are also strongly sexually dimorphic and may be sexually distinguished by the analyses of their horncores, pelvises, and metapodials (Albarella 1995; Boessneck et al. 1964; Davis 2000; Hatting 1995; Prummel & Frisch 1986). Domesticated sheep osteology is also subject to modification by castration, such as the elongation of long bones and changes in horncore morphology (Davis 2000; Hatting 1975). Expectedly, domesticated goats (*Capra hircus*) are also strongly sexually dimorphic (Zeder 2001) and

zooarchaeologists distinguish their remains by examining the morphology and biometry of their horncores, pelvises, and metapodials (Boessneck et al. 1964; Prummel & Frisch 1986).

Domesticated goat (*Capra hircus*) metapodials are even more dimorphic than domesticated sheep (*Ovis aries*) metapodials and easier to sexually distinguish (Uerpmann 1973). As with other livestock, castration may alter morphometry in domesticated species and subsequently skew sex attributions. Wild (*Capra aegargus*) and domesticated goat (*Capra hircus*) populations have also been shown to vary in size based upon their region (Zeder 2001). This biometric variability is of great relevance to zooarchaeologists seeking to distinguish the sex of Inner Asian caprids (e.g. *Capra hircus*, *Capra siberica*) using criteria developed for goats (*Capra* sp.) from the populations of different areas (such as West Asia).

6.5.3. Estimating Caprine Age

Payne's dental ageing system (1973) presented a true breakthrough in caprine age-at-death estimation that continues to be used to this day. A more recent study comparing the accuracy of Payne's (1973) and Grant's (1975, 1982) system for domesticated sheep (*Ovis aries*) and goat (*Ovis capra*) (using modern samples whose ages-at-death were known) concluded that Grant's system provided higher-resolution age estimates (Greenfield & Arnold 2008). In my experience, Panye's (1973) study remains the preferred dental age-at-death estimation amongst zooarchaeologists (pers.comm. Umberto Albarella 2024; pers.comm. Angelos Hadjikoumis 2024; pers.comm. Veronica Anicetti 2024; pers.comm. Mauro Rizzetto 2024; pers.comm. Lenny Salvagno 2024; pers comm. Marina Chorro-Giner 2024). It has also been demonstrated that sheep (*Ovis* sp.) and goat (*Capra* sp.) exhibit divergent and sexually dimorphic dental wear patterns (see Noddle 1974; Zeder 2006b).

As with cattle (*Bos* sp.) and equids (*Equus* sp.), dental eruption and wear analysis may be combined with epiphyseal fusion data to help refine age-at-death estimates in caprines (*Ovis* sp., *Capra* sp.). A popular and frequently-cited study has demonstrated that fusion age ranges consistently correspond with dental age classes in caprines (*Ovis* sp., *Capra* sp.) (Zeder 2006b). The prehistoric Kyrgyz farmhouse study (i.e. Ananyevskaya et al. 2021) used both epiphyseal fusion (following Silver 1969) and dental data (following Payne 1973) to reconstruct mortality profiles (discussed below; see section "I.IV.VIII.") for sheep (*Ovis* sp.) and goat (*Capra* sp.), and argue that their primary exploitation was for wool. In the context of Inner Asia, the caprine dominance that characterizes most archaeological assemblages more frequently allows for combined epiphyseal fusion and dental age-at-death estimation than for other taxa with much more limited representation (e.g. *Bos* sp.; *Equus* sp.; *Sus* sp.; etc.). Recently, a team of researchers combined dental analysis and ZooMS to generate mortality profiles for caprines recovered from Neolithic sites across the Eastern Adriatic Coast (Sierra et al. 2023).

6.6. Antilopines

The evolutionary relationships between the antilopines of Asia are convoluted and unclear (Kingswood et al. 2001; Kuznetsova & Kholodova 2002). There are currently no genetic or genomic studies of the ancient antelopines of Inner Asia, as far as I am aware. This is unsurprising as antelopines have never been domesticated, and identifying their bones to a taxonomic category beyond “gazelle” or “saiga” or even “wild game” is often not considered integral to faunal analysis for animal economy or subsistence strategy reconstruction. Molecular paleontological studies have utilized aDNA to explore overall saiga diversity since the Pleistocene (Campos et al. 2010; Kuhn & Mooers 2010) and research into the mtDNA diversity of modern populations of saiga in Eastern Eurasia has also been conducted for conservation purposes (Rey-Iglesia et al. 2022; Zhao et al. 2013).

6.6.1. Identifying Antilopines

The same publication which provides morphometric criteria for distinguishing between domesticated sheep (*Ovis aries*) and argali (*Ovis ammon*) (i.e. Wang et al. 2020) has also provided criteria for discerning gazelle (*Gazella sp.*) and dzeren (*Procapra sp.*). Although saiga antelope (*Saiga tatarica*) are morphologically distinct from other (wild and domestic) bovids (Jing et al. 2020), morphometric criteria for distinguishing their bones from the bones of the other cervids and antelopes of Inner Asia is lacking. The morphometric studies on Central Eurasian cervids and antelopes which have been recently published (e.g. Ratajczak et al. 2021; Vasilev et al. 2023) are useful for zooarchaeologists, although they are focused on tracking morphological changes between modern antelopine species and their Pleistocene ancestors. Amongst these Inner Asian antilopines, collagen peptide markers have so far only been published for saiga (Buckley et al. 2009; Welker et al. 2016) (Tbl.7). These markers have been used to fingerprint archaeofauna from Denisova Cave in Siberia (Brown et al. 2021b).

Tbl.7 Table of published tryptic masses of collagen peptide biomarkers in Inner Asian antelope species.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Saiga tatarica	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4

**Markers taken from Buckley et al. 2009; Welker et al. 2016.*

6.6.2. Assessing Antilopine Sex

Saiga antelope (*Saiga tatarica*) are known to be strongly sexually dimorphic; male saiga are both horned and substantially larger than female saiga, which are hornless (Grey et al. 2007; Kühl 2007; Sokolov 1974). Goitered gazelle (*Gazella subgutturosa*) are similarly sexually dimorphic, with the males being larger in body and having bigger horns than the females (Blank et al. 2012; Kingswood & Blank 1996). Dzeren (*Procapra gutturosa*) males are also horned and larger than hornless dzeren females (Frey & Riede 2003; Olson 2010; Solokov & Lushchekina 1997). The sexual dimorphism exhibited by saiga (*Saiga tatarica*) is generally helpful in the attribution of sex to their archaeological remains.

However, to date no osteomorphometric criteria have been published for sexing saiga, goitered gazelle, or dzeren, though their biometric parameters are known (see Sokolov 1974; Solokov & Lushchekina 1997). Published criteria do exist for sexing mountain gazelle (*Gazella gazella*) (which is not endemic to Inner Asia) by the analysis of horncores, pelvises, atlas vertebrae, long bones, phalanges, and astragali (Horwitz et al. 1990; Munro et al. 2011). These criteria should be applied to Inner Asian assemblages with caution as morphology varies even between different regional populations of goitered gazelle (*Gazella subgutturosa*) (Hayatgheib et al. 2011), let alone different gazelle species.

6.6.3. Estimating Antilopine Age

There are currently no criteria published in English for estimating the age-at-death of saiga antelope (*Saiga tatarica)*, dzeren (*Procapra gutturosa*), or goitered gazelle *(Gazella subgutturosa)*. Dental eruption, wear, and epiphyseal fusion criteria have been published for estimating the age-at-death of mountain gazelle (*Gazella gazelle*) remains (Munro et al. 2009). In mountain gazelle at least, epiphyseal fusion and dental eruption schedules have been found to coincide directly with one another (Munro et al. 2009). I have yet to come across a faunal report which has attempted to use either to age saiga antelope (*Saiga tatarica)*, dzeren (*Procapra gutturosa*), or goitered gazelle *(Gazella subgutturosa)* remains. This is most likely due to both the limited representation of wild ungulates in many Inner Asian faunal assemblages, as well as the history and practice of faunal analysis in Inner Asian countries. I will elaborate on both of these topics in-depth further into this dissertation (see Chapters 12–19).

6.7. Cervids

Wapiti (*Cervus canadensis*), sika deer (*Cervus nippon*), and Siberian roe deer (*Capreolus pygarus*) have been recorded in faunal reports from prehistoric Inner Asia, including from key Neolithic sites of the Mongolian Plateau (Zhao et al. 2021). It is unclear if the range of sika deer (*Cervus nippon*) extended beyond Inner Mongolia during prehistory. Although reindeer (*Rangifer tarandus*) were possibly depicted in ancient Siberian art and are herded in modern times by the Tsaatan peoples of Northern Mongolia and indigenous Siberian peoples such as the Ket, Yakut, and Evenki, they do not appear to have been exploited in ancient Southern Siberia or the Eastern Eurasian Steppe in general (Fitzhugh 2021; Lee 1967; Whitaker 1984). Reindeer will thus not not be discussed further in this chapter beyond a few relevant mentions, though they will make a brief reappearance in the second chapter.

Wapiti and sika deer are two closely related cervids with wide geographic distributions that include Inner Asia (Groves 2005; Ludt et al. 2004; Junhuai 2001; Kuwayama & Ozawa 2000; Polziehn & Strobeck 2004). Subspecies of wapiti relevant to Inner Asia include the maral, or Altai wapiti, (*Cervus canadensis sibiricus*) and the izubr (*Cervus canadensis xanthopygus*) (Stepanova & Argunov 2016). Wapiti were traditionally classified as a subspecies red deer (*Cervus elaphus*) until molecular phylogenetic analyses clarified that they are actually a

separate species and they were reclassified as *Cervus canadensis* (Groves 2005; Ludt et al. 2004; Polziehn & Strobeck 2004). This distinction will not be reflected in archaeological reports and faunal lists published before the early twenty-first century. Siberian roe deer are a more distant relative of wapiti, red, and sika deer and they are larger than their close relative the European roe deer (*Capreolus capreolus*) (Danilkin 1995; Randi et al. 1998). Genetic research into modern cervid populations have also revealed that sika deer are more closely related to wapiti than European red deer are, further contradicting traditional morphological cervid phylogenies (Kuwayama & Ozawa 2000).

The aforementioned studies emphasize the importance of comparing morphological phylogenies with molecular ones, as similar physical traits arising from similar climatic and environmental adaptations can lead to the overestimation of affinity between species that are actually distinct from one another (Groves 2005). Limited genetic studies have been conducted on ancient Siberian roe deer remains, though samples from Denisova Cave have been analyzed alongside modern samples from Southern Siberia, Central Asia, and Far East Russia to investigate the relationships between Pleistocene and Holocene populations (Vorobieva et al. 2011). Genetic investigations of Asian cervids have so far proven more useful for phylogenetic clarification and conservation efforts than for reconstructing prehistoric lifeways and subsistence economies.

6.7.1. Identifying Cervids

There is a lack of morphometric criteria for distinguishing red deer or wapiti from reindeer, all of which are large cervids, though criteria exist for distinguishing red deer from domesticated cattle (*Bos taurus*) and European fallow deer (*Dama dama*) (Lister 1996; Prummel 1988). There are no published morphometric criteria for identifying large-bodied wapiti or medium-sized sika deer (*Cervus nippon*). Collagen peptide biomarkers have been published for elk/moose and red deer, though ZooMS cannot be used to discriminate between them (Tbl.8). These markers have been used to fingerprint faunal remains from Denisova Cave (Brown et al. 2021b). Although markers have not been published for Siberian roe deer (*Capreolus pygarus*), this study noted that they can be distinguished from other cervids based on a single mass shift to *m/z* 3043.4 at α2 757 that is unique to *Capreolus* sp. (Brown et al. 2021b). This is the same peptide marker (α2 757) that distinguishes sheep from goat (Buckley et al. 2010) and that is not always retained even in well-preserved collagen.

Tbl.8 Table of published tryptic masses of collagen peptide biomarkers in Inner Asian cervid species.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Alces alces	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Cervus elaphus	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Caprelous capreolus	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3043.4	3033.4

**Markers taken from Buckley et al. 2009; Buckley & Collins 2011; Jensen et al. 2020; Kirby et al. 2013; Welker et al. 2016.*

6.7.2. Assessing Cervid Sex

The relatively recent distinction of red deer (*Cervus elaphus*) and wapiti (*Cervus cananadensis*) as separate species (see Groves 2005; Ludt et al. 2004; Polziehn & Strobeck 2004) leads to questions regarding the degree of sexual dimorphism shared between them, though they are remarkably physically similar. Despite sharing a close relation, red deer (*Cervus elaphus*) are more sexually dimorphic than sika deer (*Cervus nippon*) (Geist & Bayer 1988). Red deer (*Cervus elaphus*) males are larger than the females in both species and female red deer do not have antlers, while sika deer females do. Siberian roe deer (*Capreoulus pygarus*) are less sexually dimorphic than red deer but more so than sika deer (*Cervus nippon*), with males being slightly larger than females and having antlers while females do not (Danilkin 1995). It follows that wapiti (*Cervus canadensis*), sika (*Cervus nippon*), and Siberian roe deer (*Capreoulus pygarus*) may be attributed sex by body size estimates and that antler presence / absence data may be used to infer the sex of wapiti and Siberian roe deer remains.

Morphometric criteria for canine teeth analysis for use in the attribution of sex to red deer (*Cervus elaphus*) remains have also been published (D'errico & Vanhaeren 2002), though it is also unclear how applicable these criteria are for wapiti. There are currently no other published criteria for sexing red deer (*Cervus elaphus*), wapiti (*Cervus canadensis*), sika deer (*Cervus nippon*), or Siberian roe deer (*Capreoulus pygarus*) remains. Though biometric parameters have been established for most of these species (Danilkin 1995), cervid populations have also been shown to vary in size from prehistory to modern times (Rosvold et al. 2014; Walvius 1961). There is a gap in both the literature and knowledge regarding the sex assignment of Inner Asian cervids that could be addressed through the careful examination of reference collections or samples with established taxa and sex, and the development of new criteria.

6.7.3. Estimating Cervid Age

Although no age-at-death estimation criteria have been published for Siberian roe deer (*Capreolus pygarus*), criteria do exist for roe deer (*Capreolus capreolus*) that use dental wear and eruption, tooth crown height measurements, and epiphyseal fusion (Tomé & Vigne 2003). Criteria also exist for sika deer (*Cervus nippon*) (Uchiyama 1991) as well as for red deer (*Cervus elaphus*) (Eidmann 1932; Klein et al. 1981; Mitchell 1963, 1967). Perhaps the earliest method for aging red deer (*Cervus elaphus*) by dental analysis was the measurement of dentine layers within incisor crowns (Eidmann 1932), followed by the measurement of growth layers in dental cement (Mitchell 1963, 1967) and dental crown height (Klein et al. 1981).

Studies which have evaluated the dental height crown method with flexible regression equations (QHCM) have found that dental wear in red deer (*Cervus elaphus*) is not sexually dimorphic and that QHCM equations adjusted to fit species-specific parameters are ideal for assigning broad (but not narrow) age classes to red deer (*Cervus elaphus*) remains (Steele 2006; Steele & Weaver 2012). Another study has determined that epiphyseal fusion however is sexually dimorphic, occurring earlier in female red deer (*Cervus elaphus*) than in males (Calderón et al.

2019). Several guides for aging European subspecies of red deer (*Cervus elaphus*) by dental analysis have been published (Azorit 2011; Azorit et al. 2002, 2004; Brown & Chapman 1991).

It is not clear how applicable these studies are to wapiti (*Cervus canadensis*), and no such guides appear to have been published for the wapiti including those endemic to Inner Asia, i.e. maral (*Cervus canadensis sibiricus*) and izubr (*Cervus canadensis xanthopygus*). Dental wear stages have been shown to progress quicker in sika deer (*Cervus nippon*) than in red deer (*Cervus elaphus*) (Uchiyama 1991), and wapiti (*Cervus canadensis*) are more closely related to sika deer (*Cervus nippon*) than red deer (*Cervus elaphus*) (Kuwayama & Ozawa 2000). Further research is needed to assess the applicability of methods for estimating age at death in red deer (*Cervus elaphus*) to wapiti (*Cervus canadensis*), and whether or not criteria unique to wapiti (*Cervus canadensis*) should be developed.

6.8. Suids

Genetic studies have confirmed that modern domesticated pigs (*Sus scrofa domesticus*) were independently domesticated from wild boar (*Sus scrofa*) at least twice in both West and East Asia ca. 9,000 - 10,000 years ago, and these lineages have since introgressed with one another and dispersed throughout Asia and Europe (Ervynck et al. 2001; Frantz et al. 2013, 2015; Groenen et al. 2012; Larson et al. 2005, 2013; Megens et al. 2008; Rosengren et al. 2021; Zhao et al. 2020). These studies highlight the role that Trans-Eurasian exchange networks and the so-called “Silk Road” played in the dispersal of animal husbandry and domesticated animal lineages across Eurasia. I will revisit animal subsistence economies and especially pastoralism as mechanisms of widespread trade emergence across Eurasia in prehistory, Antiquity, and the Medieval period further into this dissertation (see Chapter 16).

Domesticated pigs were not managed during the prehistoric periods of much of Inner Asia. The wild boar ancestors (*Sus scrofa*) of domesticated pigs have been found in Neolithic assemblages from the Inner Mongolian Plateau (Zhao et al. 2021) and Central Asia (Nishiaki et al. 2022). However, the prehistoric faunal assemblages of the Eastern European Steppe and Central Asia are predominantly characterized by the remains of sheep (*Ovis* sp.), goat (*Capra* sp.), cattle (*Bos* sp.), and equids (*Equus* sp.) (see see Chapters 10–15, 18–19). Boar (*Sus scrofa*) remains are uncommon, even after the Neolithic period (see Chapters 10–15, 18–19). Although domesticated pigs (*Sus scrofa domesticus*) were not widely managed in North or Central Asia outside of China until after the Industrial Revolution (see Turakhova & Dorina 2009; Krader 1955; Panikarova 2015), their remains have been recovered from Central Asian archaeological sites associated with prehistory, Antiquity, and the Medieval periods (see Chapters 18–19).

6.8.1. Identifying Suids

The morphometric discrimination of wild boar, domesticated pigs, intermediate suids, feral pigs, and hybrid suids has a complicated history (see Rowley-Conwy et al. 2012 for an extensive

overview). Domestication, geographical distribution, and climatic changes have all impacted the size of suids, a phenomenon that has been studied extensively in the suids of Eastern Asia (Albarella et al. 2009; Matsui et al. 2005; Rowley-Conwy et al. 2012; Yamazaki et al. 2005). Traditional metric approaches to discerning between wild, domesticated, and semi-domesticated suid remains have been most successful when two populations can be compared and contrasted in a localized region, as opposed to assemblages composed of a single population (Rowley-Conwy et al. 2012).

Dental and cranial geometric morphometrics have been demonstrated to be very effective for the discernment of wild and domesticated suids (Evin et al. 2013, 2014; Owen et al. 2014) . Non-metrical methods such as the assessment of the frequency of linear enamel hypoplasia and tooth microwear analysis have also proven to be insightful, while attempts to argue for domesticated versus wild status using through the estimation of age-at-death have proven to be more problematic (Rowley-Conwy et al. 2012). The unreliability of non-geometric morphometric methods alone has led some zooarchaeologists to decry suids as “the most difficult of the major domestic animals to categorize as ‘wild’ or domestic’ (Rowley-Conwy et al. 2012). Collagen peptide markers have been published for domesticated pig (Buckley et al. 2009, 2017; Buckley & Collins 2011; Welker et al. 2016) which may be used to identify suids generally (Tbl.9).

Tbl.9 Table of published tryptic masses of collagen peptide biomarkers in Inner Asian suid species.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Sus domesticus	1105.6	1180.6	1196.6	1453.7	1550.8	1647.8	2131.1	2820.4	2883.4	2899.4	3017.4	3033.4

**Markers taken from Buckley et al. 2009, 2017; Buckley & Collins 2011; Welker et al.2016.*

6.8.2. Assessing Suid Sex

Although wild boar (*Sus scrofa*) are sexually dimorphic in size of body and skull (Genov et al. 1995; Groves & Grub 1993; Moretti 1995; Pérez-Barbería et al. 2002), their teeth (specifically canines) are more useful for sex determination than their bones (Albarella et al. 2006; Mayer & Brisbin 1988; Rowley-Conwy et al. 2012; Uerpmann 1973). Problems arise with inclusion of male juveniles however, and the high occurrence of mandibular fragmentation in archaeological assemblages complicates identifying juvenile specimens (Rowley-Conwy et al. 2012). Post-cranial metrics are also not very helpful for attributing sex to domesticated pigs (*Sus domesticus*) (Albarella 2004). Measurements of distal humeri, for example, are not useful in the discernment of male from female domesticated pigs (*Sus domesticus*) (Albarella 2004). The analysis of canine morphology is currently the most useful approach determining the sex of domesticated pig remains (*Sus domesticus*), and criteria for doing so were published in the late twentieth century (Mayer & Brisbin 1988).

6.8.3. Estimating Suid Age

Nineteenth century studies attempting to age live pigs (*Sus domesticus*) by the examination of their dentition were rife with issues ranging from poor scientific and academic practice (e.g.

Baden-Powell 1889; Girard 1834; Huidekoper 1891; Nehring 1888; Simmonds 1854) to difficulties examining the unruly pigs (*Sus domesticus*) themselves (Cornevin & Lesbre 1894; see also Legge 2013). Many of the studies which built upon these early studies were similarly flawed (e.g. Habermehl 1975; McCance et al. 1961; Teonge & McCance 1973; Silver 1963; Wenham & Fowler 1973), a deep injustice to the pigs who were intentionally starved to produce lackluster data (i.e. McCance et al. 1961; Reiland 1978; Teonge & McCance 1973). A notable error includes the assignment of an early eruption time to the third molar, a misconception that was consistently recycled from Simmonds (1854). A very thorough overview of these problematic studies has already been published (see Legge 2013).

Studies on aging wild pigs (*Sus scrofa*) via dental analysis (e.g. Matschke 1976; Bull & Payne 1982; Bridault et al. 2000; Boitani & Mattei 2002; Carter & Magnell 2007; Genov et al. 2002; Magnell 2006; Magnell & Carter 2007) were not conducted until after the mid-twentieth century. Zooarchaeologists have modified Grant's (1982) system to estimate the dental age-at-death of domesticated pigs (*Sus domesticus*, including feral, but written as *Sus scrofa*) (e.g. Rolett & Chiu 1994). Umberto Albarella's landmark PhD dissertation on pig domestication and management in Southern Europe also used Grant's (1982) system to record tooth wear following a modified version of Bull & Payne (1982) (Albarella 2004). Epiphyseal fusion criteria for domesticated pig (*Sus domesticus*) and wild boar (*Sus scrofa*) have also been published (Bridault et al. 2000; Zeder et al. 2015). No studies have been published on aging suids (*Sus* sp.) specifically from Inner Asia, which may be significant as suid dental eruption has been found to vary both by region (Anezaki et al. 2009) and sex (Zeder & Lemoine 2020).

6.9. Faunal Analysis of Inner Asian Taxa: Conclusion

"One of the major challenges in identifying the spread of domesticates in Central and East Asia is distinguishing domestic species from wild…Body size is not a reliable determinate…" (Janz et al. 2020)

Although reference collections can greatly assist zooarchaeologists with taxonomic identification, the subjective nature of identification (i.e. attribution) largely prohibits replicability, even with comparative specimens and morphometric criteria. The accuracy of faunal reports is difficult to assess and taxonomic identifications are generally accepted as a matter of faith (Wolverton 2013). While morphometric criteria exist for distinguishing domesticated cattle (*Bos taurus*) from aurochsen (*Bos primigenius*), overlaps in size between the two species (and their hybrids) complicates doing so with accuracy. Horse (*Equus* sp.), sheep (*Ovis* sp.), goat (*Capra* sp.), and suid (*Sus* sp.) remains are also notoriously difficult to morphologically classify as wild or domesticated. Consequently, several faunal reports from prehistoric Inner Asian contexts present conflicting information about archaeological animal economies. ZooMS has also not been able to be used to discriminate between the wild and domesticated variants of these taxa.

There is an overall lack of morphological criteria for many of the relevant wild taxa of Central Eurasia, including antelopines (*Gazella subgutturosa, Procapra gutturosa*, *Saiga tatarica)* and cervids (*Capreolus pygarus*, *Cervus canadensis*, *Cervus nippon*). Accurately identifying antelope and deer remains in archaeological Inner Asian assemblages is not easily achieved

with morphometric methods alone. ZooMS can be used to discriminate between *Caprelous* sp. and other cervids, but currently cannot be used to distinguish these cervids from antilopines–even though collagen peptide markers have been published for saiga. This may change with time, as there are currently very few markers that have been published for Inner Asian species of deer and antelope.

The development of methods which would allow the attribution of absolute ages (e.g. for mandibular wear stages) to faunal remains would be a worthwhile endeavor, valuable especially in the analysis of larger assemblages where a higher resolution of data are desirable. Conversely, smaller and fragmented assemblages present significant challenges for zooarchaeological research (Grayson 1984; Klein & Cruze-Uribe 1984) and the correlation of O'Connor's (1988) broad age stages with Grant's (1982) tooth wear stages would also be of great value. It is for this reason that Umberto Albarella and I created the open-access Bubona dataset (Hill & Albarella 2024; see Appendix 01), and are currently working on publishing reference tables that may be used to assess dental age class probability in archaeological cattle.

The availability and robusticity of aging criteria, regional variation in animal development and physiology, sexual dimorphism, and temporal context are all factors which may affect the results of the age-at-death estimations of archaeological animals. This especially holds true for Inner Asia, where many species are currently understudied. Zooarchaeologists must be mindful when selecting aging (and sexing) methods to produce mortality data, as well as when examining and comparing mortality data sets from different publications. When taxonomic, sex, and age-at-death data are able to be attributed to faunal remains, mortality profiles may be reconstructed for insights into human-animal relationships. This should always be done with an understanding of the ecological niches of the animals identified, as I will briefly explore in the next chapter.

7. Ecological Niches of Inner Asian Taxa

7.1. Introduction

"All considerations of domestication, whether focusing on crops or livestock, acknowledge that it involves a two-way relationship between humans and target…populations…In animals…candidacy for domestication… center almost exclusively on behavioral characteristics." (Zeder 2012)

Understanding both ecological and cultural contexts is critical when interpreting faunal assemblages or reconstructing ancient human-animal relationships. In this chapter I clarify the ecological requirements, such as food and water intake, and social behaviors that dictate the husbandry of the five key domesticated mammals of ancient Inner Asia: cattle (*Bos taurus*), horse (*Equus caballus*), sheep (*Ovis aries*), goat (*Capra hircus*), and camel (*Camelus bactrianus*). I also discuss the natural social organization of each species to contextualize how they are managed in mass by herders. I outline their natural lifespans and contrast them with the known culling practices of the humans who manage them. Additionally, I discuss the varying degrees of mobility, resiliency, and adaptability characteristic of each key species in relation to their value to herders and their potential significance in archaeological assemblages.

7.2. Domesticated Cattle (*Bos taurus*)

"The nomads' cattle were not characterized by high productivity. However, Mongolian livestock was well-adapted to the rigorous climate.There was no need to sustain cows with warm winter sheds and great reserves of hay. Cattle were also used as draft animals." (Kradin 2015b)

Cattle are large, ruminating bovines with a life expectancy of ca. 20 years and substantial food and water requirements (Dyer 2012; Hoffman & Valencak 2020; Sahu et al. 2020). Adult cattle require at least 25 liters of water per day during the cold season and at least 55 liters of water per day in the hot season; these requirements double if the animal is lactating (Dyer et al. 2012; Marwick 2007). Cattle consume some water when they graze on grass, while hay and grain-fed cows need extra water to make up the difference. A single cow or bull will typically graze 50 - 55 kg of wet forage or 20 - 25 kg dry pasture throughout the day, with morning and midday feeding peaks, although water access, temperature, humidity, and herd status greatly affect these feeding patterns and quantity of food intake (Sahu et al. 2020). Of all of the key domesticated animals featured in Inner Asian herds, cattle have the highest water and food intake requirements.

Cattle are social animals which exhibit dominance behavior and are willing to submit to humans who have earned their trust (Fjin 2011). Mother cows bond with their calves through licking, grooming, and cross-suckling, and can occasionally be coaxed into nursing orphaned calves (Fjin 2011; Sahu et al 2020). Newborn calves continue to nurse for at least one year before transitioning to grazing and socializing with other calves (Fjin 2011). Khangai herders typically castrate submissive male calves during their second year, selecting the most dominant male calves to be future bulls (Fjin 2011). As early as their second year, bulls can be mated, cows can

become pregnant and milked daily, and castrated males can be trained as draught animals- though it is better to wait until their third year (Fjin 2011). Although the natural life expectancy for cattle is ca. 20 years they are vulnerable to wolves and disease, and are also frequently culled at 3-10 years age based upon their productivity, health, or temperament (Fjin 2011; Hartwig 2009; Hoffman & Valencak 2020). The mobile management of cattle is commonly practiced throughout Eurasia (and the world), but their food and water intake requirements would greatly complicate long-distance management in greater numbers. Resource availability is a prerequisite for successfully managing cattle.

7.3. Domesticated Horses (*Equus caballus*)

"Of all the species, the horse was of major military and economic importance…they were used for riding and transporting goods…horses played an important role in the exploitation of pastures in the winter…they are symbolically embodied in folklore and legend. The status of pastoral people was determined by the number of horses they owned…" (Kradin 2015b)

Domesticated horses are large hind-gut fermenters (as opposed to ruminants) known to be more resilient, adaptable, and longer-lived than cattle, with a maximum lifespan of ca. 40 - 55 years (Fleurance et al. 2012; Hartwig 2009; Hoffman & Valencak 2020; Horvath et al. 2022; McGowan 2022; Snedden & Argenzio 1998). Horses have more efficient digestive systems than cattle and can draw from internal stores of water to sustain themselves during bouts of dehydration (Snedden & Argenzio 1998). Horses can also accumulate stores of summer body fat which they can access for energy in the winter (Gudmundsson & Dyrmundsson 1994). An adult horse will typically consume ca. 20 - 55 liters (or more) of water and ca. 10 kg of dry pasture or ca. 5 kg in wet forage a day (Dubberstein & Johnson 2009; Marwick 2007; Rodiek 2001; Siciliano 2013). Unlike cattle, horses cannot subsist on a primarily grain-based diet because their large intestines will rapidly ferment the soluble carbohydrates, which is disastrously harmful for them (Rodiek 2001).

Horses are also social and form dominance-based hierarchies (Bailey 2016; Fjin 2011; Sigurjónsdóttir 2003). Stallions are notoriously aggressive towards other males when mares are present and must be managed accordingly (McDonnell & Murray 1995). Many herders, including Khangai herders, split their horses into separate herds (or *bands*) of mares, foals, and a single stallion (a harem) and non-harem stallions and geldings (a bachelor band) (Fjin 2011; McDonnell & Murray 1995). As with cattle, submissive males are selected for castration during their second Autumn (Fjin 2011). Interestingly, it has been observed that stallions will temporarily concede higher status to a gelding *once a human has mounted them*, presumably because of the joint increase in size and technical ability represented by the pair (Fjin 2011). Unlike cattle, horses are seasonally polyestrous and mares generally give birth in summer and spring (Crowell-Davis 2007). Mares can become pregnant and be milked in their second year, but it is safer for them to give birth in their fourth year (Derisoud et al. 2021). Mare's milk is more nutritious than cow's milk, though mares produce far less milk than cows do (Malacarne et al. 2002).

Horses make for better transport than cattle, which are better suited for traction. Stallions, geldings, and mares alike can be ridden once they've been broken in. Like cattle, horses are susceptible to both disease and predation by wolves. Horses are better equipped to defend themselves than cattle and are kept with less protective measures, at least in the Khangai mountain region (Fjin 2011). Perhaps the most widespread reason for the premature culling of horses is disease and poor health, though they are also killed in the case of unproductivity and for food (Fjin 2011; Hartwig 2009; Hoffman & Valencak 2020). Horses possess great cultural significance for humans, especially in Inner Asia, and often play a role in human ritual- both as living creatures and as dead animals. I will discuss the ritual and social significance of horses further into this dissertation (see Chapters 16–17). Ecologically, domesticated horses do not require as much food or water as cattle do and the presence of their remains in archaeological assemblage can be associated with mobility.

7.4. Domesticated Sheep (*Ovis aries*)

"Sheep formed the majority of the nomads' herds in Inner Asia…sheep required no special care. They could find and eat grass all year, drink muddy brackish water, and eat snow in winter. After the hunger of winter, sheep quickly restored their weight…Sheep were the principal source of milk and meat for nomads… everyday clothes were made of sheepskin, and felt was manufactured from sheep's wool…" (Kradin 2015b)

Domesticated sheep are medium-sized ruminants which can live to be ca. 25 years old if not prematurely culled by humans or killed by predators (Hoffman & Valencak 2020). Their digestive efficiency is roughly equivalent to that of cattle, and less than that of goats (Devendra 1989; Reid et al. 1990). Adult grassland sheep require ca. 2-6 liters of water a day while saltbush sheep require 4-12 liters, which is more than goats on average (Devendra 1989; Marwick 2007). Sheep and goats require roughly the same daily intake of feed (ca. 0.025–0.035 kg) but sheep are less selective in their feed than goats, the latter of which are better able to distinguish between different tastes (e.g. sweet, salty, bitter, etc.) (Devendra 1989; El Aich & Rittenhouse 1988).

Socially, domesticated female sheep (ewes) are gregarious and do not form strong dominance hierarchies, so much as large and stable communities with strong maternal bonds to offspring (lambs) (Fisher & Matthews 2001; Ozella et al. 2020). Domesticated males (rams) form smaller groups that do observe a dominance hierarchy, and Khangai herders separate them from castrated males (wethers) (Fisher & Matthews 2001; Fjin 2011). Sheep can become pregnant and milked after their first year, at which time they may also be clipped for wool. Sheep require far less resources than cattle and are more easily managed than goats, although they do adapt some goat behavior when kept together (Fjin 2011). Sheep do not produce nearly as much milk or meat as cattle, but they are prized for their wool and their adaptability in extreme environments.

7.5. Domesticated Goats (*Capra hircus*)

"The nomads of Inner Asia also kept a small number of goats…Goats were even easier to keep than sheep; in places where grass quality was poor, they took the place of sheep in their use by nomads. Goats were able to orient themselves well in varied terrains and led the way for the entire herd. Though goat's milk offered the highest fat content…breeding goats was considered less prestigious than breeding sheep." (Kradin 2015b)

Domesticated goats are medium-sized ruminants which can live to be ca. 20 years old, but are often culled by humans at ca. 5 years old (Hoffman & Valencak 2020; Spector 1956). An adult goat requires ca. 0.025 - 0.035 kg of food and 4-5 liters of water a day (or twice that amount if lactating) (Devendra 1989; Schlink et al. 2010). Goats are able to store fat in their tails as energy reserves as well as reabsorb water in their lower guts prior to defecation, and are well-suited for hot and arid environments (Berihulay et al. 2019; Schlink et al. 2010). Although goats are more efficient digesters than sheep or cattle, they are opportunistic eaters with higher nutrient requirements (Devendra 1989; El Aich & Rittenhouse 1988; Lu 1988; Saraswat & Sengar 2000; Schlink et al. 2010; Singh 2018). Goat milk is noted for being more nutrient rich than cow milk and is valued as an ideal alternative to human breast milk (Ceballos et al. 2009; Devendra & Liang 2012; Hoffman & Valencak 2020; Nayik et al. 2022; Park et al. 2007).

Domesticated goats are notoriously curious and reactive, and they need to be watched more carefully than sheep as they are more likely to wander off (Dweyer 2022; Fjin 2011; Miranda-de la Lama & Mattiello 2010). Although quite different in temperament, domesticated goats exhibit social behaviors very similar to domesticated sheep. Female goats (does) bond strongly with their offspring (kids) and loosely organize themselves together, while male goats (billies) organize themselves together in accordance with a dominance hierarchy (Barroso et al. 2000; Shackleton & Shank 1984). Khangai herders also separate billies from male goats castrated in their second year (wethers), the latter of which are kept with ewes and lambs (Fjin 2011). Billys, wethers, and ewes can all be combed for cashmere (provided they are not of the Angora breed). The ability of domesticated goats to adapt to extreme environments and provide cashmere, hide, meat, and milk has led to them being prized by livestock herders around the world.

7.6. Bactrian Camels (*Camelus bactrianus*)

"The camel was the last of the important livestock of Inner Asia nomads… its abilities to survive without water and food up to ten days, as well as to drink water with high salt content and eat plants unsuitable for other species, would have been especially important to nomads…camels were mainly used to transport goods…Camels also comprised an important source of wool and milk products…dried camel milk excrement was an important fuel source…nevertheless, camels had drawbacks." (Kradin 2015b)

Camels ruminate but are not true ruminates by standard of physiology, behavior, or taxonomy (Fowler 2008; Al-Jassim & Hogan 2013). Bactrian camels (*Camelus bactrianus*) are primarily browsers that eat ca. 5kg dry matter a day, though they will also graze and eat fodder or grain, and can go up to a week without food (Dorman 1984; Irwin 2010; Marsh 1856). When camels do graze, they will only consume a portion of a plant as they wander; this grazing style is

markedly different from cattle, who are intensive and stationary grazers, or from caprines, which will graze down to the roots of a plant (Khomeiri & Yam 2015). Bactrian camels also require much less water than cattle, caprines, or horses and can go weeks at a time without drinking water (Dorman 1984; Irwin 2010; Marsh 1856; Patil et al. 2013; Rubel 1969). They are extremely resilient and can live for up to 35 years (Faye 2014; Hoffman & Valencak 2020; Khomeiri & Yam 2015).

Camels are known to be social as well as emotive, endearing, intelligent, and even spiteful when mistreated (Fjin 2011; Irwin 2010; Marsh 1856). Their social organization is similar to that of the other key domesticated animals discussed so far, with females and calves grouping together separately from males (Milková et al. 2005). Bactrian camel mothers have been observed to be more maternal than dromedaries and will sometimes nurse calves that are not their own (Milková et al. 2005; Nath et al. 2016). Bactrian camels do not produce as much milk as the dromedary camels (*Camelus dromedarius*) of West Asia, but they do produce more wool and their wool is considered to be of a higher quality (Alhadrami & Faye 2022; Khomeiri & Yam 2015). Male camels are much more frequently culled by humans than females, often before they reach one year of age, though modern slaughter rates in Central Asia are amongst the lowest recorded in the world (Faye 2013). Male and female Bactrian camels can be ridden or raced and provide wool, meat, and traction (Khomeiri & Yam 2015; Marsh 1856). Their presence in an archaeological assemblage is a strong suggestion of aridity and mobility, especially if they dominate in abundance. Their remains are unlikely to be found in taiga zones, as they require more open spaces and arid environments; they are poorly suited for cold and damp environments (Kradin 2015b).

7.7. Ecological Niches of Inner Asian Taxa: Conclusion

“The nomads’ mode of life and culture did not change during preindustrial times…most of their domestic animals are horses, cows, sheep, and they also have rare animals such as camels…they move according to the availability of water and pasture…” (Kradin 2015b)

The ecological niches of key herding animals must be understood and taken into consideration when interpreting faunal assemblage data. The five key domesticated mammals of Inner Asia that I have discussed in this chapter have different ecological requirements and present different challenges to livestock herders. Cattle are large, stationary grazers that require substantial amounts of food and water. They provide valuable traction, meat, food, hide, and milk but cannot be well-managed without adequate resource availability. Cattle cannot be efficiently ridden (and are difficult to mobilize in large quantities. Horses are large, efficient digesters which are more resilient and easier to mobilize than cattle. They hold great cultural and social significance for humans and can be ridden long distances, but also require substantial resources and are more difficult to milk.

Sheep are smaller and require less food than cattle or horses while providing valuable wool, meat, and milk, but they cannot be used as effectively for traction or transport. Sheep are easily managed but more vulnerable to predation than horse or cattle and they do not live as long. Goats are more adventurous and naturally curious than sheep; they are fussier eaters, but also

more self-sufficient in their feeding, and are better adapted to arid environments. Goats provide similarly valuable products as sheep, producing cashmere instead of wool, and the two species are frequently herded together. Sheep and goats can overgraze a pasture if not managed mobily, as opposed to camels, which have the lowest ecological requirements of all key species discussed. Camels are the most well-adapted to extremely arid environments as well the least disease prone, and the most suited to cross vast swathes of land. Camels can be utilized for transportation, traction, meat, milk, wool, and hide, but require open landscapes and are not suitable for the forests of the taiga.

Each of these key species presents unique value as well as challenges, and while their inclusion in an archaeological assemblage can be used to infer economic and environmental circumstances it is difficult to make any solid conclusions based on taxonomic presence or abundance alone. The preference for sheep husbandry that has consistently characterized many Inner Asian populations probably developed due to the docile behavior of sheep and the comparative ease of their management, combined with their contribution of nutritionally and economically valuable products. The consistent pairing of sheep with a much smaller ratio of goats is likely because goats also provide valuable products and can help sheep become more resilient, but are more difficult to manage in larger numbers. An increase of goats at the expense of sheep can be linked to increased aridity or altitude; goats predominate over sheep in the herds of the Gobi desert, for example.

Cattle are also docile and provide more meat and dairy than caprines as well as traction and labor that is of great value to herders, but they are not as easy to mobilize and have far greater food and water requirements. This likely explains why cattle generally have lower representation than caprines in Inner Asian herds, and why their increased representation has a positive correlation with sedentarism. Horses are more difficult to manage and milk than cattle or caprines, but they are resilient and provide a prestige and symbolic value that the former do not, especially because they can be ridden and raced. Their presence in Asian cosmologies and rituals dates back to ancient times and it is no wonder that they continue to be prized and represented in herds, but are difficult to sustain in large numbers.

Bactrian camels are the most resilient of all the species discussed and have the lowest ecological requirements. They arguably provide the most secondary products and services, and they do not overgraze as caprines do. It is not entirely clear why there is a consistently very low representation of camels in the Inner Asian herds managed in regions with suitable aridity and space, especially amongst highly mobile communities. Camels can be raced, ridden, and milked just as horses can, but also provide wool where horses do not. Both animals have been noted for their intelligence, loyalty, and beauty and have been featured in art, folklore, and poetry. It may be the case that camels simply are not ecologically productive (pers.comm. Will Taylor 2024), and are slow breeders (Kradin 2015b). I will revisit the notable absence of camel remains recovered from archaeological contexts where they could be expected, such as Silk Road Period Central Asia, further into this dissertation. I will dedicate the next chapter instead to exploring the management practices of these key domesticated animals in Inner Asia.

8. Inner Asian Animal Economies

8.1. Introduction

“Animal husbandry has been one of the main subsistence patterns for many cultures around the world since the Neolithic period.” (Kardulias 2015)

Animal economies, or the human management and exploitation of non-human animals, provide critical insight into human behavior, culture, and lifeways (Rowley-Conwy et al. 2017). In Inner Asia *pastoralism* is frequently cited as one of the most common animal management strategies. In this chapter I will first discuss different definitions, modes, and archaeological markers of pastoralism. I will also explore the historical and modern herd compositions and animal husbandry practices of Southern Siberia, Mongolia, Kazakhstan, and Uzbekistan. Finally, I will discuss modern and historical Inner Asian animal economies alongside their relation and relatability to archaeological cultures and faunal reports.

8.2. Defining Pastoralism

“There are no features of culture or social organization that are common to all nomads or even that are found exclusively among nomads."(Spooner 1973)

A multitude of terms and definitions have emerged to describe Inner Asian peoples who herd animals. Barfield defined *nomads* as highly mobile peoples who do not necessarily engage in pastoralism, and *pastoralists* as economic specialists who raised livestock and need not be nomadic (Barfield 1993). For Barfield, *nomadic pastoralists* engaged in mutually beneficial relationships with domesticated animals which required periodic movement, and he emphasized the uniqueness of the lifeways which characterized the horse-riding *nomadic pastoralists* of the Eastern Eurasian Steppe (Barfield 1993). *Nomadic pastoralists* in Asia have elsewhere been defined as animal herders who migrate seasonally (Goldstein & Beall 1994) as well as *mobile livestock herders* (Dyson-Hudson & Dyson-Hudson 1980). Humphrey & Sneath reflected upon the robusticity and sustainability of the *mobile pastoralist* practices of Asian *nomads* (Humphrey & Sneath 1999), just as Asian *nomads* have been defined in more recent publications as highly specialized *mobile pastoralists* (Spengler et al. 2021).

Khazanov argued against defining *nomads* based upon their mobility regardless of their economy and defined *pastoral nomads* as peoples engaged in extensively mobile food-producing economies which required year-long herd maintenance of free-grazing and stable-less herds, who periodically migrated within established grazing territories, and who predominantly produced for subsistence instead of markets (Khazanov 1994). Jones (2005) and Lattimore (1962) emphasized the role of trade with agricultural communities for both necessities and luxuries within *pastoral nomadic* lifeways as practiced by Asian *herdsmen* (Jones 2005; Lattimore 1962). Fjin intentionally adapted Lattimore’s herdsmen to *herders*, who she defined as any people who take the role of directing the animals they herd in her ethnographic study of *Inner Asian nomads* (Fjin 2011).

The aforementioned terms *nomad, pastoralist, pastoral nomad, nomadic pastoralist, mobile pastoralist, mobile livestock herder, herdsmen*, and *herder* have been woven into decades of anthropological and archaeological literature, often seemingly interchangeably, and often without explanation. Pastoralist terminology will not be resolved in this dissertation, though the curious reader is directed to Dyson-Hudson & Dyson-Hudson (1980) for an in-depth exploration of nomadic pastoralist terminology. For simplicity's sake, pastoralism will here be defined as the mobile management of domesticated animal herds (Dong 2016) while maintaining an awareness that degrees of mobility and relationships with domesticated animals vary greatly between pastoralist communities.

8.3. Modes of Pastoralism

"Nomads, or highly specialized mobile pastoralists, are prominent features in Central Asian archaeology, and they are often depicted in direct conflict with neighboring sedentary peoples. However, new archaeological findings are showing that the people who many scholars have called nomads engaged in a mixed economic system of farming and herding." (Spengler 2021)

Reflecting upon the ever-increasing number of attempts to narrow down a precise definition of pastoralism, Khazanov (1994) remarked upon the futility of trying to determine exactly what a pastoral economy *is* and emphasized the importance of identifying the *ratios* of pastoralism and agriculture that characterize the economy of individual communities. Noting that the number of nomadic or mobile pastoralist subsistence strategies is virtually inexhaustible, he outlined two major pastoral economies: *pastoral nomadism proper* and *semi-nomadic pastoralism* (Khazanov 1994). For Khazanov, *pastoral nomadism proper* is characterized by the total absence of agriculture as practiced by the *pure nomads* living in parts of "North Eurasia, High Inner Asia, and the Eurasian Steppes" (Khazanov 1994).

Khazanov (1994) defined *semi-nomadic pastoralism* as extensive pastoralism with a periodic rotation of pastures and a secondary reliance on agriculture, and noted that this economy is far more common in the world than *pastoral nomadism proper*. He even outlined a history and model of *Eurasian steppe type pastoral nomadism*, noting that *pure nomadism* and *semi-nomadism* were more fluid in this region than in other areas of the world, with communities easily switching back and forth between the two (Khazanov 1994). The perception of certain Asian peoples as pure nomads, and the resultant impact on Asian archaeology, will be discussed in the later in this section.

Other modes of pastoralism that are of interest to archaeologists include *agropastoralism*, *transhumance*, *vertical pastoralism, horizontal pastoralism,* and *dairy pastoralism*. *Agropastoralism* has been applied to predominantly sedentary communities who engage in farming and livestock management (Spengler et al. 2021). *Transhumance* has been both equated with *pastoral nomadism* (see Chang 2015) and distinguished from it by the merit of being practiced by livestock herders who are seasonally mobile but live in settled agricultural communities (Jones 2005). In this schematic, *agropastoralists* and *transhumant pastoralists* are

separated by their degrees of mobility, with neither being consistently mobile enough to be considered *nomadic pastoralists*.

This spectrum of economic mobility is, of course, a soft construct that is convenient for discussing subsistence strategies and lifeways, but (like most models) falls apart under close examination (see Dyson-Hudson & Dyson-Hudson 1980). *Vertical pastoralism* refers to short-distance transhumance through different altitudes, while horizontal pastoralism refers to long-distance, longitudinal transhumance (Barfield 1993). *Dairy pastoralism* is used in archaeological literature not as a metric of pastoral mobility, but in reference to the exploitation of dairying animals as well as the production and consumption of secondary milk-based products (e.g. Scott et al. 2022; Wilkin et al. 2020).

Reconstructing the pastoralist economies of ancient populations is a difficult task. Archaeologists cannot simply subscribe modern subsistence practices to prehistoric peoples in a presumably analogous transference (though, these will be explored). Instead, it is in the examination of material culture and the remains of once-living community members (including animals) and resources (including animals) that evidence of subsistence can be uncovered. I will discuss the archaeological markers of pastoralism in the subsection below.

8.4. Archaeological Markers of Pastoralism

“At the core of understanding domestic animal use and dispersal events across Eurasia is a significant methodological hurdle – how can we distinguish domestic animals from their wild relatives?” (Taylor et al. 2020c)

Identifying pastoralist activity in the archaeological record requires pursuing two major lines of evidence: mobility and domesticated animal reliance (Chang & Koster 1986; Honeychurch & Makerawicz 2016). Mobility is an especially complicated phenomena to detect and reconstruct, though archaeologists have endeavored to do so by identifying pastoralist infrastructure such as settlement patterns, seasonal encampments, portable housing structures and tools, herd enclosures, and rock art (Honeychurch & Makerawicz 2016). The remains of domesticated animals can contribute to our understanding of both mobility and husbandry, as certain animals (such as yaks, camels, and horses) have long been utilized for long-distance transportation (see Chapters 09–19). Seasonal animal movement and management can also be detected and reconstructed using combined stable carbon, oxygen, nitrogen, and strontium isotope analyses of animal remains (see Chapter 04; see also Bendrey et al. 2015; Honeychurch & Makerawicz 2016; Lazzerini et al. 2019, 2021; Makarewicz 2014, 2017; Makarewicz & Tuross 2006; Ventresca Miller et al. 2019; Rosengren et al. 2021).

Reliance on domesticated animals (as well as additional subsistence strategies, such as fishing) can be inferred directly from the faunal remains recovered from an archaeological site. Accurately distinguishing domesticated taxa from wild taxa by morphology alone is a significant challenge (see Chapter 02; see also Chuang & Bonhomme 2019; Clutton-Brock et al. 1990; Geigl & Grange 2012; Halstead et al. 2002; Helmer 2000; Hermes et al. 2021; Payne 1991;

Taylor et al. 2020c; Twiss et al. 2017). Zooarchaeology by Mass Spectrometry is also an ineffective method for distinguishing wild from domesticated mammals (see Chapter 05). The combination of zooarchaeology and ZooMS (e.g. Sierra et al. 2023; Taylor et al. 2021a) can lead to the identification of ideal candidate specimens for higher resolution taxonomic identification methods such aDNA analysis (e.g. Hermes et al. 2021), though these methods are costly, require specialized training, and are not accessible to all researchers (see Chapter 04).

ZooMS may not be an effective method for separating wild from domesticated mammals, but it is very useful for distinguishing sheep (*Ovis* sp.) from goat (*Capra* sp.) (Buckley et al. 2010; see also Brown et al. 2021b; Sierra et al. 2023; Tarlykov et al. 2021; Taylor et al. 2018, 2020a, 2021a)–an endeavor that is notoriously difficult using osteometry and morphology (see Chapter 06; see also Bartosiewicz 1999; Boessneck 1969; Halstead et al. 2002; Lloveras et al. 2022; Payne 1973, 1985; Reitz & Wing 200). Zooarchaeologists have classically reconstructed culling profiles from archaeological caprine assemblages to infer pastoralist strategies (Arbuckle & Atici 2013; Gillis et al. 2022; Hesse 1982; Redding 1981, 1984). However, multiple studies have demonstrated that archaeological interpretations of mortality data do not consistently represent animal husbandry practices or secondary product specialization with accuracy (Cribb 1985, 1987; McCormick 1992; Russell 2004). The over-interpretation of mortality data does not mean that mortality data are not valuable (it absolutely is), but is more of an indication that researchers need to be more critical in their interpretations (pers.comm. Will Taylor 2024).

Instead of using sheep and goat mortality profiles to argue for or against various modes of animal husbandry or pastoralism at individual sites, it may be more useful to compare and contrast different sheep and goat herd composition ratios and mortality data from different regions through time. Importantly, it should be stated again that while ZooMS can establish which bone specimens are sheep or goat in origin, the method cannot currently be used to determine whether they belonged to domesticated caprines or wild species, e.g. argali or ibex. When researchers can be reasonably confident about the taxonomic attributions for an animal assemblage, whether through morphology, biomolecular verification, or context (or all three, ideally; see Taylor et al. 2020c), more nuanced inferences about archaeological animal economies can be made- provided there is an appropriate framework with which to interpret the data. I will discuss the availability of proper frameworks for reconstructing Inner Asian animal economies in the next section.

8.5. Modern & Historical Animal Economies

“Mortality and taxonomic abundance measures are proxies for past processes that zooarchaeologists hope to monitor, such as hunting strategies, domestic animal management, and impacts of climate change on subsistence.” (Gifford-Gonzalez 2018)

Faunal mortality data from individual archaeological sites would probably be better viewed through the lenses of local herding practices and human-animal relationships, as opposed to being filtered through models that were developed based off of data from vastly different regions and time periods (e.g. Greenfield 1988, 2005; Payne 1973; Redding 1981, 1984; Vigne &

Helmer 2007). This is especially true considering the aforementioned issues involved with reconstructing and interpreting culling profiles (Brochier 2013; Cribb 1985, 1987; McCormick 1992; Russell 2004). The next subsections will discuss the historical and modern animal husbandry practices of Southern Siberia, Mongolia, Kazakhstan, and Uzbekistan, with the intention of elucidating more regionally and culturally appropriate frameworks for analyzing taxonomic abundance and mortality data from Inner Asian assemblages.

8.5.1. Southern Siberia

Animal husbandry was strictly regulated during the Soviet era and herders had fixed, unforgiving meat, wool, and dairy product quotas to fill (Andhearn 2021; Brunswick 1960; Fjin 2011; Jenkins 1956; Jones & Smogorzewska 1982; Strauss 1970; Vaĭnshteĭn 1980). Historical herd composition throughout much of Eastern Eurasia fluctuated before, during, and after Soviet rule, driven by both economic and socio-political changes (Krader 1955; Vaĭnshteĭn 1980). There are limited ethnographic accounts of herding lifeways to contextualize and understand these changes within Southern Siberia, especially compared to Mongolia, but data does exist (e.g. Lee 1967; Stépanoff et al. 2017).

Certain groups of modern Yeniseian peoples in the Ob-Yenisei river basin, such as the Ket, still maintain hunter-gatherer and fishing lifeways and only some of them engage in the herding of domesticated animals (Lee 1967) (Tbl.10). The Ket peoples on the left bank of the Yenisei River have adopted reindeer herding (with an increased reliance in the northern region) while the Ket on the right bank of the Yenisei have not (Lee 1967). Notably, reindeer herding was not believed to have been practiced by ancient peoples in this region of Southern Siberia and is believed to be a modern adaptation that was met with resistance (Lee 1967).

Tbl.10 Table of seasonal activities of the modern Ket people on the bank of the Yenisei River (Lee 1967).

Season	Location	Activity
Spring	Spring & Autumn camps	Fishing along streams & tributaries, reindeer sheltering
Summer	Summer camps	Fishing along the Yensei, duck hunting, fish & meat salting and drying, fat storing, making winter clothing, releasing reindeer into taiga
Autumn	Spring & Autumn camps	Reindeer herded back into camps, bear hunting, fish & meat salting and drying, fat storing, making winter clothing
Winter	Winter hunting sites	Squirrel and wild reindeer hunting expeditions in the taiga

Southwards from the Ket, the modern indigenous Khakas peoples who live on the left bank of the Yenisei River in the Khakassk-Minusinsk Basin practice a mixed subsistence strategy (Turakhova & Dorina 2009). Khakas peoples today primarily breed cattle and pigs and forage for wild plants, roots, nuts, and mushrooms (Panikarova 2015). Secondary economic activities of the modern Khakas peoples include fishing, cultivating cereals and vegetables, and raising chickens, sheep, and horses (Panikarova 2015). Traditional, pre-Soviet Khakas lifeways were centered upon the year-long mobile management and breeding of horned cattle, sheep, and horses supplemented by minimal barley cultivation, squirrel hunting in autumn, and the hunting of small game, cervids, and bears in winter and spring (Tutarkova & Dorina 2009). Khakas peoples hunt in the taiga on horseback with their dogs, whereas Ket peoples leave their dogs at

camp so as not to frighten the reindeer (Tutarkova & Dorina 2009; Lee 1967). Ket people also avoid hunting bears in the winter, when there is an abundance of snow, whereas winter is a prime bear-hunting season of the Khakas peoples (Tutarkova & Dorina 2009; Lee 1967).

South of the Minusinsk Basin, the peoples of the neighboring Sayan and Tannu-Ola Mountain steppe region of Tuva actively manage several domesticated animals. During the Soviet era the herds managed by Tuvinian peoples (and regulated by the socialist state) were dominated by sheep and goat, followed by horse and cattle, and a minimal representation of camel and yak (Vaĭnshteĭn 1980). Post-Soviet Tuvinian herds increased in cattle at the expense of horses, and pivoted from camels and yak to reindeer (Tbl.11) (Vaĭnshteĭn 1980). It should be mentioned that local variations in herd composition have been noted throughout Tuva, with the pastoralist hunters of the taiga steppe zone favoring horses above all other animals and forsaking both yak and camel entirely. Yaks are instead bred extensively in the mountains and foothills (Vaĭnshteĭn 1980).

Tbl.11 Table of historical Tuvan herd compositions (Vaĭnshteĭn 1980).

Period	Sheep	Goat	Horse	Cattle	Yak	Camel	Reindeer
Soviet Tuva	~50%	~25%	~15%	~9%	~0.5%	~0.5%	0%
Post-Soviet Tuva	48%	27%	9%	15%	0%	0%	1%

The subsistence strategies and herd compositions of Southern Siberia have varied and fluctuated throughout time, dependent upon geographical, environmental, and cultural conditions. Modern and historical pastoralists in the southernmost regions of Southern Siberia have consistently (but not exclusively) prioritized managing greater numbers of domesticated sheep and goat, then horse and cattle, with a minimal reliance on yak, camel, or reindeer. Certain groups have focused nearly exclusively on managing domesticated horses or reindeer, or have (to this day) decided against domesticated animal management entirely, and pig husbandry has been adopted in certain communities.

The Soviet influence upon all these lifeways cannot be denied, even upon hunter-gatherer-fisher groups such as the Ket (Lee 1967). It is difficult to say how analogous the seasonal hunting and fishing practices of the Ket peoples, the mixed subsistence lifeways of the Khakas peoples, or the historical herd compositions of non-homogeneous Tuvan pastoralist peoples, are to those of the Eneolithic peoples of the Minusinsk Basin or Altai Mountains. The data presented above probably provide a better baseline than subsistence models derived from the ancient agropastoralists of Western Asia or Africa, for example, being derived from people who share more closely related landscape, culture, diet, and history.

8.5.2. Outer Mongolia

Modern Mongolian herders in the Khangai Mountain region do not view animals as possessions that they control so much as beings in their own rite that they integrate and form a joint society with, built upon mutual trust (Fjin 2011; Stépanoff et al. 2017). Khangai pastoralists observe a cyclical, seasonal rhythm of migration and economic activity centered around animal birthing, milking, clipping, combing, racing, castrating, and slaughtering (Tbls.12–13) (Andhearn 2021;

Fjin 2011). Cattle, horses, sheep, and goats are largely allowed to roam and graze freely throughout the seasonal pastures, and the animals willingly submit to and remain amongst the herders (Fjin 2011; Stépanoff et al. 2017). Beyond the Khangai mountains, dairying is still a predominant economic activity and the pastoralists of the Mongolian steppe primarily (but not exclusively) milk goats while the herders of the Gobi Desert primarily milk camels (Andhearn 2021). Historical herd composition estimates for Khangai Mountain region suggest a higher reliance on cattle than in the steppe, the Gobi desert, or the Mongolian Altai Mountain region, as well as the lowest reliance on camels (Tbl.14) (Krader 1955).

Tbl.12 Table of livestock management activities of modern herders in the Khangai Mountains (Fjin 2011).

Cattle / Yaks / Cattle-Yak Hybrids			
Age	**Male (*Bukh*)**	**Castrated Male (*Shar*)**	**Female (*Ünee*)**
First Year (*Togal*)	Kept with mother, not eaten	N.A.	Kept with mother, not eaten
Second Year (*Byaruu*)	Still nursing, or beginning to graze	Still nursing, or beginning to graze; castrated in Autumn	Still nursing, or beginning to graze
Third Year + (*Guna, Gunjin*)	Kept as bull, left to graze or killed for food; changed every 3-4 years	Trained for traction & transport, or killed for food	Milked daily, or killed for food
Domesticated Horses			
Age	**Male (*Azraga*)**	**Castrated Male (*Mor'*)**	**Female (*Güü*)**
First Year (*Unaga*)	Kept with mother, not eaten	N.A.	Kept with mother, not eaten
Second Year (*Daaga*)	Broken in for riding	Castrated in Autumn, broken in for riding	Broken in for riding
Third Year (*Shudlin*)	Kept as harem stallion, or killed for food	Kept in a bachelor band, or killed for food	Kept in a harem, or killed for food
Fourth Year + (*Khyzaalin*)	Replaced every four years	Used for travel & herding	Pregnant, milked
Domesticated Sheep			
Age	**Male (*Khuts*)**	**Castrated Male (*Ireg*)**	**Female (*Em, Khon'*)**
First Year (*Khurag*)	Socialized, not eaten; kept as future ram	Socialized, not eaten; castrated in Spring	Socialized, not eaten
Second Year + (*Tylög*)	Kept in a separate herd; clipped for wool or killed for food	Clipped for wool or killed for food	Pregnant, milked for one month in summer; clipped for wool or killed for food
Domesticated Goat			
Age	**Male (*Ukhna*)**	**Castrated Male (*Serkh*)**	**Female (*Em, Yamaa*)**
First Year (*Ishig*)	Socialized, not eaten; kept as future ram / billy	Socialized, not eaten; castrated in Spring	Socialized, not eaten
Second Year + *(Borlon*)	Kept in a separate herd; combed for cashmere or killed for food	Combed for cashmere or killed for food	Pregnant, milked for one month in summer; combed for cashmere or killed for food

Tbl.13 Table of seasonal livestock management practices of herders in the Khangai Mountains (Fjin 2011).

Season	**Location**	**Activity**
Spring	Spring pastures	lambs / kids born & castrated, calves & foals born, goat cashmere cropped, horse manes cropped
Summer	Summer pastures	calves & foals born, mares & cows milked, sheep & goats milked, sheep wool clipped, horses raced, dairy products made
Autumn	Autumn pastures	cattle & horses castrated, mares & cows milked, livestock slaughtered
Winter	Winter reserve pastures	limited activity

Tbl.14 Table of nineteenth century Mongolian herd composition data (Krader 1955).

Region	Sheep	Goat	Cattle	Horse	Camel
Eastern Steppe	59%	14%	12%	13%	3%
Khangai Steppe	58%	17%	13%	11%	1%
Gobi Desert	51%	28%	5%	9%	8%
Mongolian Altai	56%	29%	6%	7%	3%
(Outer Mongolia)	55%	22%	9%	10%	4%

Domesticated sheep (*Ovis aries*) are not herded with argali (*Ovis ammon*) just as domesticated goats (*Capra hircus*) are not herded with ibex (*Capra siberica*), but domesticated sheep and goat are herded together and learn species-specific survival skills from one another (Fjin 2011). Wild horses (*Equus przewalskii*) are not herded or kept with the harem and bachelor bands of free-ranging domesticated horses managed by men, though domesticated cattle (*Bos taurus*) and yak (*Bos grunniens*) are kept in a respective 4:1 ratio by the women who manage them (Fjin 2011). Cattle-yak hybrids (*khainag*) are prized for their temperament, winter resilience, thick milk production, and robusticity, but are unable to breed after two generations of hybridization and are killed for food after their second year (Fjin 2011).

It is unknown if these same multi-species herd compositions and cross-breeding ratios or culling practices also characterized the prehistoric herds of the Khangai Mountain region, but it seems likely. Mongolian pastoralists largely abandoned the collectivist herding practices imposed upon them after the collapse of the Soviet Union and have since returned to their traditional “folk” methods, which have been practiced since at least the 13th century (Fjin 2011). The ethnographic data provided by Fjin (2011) is very valuable for the interpretation of archaeological animal assemblages recovered from mountain and steppe landscapes adjacent to the Altai, Sayan, and Khangai regions, and beyond.

8.5.3. Kazakhstan

Pastoralist and agricultural practices in Kazakhstan were as overhauled and scarified by the collectivist policies of the Soviet Union as they were in Southern Siberia and Mongolia (Ferret 2018; Kerven et al. 2008, 2021; Khazanov & Shapiro 2005; Olcott 1983; Robison et al. 2020). Pre-industrial, pre-Soviet Kazakhstan has long been romanticized (and politicized) as a nation of freedom-loving nomads roaming the open grasslands on horseback, though the factuality of this has been contested (Chang 2015, 2022; Ferret 2018; Spengler et al. 2021). Arguments against broad, uniform mobile pastoralism without agricultural activity from ancient to historical times in Kazakhstan draw from the fact that seeds of cultivated plants (such as grapes) have been recovered from archaeological contexts (Spengler et al. 2013, 2017), isotopic evidence supports millet consumption during the Bronze Age (Ananyevskaya et al. 2018), and modern ethnographical studies portray small-scale agropastoralism (Hauck et al. 2016) (Chang 2022; Spengler et al. 2021).

From at least the Late Medieval and Early Modern periods onwards, certain highly mobile Kazakh communities have been managing herds of domesticated animals on horseback (Ferret 2014, 2018; Kerven et al. 2021; Khazanov & Shapiro 2005; Krader 1955; Olcott 1983).

Historical, pre-Industrial Kazakh pastoralists were seasonally mobile and moved as camps of patrilineal extended family groups (*aul*) through the steppe and desert, along with their livestock (Kereven et al. 2021). Mobility could be horizontal, with herders heading south in the winter, or vertical, with herders heading from the plains to the mountains in the summer (Ferret 2018). The size of an *aul* was determined by the size of the herd and their environment, and seasonal pastures were chosen based upon temperature, topography, aridity, wind, snow, insects, and water and resource availability (Ferret 2018; Kereven et al. 2021).

Kazakh pastoralists of the late nineteenth century and onwards more commonly wintered in fixed brick-and-mud structures (*qystau*) than they engaged in year-round full mobility, and some did also practice agriculture (Ferret 2014, 2018; Kereven et al. 2021). Soviet collectivization in the twentieth century led to wide-spread famine and death in Kazakhstan, and eventually resulted in a transition to more sedentary lifeways (Arzhantseva et al. 2017; Ferret 2018). Certain groups in Kazakhstan still practice forms of mobile pastoralism, such as the herders of the Raĭymbek District (Almaty Province) in Southeastern Kazakhstan (Tbl.15) (Ferret 2018). Information about the seasonality of castrating, shearing, and culling of animals in these herds, or foraging and agricultural practices, is unfortunately unavailable.

Tbl.15 Table of vertical pastoralist practices in modern Almaty Province of Kazakhstan (Ferret 2018).

Season	Location	Activity
Spring	Spring pastures (*kökteu*)	Herding in low-altitude plains
Summer	Summer pastures (*zhaĭlau*)	Herding in high mountain pastures, milking, dairy-product making
Autumn	Autumn pastures (*küzeu*)	Herding in low-altitude plains
Winter	Winter quarters (*qystau*)	Herding on south-facing, sunny mountain slopes

During the nineteenth century, horses had the highest recorded predominance in the herds of Northeast Kazakhstan, as well as the lowest recorded predominance of camels (Tbl.16) (Krader 1955). Caprines were the animals with the highest representation in all nineteenth century herds as recorded by Krader (1955), presumably with a substantially higher reliance on sheep than goats. The herd composition data recorded by Krader throughout early twentieth century Kazakhstan mirrors the nineteenth century data overall, though with a reduction in horses, an increase in cattle, and an added, minimal reliance on pig husbandry (Tbl.17) (Krader 1955). These changes are largely not reflected in the earlier data collected by Ferret (2018) for the largely mobile and wealthy district of Dhzarkhent in Southeast Kazakhstan, which is more parsimonious with Krader's (1955) nineteenth century data. Notably, a reduction in camel is evident in both sets of data (Ferret 2018; Krader 1955) (Tbls.16–18).

Tbl.16 Table of nineteenth century Kazakh herd composition data (Krader 1955).

Context	Sheep	Goat	Caprine	Cattle	Horse	Camel
West Kazakhstan, 1846	/	/	67%	11%	17%	5%
West Kazakhstan, 1849-50	65%	8%	/	10%	14%	4%
West Kazakhstan, 1852	/	/	72%	12%	10%	6%
Northeast Kazakhstan, 1876	/	/	58%	11%	31%	~.5%

Tbl.17 Table of twentieth century Kazakh herd composition data (Krader 1955, Ferret 2018).

Context	Sheep	Goat	Cattle	Horse	Camel	Pig
Kazakhstan, 1920	51%	8%	24%	12%	2%	2%
Southeast Kazakhstan, 1907	69%	12%	9%	10%	~.5%	/
Southeast Kazakhstan, 1910	73%	8%	8%	11%	~.5%	/

Tbl.18 Table of twenty-first century Kazakh herd composition data (Ferret 2018).

Region	Sheep	Goat	Caprine	Cattle	Horse	Camel	Pig
Kazakhstan, 2012	57%	10%	/	21%	6%	~.5%	5%
Almaty, 2012	/	/	71%	19%	6%	1%	3%
Raĭymbek, 2012	/	/	73%	17%	10%	/	/
Zhalanash, 2012	74%	4%	/	14%	8%	/	/

Beyond Almaty, herd composition throughout all of modern Kazakhstan as represented by agricultural census data (2006) is somewhat uniform but still dependent upon the province (Ferret 2018) (Fig.3). In the provinces of Northern Kazakhstan, cattle comprise more than half of the livestock reared and pigs are as prevalent as sheep and goat. Reliance on cattle is greatly diminished in all other provinces, though cattle still predominate in every other province besides Mangystau in the Southwest, where they are underrepresented. Camel reliance is the strongest in this province, followed by its neighboring Atyrau in the true West, and is minimal or nonexistent in all other provinces. Unlike camels, horses are solidly represented in all provinces. Pigs are prevalent in the Northern provinces, and less so in the others.

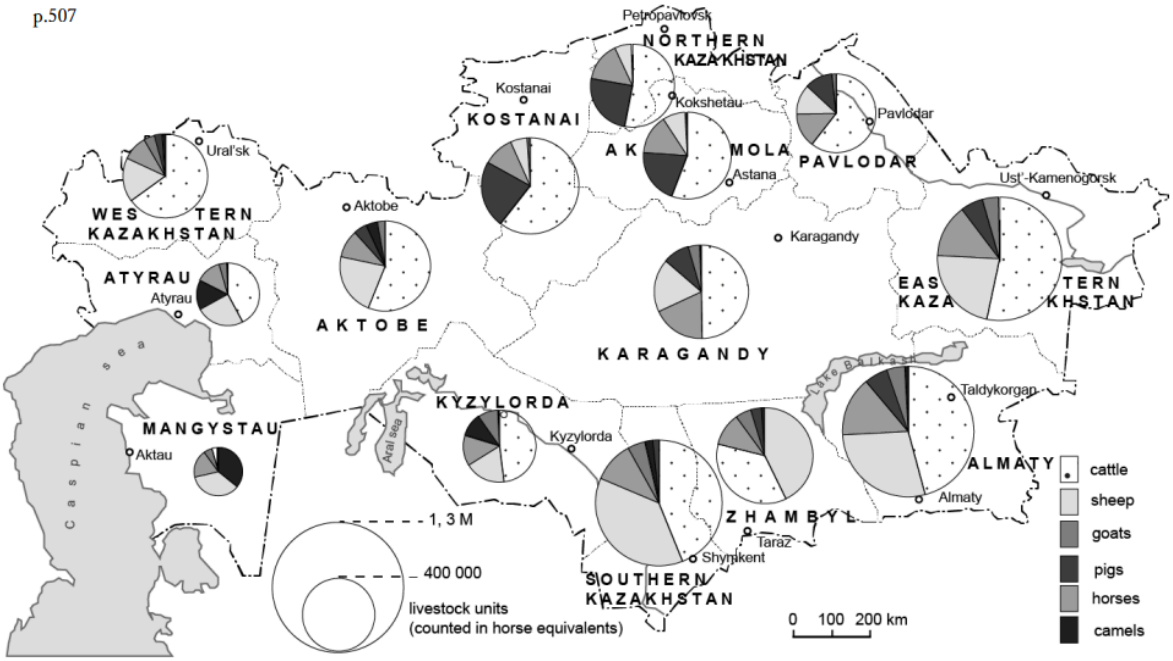


Fig.3 Map of regional herd compositions as recorded across modern Kazakhstan (Ferret 2018).

The herd composition data presented by Ferret for Almaty in 2012 (Tbl.18) does clash significantly with the 2006 census data included in the same publication (Fig.3) (Ferret 2018), though this is not exceptionally relevant for the purposes of this dissertation. Domesticated pigs would not have been reared by any archaeological cultures of Kazakhstan and camel prevalence would have varied based on environmental and geographical factors. Highly mobile ancient pastoralists would not have managed herds predominated by cattle, and any archaeological assemblages predominated by cattle remains would suggest more sedentary lifeways. Importantly, assemblages dominated by caprine remains should not be taken as solid evidence of mobile pastoralism or the absence of agricultural activity. I will explore the ecological niches of key domesticated animals as well as their relation to social structures and subsistence strategies further into this chapter.

8.5.4. Uzbekistan

Compared to the historical peoples of Kazakhstan, the historical peoples of Uzbekistan were not especially mobile. A lack of suitable pastureland led to a widespread preference for sedentary agriculture and the relegation of livestock management to specialists (Khazanov & Shapiro 2005; Krader 1955). The imposition of Soviet regulation in the twentieth century further reduced mobility, including amongst the agropastoralists and shepherds who were pushed to produce cotton and pelts that they did not know the true market value of at the expense of the integrity of their own pastures (Zanca 2000). Twentieth century herds in Uzbekistan were composed of more cattle than those generally recorded in the historical herds of Southern Siberia, Outer Mongolia, and Kazakhstan (Tbl.19); this is likely related to their comparatively lower mobility. However, cattle representation has decreased since the collapse of the Soviet Union and de-collectivization, as Uzbek peoples have largely lost their pre-collectivization cattle-rearing knowledge (Evers & Wall 2006).

Tbl.19 Table of twentieth century Uzbek herd composition data (Krader 1955).

Region	Sheep	Goat	Cattle	Horse	Ass/Mule	Camel
(Uzbekistan)	44%	17%	26%	9%	6%	2%

Knowledge-loss is not restricted to cattle or even livestock rearing within rural Uzbekistan; agriculture has been equally affected and rural Uzbek peoples have struggled to maintain their lifeways following decollectivization (Evers & Wall 2006; Ibragimov et al. 2007; Zanca 2000). The resultant discontinuity of pre-Soviet animal management practices and the inability to return to them (as opposed to the return to folk pastoralism in post-Soviet era Mongolia), coupled with the lack of new, effective management practices before 2010, means that ethnographical data would be unlikely to provide valuable insight into pre-modern animal economies. There is not an abundance of ethnographic literature to begin with, probably because Uzbek peoples have historically practiced forms of sedentary agropastoralism, as opposed to the transhumant or mobile pastoralist lifeways which tend to attract ethnographers.

Unfortunately, there is little more than limited livestock census data available to provide insight into the modern and historical animal economies of Uzbekistan. More recent studies featuring

the meat productivity of karakol sheep (Bobokulov et al. 2021) and the meat and wool yields of new sheep breeds (Ruzibaev 2019) signify positive economic growth in Uzbekistan, but do not contain information about actual animal husbandry and are not helpful for the understanding of pre-2020 animal economies. A very recent overview of livestock production in Uzbekistan from 2010 to 2020 is equally encouraging, though equally unhelpful (Dehqonboyevich & Khamza-Kizi 2021). It is unclear what historical animal husbandry might have looked like in pre-Soviet Uzbekistan regarding sheep-to-goat ratios, the shearing, combing, or dairying of livestock, camel or donkey exploitation, or general culling practices.

8.5.5. Modern & Historical Animal Economies: Conclusion

The data collated for these comparisons is not meant to serve as a rigid baseline, and it cannot be known how truly relatable these datasets are, or how many different modes and scales of animal husbandry and degrees of mobility are represented (or not) within each data point. What is clear however is that throughout historical and modern Inner Asia, the domesticated animal herds managed by mobile, transhumant, agricultural, and mixed-strategy herders have broadly (not exclusively) followed the same overarching pattern (Tbl.20). Caprines, primarily sheep with a significantly smaller representation of goats, dominate herd compositions and typically comprise over half of the herd, often at least 75%. This 3:1 ratio of sheep-to-goat is in keeping with what has been observed in prehistoric assemblages across the Eastern and Western Eurasian Steppe, including at Bronze Age Obishir V in Kyrgyzstan (Taylor et al. 2021a). Horses and cattle are also represented in substantial numbers, comprising roughly 10% each (ca. 20% total). Increased cattle representation often correlates with decreased horse representation and a lower degree of mobility. Camels and yaks often make up the difference, with camels being more prevalent in the desert and yaks in the mountains.

Not all historical or modern Inner Asian communities have managed their herds this way, with many choosing not (or being unable) to herd certain key animals all together. In some areas, seasonal hunting, fishing, and foraging lifeways still prevail over domesticated animal husbandry and / or agriculture; in others, seasonal transhumance is not observed at all. The production-oriented policies of Soviet collectivization and the subsequent de-collectivization and privatization of domesticated animal herds have irreversibly affected the subsistence practices and lifeways of Siberian, Mongolian, Kazakh, and Uzbekh herders. Sedentary lifeways, reindeer herding, cattle and pig-rearing, and crop farming have become more prevalent with time in certain communities, though it is worth mentioning that some of them were already partially or fully sedentary and reliant on agriculture. Modern changes in herd composition, such as an increase of goats to produce secondary products that are profitable in modern markets, or a decrease of cattle due to pre-Soviet knowledge-loss, are not analogous to changes observed in the stratigraphic abundances of animal remains in the archaeological record.

At the same time, the animal husbandry practices and economic activities recorded in modern ethnographies and historical livestock census data are valuable resources for reconstructing and understanding the subsistence practices and animal economies of the archaeological populations which once inhabited these same regions. This is especially true for the

ethnographic data provided for the fixed, species-specific economic activities related to animal age in the Khangai mountain region of Mongolia. These data most likely provide better lenses to view herd composition and mortality data through, than those crafted for the interpretation of West Asian, African, and European archaeological animal assemblages.

Tbl.20 Table of historical Inner Asian herd composition data (Ferret 2018, Krader 1955, Vaĭnshteĭn 1980).

SOUTHERN SIBERIA					
REGION	**Sheep**	**Goat**	**Cattle**	**Horse**	**Camel**
Tuva	48%	27%	15%	9%	0%
OUTER MONGOLIA					
Eastern Steppe	59%	14%	12%	13%	3%
Khangai Steppe	58%	17%	13%	11%	1%
Gobi Desert	51%	28%	5%	9%	8%
Mongolian Altai	56%	29%	6%	7%	3%
(Outer Mongolia)	55%	22%	9%	10%	4%
KAZAKHSTAN					
Northeast Kazakhstan	58%		11%	31%	~.5%
West Kazakhstan	65%	8%	10%	14%	4%
Southeast Kazakhstan	73%	8%	8%	11%	~.5%
(Kazakhstan)	51%	8%	24%	12%	2%
UZBEKISTAN					
(Uzbekistan)	44%	17%	26%	9%	2%

8.6. Inner Asian Animal Economies: Conclusion

“All nomadic interests were invested in livestock, their source of life and indicator of success.” (Kradin 2015b)

Although a multitude of economic strategies involving livestock management have developed in the region overtime, pastoralism is the most frequently referenced and remains a topic of fascination in archaeological, anthropological, and historical literature. Definitions of pastoralism have proven to be as ephemeral and inconsistent, though several expressions of pastoralism have been reconstructed from the archaeological record. Detecting ancient pastoralist activity is a challenging endeavor dependent upon reconstructing mobility and domesticated animal reliance, both of which can be exceptionally complicated to identify with confidence. Historical and modern herd composition records, as well as ethnographic data, are valuable resources and provide insight into the kinds of economic activities and strategies that different archaeological herd compositions, sex ratios, and age-at-death distributions might indicate.

Archaeological herd composition data has classically been interpreted to infer human behavior in accordance with models developed for West Asian, Mediterranean, and European animal economies; Inner Asian assemblages would probably be better interpreted through taxonomic and culling “templates” that actually reflect local animal management practices. Zooarchaeology can provide evidence for the presence of domesticated animals, and both

zooarchaeology and ZooMS can be used to identify samples for subsequent aDNA analyses. Importantly, while aDNA can establish lineage, lineage does not always clarify behavior and relationships, and what it means to be “domesticated” is a nuanced conversation (pers.comm. Will Taylor 2024). In the next chapter I will overview different theoretical models of domesticated animal husbandry and pastoralist emergence in Inner Asia, as well as the culture-driven shifts in archaeological thought regarding them.

9. Archaeological Theories of Pastoralism

9.1. Introduction

“For several reasons, the study of pastoralism is an ideal way to explore ecological relationships because it involves symbiotic connections between humans and domesticated animals, with a series of cascading effects in political, social, economic, and religious organization.” (Kardulias 2015)

Having explored the ecological niches and associated management practices of key domesticated animals, as well as how these are reflected in historical and modern herds, I will now focus on how animal husbandry came to be embodied in the lifeways of the ancient peoples of Inner Asia. This chapter will first discuss key concepts in Soviet era archaeological theory and practice which have inevitably shaped the initial corpus of available archaeological data as well as the perception of pastoralist communities and identities. Such a discussion is necessary to contextualize the theoretical models of pastoralist emergence that have arisen in archaeological thought and literature.

9.2. Soviet Archaeological Theory & Practice

“Archaeology plays an important part in establishing Marxist views on history.” (Mongait 1963)

The origins of Russian archaeology have been traced back to the early eighteenth century antiquarian endeavors of Tsar Peter the Great and the Historical and Antiquarian Society (Bulkin et al. 1982; Gryzanov 1969). Eighteenth century Russian archaeology initially lacked the scientific theory or practice necessary to develop much farther beyond antiquarianism and discourse, although there was public interest in monumental architecture and royal investment in both historical preservation and methodology. A number of archaeological organizations were subsequently established in the nineteenth century, such as the Russian Archaeological Society, the Imperial Archaeological Commission, the Russian Archaeological Society at St. Petersburg, the Imperial Russian Geographical Society, the Moscow Archaeological Society, and the Society of History, Archaeology and Ethnography (Field & Price 1947; Hooson 1968; Kradin 2011; Victorovich 2016). By at least the early nineteenth century there was a growing awareness that archaeological artifacts could be broadly differentiated by cultural tradition and region (Mongait 1967; Victorovich 2016).

Russian archaeological practice was restructured in the mid-nineteenth century when Swedish archaeologists developed typological classification systems for material culture (Daniel 1943; Gräslund 1987; Heizer 1962; Trigger 1983). The adaptation of “closed find” typology allowed Russian archaeologists to reinterpret archaeological finds through refined chronological frameworks, effectively transforming pre-Soviet Russian archaeology into a historical science firmly rooted in the stadialist “Three Age System" of Stone, Bronze, and Metal Ages (Heizer 1962). The late nineteenth century influence of Marxism and especially dialectical materialism led to an emphasis on the role of labor and economic productivity in human social organization, while the influence of Swedish and German cultural-historical approaches emphasized cultural

differences and the role of human migrations in cultural change (Akin 2015; Mongait 1967; Trigger 1983). Archaeological cultures were delineated based upon epoch, materia, and technology, especially by the prominent Vasilii Aleksejevich Gorodtsov and his pupils, and often equated with ethnicity (e.g. Gorodtsov 1901; see also Mongait 1967 and Platanova 2007). Pre-Soviet paleoethnologists such as Sergej Ivanovich Rudenko focused instead on the empirical study of cultural diffusion and embraced statistics, ethnology, and ethnography (Platanova 2007).

The October Revolution directly facilitated the emergence of a new school of archaeological thought and practice in early twentieth century Russia (Avdiyev 1945; Davis 1983; Field & Price 1947; Klejn 2012; Kradin 2011; Platonova 2007). A new archaeological commission, the State Academy of the History of Material Culture (AIMK), was implemented to replace the old archaeological commission (Field & Price 1947; Klejn 2012; Platonova 2007). Archaeology was placed firmly under the authority of the new Soviet regime which appropriated history as a vehicle to justify its socialist agenda and advance its determinist ideology, and archaeologists were expected to fall in line (Davis 1983; Klejn 2012; Kradin 2011; Platonova 2007). The old school of Russian archaeologists, especially the paleoethnologists who studied cultural development outside of a strictly Marxist paradigm, were heavily criticized and discredited as part of a politically motivated campaign to purge, imprison, and execute scholars en masse (Klejn 2012; Platonova 2007). Cultural diffusionism, migrationism, and the Three-Age Model were dismissed as “bourgeois archaeology” and replaced with models of social evolution, economic production, and the emergence of class conflict (Bulkin et al. 1982; Klejn 2012; Shnirelman 2005; Slezkine 1996).

The echoes of both pre-Soviet and Soviet archaeological thought, especially Marxism, ascension theory, historical materialism, technical stadialism, social determinism, and the rejection of synchronic variability, can be found in the twentieth century theories developed by Russian scholars. Put simply, it was the invention of tools and the advent of labor that was believed to have transformed primates into humans. Human societies were then perceived through archaeological epochs defined by their development of material culture related to their modes of economic production. Archaeological epochs were in-turn obliged to correspond with fixed stages of social organization that followed a predetermined trajectory. The Paleolithic, for example, was equated with the era of pre-class societies which progressed from primitive hordes to matriarchal or patriarchal clans before unraveling and reemerging as class-based societies after the Paleolithic (Davis 1983). Clans should feature in the Upper Paleolithic but not the Lower Paleolithic, and nuclear families should not feature in either. Decaying clans should then reorganize themselves as stratified slave-owning societies, feudal societies, capitalist societies, and finally socialist societies (see Tishkin 2016). Human societies were not only believed to develop uniformly but also independently of factors such as environment, belief systems, or cultural transmission; they were thought to be driven instead by production, social stratification, and clashes between social classes (Klejn 2012; Kradin 2002).

The passage above is a generalization that does not encompass or define all of early to middle twentieth century Russian archaeological thought, especially considering the diversity of

scholastic approaches and the many reversals and revisions in Stalin's own ideology, and thus the USSR's ideology, that dictated archaeological practice during the Soviet Era. That being said, many of the key concepts that underpin the paradigm simplified in the previous passage were deeply entangled within Russian archaeology and influenced how both the prehistoric cultures and pastoralist lifeways of Inner Asia have been conceptualized and analyzed. Perhaps the most relevant of these concepts were Nikolai Yakovlevich Marr's autochthonic theory of ethnogony and Vladislav Iosifovich Ravdonikas's ascension theory. Both of these concepts are explored below alongside their influence on the perception of ancient and modern pastoralists.

9.2.1. Soviet Ethnogenesis, Marrist Ethnogony, & Nationalist Ethnogenic Myths

"Childe, of course, was able to use Marxism for archaeology, but thoughtfully and liberally. Was it perhaps the misfortune of Soviet archaeologists that we, on the contrary, attempted to put archaeology to the service of Marxism?" (Klejn 2012)

The concept of *ethnogenesis*, or the process by which distinct ethnic groups emerge over time, has a deeply complex history within Russian archaeological scholarship. Ethnogenesis was initially perceived as an antidote to the dynamic archaeological culture concepts which contradicted the linear stages of cultural evolution aligned with Marxist and Marrist ideology (Kohl 1998; Shnirelman 2005; Tiesler 2021). Soviet ethnogenesis, armed with Nikolai Yakovlevich Marr's theories of *ethnogony* and class-based linguistics, attributed population turnovers to internal socio-economic transformations as opposed to cross-cultural contact and exchange (Chang 2005; Shnirelman 2005; Slezkine 1996; Thomas 1957; Tiesler 2021). Marr's *ethnogony* was the study of the conception and evolution of ethnic groups in general, whereas Soviet *ethnogenesis* focused on how one ethnic identity became exchanged for another. Early twentieth century Soviet scholars were encouraged to identify a shared autochthonic and socio-cultural foundation that would unify the people of the USSR and ease tensions between its many ethnic groups (Kohl 1998; Shnirelman 2005; Slezkine 1996). Ethnogenic studies of regional ethnic groups became a popular way to contain and connect archaeological cultures with historical populations in a politically advantageous and ideologically correct way (Chard 1963; Chang 2015; Shnirelman 2005). To stray too far from Marrist ideology was to risk persecution (Shnirelman 2005; Slezkine 1996; Thomas 1957).

Closing in on the mid-twentieth century, the Marrist ethnogenic initiative developed into a quest to prove that Russians were the true, autochthonic descendants of ancient Slavic peoples and to promote their ethnic superiority, especially over Germans and "Indo-Europeans" (Klejn 2012; Kohl 1998; Shnirelman 2005; Slezkine 1996; Tiesler 2021). Soviet nationalist ethnogenesis began to embrace the archaeological culture concept that, alongside socioeconomic Marrism, it was originally employed to refute (Klejn 2012; Kohl 1998; Shnirelman 2005; Slezkine 1996). Although Marrism subsequently oscillated in and out of favor until the fall of the Soviet Union (Klejn 2012; Thomas 1957), nationalistic ethnogenesis continued to be embraced in the form of the "ethnogenic myths" that were constructed to provide identities to displaced communities (Shnirelman 2005; Slezkine 1996). Contemporary scholastic endeavors and political narratives have since attempted to ethnically link the modern peoples of Kazakhstan not only with historical Kazakh nomads but also the nomadic confederacies of the Iron Age, for example (see

Chang 2015). This ethnogenic myth can be compared to the earlier Soviet scholarship which sought to legitimize the USSR at the height of its nationalism by ethnically linking Russian and Central Asian people with the same aforementioned nomadic confederacies (Slezkine 1996).

Ethnogenesis is not a theory of pastoralist emergence or domesticated animal husbandry in its own right, but its Soviet legacy is maintained in the descriptors that have been used to define the ancient populations of Inner Asia as well as the contemporary narratives which seek to directly relate modern peoples back to them. Through the lens of Soviet ethnogenesis, a pastoralist community should have both ethnically descended and evolved socially from the "primitive hordes" and slave-owning groups that predated them *in the same region* (though, the role of migrationism was re-visited after the mid-twentieth century). The complex interplay of Soviet thought regarding archaeological culture and *ethnos* through time has also directly impacted the nature of research and reporting for many key Inner Asian archaeological sites, as will be discussed in depth in the next chapter. The next subsection of the current chapter will move on to nomadic feudalism, a concept equally devoted to linear and socioeconomic models of cultural evolution. Nomadic feudalism, like Marrist ethnogony and Soviet ethnogenesis, has contributed to the cultural perception and nationalist rhetoric surrounding ancient pastoralists both within archaeology and outside of it.

9.2.2. Ascension Theory, Nomadic Feudalism, & Practical Archaeology

"It is not what is made but how, and by what instruments of labour, that distinguishes different economic epochs." (Marx 1873)

Ravdonikas's early twentieth century ascension theory could be called a tenant of Soviet era archaeology (Ravdonikas 1930, 1932; see also Bulkin et al. 1982). Ascension theory follows a Marxist and deterministic axis of stadial social evolution both inspired by Marrism and directly from derived nineteenth century models of human organization (e.g. Morgan 1877; Engels 1844) corresponding with "savage, barbarous, and civilized" stages of development. Within this framework economic growth leads to revolutionary social development and eventually ethnic transformation (Klejn 2017); this is very much in keeping with Marr's theories of language, linguistics, and ethnogony.

Ascension theory eventually graduated into Soviet models positing that Lower Paleolithic hordes progressed into Upper Paleolithic matriarchal clans, which transitioned into patriarchal clans by the Neolithic period (see Tishkin 2016). Clans fell apart and re-emerged as village communities before the unfolding of class-based systems in the Metal Ages. Slave-owning societies emerged in Antiquity, became feudal societies in the Middle Ages, and then advanced into capitalism and finally socialism. Criticisms of this model from Russian archaeologists would not be found until the late twentieth century (e.g. Grigoryev 1972; Khlobystin 1972; see also Tishkin 2016).

It follows then that the archaeology of inequality and social stratification was of great interest to Soviet archaeologists, especially regarding the ancient and modern pastoralist cultures of the Eurasian Steppe (Kradin 2011). Pastoralists, as known and understood by Russian scholars, herded domesticated animals but were not beyond cultivating plants and engaging in agriculture

(Chang 2015). Soviet archaeologists were confronted with several ideological outliers in their studies of historical mobile pastoralists who did not engage in agriculture but maintained patriarchal and stratified social structures (Chang 2015), who did not construct settlements but left behind manifold burial sites filled with goods distributed by status (Kradin 2011), who had economically relied on animal pastoralism for centuries and also considered their animals to be private property, despite not being sedentary peoples (Kradin 2003), and who thus could not be defined as agricultural, industrial, or post-industrial nor be neatly categorized into any socio-economic stages of cultural evolution (Chang 2015; Gellner 1988; Kradin 2003, 2019). “Nomadology" subsequently become a subject of intense study amongst Soviet scholars which culminated in the theory of *nomadic feudalism* (see Gellner 1988; Kogan 1980; Kradin 1992, 2019; Markov 1989, 1998, 2001; Masanov 1995; Popov 1986; Vasyutin & Dashkovsky 2009).

Early nineteenth century Soviet archaeologists reasoned that ancient Central Asian pastoralists may have been either tribal, pre-state peoples or slave-owning state peoples who eventually progressed into (nomadic) feudalism during the Middle Ages (Kradin 2002, 2003, 2015a, 2019). Various interpretations of nomadic feudalism assume cattle, land, or social power and influence to be the primary foundation of economic production amongst the mobile pastoralists of Central Asia (Kradin 2002, 2015a). Consequently, the question of *how mobile* ancient pastoralist communities were and whether or not they practiced agriculture was not even considered. Archaeological investigations into Iron Age settlements of Kazakhstan, for example, would not survey for evidence of semi-permanent architecture or involve archaeobotanical and zooarchaeological collection and analysis until the very late twentieth century (Chang 2015). The idea that “feudal pastoralists” remain locked in a lower stage of social evolution also created unwarranted and strongly negative implications about their worth, respectability, and humanity.

The assumption that the ancient pastoralists of Central Asia must have been as mobile and disengaged in agriculture as certain historical pastoralist groups has directly impacted how archaeological excavations have been conducted, restricted the lines of evidence that have been collected, and narrowed the scope of the research questions that have been investigated. This has not only biased subsequent interpretations, but limited the availability of data to researchers seeking to interpret these sites and assemblages through different lenses. All of which has, inevitably, impacted theories surrounding the emergence of pastoralism and introduction of domesticated animals into the region. I explore key theories below.

9.3. Models of Domesticated Animal Dispersal & Pastoralist Emergence

“...herding / animal husbandry creates a viable ecological niche for humans where none would have existed otherwise.” (Kardulias 2015)

Cattle, sheep, and goats were initially domesticated in Neolithic Western Asia, well away from even the most Western reaches of Southern Siberia, Mongolia, Kazakhstan, or Uzbekistan (see see Chapter 06). Modern domesticated horses originated from the Volga-Don region of the Western Eurasian Steppe, also far removed from Inner Asia (see Chapter 06). A number of

theories have been proposed by scholars throughout the past several decades endeavoring to explain how and when these domesticated animals reached Inner Asia, as well as the emergence of pastoralist husbandry. Their theories are influenced by both their cultural backgrounds as the popular ideologies and reigning academic trends of their time. Certain theories share a good deal of overlap, some are only loosely related in subject or topic, and others are completely at odds with one another. Recent developments in biomolecular archaeology (see Chapter 04) have prompted new arguments and challenged older ones, bringing clarity on one hand and controversy on the other. This section will briefly overview the evolution of several theories surrounding the origins of domesticated animal husbandry in Inner Asia, without arguing in favor of one or the other.

9.3.1. A Note on Western Perspectives

"For far too long, Eurasian archaeology has permitted such loose associations between material culture horizons, language groups, and migration events." (Taylor 2021)

The theories developed by Western scholars to explain how domesticated animals and pastoralist husbandry reached Inner Asia are more interdisciplinary in nature than the Soviet theories and concepts that influenced them. It should be noted that Western studies have also benefited from certain advances in Soviet archaeology, such as the study of taphonomy (see Chapter 02) and use-wear analysis of lithics (Bulkin et al. 1982). Western theories of pastoralist emergence, transmission, and intensification however have tended to focus less on the social organization of pastoralists and more on the ecological incentives for (and impacts of) animal management practices, scales of economic investment, comparative herd compositions, and human-animal relationships more broadly (Chang 2015; Dyson-Hudson 1972).

Major Western theories are centered around models and concepts of human migration, cultural diffusion, exchange networks, environmental adaptation, resource dependency, and technological innovation. Western theories have (more recently) incorporated multiple biomolecular lines of evidence and continue to be revised and transformed by them as more studies are conducted and more data are produced. In this subsection, I will briefly outline prevalent Western theories as they developed through time, in accordance with their central themes, and the issues surrounding them. Importantly, these themes share a great deal of overlap and are not intended to be perceived as isolated camps of thought.

9.3.2. Steppe Migration Theories

"We have been slow to recognize that long-distance migrations are complex, multi-generational human processes…we failed to see that long-distance migrations created new social dynamics…too often we dismissed long-distance migration as "always simplistic"...this was because many of us retained the "invasion" theory of migration as a foil for alternative theories of culture change…" (Anthony & Daniels 2022)

Migrationism was vehemently opposed in Soviet schools of archaeological thought until after the mid twentieth century (Bulkin et al. 1982; Klejn 2017; Shnirelman 2005; Slezkine 1996), but was subsequently instrumental in the development of both Eastern and Western theories about pastoralist expansion throughout the Eurasian Steppe (Anthony & Daniel 2022; Frachetti 2012).

Although migrationism (and cultural diffusionism) fell out of favor in the West with the emergence of post-processual archaeology towards the end of the twentieth century (Frachetti 2012), it was Marija Gimbutas's Kurgan culture migration hypothesis (Gimbutas 1956, 1963a, 1963b, 1970, 1977, 1980, 1993) that would help to shape initial theories surrounding Steppe pastoralism and that would continue to be revisited decades later (Anthony & Daniel 2022).

Gimbutas (who was trained in the Soviet Union) speculated that Indo-European languages and lifeways crashed into prehistoric, agricultural Europe in three violent waves of Pontic-Caspian warrior nomad invasions (Gimbutas 1956, 1963a, 1963b, 1970, 1977, 1980, 1993). Ironically, while many Western scholars rejected Gimbutas's migrationism-based theories (Anthony 1986, 1990; Anthony & Daniel 2022; Chapman & Dolukhanov 1992; Frachetti 2012; Renfrew 1987), Russian archaeologists such as Nikolay Merpert whole-heartedly embraced them (Anthony & Daniel 2022; Merpert 1974). There were, of course, also Western scholars who agreed with Gimbutas (Mallory 1989) and later Eastern scholars who did not (Koncha 2001; Manzura 1999; Nikolova 2003; Stefanovich 2003).

David Anthony has criticized Gimbutas's Kurgan hypothesis for being too simplistic, overly focused on invasion, and ultimately unhelpful (Anthony 1986, 1990, 2023a; Anthony & Daniel 2022). Anthony reinterpreted the data to instead suggest that Indo-European lifeways disseminated into Bronze Age Europe as Yamnaya pastoralists migrated southwest from the Pontic-Caspian Steppe (Anthony 1986, 1990, 2023a, 2023b; Anthony & Daniel 2022). The spread of pastoralism from the Western Eurasian Steppe into Europe is in itself beyond the scope of this dissertation, but the role of Yamnaya migrations in pastoralist diffusion is not.

The Yamnaya peoples are now widely considered to be the first pastoralists of the Eurasian Steppes (Anthony 2023b; Frachetti 2012), a conclusion that has come from decades of research by scholars such as Gimbutas and Anthony into the origins of Indo-European languages and cultures. Multiple scholars, including Anthony, have maintained that the Yamnaya were not only pastoralists, but highly mobile nomadic pastoralists (Anthony 2023b; Frachetti 2012; Gimbutas 1977; Merpert 1974; Scott et al. 2022; Shilov 1975; Shishlina 2008). Some researchers have credited a fully mobile herding and dairying economy to the vast expansion of the Yamnaya peoples, who rode on domesticated horses and whose wagons were pulled by domesticated oxen, both east and west through the Eurasian Steppe (Anthony 2023b). It has also been suggested that a need for more pasture for domesticated animal herds may have driven Yamnaya expansion (Scott et al. 2022).

The long-distance, eastward migrations of Western Steppe cultures such as the Yamnaya has been both linked to (Frachetti 2012; Scott et al. 2022; Wilkin et al. 2020) and directly attributed to (Danilenko 1974; Svyatko et al. 2009; Vadetskaya 1986) pastoralist emergence in Southern Siberia during the Eneolithic. It should be stated that the older archaeological evidence for a direct Yamnaya transmission of pastoralism from the Western Steppe to the Eastern Steppe is weak (Frachetti 2012). The flexed Afanasievo burial position that has been attributed to a Yamnaya or Western Steppe origin has also been found in Early Bronze Age burials from Central Asia (Avanesova & Dzhurakulova 2008; Frachetti 2012; Lyonnet 1996).

The descent of Afanasievo-associated individuals from migrating Yamnaya peoples has problematically been inferred from Soviet studies of cranial osteometery and biodistance (e.g. Alekseev 1961; Alekseev & Gokham 1984; Frachetti 2012; Syvatko et al. 2009). Ceramic typology has also been cited (Danilenko 1974), an equally unconvincing line of evidence which has further been compromised by issues surrounding Yamnaya typology (Chernykh 2009; Frachetti 2012; Telegin 2002; Rassamakin 1999). I will explore issues related to cranial osteometry, material culture typology, and Afanasievo association in depth in the next chapter. More recent studies however have confirmed a close genetic relatedness between Yamnaya individuals and Afanasievo individuals (Allentoft et al. 2015; Jeong et al. 2020; Mathieson et al. 2015).

Although it is now clear that Western Steppe peoples did migrate into Southern Siberia, it is difficult to say whether or not pastoralism was being practiced in the region before these populations arrived because there is very little faunal data available (Alekhine et al. 1995; Frachetti 2012). The faunal data that is available is questionable, an issue which I will address at length in the next chapter of this dissertation. The absence of reliable and abundant faunal data not only from Eneolithic Southern Siberia but also Inner Mongolia and Central Asia has left room for multiple theories surrounding pastoralist emergence, not all of which are centered upon migrationism. In the next subsection, I will discuss theories of pastoralist emergence and domestic animal dispersal that focus on cultural diffusion and exchange networks.

9.3.3. Cultural Diffusion & Exchange Network Theories

“The greater the distance between groups in time and space, the more unlikely it is that diffusion would take place between them.” (Sanders & Price 1968)

Researchers who have not embraced Steppe migration theories have looked instead to cultural diffusion and exchange networks (e.g. Frachetti 2011, 2012, Janz et al. 2020; Honeychurch et al. 2021). I will use this subsection to briefly discuss each of their theories in turn, as well as their relation to one another, beginning with Michael Frachetti’s Multi-Regional Emergence Theory. It should first be noted that while cultural diffusionism was long shunned in twentieth century Russian archaeological and historical thought, it was not completely banished from it. Initial Russian contributions to diffusionist approaches in ancient and medieval Central Asian contexts (e.g. Trepavlov 1993) have more recently been revisited by Western scholars (e.g. Rogers 2007) and have helped to shape the broader corpus of diffusionist theory in relation to the Eurasian Steppe (Kradin 2019).

9.3.4. Frachetti’s Multi-Regional Emergence Theory (2011)

“If western steppe pastoralists were not the likely source of Afanas’ev pastoralism in the eastern steppe, what was the springboard of eastern steppe herding economies? Where can we trace their source of domestic animals, and what brought on the intensification of mobile pastoral strategies in the Altai and southwest Siberia?” (Frachetti 2012)

Frachetti's (2011) theory moves away from examining the role of long-distance migrations across the Eurasian Steppe and focuses instead on the long-term interactions that may have taken place between ancient human networks connected throughout the Hindu Kush, Pamir, Tian Shan, Dzhungar, and Altai Mountains (Frachetti 2012). Frachetti (2011) argues that the extreme environmental conditions of the "Inner Asian Mountain Corridor" (IAMC) have limited population growth and led to specialized subsistence strategies, but have not isolated human communities to the extent depicted in either Eastern (Isakov 1991; Vinogradova 1993) or Western (Moore et al. 1994; Stein 1925) literature.

Multi-regional emergence theory proposes that domesticated sheep and goats may have been introduced into the IAMC by nearby agropastoralist communities and subsequently diffused throughout the mountain corridor via transhumant pastoralist migrations and into Inner Asia ca. 3500 BC (Frachetti 2012). This is supported by the genetic homogeneity of Central Asian domesticated sheep breeds that is not shared with domesticated European (Western Steppe) sheep or reflected in wild Eurasian sheep, which are genetically distinct (Frachetti 2012; Hiendleder et al. 1998, 2002). Genetic markers shared between West Asian and Inner Asian domesticated sheep, but not between European domesticated sheep breeds, have also been cited to argue for a direct transmission through the IAMC (Chessa et al. 2009; Frachetti 2012).

Frachetti also argues that Afanasievo-associated herd compositions mirror the Early Bronze Age herd compositions of the IAMC (Frachetti 2012), although the Afanasievo herd composition data he cites either comes from burial contexts or from settlement sites that are both limited and thoroughly unreliable (see the next chapter of this dissertation). A prevalence of sheep and goat over cattle in the modern herds of Sarazm in Tajikistan is then argued to be indicative of mountain pastoralism as opposed to sedentary agriculture and suggestive of contact with mountain communities (Frachetti 2012), even though this same prevalence has been repeatedly recorded in the historical and modern (mobile and sedentary) herds of Kazakhstan, Uzbekistan, and the Gobi desert as well as the mountainous regions of Inner Mongolia and Southern Siberia (Ferret 2018; Krader 1955; Vaĭnshteĭn 1980). That is not to say that Frachetti is incorrect about the contact between mobile mountain pastoralists and their agropastoralist neighbors in the IAMC, so much as the herd composition data he uses as evidence is insubstantial.

Archaeobotanical evidence from Early Bronze Age Begash in Kazakhstan does suggest that wheat was being transported from Southwest Asia along the IAMC and into China, and that millet was being transported from China into the IAMC (Frachetti 2012). Frachetti's multi-regional emergence theory posits that it was these kinds of regional interactions and exchanges, as opposed to long-distance migrations from the Western Steppe, that led to the diffusion of Inner Asian pastoralism (Frachetti 2012). Mongolia is unfortunately excluded from IAMC theory, despite being an adjacent region of critical cultural importance with an extensive pastoralist history. Janz et al.'s (2020) desert wealth exchange theory however does explore the spread of pastoralism throughout Mongolia through a cultural diffusionist lens and is discussed below.

9.3.5. Janz et al.'s Desert Wealth Exchange Theory (2020)

"Based on evidence of interaction between Gobi Desert groups and agrarian villages…we see this desert region as the geographic core of cultural transformations among indigenous populations…the movement of goods held extreme significance for the spread of pastoralism…the role that Gobi Desert groups played in the formation of early trade networks is vital for understanding the spread of pastoralism in Mongolia." (Janz et al. 2020)

While Frachetti focuses on the roles of Inner Asian mountain ranges in pastoralist transmission and exchange, Janz et al. (2020) focus on the role of the Gobi Desert. The influence of Yamnaya and Afanasievo lifeways on the Eneolithic and Early Bronze Age subsistence strategies of Mongolian peoples occupying the Altai and Khangai mountains is acknowledged, but the absence of evidence for pastoralism throughout the rest of Mongolia until the Late Bronze Age is also emphasized (Janz et al. 2020). The emergence and expansion of pastoralism eastward across the Gobi Desert is attributed to cultural diffusion, once again citing shared burial postures (face down as opposed to flexed), material culture, genetic traits, and cranial features amongst indigenous archaeological cultures (Janz et al. 2020). Evidence provided for Bronze Age pastoralism includes monumental burial architecture associated with domesticated animal remains, milk proteins recovered from human dental calculus, and milk residue recovered from pot sherds (Janz et al. 2020).

Late Bronze Age Gobi Desert groups are portrayed in Janz et al.'s (2020) Desert Wealth Exchange Theory as dairy pastoralists who produced and traded stone beads and who likely adapted pastoralism as part of an economic strategy to mobilize their wealth as complex trade networks connecting Mongolia and China began to emerge (Janz et al. 2020). Janz et al. (2020) admit that more data are needed to fully explore this wealth exchange theory and identify the origin of pastoralism in the Gobi Desert, especially large scale organic residue analysis to identify dairying and comparative lithic analysis to identify technological relationships and overlaps between Bronze Age Gobi Desert groups and their neighbors.

Other scholars have questioned some aspects of Janz et al.'s (2020) model, such as whether the human and animal burial data reflect a much older tradition of animal husbandry that simply has not been preserved in or recovered from the archaeological record (Honeychurch et al. 2021). Honeychurch et al. (2021) references studies which have analyzed pollen, charcoal, sediments, and phytoliths and concluded that widespread anthropogenic landscape modification (which could be associated with pastoralist practices) was unfolding across Mongolia prior to the timing of these burials. They also caution against treating Afanasievo populations as isolated communities and raises the possibility that the interactions between Afanasievo pastoralists (and their domesticated herd animals) and indigenous Mongolian hunter-gatherers led to the formation of rudimentary, experimental animal husbandry during the Eneolithic period which was refined and expanded overtime (Honeychurch et al. 2021). Honeychurch et al.'s (2021) counter-proposal of early "learning curve" pastoralism to Janz's desert wealth exchange theory is explored below.

9.3.6. Honeychurch et al.'s Learning Curve Theory (2021)

"We propose an early introduction of herd animals by the Afanasievo communities in central Mongolia followed by an extended interval best understood as a 'learning curve' period…Experiments with early animal traction and portable dwellings enhanced an existing mobility ethic…in which more intensive pastoralism developed and flourished." (Honeychurch et al. 2021)

Honeychurch et al.'s (2021) learning curve theory proposes that migrating Afansievo populations introduced domesticated herd animals to the primarily hunter-gatherer communities of Western and Central Mongolia, who probably perceived them as fascinating oddities as opposed to food sources. These animals were likely distributed as gifts amongst different indigenous groups who may have rejected, neglected, appreciated, or revered them; those who invested in their care, keeping, reproduction and exploitation would have had to cope with a steep learning curve, zoonotic disease and their own lactose intolerance (Honeychurch et al. 2021). Eneolithic Mongolian communities would have slowly learnt how to cater to domesticated animal needs and organize the logistics of management and cohabitation with them over time (Honeychurch et al. 2021).

Honeychurch et al. (2021) further identify six factors that they attribute to the subsequent pastoralist intensification identified in the Late Bronze Age archaeological record throughout Mongolia, the first of which is the gradual development and diffusion of the aforementioned animal husbandry knowledge. The second proposed factor is the adaptation of dairying technology which transformed raw milk into food products that would have been more digestible for lactose intolerant individuals and populations. Portable dwelling technology enabling seasonal transhumance is the third factor, the monumental architecture and burials which marked the emergent pastoralist territories is the fourth, and the use of domesticated horses for transport across these territories is the fifth.

The sixth and final suggested factor is the ancient aridification of the Gobi Desert and the extreme climate regimes which characterize much of Mongolia which would have greatly complicated sedentary agriculture, and could have led to an economic and cultural preference for animal husbandry and pastoralism. This environmental factor is listed as being of minimal significance compared to the human factors driving cultural and technological diffusion (Honeychurch et al. 2021). Both Anthony (2023b) and Frachetti (2012) have also acknowledged but downplayed the influence of climatic change and aridification on Eurasian pastoralist intensification, and there do not appear to be any widely circulated theories advocating environmental adaptation as the primary catalyst of pastoralist emergence and transmission in North or Central Asia.

Taylor (2021) has lauded Honeychurch et al.'s (2021) contributions while also offering several constructive criticisms of their model of pastoralist diffusion in Mongolia. Taylor points out several issues surrounding the term "Afanasievo", such as shifting definitions and identifications based upon ceramic typology, lithic technology, burial traditions, and ethnicity (Taylor 2021); I will explore these issues in-depth in the next chapter of this dissertation. Taylor also raises the issue that there is no proof of domesticated horses having been present in Eneolithic Mongolia

and so their exploitation cannot be confidently associated with Afanasievo animal management practices (Taylor 2021).

Taylor (2021) further points out that the attribution of wild or domesticated origins to faunal remains from Afanasievo-associated assemblages in Mongolia are questionable. This is in fact a problem that reaches far beyond the scope of Mongolian Altai assemblages, or even Afanasievo assemblages, and is an issue which will be repeatedly revisited throughout this dissertation. Taylor (2021) concludes his evaluation with a statement highlighting the need for archaeologists to both produce and compare more reliable data, and to incorporate more biomolecular lines of evidence into their research. I will briefly review zooarchaeological practice in both Russia and Mongolia below.

9.4. Faunal Data Collection & Analysis

"Culture shapes our reading of animals just as much as animals shape our reading of culture" (Baker 1993)

Archaeological theory and method directly impact the collection and analysis of faunal data from archaeological sites. As new methods emerge and new excavations take place, older zooarchaeological assemblages and datasets can be revisited to address research questions and refine our understanding. Whether or not animal bones are collected from animal sites, analyzed, their data reported, and retained in collections is largely dependent upon the research culture and the theoretical prism said culture is being filtered through. Before entering into new discussions and reviews of the archaeology of pastoralism in Bronze Age Southern Siberia and Mongolia, I will first briefly discuss the history of zooarchaeology in Russia and Mongolia.

9.4.1. Russian Zooarchaeology

"Animal bones represent a large-scale type of finds, at the very least in the urban strata, which makes it possible to reconstruct the composition of the herd. Archaeozoological remains fundamentally change our knowledge concerning domestic animals..." (Chernaya 2016)

Soviet era archaeological reports often emphasized stages of social evolution and the material typology of tools and artifacts over subsistence strategies, a priority which came at the expense of the collection and analysis of faunal and archaeobotanical data. It is not uncommon to find multiple reports cataloging the lithic, ceramic, and metal finds recovered from the same site without encountering any faunal data, or perhaps a poorly characterized faunal list nested amongst the cultural material finds. Stratigraphic context is rarely available, and when it is, the stratigraphy is often compromised by haphazard excavation methodology and characterized by mixed assemblages. Poor methodology in Russian archaeology has in part been attributed to the influence of the *archaeological history* approach, which emphasized the historical nature of archaeology at the expense of objectivity and scientific rigor (Bulkin et al. 1982). This style of reporting has unfortunately outlived the Soviet Union and continued well into the twenty-first century.

These issues are not unique to Russian archaeology; archaeology around the world has continued to be developed and refined, and strong criticisms can be made of the older methods and theories of any other country. I am highlighting the major issues that have shaped the older body of Russian archaeological data because of their relevance to and impact upon my own doctoral research, but I do not mean to imply that the rest of the world practiced a superior form of archaeology. It should also be noted that not all older Russian archaeological reports lack faunal and archaeobotanical data; Bibikov (1953) contained both for example, and also generated population, grain yield, and pasturage requirement estimates (see Anthony 1995). The renowned Soviet archaeologist Mikhail Petrovich Grzaznov was also noted for his rigorous excavation methodology as well as his consistent criticism of his less-critical colleagues' methods, his implementation of mathematical approaches, and his pioneering of lithic use-wear analysis (Klejn 2017). Sergei Aristarkhovich Semenov has also been lauded for his methodological advances in understanding archaeological tool functions (see Anderson et al. 2005).

Faunal analysis in modern day Russia has come a long way, and its importance has been increasingly recognized with time (see Chernaya 2016). Although there are no specialized zooarchaeology training programs in Russia, some 200 people are currently practicing after having learnt faunal analysis through field work and graduate school training (pers.comm. Alexey Kasparov 2023). There are no specifically zooarchaeological reference collections in Russia, though scholars such as Natalia Mikhailovna Ermolova at the Russian Academy of Sciences in St. Petersburg have curated their own (pers.comm. Alexey Kasparov 2023). Russian scholars also have access to impressive zoological and biological collections at various universities, museums, and institutes such the Zoological Institute in Novosibirsk (pers.comm. Alexey Kasparov 2023). Russian zooarchaeologists will typically compare faunal remains to these collections as opposed to osteological atlases, though a Russian reference guide has been produced by Gromova (pers.comm. Alexey Kasparov 2023).

Taxonomy is most often attributed to archaeological animal bones which a zooarchaeologist has received after excavation, as they are typically not included in field work (pers.comm. Alexey Kasparov 2023). Beyond taxonomic identification, Russian zooarchaeologists estimate sex and age using predominantly Russian methods and sources (pers.comm. Alexey Kasparov 2023). For aging, Klevezal's (1996) method of counting dentin layers is perhaps the most common, though the methods published by Payne (1973) and Grant (1982) are also used (see Chapter 02) (pers.comm. Alexey Kasparov 2023). Bones are measured in accordance with van Den Driesch (1976) (pers.comm. Alexey Kasparov 2023), as is common practice in zooarchaeology around the world (see Chapter 02) . Skeletal part frequency is most quantified using NISP, MNI, and MNE (pers.comm. Alexey Kasparov 2023), as is also the case for most of the world (see Chapter 02). Biomolecular methods have been less commonly employed, though stable isotopic analysis and radiocarbon dating of animal bones (see Chapter 03) has been conducted for decades.

9.4.2. Mongolian Zooarchaeology

"...archaeology that has been mainly interested in burials, ritual sites and objects of fine craftsmanship. Botanical remains and animal bones have not been given the same attention..." (Houle 2010)

A lack of archaeological, especially faunal, data from Early Bronze Age habitation sites in Mongolia has left researchers attempting to contextualize the emergence of pastoralism in a vacuum (see Taylor et al. 2020c). Very recently, the work of William Taylor has begun to address this gap. In contemporary times, approximately 60 archaeological excavations take place in Mongolia every year; half of these are international projects conducted in cooperation with the USA, Germany, Russia, and China (pers.comm. Tuvshinjargal Tumurbaatar 2024). Zooarchaeologists are typically included in both local and international projects, though in Mongolia zooarchaeologists tend to be field archaeologists who also specialize in fauna analysis (pers.comm. Tuvshinjargal Tumurbaatar 2024).

Although many Mongolian archaeologists consider faunal analysis to be of great importance, zooarchaeological training is largely unavailable in Mongolia (pers. comm. Tuvshinjargal Tumurbaatar 2024). There are currently no courses in faunal analysis at any Mongolian University, though many archaeological faunal reference collections from ancient burial sites are available (pers.comm. Tuvshinjargal Tumurbaatar 2024). Despite ongoing international collaboration, very few Western zooarchaeologists participate in Mongolian archaeological field work. Mongolian archaeologists almost exclusively publish their work in the Mongolian language, most commonly in the "Studia Archaeologica" journal of the Institute of Archaeology, Mongolian Academy of Science (pers. comm. Tuvshinjargal Tumurbaatar 2024).

There are currently only four zooarchaeologists working at the Mongolian Academy of Science: Bayarsaikan M., Delgermaa D., Madakh D., and Tuvshinjargal T. (pers.comm. Tuvshinjargal Tumurbaatar 2024). Bayarsaikan's (1998, 1999) publications of his craniometric studies on archaeological animal heads in the "Studia Archaeologica" journal could be said to mark the beginning of faunal analysis in Mongolian archaeology (pers. comm. Tuvshinjargal Tumurbaatar 2024). Mongolian zooarchaeologists generally use faunal remains recovered from Mongolian burial sites as a reference to attribute taxonomy, including domesticated versus wild (pers.comm. Tuvshinjargal Tumurbaatar 2024). The osteological atlases of Joachim Boessneck (e.g. Boessneck 1970; Boessneck et al. 1964) and Melinda Zeder (e.g Zeder & Lapham 2010; Zeder & Pilaar 2010) are also used to distinguish sheep from goats (pers.comm. Tuvshinjargal Tumurbaatar 2024).

Quantification of skeletal parts has often been neglected, though MNI and NISP are becoming more commonly reported (pers.comm. Tuvshinjargal Tumurbaatar 2024). Sex and age estimation is achieved using a mix of Western (e.g. Payne 1973) and Russian materials (e.g. from Veniamin Iosifovich Tsalkin; works unspecified) (pers.comm. Tuvshinjargal Tumurbaatar 2024). Traditional Mongolian livestock aging methods are avoided due to their reliance on live animals (pers.comm. Tuvshinjargal Tumurbaatar 2024) (see Gillis 2017 for issues associated with aging methods derived from living animals). The isotopic and biomolecular analyses of archaeological animal remains, including radiocarbon dating, are only conducted in

collaboration with archaeologists from outside Mongolia (e.g. Kovalev 2008; Taylor et al. 2019). I will review some of these studies on a case-by-case basis, after establishing the radiocarbon dating work which has been done on Bronze Age animal remains and archaeological materials more broadly.

9.5. Archaeological Theory of Pastoralism: Conclusion

"A coherent understanding of animal domestication and exchange can only emerge through…a multidisciplinary approach to the archaeological record, and building explanatory models that reflect the interconnected nature of ancient Eurasia." (Taylor et al. 2020c)

Faunal data collection and interpretation from Inner Asian archaeological sites have been strongly impacted by Soviet archaeological theory. Scholars around the world have built on these data and proposed a number of theories and models for the adaptation of pastoralism and domesticated animal husbandry in Inner Asia. Steppe migration theories have traditionally focused on the role of Western Steppe (particularly the Yamanaya) expansion into the Eastern Steppe, especially as the predecessors of the Afanasievo peoples. Cultural diffusion and exchange network theories have focused instead on the interactions between local communities and the transference of knowledge and technology across vast networks. The role of Afanasievo peoples and the Altai Mountains has been emphasized in most theories surrounding pastoralist emergence, although a number of issues involving inconsistent use of terminology, an overreliance on material culture typology, and a lack of reliable faunal data complicate our understanding of what the term Afanasievo really refers to. A thorough examination of the Bronze Age archaeological cultures, settlement sites, and animal economies of Southern Siberia and Outer Mongolia will be the focus of the next several chapters of this dissertation.

10. Bronze Age Southern Siberia (ca. 3000–900 BCE)

10.1. Introduction

"..It is not every European country that can claim that its archaeological sites have been investigated as thoroughly, with the object of throwing light on the successive stages of its cultural development, as the sites in the Minusinsk basin. But unfortunately there has not been the same detailed investigation in every part of Southern Siberia." (Gryaznov 1969)

In this chapter I will focus on the archaeological cultures of Southern Siberia, here defined as encompassing the Altai and Sayan mountains, the Altai plain, the Kuznetsk and Minusinsk Basins, and Tuva (Gryaznov 1969) (Fig.4), from the Eneolithic period to the Late Bronze Age. I will first open with a discussion of the Russian archaeological theories, methodologies, and practices which were instrumental in the delineation of prehistoric ethnic units and the collection of associated faunal data. I will then outline the major archaeological cultures of Southern Siberia (ca. 3000 - 900 BCE), i.e. the Afansievo, Okunevo, Karakol, Yelunino, Andronovo (Fyodorovka), and Karasuk.

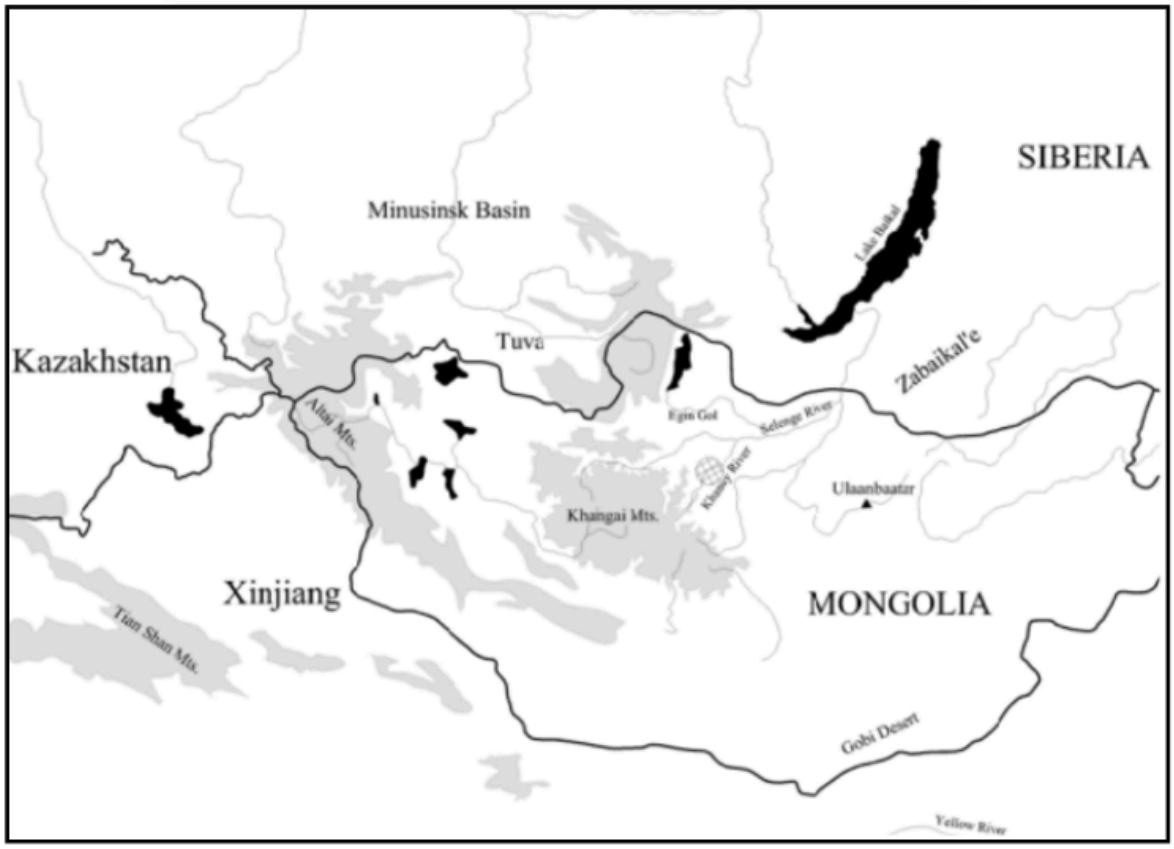


Fig.4 Map of Southern Siberia and adjacent regions in Inner Asia (Houle 2010).

10.2. The Archaeology of Ancient Southern Siberian Ethnic Units

"Whatever we may think of the methods adopted…we do owe to this period a body of archaeological material of inestimable value…" (Gryzanov 1969)

The cultural descriptors, or ethnic units, constructed to classify the prehistoric human populations observed in the archaeological record of Southern Siberia are a product of Russian archaeological and historical theory, practice, and literature. In this context it is important to clarify the distinction between what is meant by an ethnic group in the West and an *ethnos* is Russian scholarship. Ethnicity as conceived by Western schools of archaeology is rooted in the twentieth-century historical-cultural model posited by Gustav Kossina (1911) and was made popular by the works of V. Gordon Childe, wherein an ethnic unit was seen as a self-identifying, homogeneous community and a direct association is assumed between ethnic units, material culture, and physical traits (Jones 1997). Although Western scholars have since entered into much deeper conversations about complex and heterogeneous ethnicity, those conversations are beyond the scope of this dissertation. While the historical-cultural model of Kossina also shaped Russian archaeological theory, pre-Soviet ethnography and the emergence of Marxist archaeology and Marrism culminated in the unique conception of *ethnos* (see Chapter 09).

An *ethnos* is conceived to be self-aware and to maintain a continuity of both shared culture and character through time (Anthony 1995), while also being contained within a package of shared ancestry, material culture, and world view. Modes of social organization and economic production have been emphasized in the studies of different ethnoses more than subsistence strategies and human-animal relationships. The assumed relationship between physical appearance and material culture has directly impacted the Russian designation of Southern Siberian archaeological cultures. Craniometry and archaeological typology have been classically (and problematically) employed to identify Southern Siberian ethnic units, reconstruct their ethnogenic emergence from one another (see Chapter 09), and retrace their migrations and interactions with one another. Archaeological history approaches and a comparative disinterest in subsistence studies and faunal analysis has delayed the understanding of ancient animal economies of sites associated with Southern Siberian archaeological cultures. Problematic chronological contextualization has further compromised studies into both the ancient human and animal communities of Southern Siberia. All of these issues are explored in-depth below.

10.2.1. Craniometry, Racial Science, & Scientific Racism

"More than any other discipline in the realm of scientific anthropological research, craniometric analysis and those involved in the fields of craniology and craniometry have had to live in the shadows of the discipline's less than honourable history." (Stephens 2011)

The use of physical anthropology as a "racial science" by Russian scholars to classify ethnicity and investigate ethnogenesis predates the Soviet era, and has outlived it as well (Alekseev 1974a, 1977, 1978, 1979, 1984a, 1989a,b, 1991; Chard 1962; Jochelson 1924; Mogilner 2013; Zakh & Bagashev 1998). Craniometry, or "the study of human cranial measurements for use in

anthropological classification and comparison" (Stephens 2011), was part and parcel in a nineteenth and twentieth-century Russian education in medicine and natural science (Mogilner 2013). Craniometry inevitably found its way into archaeology in both the East and the West (Alekseev & Debets 1964; Stephens 2011), unfortunately in part through the unethical exchange of human crania as exotic curiosities in scientific circles and the pseudoscientific exploitation of cranial diversity in perpetuation of racist and nationalist ideologies (Mogilner 2013; Stephens 2011).

Twenty-first century applications of craniometry have come a long way following the widespread scientific rejection of nineteenth and twentieth century racial essentialism and discrete biological typology (Hefner & Spradley 2018; Spradley & Jantz 2021; Stephens 2011). The adaptation of standardized craniometric measurements, multivariate statistics, computer-based analyses, geometric morphometrics, computational tomography, and advanced imaging techniques in addition to the implementation of ethical practices have further refined the technique (Rogers 1984; Spradley & Jantz 2016; Spradely & Stull 2018; Stephens 2011). Craniometry is used to this day to estimate ancestry in both archaeological and forensic contexts (Spradely 2016; Stephens 2011), though not without controversy (Armelagos & van Gerven 2003; Armelagos & Goodman 1998; Smay & Armelagos 2000; Spradley & Weisnsee 2013). Twenty-first century anthropologists have largely concluded that craniometry may be more appropriately said to estimate population affinity instead of ancestry, measuring degrees of *similarity* as opposed to race or ethnicity (Spradley & Jantz 2021).

Russian archaeologists have classically reconstructed ancient Eurasian cultural groups, ethnic histories, and ethnogenic narratives from craniometric studies, which is referred to simply as "anthropology" or "palaeoanthropology", even when discussing the Bronze and Iron Ages (e.g. Alekseev 1954, 1956, 1958, 1959, 1961a, b, c, 1961, 1962, 1963, 1972, 1974b, 1975, 1984b, 1986; Alekseev & Mamonova 1988; Alekseev & Trubnikova 1984; Alekseev et al. 1987, 1990; Bagashev 2000; Chikisheva 2010; Debets 1932; Molodin & Alkin 2012; Pozdnyakov 2004; Rykun 2005; Solodovnikov 2006; Solodovnikov & Tur 2003; Zubova 2005, 2008; see also Chard 1962). More recent craniometric studies of ancient Southern Siberian cultures by Russian scholars have incorporated data from older ones, and their inclusion into modern research warrants healthy skepticism. Scholars have criticized the use of craniometry to attribute a Western Steppe ancestral origin to Afansievo peoples (Frachetti 2012) and to attribute Afansievo ancestry to other archaeological populations, pointing out that craniometric data should not be used to infer population history or ancestry while excluding (or ignoring) other lines of archaeological evidence (Honeychurch 2021).

Craniometry is subjective (Good et al. 2010), arguably assesses probability instead of reality (Stephens 2011; White & Folkens 2000), and cannot account for nor capture the complex interplay between human biological diversity, ancestral admixture, and population variation. This is not to say that craniometry should be abandoned all together, but archaeologists must move beyond the older Southern Siberian (and Eurasian) ethnic units, culture descriptors, and historical narratives which have propagated in the literature–as well as the overreliance on craniometric data which has shaped them. It is not even that the conclusions reached by

craniometric analysis are necessarily inaccurate (often they are not), so much as with any line of archaeological evidence, proper contextualization and the inclusion of multi-proxy perspectives are essential. Genetic and genomic analyses of ancient human DNA have greatly contributed to the clarification of Southern Siberian population histories (e.g. Allentoft et al. 2015; Mathieson et al. 2015; Jeong et al. 2020; Narasimhan et al. 2019; Rogers 2016; Wang et al. 2021).

10.2.2. Material Culture Typology & Descriptive Archaeology

"Typology is a pet subject for the Russian archaeologists... Many scholars are sure that classification is the best theory. Vasyutin has long been trying to create a universal typology of pastoral empires." (Kradin 2019)

In early twentieth century Russia, the term "archaeology" was temporarily replaced with the term "history of material culture" (Bulkin et al. 1982). This shift in terminology and thought coincided with and is well-reflected in Gorodstov's (1927, English translation 1933) influential treatise on the typology of archaeological objects. Gorodstov (1927, 1933) attributed the origins of scientific typology to nineteenth century French academia (via de Blainville 1816, mistranslated as "Blenwell"; see Gräslund 1987) but criticized subsequent Western attempts to blindly incorporate it into archaeology. Gorodstov (1927, 1933) outlined a typological method and theoretical framework for archaeologists where cultural materials should be divided and subdivided into a sequential array of functional *categories*, material *groups*, morphological *orders* or *genera*, and their resultant *types*. Material culture typology has been a hallmark of both Russian (Anthony 1955; Bobrov 1988; Bulkin et al. 1982; Gening 1989; Klejn 1970, 1982; Kudryavsteva 1985; Smirnov 1964; Zakharuk 1990) and Western (see Bulkin et al. 1982) archaeology ever since.

For many Russian archaeologists typology was not a methodology resulting in useful artificial constructs, but in actual facts that existed independently of the archaeologist (Anthony 1955; Badou & Jannson 2015; Klejn 1982). Archaeological typology eventually culminated in a widespread empiricist school of *descriptive archaeology* in late twentieth-century Russia, a highly systematic approach to material culture analysis which has been criticized for being unnecessarily restrictive and overly mechanical (Bulkin et al. 1982). This is dynamically opposed to *historical archaeology* as a mode of typology, which is more focused on the chronological and temporal contextualization of cultural materials than the qualification of their inherent properties (Rouse 1960). Resultant descriptive (and historical) typologies for lithic, ceramic, and metal artifacts have been used to both define and identify archaeological cultures within Southern Siberia (Derevianko & Molodin 1994; see Gryaznov 1969 and Honeychurch 2021) and argue for their expansion into Mongolia and East Asia (Jaang 2015; Honeychurch 2021; Novgorodova 1989; Vadetskaya et al. 2014; Yesin et al. 2012).

Typological arguments inevitably resurrect the old maxim that *pots are not people*, which reminds scholars that material culture is not the same thing as ethnicity. The presence of a certain material culture "type" does not necessarily correlate with group identity or direct technological transmission from a specific population (Christian 2011). Subjectivity and ambiguity are also issues inherent within archaeological typology (Hill & Evans 1972; Whittaker et al. 1998), as with craniometry. Descriptive typological arguments invite further criticism for

their disregard of chronological context and subsequent tautological reasoning; i.e. *(subjectively qualified) material type x has been found in sites (subjectively) associated with culture type x, and so the (subjectively qualified) presence of material type x must indicate the presence or influence of culture type x*.

Archaeological typology, descriptive or otherwise, still has much to contribute and material culture finds are of extreme importance. The designation of ethnic units, the attribution of ancestry, and the reconstruction of population migrations however should not be put forth based upon archaeological typology alone, or upon combined archaeological typology and craniometry- most especially without secure chronological contextualization. The incorporation of biogeochemical and biomolecular lines of evidence, such as radiocarbon dating, aDNA analysis, and stable isotopic analyses, are invaluable to such endeavors (see Chapters 03–04; see also Badou & Jannson 2015; Taylor et al. 2020). I will discuss specific issues and pleas for clarification further along this chapter, as relevant for each cultural descriptor (e.g. ethnic unit). I first review the radiocarbon dates produced by Russian scholars in Southern Siberian archaeological contexts.

10.2.3. Chronology & Radiocarbon Dating

"The traditional chronology of the steppe cultures was originally established on the basis of cross cultural synchronization with Chinese bronzes, with European sites, and on 1 occasion with "Mycenaean" ornaments ...The traditional chronology, however, has appeared to be in conflict with the dating sequence derived on the basis of 14C dates…" (Svyatko et al. 2009)

Intrusive and mixed burials have greatly complicated Russian efforts to reconstruct prehistoric chronology in Southern Siberia (Gryaznov 1969), which was initially dependent upon comparisons to adjacent archaeological sites (Poliakov & Lazaretov 2020). Perhaps the earliest attempt at distinguishing the archaeological epochs of Southern Siberia was made in the nineteenth century by the German-Russian scholar Friedrich Wilhelm Radloff (Vasily Vasilievich Radlov). Radloff's chronology was the result of his seven years of excavating kurgans and archaeological monuments, and did not differentiate between the various stages of the Bronze Age (Gryaznov 1969). Radloff's rudimentary chronology was followed by the twelve-period chronology of Sergei Aleksandrovich Teploukhov (1927) which covers the Eneolithic through Mongol period (see Gryaznov 1969; Klejn 2017; Poliakov & Lazaretov 2020). Although Teploukhov would later be arrested and would not survive his imprisonment, his chronology is still used (with some modification) to this day (Klejn 2017; see Poliakov & Lazaretov 2020). Gryaznov applied Teploukhov's periodization to the whole of the Eastern Eurasian Steppe (Klejn 2017; Poliakov & Lazaretov 2020).

Although conceived through the lens of linear cultural evolution, with each period corresponding to stages of social development, Teploukhov's (1927) chronology is still applicable and useful even when such concepts have been discarded (as demonstrated by Poliakov & Lazaretov 2020). This framework has been available since the mid-twentieth century, though it has not always been applied with consistency. Scholars have contextualized the same prehistoric archaeological cultures within different archaeological periods, often without defining what is

meant by either. The Afansievo for example have been referred to as both an Eneolithic (Gryaznov 1969; Hermes et al. 2020b; Rogers et al. 2020; Syvatko et al. 2009; Vasil'ev & Seminov 1993) and Bronze Age (Jeong et al. 2020; Jia et al. 2010; Zaitseva & van Geel 2004) archaeological culture (see also Honeychurch et al. 2021). The Okunevo have also been described as being a Bronze Age culture (Blyakharchuk & Chernova 2013; Hollard et al. 2018; Jia et al. 2010; Lazeretov 2019; Outram et al. 2018; Syvatko et al. 2009; Vasil'ev & Seminov 1993; Wang et al. 2023; Yu et al. 2020; Zaitseva & van Geel 2004; Zotkina et al. 2023) as well a culture that predated the Bronze Age and continued into it (Gryaznov 1969; Jacobsen-Tepfer 2015; Semenov 1997; Zeng et al. 2023). This is partially a result of revised radiocarbon dating but not entirely, as can be seen by the number of publications from after 2009 and even 2021 (the relevance of this is explained below; see Tbl.21).

Poor stratigraphic contextualization of human skeletons, archaeological objects, and faunal remains can often be resolved with direct radiocarbon dating (see Chapter 03). Unfortunately widespread skepticism, apprehension regarding calibration, and a lack of facilities of suitable quality during the Soviet era delayed the adoption of radiocarbon dating in Russia (Anthony 2001; Christian 2011; Poliakov & Lazaretov 2020). An early example of radiocarbon dating by Soviet archaeologists in Southern Siberian contexts is the dating of wooden beams from Altai kurgan burials that took place from 1956 - 1961 (Butomo 1965; Syvatko et al. 2009), less than a decade after the incorporation of radiocarbon dating into Western archaeological practice (Arnold & Libby 1949). Many of the subsequent radiocarbon studies of Southern Siberian archaeological materials have been similarly derived from wood and charcoal samples (e.g. Alekseev et al. 2001; Dolukhanov et al. 1970; Görsdorf et al. 2001; Semenstsov et al. 1998; Semyontsov et al. 1972; see Syvatko et al. 2009). These dates are not reliable, due to the application of LSC instead of AMS methods and the old wood effect (Poliakov & Lazaretov 2020; Poliakov et al. 2019; Svyatko et al. 2009; see also Chapter 03).

New AMS radiocarbon dates derived from human and animal bone have been published by Russian (e.g. Poliakov & Lazaretov 2020; Poliakov & Svyatko 2021; Syvatko et al. 2009; see also Poliakov et al. 2019) and American (e.g. Hermes et al. 2020b, 2021) scholars, which is a very positive step forward for Southern Siberian archaeology. Russian scholars have expended great effort to consistently produce AMS radiocarbon dates and clarify the chronology of the Minusinsk Basin in particular (e.g. Poliakov & Lazaretov 2020; Poliakov & Svyatko 2021; Syvatko et al. 2009). American scholars have focused instead on the Altai region (e.g. Hermes et al. 2020b, 2021). There is still much chronological clarification needed (see Poliakov & Lazaretov 2020; Poliakov & Svyatko 2021; Sokolova 2012), as will be addressed below for each archaeological settlement site and associated faunal assemblage.

Tbl.21 Table of Bronze Age Minusinsk Basin chronologies (Syvatko et al. 2009; Poliakov & Svyatko 2021).

Culture	Period	Traditional Dates	Radiocarbon dates (pre-2009)	Radiocarbon Dates (2009)	Radiocarbon Dates (2021)
Afanasievo	Eneolithic	ca. 2500–2000 BCE	ca. 3700–2500 BCE	ca. 2900–2500 BCE	ca. 3000–2500 BCE
Okunevo	Early Bronze Age	ca. 1900–1600 BCE	ca. 2500–1900 BCE	ca. 2500–1900 BCE	ca. 2600–1700 BCE
Andronovo	Middle Bronze Age	ca. 1600–1300 BCE	ca. 1900–1500 BCE	ca. 1900–1500 BCE	ca. 1700–1500 BCE
Karasuk	Late Bronze Age	ca. 1300–800 BCE	ca. 1500–900 BCE	ca. 1500–900 BCE	ca. 1500–900 BCE

**All radiocarbon dates are calibrated.*

10.3. The Archaeological Cultures of Southern Siberia

“Here for many centuries wandering tribes of hunters and fishermen lived in the forests side by side with the stock-farming tribes who pursued a sedentary, and later a nomadic, way of life on the steppes.” (Gryzanov 1969)

Many prehistoric human populations have inhabited Southern Siberia and have left traces of their presence throughout time in the archaeological record of the Bronze Age. These archaeological cultures have been grouped by archaeologists and historians into the Eneolithic / Early Bronze Age Afanasievo, Okunevo, Karakol, and Yelunino, the Middle Bronze Age Andronovo, and the Late Bronze Age Karasuk. The definitions and delineations of both the cultural descriptors and the archaeological epochs used in academic literature quickly break down under scrutiny and are used here for continuity, coherence, and convenience. Chronological groupings are very useful but not without limits (see Tishkin 2016), and the division of cultural periods based upon the known utilization of different metal alloys leaves much to be desired in discussions of human-animal relationships. I have chosen to structure my review around such a chronological model in order to facilitate the theme and flow of my discussion, and do not present my delineations as solid facts. The approximate timeframe of each period will be defined as they are introduced, beginning with the Eneolithic period below. Associated archaeological cultures, settlement sites, faunal assemblages, and inferences regarding animal economies will also be detailed.

10.3.1. Eneolithic & Early Bronze Age Cultures of Southern Siberia (ca. 3000–2500 BCE)

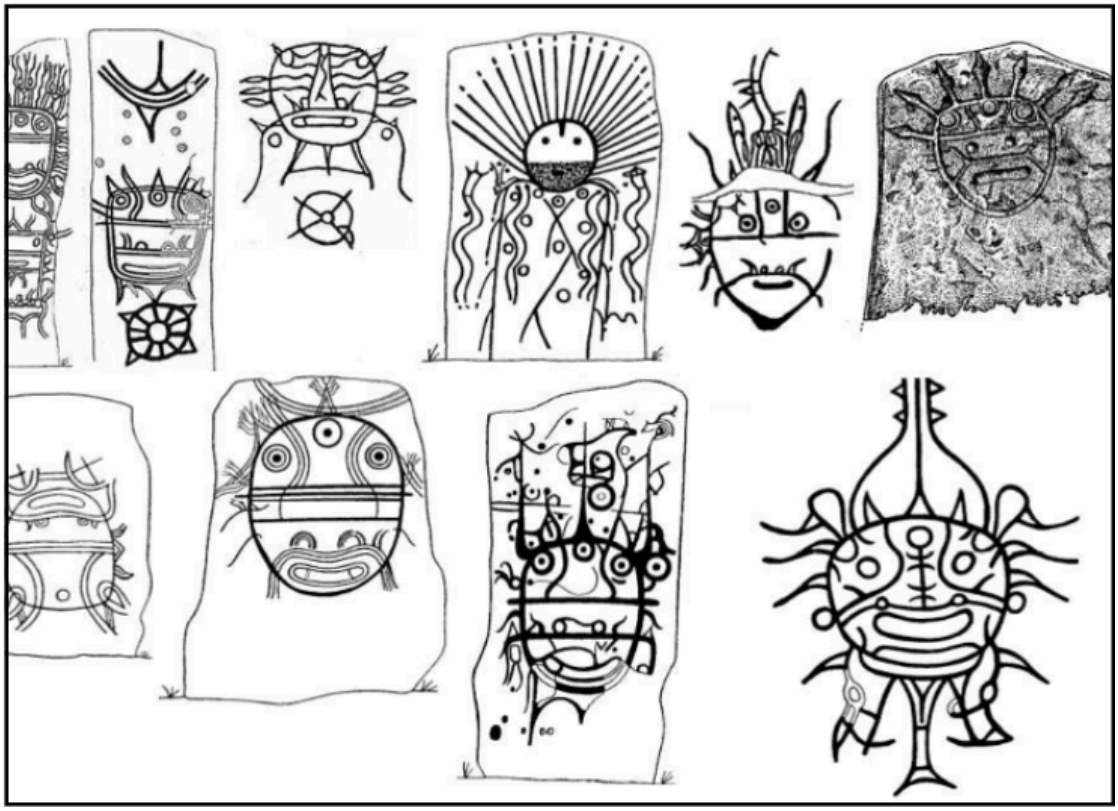
“In conclusion, it should be stressed again that any model or design are quite conventional analogues of a real process. Their choice is determined by the knowledge and desire of a researcher, as well by the tasks of his work.” (Tishkin 2016)

The Eneolithic & Early Bronze Age period of Southern Siberia, for the purposes of this dissertation, is roughly concurrent with ca. 3000 - 2500 BCE (Poliakov & Svyatko 2021). The Eneolithic here is characterized by the initial emergence of agriculture and animal husbandry, as well as the continued use and refinement of stone tools (Bobrov 1988; Gryaznov 1969). The transition from the Eneolithic to the Early Bronze Age is poorly understood and I have chosen to incorporate what many scholars would deem the Early Bronze Age into my presentation and discussion of the Eneolithic, for reasons elaborated further into this discussion. What we know of Eneolithic and Early Bronze Age art from Southern Siberia consists mostly of stone monoliths and slabs carved with masks, beasts, birds, human anatomy, and celestial symbols flowing into one another (Gryaznov 1969; Jacobsen-Tepfer 2015; Sokolova 2012), forming evocative rock imagery reminiscent of mythical chimeras from a prehistoric dream (Fig.5).

The predominant cosmological motif inferred from this period has been deemed the “Animal Mother” and has been interpreted to represent both a female liminal guardian and the source of all creation, wielding the powers of life and death in natural balance (Jacobsen-Tepfer 2015). The gradual reduction of the Eneolithic “Animal Mother” to the “Mother of Animals” and finally “the Guardian of the Road to the Land of the Dead” as well her eventual overshadowing by the

“Male Hero Hunter” as perceived in Late Bronze Age Southern Siberian art (Jacobsen-Tepfer 2015) may coincide with changes in prehistoric animal economies, hunting versus herding reliance, and ritual animal use. This is an intriguing idea, but both the quality and quantity of faunal data from the region must be significantly improved and securely dated before any robust investigation can be undertaken.

Fig.5 Illustrations of Late Bronze Age Southern Siberian rock art (Jacobson-Tepfer 2015).



Two archaeological cultures have been associated with the Eneolithic and Early Bronze Age of the Minusinsk Basin in Southern Siberia- the Afanasievo and the Okunevo. The Afanasievo were believed to be Eneolithic pastoralist-metallurgists who migrated from the Western Steppe, while the Okunevo were assumed to be an autochthonic population of Early Bronze Age (or earlier) hunter-fishers (Gryaznov 1969; Jacobsen-Tepfer 2015; Semenov 1997; Syvatko et al. 2013) who later reared livestock and practiced copper and bronze metallurgy (Frachetti 2012), possibly as a result of contact with the Afansievo or Western Steppe pastoralists (Gryaznov 1969; Maksimenkov 1975; Outram et al. 2018).

AMS radiocarbon dating has established a century-long chronological overlap of Afanasievo and Okunevo populations in the Minusinsk Basin (Poliakov & Svyatko 2021). This overlap involved an early material culture intersection (Blyakharchuk & Chernova 2013; Poliakov & Lazaretov 2020; Zaika 2021) which included the depiction (and possibly cosmological contextualization) of animals (Esin 2010; Jacobsen-Tepfer 2015). The suggestion that early Okunevo populations adapted animal husbandry from the Afansievo (Gryaznov 1969;

Maksimenkov 1975; Outram et al. 2018) has also strongly influenced my combination of the Eneolithic and Early Bronze Age in this dissertation.

Scholars have classically differentiated the two archaeological cultures based upon craniometry (Alekseev 1961c; Kozintsev 2009), with Afansievo being designated “Europoid” and the Okunevo “Mongoloid” (Blyakharchuk & Chernova 2013; Gryaznov 1969), as well as material culture such as ceramics (Gryaznov 1969; Jacobsen-Tepfer 2015; Jia 2010; Semenov 1997; Sokolova 2012; Stepanova 2017), metal objects (Gryaznov 1969), and rock art (Gryaznov 1969; Jacobsen-Tepfer 2015; Sokolova 2012). Round-bottomed ceramic jars made from low / moderate ductile clays and grog have been associated with the Afansievo and flat-bottomed jars made from high ductile clay and grit with the Okunevo (Gryaznov 1969; Jacobsen-Tepfer 2015; Jia 2010; Stepanova 2017).

The aforementioned carved stone monoliths and slabs have been generally attributed to the Okunevo, as have walking wolf-men and figures in long headdresses, while imagery of thin cattle and long-haired women have been associated with the Afansievo (Jacobsen-Tepfer 2015). Afanasievo and Okunevo-assigned material culture has proven to be more fluid than initially presented in the archaeological literature. Mixed ceramic, metallurgic, and artistic “types" have been recorded from archaeological sites (in non-intrusive contexts) such as Tas Khazaa (Lipsky 1957), Razliv X (Pshentitsya & Pyatkin 2006), Uibat III and V (Lazartov 1997), and Verkh-Askiz (Khavrin 1997) (see Jacobsen-Tepfer 2015 for an in-depth discussion of the mixed material culture types and related issues, including the mixing of artistic animal depictions).

Genetic and genomic studies do however support a clear separation between individuals associated with Okunevo versus Afanasievo contexts (Hollard et al. 2018; Jeong et al. 2018, 2019; Wang et al. 2023), as well as genetic relationship between Okunevo and indigenous American populations that is not shared with Afansievo-associated individuals (Kim et al. 2018; Wang et al 2023; Yu et al. 2020; see also Kozinstev 2020). Such associations have also been previously suggested by craniometric studies (Alekseev 1961c; Kozintsev 2009, 2020; Kozinstev et al. 1999).

What exactly Afanasievo or Okunevo means is difficult to define, and scholars rarely attempt to do so when writing about them (see Taylor 2021; Tishkin et al. 2021). Understanding the intersection (and separation) of genetic relatedness and the transmission (and fluidity) of subsistence strategies, food production technology, cosmological belief, ritual culture, artistic stylization, and lifeways in general is an equally challenging endeavor. It is through the examination of animal domestication, depiction, ritual use, hunting and herding strategies, and secondary product manufacture that the ancient human-animal relationships of different prehistoric communities can be compared and contrasted throughout different regions and time periods. I will now outline the “cultural complexes” that have been attributed to both Afansievo and Okunevo archaeological populations below, alongside the less well-known Karakol and Yelunino of the Altai Mountain region.

The Afanasievo (Афанасьевская культура) (ca. 3000 - 2500 BCE)

Teploukhov excavated three ancient burial sites at Mount Afanasieva (Afanasieva Gora) in the early twentieth-century and subsequently attributed them to a newly-found *Afanasievo* culture (Gryaznov 1969). The term Afanasievo is used to this day to refer to a distinctive Eneolithic complex of material culture, human-animal relationships, and mortuary practices concentrated in the Altai Mountains and Minusinsk Basin (Grushin & Stepanova 2010; Khavrin 2010; Kilunovskaya & Semenov 2019; Kirginekov 2010; Linduff 2015; Poliakov et al. 2019; Poliakov & Lazaretov 2020; Semenov 1975; Stepanova 2010;; Vadetskaya et al. 2014). Afanasievo-associated burial sites also extend into the Khangai Mountains and adjacent regions of Central Mongolia (Alekhin et al. 1995; Gryaznov et al. 1979; Hermes et al. 2021; Honeychurch et al. 2021; Krasnienko 2010; Seferiades 2004; Shulga 2012; Vadetskaya et al. 2014; Volkov 1995).

Stark differences perceived in the archaeological materials of different regional Afanasievo assemblages (see for example Stepanova 2010, and more tangentially Poliakov & Lazaretov 2020) have led Russian archaeologists to question whether the overarching term Afansievo should be retired and replaced with separate archaeological culture terms, such as “Saldyar” in the Altai Mountain region (Surazakov & Tishkin 2007; Tishkin 2018; Tishkin & Seregin 2012; Tishkin et al. 2021). Western archaeologists have in turn called for clarity and transparency when using the term Afanasievo in future reporting (Taylor 2021).

Modern population genomic studies have not investigated whether or not a major divergence exists between Altai and Minusinsk Afanasievo-associated individuals and seemingly assume a Yamnaya ancestry for both (e.g. Allentoft et al. 2015; Mathieson et al. 2015; Jeong et al. 2020; Narasimhan et al. 2019; Wang et al. 2021). Notably, Russian archaeological literature concluded a Yamanaya ancestry for Afanasievo individuals long before it was confirmed by molecular anthropology (e.g. Gryaznov 1969; Alekseev 1961b; Alekseev & Gokham 1984). One genetic study does support a close relation and common ancestry for both Altai and Minusinsk Afanasievo individuals (Keyser et al. 2009), though it utilizes only mitochondrial DNA.

The Afanasievo archaeological cultural “package” of rounded pottery, copper metallurgy, mobile pastoralism, and burial mounds is believed to have disseminated through Southern Siberia (Bobrov 1988; Poliakov & Lazaretov 2020; Vasil'ev & Seminov 1993) and possibly into pockets of Inner Asia such as Mongolia (see Honeychurch et al. 2021; Semenov 1997; Taylor et al. 2019; Volkov 1995) and Xinjiang in Northwest China (Han 1998; Kovalev 2017; Mallory 1989, 1998; see Anthony 2001 and Hemphill & Mallory 2004). Perhaps most relevant to this dissertation is the long-held conclusion that Afansievo-associated peoples introduced domesticated animals and pastoralist lifeways into Inner Asia (Gryaznov 1969; Hermes et al. 2020b, 2021; Honeychurch et al. 2021; Maksimenkov 1975; Outram et al. 2018; Poliakov & Lazaretov 2020; see also Chapters 01, 09). I will review Afansievo settlement sites and animal economies in the upcoming chapters of this dissertation.

The Okunevo (Окуневская культура) (ca. 2600 - 1700 BCE)

The cultural descriptor “Okunevo” was derived from the Okunev *ulus* (camps) in Khakassia where Tephoukhov (1928) first excavated Okunevo-associated burials. Okunevo burials were initially attributed to an early phase of the Andronovo (a deeply problematic cultural term explored at length further into this chapter) (Komarova 1947), then to a late phase of the Afansievo (Kyzlasov 1971), and eventually recognized as a distinct archaeological culture (Maksimenov 1965, 1975) (see Bobrov 1988; Gryaznov 1969; Gryzanov & Vadetskaya 1969; Outram et al. 2018; Semenov 1997). While it was the intrusion of Okunevo tombs into Afansievo burials that initially contributed to this confusion (Gryaznov 1969; Maksimenov 1975; Sokolova 2012), some Russian studies continued to assert a Western Steppe origin for the Okunevo (e.g. Gromov 1997; Lazaretov 1997; Lazaretov et al. 2012; Slavnin & Sherstova 1999; see Kozintsev 2020, 2023). Other Russian craniometric studies have long pointed towards a Neolithic Siberian forest steppe ancestry for the Okunevo (e.g. Bokobvenko 1996; Chebotaev 1992; Chikisheva 2012; Dremov 1980; Kozintsev 2009; see again Kozintsev 2020) and their findings have now been confirmed by modern genomic and genetic studies (e.g. Allentoft et al. 2015; Hollard et al. 2018; Kim et al. 2018; see Kozintsev 2020, 2023). Some genetic admixture between Afansievo and Okunevo archaeological populations is certainly possible, but it is clear that the Okunevo did not descend from the Afansievo or any other Western Steppe peoples.

Russian archaeologists have also used AMS radiocarbon dating to subdivide Minusinsk Okunevo chronological contexts into three phases (Poliakov & Lazaretov 2020; Poliakov & Svyatko 2021) (Tbl.22). Though concentrated in the Minusinsk Basin, Okunevo-associated tombs have also been discovered in Tuva (Gokhman 1980; Gryaznov 1969; Lazaretov & Poliakov 2018; Outram et al. 2018; Semenov 1997, 2018; Sokolova 2012; Stambulnik & Chugunov 2006; Zhogova et al. 2023). These findings are sometimes grouped under a regional Okunevo-like variant deemed “Chaa-Khol” (e.g. Kozinstev 2020, 2023). I am including the “Chaa-Khol” Tuva variant in my examination of Okunevo settlement sites and animal economies due to the scarcity of available data and the general consensus of their shared material culture. It should be noted however that divergence has been noted in the cranial morphology of “Chaa-Khol” individuals as compared to the Okunevo, leading to speculation that they are descended from Western Steppe populations or even the Afanasievo (Kozinstev 2009, 2023).

Tbl.22 Table of Minusinsk Basin Okunevo radiocarbon dates (Poliakov & Lazaretov 2020).

Phase	No. of Radiocarbon Dates	Radiocarbon Dating Results (2020)
Uibat	14	ca. 2600 - 2300 BC
Chernovaya	29	ca. 2200 - 2000 BC
Razliv	02	ca. 1900 - 1700 BC

**All radiocarbon dates are calibrated.*

Some researchers also consider the “Karakol” archaeological culture to have been an Altai variant of the Okunevo (e.g. Jacobsen-Tepfer 2015), and recent mitochondrial aDNA analysis (Gubina et al. 2016) has suggested that individuals associated with the two archaeological cultures shared a haplogoup (Eastern Eurasian haplogroup D). A common origin for Okunevo

and the Karakol-associated individuals has yet to be demonstrated and they are more often viewed as related but distinct archaeological cultural phenomena (Outram et al. 2018; Pilipenko et al. 2016). This is inline with the earliest interpretations of the archaeological data (i.e. material culture and cranial morphology) (e.g. Kubarev 1988; see also Gublina et al. 2016; Pilipenko et al. 2016). Accordingly, I will explore the Karakol cultural complex separately from the Okunevo below.

The Karakol (Каракольская культура)

The Eneolithic and Early Bronze Age archaeological cultures that I have discussed so far have been largely concentrated in the Minusinsk Basin. Remains of the Karakol archaeological culture have alternatively been contained to the Altai Mountains, unless one considers them to be a regional variant of the Okunevo (see section “III.III.I.II.” above). As is standard for Eneolithic and Bronze Age contexts, evidence of the Karakol archaeological culture is mostly limited to rock art (see Jacobsen-Tepfer 2015; Pakhunov et al. 2017) and burial features (see Gubina et al. 2016; Kubarev 1988, 2009, 2013; Kubarev et al. 1992; Molodin 1997, 2006). There is less available information regarding Karakol archaeological contexts and excavations compared to those associated with the Afansievo and Okunevo. There also do not appear to be any AMS radiocarbon dates associated with Karakol contexts.

Karakol stone slab art is fantastically anthropomorphic (Jacobsen-Tepfer 2015; Pakhunov et al. 2017) and very reminiscent of Okunevo rock art, with a unique expression of animalistic “spirit figures” with horns, feathered headdresses, winged and clawed appendages, and avian bodies (Jacobsen-Tepfer 2015). Karakol tombs such as at Ozernoye and Karakol (from which the cultural descriptor is derived) were often constructed from stone slabs featuring striking petroglyphs (Pakhunov et al. 2017) and the divergence from typical Karkol stylization exhibited at the burial site of Bertek-56 in the Ukok Plateau has weakened its Karakol attribution (see Pilipenko et al. 2016). A mitochondrial DNA sample derived from a Bertek-56 individual was included in Gubina et al. (2016) and considered to be Karakol-associated. Molodin (2006) reported a total absence of Krakol settlement sites. Little is known about Karakol human-animal relationships or animal economies.

The Yelunino (Елунинская культура) (ca. 2016-1775 BCE)

The Yelunino (or Elunino) were an archaeological culture concentrated in the Altai Mountain region (especially Rudny Altai) of Central Asia as well as the forest-steppe region (Upper Ob) of Western and Southern Siberia (Kiryushin & Solodovnikov 2010; Kozinstev 2008; Solodovnikov 2006; Solodovnikov & Tur 2003). Craniometric studies have linked Yelunino individuals to the “Chaa Kol” Okunevo (and both with certain Scythian populations which formed after them) as well as Western European populations (Kozinstev 2008). Ceramic studies on the other hand have attributed Yelunino material culture origins to Eastern Kazakhstan and Dzungaria (Kovalev et al. 2008; see Kiryushin & Solodovnikov 2010). The Yelunino have been speculated to have formed complexes around the Altai tin deposits which facilitated local expressions of bronze metallurgy (Novozhenov 2022), and to have been driven away from them by the arrival

Andronovo communities in spoke-wheeled chariots (Chikisheva 2010). Yelunino settlement sites seem to cluster in the Altai Krai of Western Siberia (e.g. Berezovaya Luka, Kolvyan-I, Kolyvanskoe-I, and Pavlovka-I) and Eastern Kazakhstan (e.g. Shauke 8b). No details are available regarding the Yelunino use of animals.

10.3.2. Middle Bronze Age Cultures of Southern Siberia (ca. 1700–1500 BCE)

"The change to a pastoral and agricultural economy required some redistribution of land between different clans (kinship groups) and tribes…The final result was that the immense area of steppe land stretching from the Urals to the Yenisey and from the deserts of Central Asia to the Siberian taiga was settled by tribes sharing a related culture which was uniform over extensive stretches of territory." (Gryzanov 1969)

The Middle Bronze Age is here defined as spanning ca. 1700 - 1500 BCE (Poliakov & Svyatko 2021) and is supposedly characterized by an economic shift to *productive* agriculture and animal husbandry (Gryaznov 1969; Jettmar 1950). This shift has been speculated to coincide with both the holding of feasts which involved the ceremonial slaughter of domesticated animals as well as the increased incorporation of dairy and vegetable products into the common diet (Gryaznov 1969), although much of the archaeological evidence pulled into this argument originates in the Bronze Age burials of Kazakhstan. Evidence for the Middle Bronze Age intensification of animal husbandry in Southern Siberia is also limited to conjecture based upon ceramic abundance and diversity observed in burial contexts (Gryaznov 1969) as opposed to the recovery and comparative study of any actual domesticated animal remains.

A decreased reliance on hunting has also been extrapolated from a low recovery of arrowheads associated with his period (Jettmar 1950). Unfortunately there are no artistic motifs, depictions, or stylizations of animals associated with the Middle Bronze Age in Southern Siberia (Jacobson-Teffer 2015) to help elucidate the matter. Stable isotopic studies do support a shift from a C3-plant based (i.e., non-millet) diet during the Middle Bronze Age to a more varied and millet-inclusive diet by the Late Bronze Age, alongside a continued reliance on freshwater fish (Svyatko et al. 2013). Only one archaeological culture is associated with the Middle Bronze Age in Southern Siberia, although the singular term "culture" here is hardly appropriate. I will explore this issue at length below in my discussion of the Andronovo (Fyodorovka).

<u>The Andronovo (Federova) (Андроновская культура [Федоровка]) (1700 - 1500 BCE)</u>

Of all of the cultural descriptors applied to Southern Siberian archaeological populations, "Andronovo" is easily the most convoluted, paradoxical, and problematic. Andronovo does not even refer to a single archaeological culture but a conglomerate of them which spanned the Southern Ural Mountains of Western Siberia and Kazakhstan, the Yensei River Valley of Southern Siberia, Xinjiang in Northwestern China, and Tajikistan and Uzbekistan in Central Asia (Grigoriev 2021). The earliest reports of an Andronovo-type culture refer to burials excavated in the Southern Transurals and date as far back as the later mid-nineteenth century (e.g. Zyryanov 1863), though they were not initially attributed to a culture called "Andronovo".

Decades later the excavation of a cemetery near the village of Andronovo in Southern Siberia led Teploukhov (1927) to propose the existence of an Andronovo culture, much as he did for the Afanasievo burials he excavated in Mount Afanasieva, and he connected the two archaeological cultures based upon ceramic typology (Grigoriev 2021). The very same year, Gryaznov published the results of his excavation of a series of burials in Western Kazakhstan (Gryaznov 1927). Again based upon ceramic typology, Gryaznov (1927) associated the burials with a western expression of the Andronovo culture described by Teploukhov (1927) and noted an affinity with the Srubnaya culture of the Western Steppe (Gryaznov 1927; see Grigoriev 2021). The culmination of their scholarship was the belief in a widespread Andronovo culture that could be subdivided into an eastern “Fyodorovka” variant similar to the Afanasievo and a western “Alakul” variant similar to the Srubnaya (Grigoriev 2021).

Shortly thereafter, Krivtsova-Grakova (1933) misattributed a two-period ceramic assemblage from the site of Alexeevskoe in Northern Kazakstan to a single Bronze Age Andronovo context (Grigoriev 2021). Krivtsova-Grakova (1933) concluded that the eastern “Fyodorovka” variant originated in the west before expanding east and that the later ceramics of the western “Alakul” variant exhibited cordoned wear. Building off of her schematic Salnikov (1948, 1951) developed a linear model of Andronovo material cultural evolution, where the “Fyodorovka” phase preceded the “Alakul” phase, to contextualize his excavations in the Southern Transurals (Grigoriev 2021).

This linear model was widely adapted by archaeologists working in Central Asia and they took the liberty of modifying and expanding the names and stages to fit their local contexts, leading to the emergence of a number of regional Andronovo periodization and material culture models (e.g. Chernikov 1960; Evdokimov & Varfolomeev 2002; Margulan et al. 1966; Potemkina 1985; Zdanovich 1988; see Grigoriev 2021). Unfortunately this was further complicated by the eventual rejection and modification of Salnikov’s (1948, 1951) model by the archaeological community (beginning with Stokolos 1972) alongside the discovery of the Bronze Age Petrovka culture in Kazakhstan (Grigoriev 2021). The assumed relationship between the “Fyodorovka” and the “Alakul” fell apart, yet the two cultures are still solidified under the entangled term “Andronovo”.

In the context of Southern Siberian prehistory, only the “Fyodorovka” archaeological culture has been identified, and reliable AMS radiocarbon dates have been provided by Poliakov & Svyatko (2021). However, the Southern Siberian (Yensei) expression of “Fyodorovka” clashes with the “Fyodorovka” of the Transurals in funerary archaeology, being indicative of “Alakul” burial style– although no “Alakul” presence has been identified in the region (Grigoriev 2021). This has led to the continued use of the problematic term “Andronovo” in Southern Siberian archaeology, though often with “Fedorov”, or “Fedorova” in parenthesis. Material culture and human remains attributed to Andronovo (Fedorova) populations in Southern Siberia appear to be limited to the Minusinsk Basin (Gryaznov 1969; Poliakov & Lazaretov 2020; Vasil'ev & Seminov 1993). The origins of this culture are still entirely unclear (Grigoriev 2021), and only one settlement has been associated with them in the context of Southern Siberia.

10.3.3. Late Bronze Age Cultures of Southern Siberia (ca. 1500–900 BCE)

“About the 13th century B.C. the Andronovo culture seems to have been superseded throughout its whole area of diffusion by a new culture which is known as the Karasuk culture.” (Gryzanov 1969)

The Late Bronze Age unfolded from ca. 1500 to ca. 900 BC, again in accordance with the chronology provided by Poliakov & Svyatko (2021). Gryzanov (1969) proposed that this period reflected another economic transition, this time from the sedentary agropastoralism he attributed to the Middle Bronze Age to semi-nomadic and transhumant pastoralism (see Chapter 09). Although Gryzanov based his speculation upon what he admitted was indirect archaeological evidence (Gryzanov 1969), an emphasis on mobility and pastoralism is clearly reflected in the rock art of this period (Jacobson-Teffer 2015). The earliest Late Bronze Age rock art of Southern Siberia featured a dramatic shift from fantastic depictions of anthropomorphic spirits, surreal masks, and (often birthing) women to simple and realistic portrayals of humans engaged in combat, hunting wild animals (e.g. ibex), and herding domesticated animals alongside yaks loaded with cargo and wheeled vehicles pulled by draught animals (Jacobson-Teffer 2015).

Towards its end, the Late Bronze Age also coincided with a pronounced transition in the artistic depiction of cervids. The majestic and lively elk/moose and deer of earlier rock art were denatured and exaggerated into wolf-like, intertwining cervids of symbolic power (Jacobson-Teffer 2015). These bizarre, lifeless, and emblematic cervids were even intentionally, and seemingly aggressively, transposed over the cervids of earlier Bronze Age rock art (Jacobson-Teffer 2015). While this transformation was most dramatic in the depiction of stags, animals such as argali and ibex also assumed liminal, bird-like, and ornamental stylizations at the expense of their natural vitality (Jacobson-Teffer 2015). Notably, this Altai-Sayan artistic phenomena is concentrated in the rock art of prehistoric Tuva and Mongolia and has been associated with a new-found sense of power (and status) that could have come with mounting and riding horses for the first time (Jacobson-Teffer 2015).

Mobility was clearly limited however as a new reliance on cereal cultivation is supported by finds of bronze sickles in Late Bronze Age contexts (Jettmar 1950) as well as their absence in Middle Bronze Age contexts (Syvatko et al. 2021). The initial emergence of millet consumption during this period in Southern Siberia has also been repeatedly demonstrated in stable isotopic studies (e.g. Syvatko et al. 2007, 2013, 2021) and more indirectly by dental pathological studies (e.g. Syvatko 2014). This seems at odds with both Russian (e.g. Gryzanov’s 1969) and Western (e.g. Jettmar 1950, 1970; Legrand 2006) assertions that agriculture in prehistoric Southern Siberia reached its peak in the Middle Bronze Age before declining in favor of metallurgy and cattle husbandry with the advent of the Late Bronze Age. It is certainly at odds with the idea that the Late Bronze Age in Southern Siberia coincided with the attainment of “the full mobility of the nomadic way of life” (Jettmar 1970).

It should also be noted that older Russian narratives which attributed millet consumption to Middle Bronze Age “Andronovo” peoples in Southern Siberia (e.g. Slavnin & Sherstova 1999) continue to be circulated in modern literature (e.g. Blyakharchuk & Chernova 2013), even after the publication of multiple isotopic and archaeological studies which refute this (e.g. Jettmar

1950; Syvatko et al. 2007, 2013). The overwhelming body of evidence suggests that millet cultivation was initially practiced in Southern Siberia by the “Karasuk” peoples, and not the Andronovo (Fyodorovka) populations which preceded them. I will explore the Late Bronze Age Karasuk archaeological culture complex and their subsistence strategies, with an emphasis on their Southern Siberian context, below.

The Karasuk (Карасукская культура) (ca. 1500 - 900 BCE)

Similar to the cultural descriptor “Andronovo”, “Karasuk” is more appropriately attributed to a widespread group of North and Central Asian archaeological cultures (Poliakov & Lazeratov 2020). Teploukhov (1926) first applied the term “Karasuk” to the archaeological remains and materials recovered from the burials he excavated alongside the Karasuk River in the Minusinsk Basin (Teploukhov 1927, 1929). Evidence of Karasuk and Karasuk-like cultures were subsequently identified in the Altai and Tien Shan mountain regions of Siberia, Mongolia, and Central Kazakhstan (see Gyzanov 1969; Jacobson-Tepfer 2015; Jettmar 1950). Originally grouped into a single autochthonic archaeological culture that evolved from the Andronovo (Fyodorovka) complex (e.g. Teploukhov 1927, 1929; later by Gryzanov 1966; 1969), then alternatively from an external culture (e.g. Členova 1961, 1962, 1963; Khlobystina 1970; Kiselev 1951; see also Glaesser 1973; Jettmar 1950, 1970), the continued examination and AMS radiocarbon dating of Late Bronze Age finds has suggested that not one but multiple cultures are represented within the Karasuk complex (Poliakov & Lazeratov 2020). Within Southern Siberia, Late Bronze Age material culture has now been associated with four distinct chronological phases (Tbl.23).

Tbl.23 Table of Karasuk chronologies (Poliakov & Lazeratov 2020).

Teploukhov (1920’s)	Gryzanov (1970’s)	Poliakov & Lazeratov (2020)
Karasuk Phase	Karasuk, Classical Phase	Late Bronze Age Phase I
		Late Bronze Age Phase II
	Karasuk, Kamenniy Log Phase	Late Bronze Age Phase III
		Late Bronze Age Phase IV

The first phase is unique to the Minusinsk Basin and possibly the result of population migrations from Kazakhstan after the fading out of Andronovo (Fyodorovka) populations (Poliakov & Lazeratov 2020). The second phase is associated with internal innovation as well as cultural exchange with the populations of Northern China (Poliakov & Lazeratov 2020; Svyatko et al. 2021a). This third phase is also believed to be unique to the Minusinsk Basin and to have coincided with population admixture, continued contact with Chinese groups, and more pronounced change in the southern region as compared to the northern region (Poliakov & Lazeratov 2020). The fourth and final phase may have overlapped with developing Scythian cultures, though this is currently unclear (Poliakov & Lazeratov 2020).

Intensified “Karasuk” contact with Chinese communities is supported by the aforementioned isotopic and archaeological evidence of the introduction of millet cultivation and consumption

during the Late Bronze Age (Jettmar 1950; Svyatko 2014; Svyatko et al. 2007, 2013, 2021), as well as the inclusion of Karasuk-style bronze blades in Chinese graves (Taylor 2024). This evidence does not support notions that Karasuk populations began descaling agricultural practices (in comparison to the Middle Bronze Age) in favor of mobile or semi-mobile pastoralist intensification (Bokovenko 2006; Gryzanov's 1969; Jettmar 1950, 1970; Legrand 2006). In an effort to clarify at least whether or not there is evidence of domesticated animal management intensification, I will attempt to examine Karasuk-attributed settlement sites and associated faunal data in Chapter 13.

10.4. Bronze Age Southern Siberia (ca. 3000–900 BCE): Conclusion

"The reality of…culture is…complex…rigorously monogenetic interpretation is at odds with this reality…" (Glaesser 1973)

The ethnic units used to describe the Bronze Age cultures of Southern Siberian are largely a product of craniometry and material culture typology. Some of their conclusions have since been verified by biomolecular analysis, but they are also subjective and have led to a number of issues, including the perpetuation of misleading and vague cultural descriptors such as the paradoxical "Andronovo" ethnic unit. The long-standing emphasis on developing descriptive typological models for material culture, especially tools, and the reconstruction of modes of socioeconomic organization within a fixed paradigm has come at the expense of recording of faunal data. Thus, many gaps remain within the faunal records. Chronological contextualization has recently been refined with the direct AMS radiocarbon dating of human and animal bones, leading to valuable new insights into Bronze Age archaeological cultures of Southern Siberia. In the next chapter, I will overview the archaeological cultures and data of Bronze Age Outer Mongolia.

11. Bronze Age Outer Mongolia (ca. 3170–910 BCE)

11.1. Introduction

“Mongolia has seen an explosion of high-quality archaeological research and publication during the first decades of this century.” (Wright 2021)

The archaeology of the Bronze Age in Outer Mongolia is not nearly as well-formed as in the neighboring countries of Russia, Kazakhstan, or China (Kovalev & Erdenebaatar 2009), though recent innovation and research has begun to change this (Wright 2021). In this chapter I will overview the development of chronological period models for prehistoric Outer Mongolia to preface my discussion of the Afanasievo, Chemurchek, Munkhkhairkhan, Ulaanzuukh, Sagsai, Khirigsuur, Deer Stone, and Baitag archaeological cultures. For the purposes of this dissertation, Outer Mongolia broadly encompasses the territory of modern day Mongolia (Fig.6). Though prehistoric Tuvan archaeology is integral to the archaeology of this region, I will not revisit the topic in this chapter (see instead Chapter 10). I have also excluded Inner Mongolia as the prehistoric archaeology of this region appears to be independent and to reflect an extension of Chinese Neolithic archaeological culture. I will review this briefly, along with the history and development of prehistoric settlement site archaeology and faunal analysis in Mongolia.

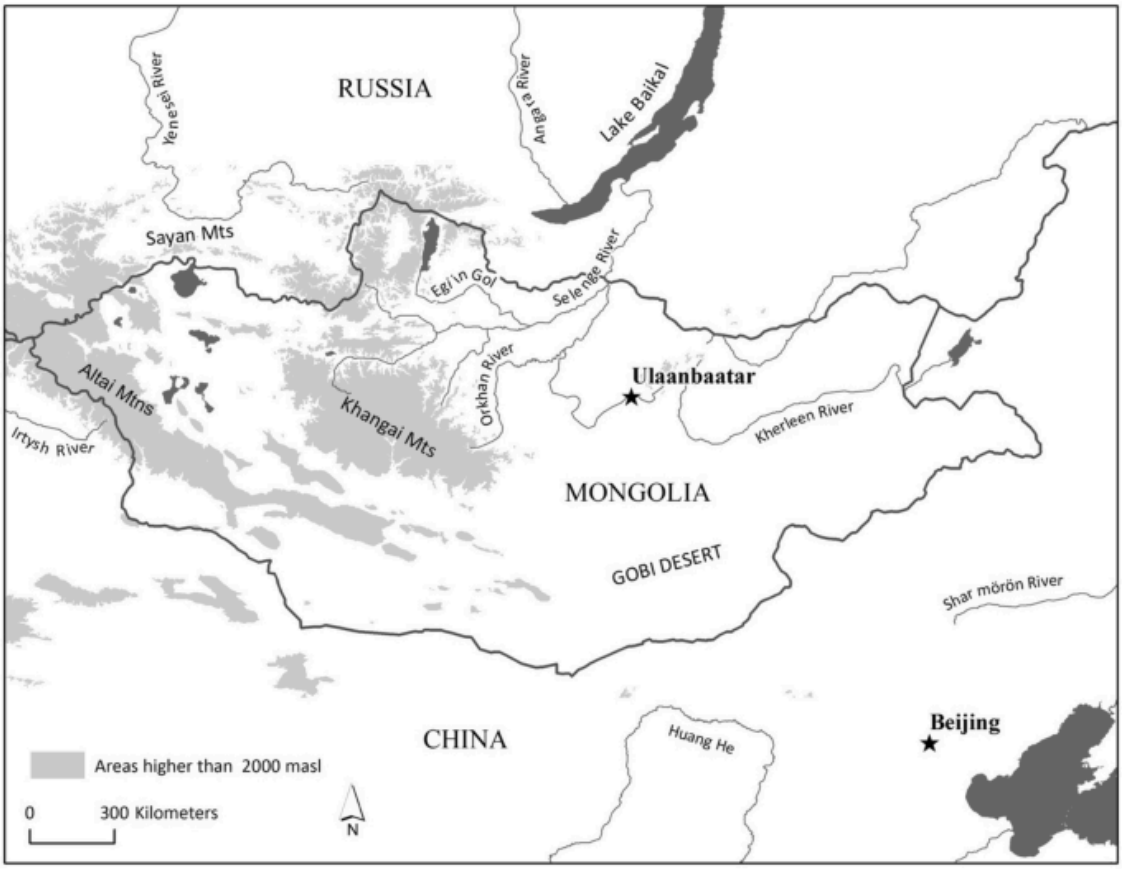


Fig.6 Map of Mongolia (Wright 2021).

11.2. The Archaeology of Prehistoric Settlement Sites in Mongolia

"The archaeology of Bronze Age Mongolia is an archaeology of monuments…Habitation and production sites are rare and low impact, and the landscape is dominated by impressive architecture made up of stone mounds, formal constructions, standing stones, rock art, complex patterns of alignments, and repeated smaller features." (Wright 2021)

Archaeologists have historically ignored the prehistoric settlement sites of Mongolia, focusing instead on monumental architecture and burial grounds (Gardner & Burentogtokh 2018; Houle et al. 2022). Prehistoric Mongolian habitation sites are challenging to identify and analyze, and have been described as "ephemeral" in nature (Wright 2016). Some of the earliest research into Bronze Age Mongolian habitation sites include Jean Luc-Houle's excavations of Late Bronze Age sites in the Khanuy Valley, which revealed early social complexity (far removed from centralized and sedentary powers) that likely shaped the sociopolitical organization of the Early Iron Age in Mongolia (see Houle et al. 2010).

The subsequent excavation of Early Iron Age habitation sites in the Tarvagatai Valley led to the development of an excavation framework specifically for mobile pastoralist domiciles which analyzes horizontal distribution patterns of material culture to reconstruct ancient activities and vertical distributions (or artifact depth) to determine archaeological units (Gardner & Burentogtokh 2018). A creative framework has also been developed for the remodeling of the microenvironments which characterized prehistoric habitation sites in Mongolia (see Wright et al. 2016). Although the importance of excavating and analyzing habitation sites and non-permanent archaeological features has been increasingly emphasized over the past decade, there is a lack of known stratified habitation sites in Mongolia available for study (Honeychurch 2015; Houle 2014; Houle et al. 2022; Wright 2021). The recently excavated ZK513 habitation site is a notable exception (Houle et al. 2022).

11.2.1. Chronology & Radiocarbon Dating

"To use radiocarbon dates to make meaningful inferences regarding cultural dynamics in early Mongolia, a number of key challenges must first be addressed." (Taylor et al. 2019)

A refined chronological framework for Bronze Age Outer Mongolia secured by reliable AMS radiocarbon dating of human bone (see Chapter 03) has only recently been provided by Taylor et al. 2019). Notably, some 200 radiocarbon dates had previously been generated from archaeological materials such as wood and human bone (see Amartuvshin et al. 2015; Amartuvshin & Jargalan 2010; Bemmann et al. 2015; Eruul-Erdene et al. 2015; Fitzhugh et al. 2012; Fitzhugh & Bayarsaikhan 2010; Frohlich et al 2009; Fitzhugh et al. 2011, 2012; Fitzhugh et al. 2013; Fitzhugh & Kortum 2012; Gantulga et al. 2016; Gunchinsuren et al. 2006; Hayashi 2013; Johanneson 2016; Kovalev & Erdenebaatar 2009; Machicek 2011; Miyamoto 2017; Miyamoto & Obata 2016; Nelson et al. 2009; Taylor 2017, 2018; Tumen et al. 2012; Turbat et al. 2003; Wright et al. 2019; Yeruul-Erdene et al. 2015; Zazzo et al 2019). Archaeologists delineated tentative periodization schemes for Bronze Age Mongolia using some of these dates, with the understanding that they were working models with many limitations (e.g. Honeychurch 2015; Houle 2014; Wright 2021) (Tbl.24).

Tbl.24 Table of Bronze Age Outer Mongolian chronologies.

Archaeological Period	Estimated Dates (Houle 2014)	Estimated Dates (Honeychurch 2015)	Estimated Dates (Wright 2021)
Eneolithic	ca. 3500–2500 BCE	N.A.	N.A.
Early / Middle Bronze Age	ca. 2500–1500 BCE	N.A.	ca. 1800–1200 BCE
Late Bronze Age	ca. 1400–700 BCE	ca. 1400–1000 BCE	ca. 1200–800 BCE
Terminal Bronze Age	ca. 700–400 BCE	ca. 1000–750 BCE	

**All radiocarbon dates are calibrated.*

Importantly, the low-resolution of many of the radiocarbon dates generated for Bronze Age Mongolia, coupled with issues introduced by the aquatic reservoir and old wood effects (see Chapter 03), has made precise chronological modeling difficult (see Taylor et al. 2019). The new radiocarbon dates produced by Taylor et al. (2019) suggest that, within Mongolia, the Bronze Age could be said to roughly correspond with ca. 3170 - 910 BCE (Tbl.25). The data also suggests that the Eneolithic Afanasievo archaeological culture was followed by the Early Bronze Age Chemurchek archaeological culture, which was in turn followed by the Middle Bronze Age Munkhairkhan archaeological culture (Taylor et al. 2019) (Tbl.25). The archaeological cultures of the Middle and Late Bronze Ages on the other hand shared significant temporal overlap (Tbl.25). Notably, the inclusion of radiocarbon dates from certain tombs, and the exclusion of certain others, by Taylor et al. (2019) into a Sagsai context has very recently been called into question (see Bemmann et al. 2024). I will revisit this objection further into this chapter, as part of my discussion of the archaeological cultures of the Late Bronze Age.

Tbl.25 Table of the Bronze Age Outer Mongolian chronology observed in this dissertation.

Archaeological Period	Archaeological Culture	AMS Radiocarbon Dates (Taylor et al. 2019)
Eneolithic / Early Bronze Age	Afanasievo, Chemurchek	ca. 3170–1915 BCE
Middle Bronze Age	Munkhkhairkhan, Ulaanzuukh	ca. 1915–1350 BCE
Late Bronze Age	Ulaanzuukh, Khirigsuur, Sagsai, Deer Stone, Baitag	ca. 1350–910 BCE

**These archaeological periods were not delineated in Taylor et al. 2019.*

11.3. The Archaeological Cultures of Mongolia

"Trajectories of social and economic development visible in the archaeology of Mongolia are just as likely to be autochthonous developments or related to trans-Eurasian east–west interaction as they are to be based on dependencies or interactions with the sedentary agricultural populations to the south of Mongolia." (Wright 2021)

Early Holocene Mongolia was both more humid and heavily forested than it is today, and its ancient human inhabitants developed a multitude of subsistence strategies uniquely adapted to their local environmental conditions (Bazarova et al. 2019; Cybiktarov 2002; Janz et al. 2017; Wright 2021; Zhao et al. 2021). In the open steppe of Inner Mongolia, the Neolithic peoples of Tamsabulag are thought to have cultivated cereals, fished, hunted wild game such as antelope and horse, and gathered wild plants (Houle 2014; Okladnikov & Derevyanko 1970; Séfériadès 2004; Zhao 2021). Domesticated cattle-breeding has also been associated with Tamsabulag (Dorj 1971; Séfériadès 2004; Volkov 1995), though these claims are no longer taken seriously.

Closer to the forest, the Neolithic peoples of Baiyinchanghan were believed to have hunted cervids but focused more on the processing of cereals and foraged plants, with little interest in small game, equids, or bovines (Zhao 2021). The Neolithic peoples of Hag in the eastern wetlands of Inner Mongolia have been speculated to have been less invested in plant processing and focused more on fishing and hunting birds, hares, foxes, and roe deer (Zhao 2021). The emergence of seemingly complex Neolithic lifeways incorporating sedentary agriculture at Tamsabulag, Baiyinchanghan, and Hag challenges the idea that prehistoric peoples of what is now called Mongolia experienced a uniform transition from hunting and gathering to nomadic pastoralism.

Although sedentary lifeways did not seem to endure in prehistoric Inner Mongolia beyond the Late Neolithic (Allard & Erdenebaatar 2005; Cybiktarov 2002), these sites emphasize the role of local climate and environment variability in the emergence of human subsistence strategies across the Mongolian Plateau (Zhao 2021; see also Janz et al. 2017, 2021; Pleuger et al. 2023). An abundance of lithic and ceramic assemblages spanning the Early and Middle Holocene suggest that mobile hunting and gathering was the predominant subsistence strategy in Outer Mongolia, with some evidence of decreasing mobility through time (Abramova 1956; Allard & Erdenebaatar 2005; Derevianko et al. 2001, 2003;; Odsuren et al. 2015; Schneider et al. 2016; Weber et al. 1998; Weber & Bettinger 2010; Wright 2021; Wright & Janz 2012).

Livestock management and mobile pastoralism does not appear to have emerged until the Eneolithic and Early Bronze Age in Outer Mongolia (Allard & Erdenebaatar 2005; Wright 2021), and this transition is currently not well-understood. More faunal data are needed, ideally from Eneolithic and Early Bronze Age settlement sites, and these data need to both be reliably radiocarbon dated and to have securely distinguished wild versus domesticated taxa attributions. The two predominant archaeological cultures associated with the Eneolithic and Early Bronze Age in Outer Mongolia were the Afanasievo and the Chumurchek, which gave way to the Munkhkhairkhan and the Ulaanzuukh in the Middle Bronze Age. The Late Bronze Archaeological cultures of Outer Mongolia include the Ulaanzuukh (which spanned the Middle and Late Bronze Ages), the Khirigsuur Culture, the Sagsai, the Deer Stone Culture, and the Baitag. The table below provides a loose model of the archaeological cultures and periods of the Outer Mongolian Bronze Age, delineated from the most up-to-date AMS radiocarbon dates (see Taylor et al. 2019) (Tbl.26).

Tbl.26 Table of the chronology for Bronze Age Outer Mongolian cultures as observed in this dissertation.

Archaeological Period	Archaeological Culture	Traditional dates (Dashtseveg et al. 2014)	AMS Radiocarbon Dates (Taylor et al. 2019)
Eneolithic / Early Bronze Age	Afanasievo	ca. 2800–2500 BC	ca. 3170–2725 BCE
Eneolithic / Early Bronze Age	Chemurchek	ca. 2500–1800 BC	ca. 2760–1915 BCE
Middle Bronze Age	Munkhkhairkhan	ca. 1800–1500 BC	ca. 1860–1345 BCE
Middle / Late Bronze Age	Ulaanzuukh	ca. 1500–1300 BC	ca. 1470–1170 BCE
Late Bronze Age	Khirigsuur	ca. 1600–300 BC	ca. 1350–885 BCE
Late Bronze Age	Sagsai	N.A.	ca. 1330–1070 BCE
Late Bronze Age	Slab Burial	ca. 1600–300 BC	ca. 1170–395 BCE
Late Bronze Age	Deer Stone	N.A.	ca. 1165–755 BCE
Late Bronze Age	Baitag	N.A.	ca. 1055–910 BCE

**These archaeological periods were not delineated in Dashtseveg et al. 2014 or Taylor et al. 2019. All radiocarbon dates are calibrated.*

11.3.1. Eneolithic & Early Bronze Age Cultures of Outer Mongolia (ca. 3170–1915 BCE)

"Occupied by hunter-gatherers since at least the end of the Pleistocene, the Altai Mountains also yield the Eastern Steppe's oldest direct evidence for domestic animal use—in the form of burials of the Afanasievo culture, apparent migrants from eastern Europe that brought with them sheep, goat, and cattle just prior to ca. 3000 BCE." (Taylor et al. 2021b)

The Eneolithic and Early Bronze Age periods of Outer Mongolia were characterized by the manufacture and use of thin red ware pottery, the erection of monumental stone architecture, the implementation of both bronze and copper metallurgy (especially ornamental), the more-or-less uniform adaptation of a shared cosmological and ritual culture, and presumably the initial transition from hunter-gatherer lifeways to livestock rearing (Volkov 1995; Wright 2021). It has been speculated that this subsistence transition was initiated by contact with Afanasievo pastoralists and their domesticated animal herds migrating into Mongolia from the Western Eurasian Steppe (Frachetti 2011; Honeychurch et al. 2021b). Scholars have also argued that the Eneolithic and Early Bronze Age peoples of Outer Mongolia were predominantly sedentary agriculturalists, and that the widespread adaptation of pastoralism did not take place until the Late Bronze Age (Koryakova & Epimakhov 2007; see also Houle 2014).

The most recent multiproxy biomolecular analyses (ZooMS and aDNA) of archaeological faunal remains from Bronze Age contexts suggest that Eneolithic and Early Bronze Age peoples of Outer Mongolia were herding livestock, but (importantly) were not yet exploiting horses for food (Taylor et al. 2020b). The archaeological evidence that is available does not suggest that horses were domesticated and being ridden in Outer Mongolia until the Late Bronze Age (Houle 2014; Taylor et al. 2020b). The much-debated question of the timing and mechanisms of domesticated horse arrival, as well as their exploitation, will be discussed in-depth further along this chapter. This subsection will instead overview the settlement sites, associated faunal assemblages, and speculated animal economies that have been attributed to the primary archaeological cultures of Eneolithic and Early Bronze Age Mongolia- the Afanasievio and the Chemurchek.

<u>The Afanasievo (ca. 3170–2725 BCE)</u>

I have already discussed the Afanasievo archaeological culture in the context of Eneolithic and Early Bronze Age Southern Siberia (see Chapter 10). Two burial sites have been excavated and associated with the Afanasievo in Central Mongolia, namely Altan Sandal ("Golden Chair") and Shatar Chuluu ("Stone Chest") (Novgorodova 1989; Tseveendorj 1975; Volkov 1980). The human remains uncovered at Altan Sandal and Shatar Chuluu were found coated in red ochre, in supine burial positions with flexed legs (Volkov 1995). Initial craniometric analyses of individuals exhumed from Mongolian Afanasievo contexts suggested a Western Eurasian Steppe ancestral affinity as opposed to an Asian ancestral affinity (Volkov 1995), and these findings were subsequently confirmed by mitochondrial and genomic analyses (Honeychurch et al. 2021a; Rogers 2016; Rogers et al. 2019; Jeong et al. 2020). The Western Eurasian Steppe ancestral affinity attributed to the individuals exhumed from Mongolian Afanasievo contexts is completely in accord with the craniometric, biomolecular, and general archaeological findings

attributed to the Afanasievo in the Altai Mountains and Minusinsk Basin of Southern Siberia (see Chapter 10).

Unfortunately, no faunal remains were recovered from either Altan Sandal or Shatar Chuluu, except for a single carnivore tooth pendant (Honeychurch et al. 2021; Tseveendorj 1975). The only other Afanasievo-associated burial in Mongolia to-date, named “Khuurai-Gov’ No. 1”, was excavated in Ulaankhus sum (district), Baian-Ölgii aimag (subdistrict) in 2004 (Kovalev & Erdenebaatar 2009). This burial did include a number of sheep (*Ovis* sp.) astragali (Kovalev & Erdenebaatar 2009). No archaeological settlement sites discovered in Mongolia (Inner or Outer) have been associated with the Afanasievo, and thus no analysis of faunal evidence can be undertaken to reconstruct Afanasievo-associated subsistence practices or animal economies in Mongolian contexts. In lieu of more robust data, the question of whether Afanasievo peoples introduced pastoralism to Outer Mongolia or pastoralism was already being practiced before Afanasievo arrival remains open.

The Chemurchek (ca. 2760–1915 BCE)

Chemurchek (alternatively “Qiemu’erqieke”, “Shamirshak”, or “Hemtseg”, or “Khemceg”, alongside various other spellings) refers to an archaeological culture believed to have spanned the Altai Mountain region of Western Mongolia and the Xingjiang region of Northwestern China (Chen & Hiebert 1995; Houle 2014; Jia & Betts 2006; Kovalev & Erdenebaatar 2009; Taylor et al. 2020b; Tumurbaatar & Makarewicz 2022). Chemurchek cemeteries were initially discovered in the Chemurchek River Valley in the Junggar Basin of Xinjiang in 1963, revealing a total of 32 graves which have since been attributed to the archaeological culture (which was named after the river valley) (Jia & Betts 2006). The supine and flexed burial positions of the individuals uncovered from these cemeteries has been related to the burial positions of the Yamanaya and Afanasievo, while the ceramic grave goods have been related to the material culture of the Afanasievo, Okunevo, and Karasuk (Chen Kwang-tzuu & Hiebert 1995*;* Jia & Betts 2006) (for Bronze Age Southern Siberian material cultural, see also Chapter 10).

Decades after the initial discovery of Chemurchek-associated burials in Xinjiang, Bronze Age burials in the foothills of the Mongolian Altai Mountain region (e.g. Khovd aimag, Baian-Ölgii aimag) were also attributed to the Chemurchek archaeological culture (Kovalev & Erdenebaatar 2009). Although sheep and horse bones have been recovered from Chemurchek burial and ritual sites of Mongolia, it is unclear whether these bones belonged to wild or domesticated animals (Houle 2014; Taylor et al. 2020b). Stone stelae featuring depictions of horses have been discovered in Western Mongolia and attributed to the Chemurchek (Molodin et al. 2024), and Chemurchek stelae featuring cattle have been discovered in both Xinjiang and Western Mongolia (Jia & Betts 2006; Molodin et al. 2024; Tumurbaatar & Makarewicz 2022). There are no settlement sites in Mongolia associated with the Chemurchek (see Houle 2014; Taylor et al. 2020b).

It is possible that Chemurchek-associated peoples herded domesticated sheep and cattle (see Taylor 2024), though it is unlikely that they managed livestock on the backs of domesticated

horses (see Taylor et al. 2020b), given that the oldest evidence for Inner Asian horse transport dates back to the Sintashta archaeological culture (ca. 1950 BCE) and the oldest evidence for horse domestication in Outer Mongolia is dated to ca. 1650 BCE (Taylor et al. 2024). It is also possible that the Chemurchek adopted animal husbandry from the Afanasievo, who they shared similar funerary customs with (for body positioning, see Chen Kwang-tzuu & Hiebert 1995*;* Jia & Betts 2006; for red ochre painting, see Kovalev & Erdenebaatar 2009). The biomolecular examination of the sheep remains from Mongolian Chemurchek burial contexts to secure either a domesticated or wild origin is the best direction forward, in lieu of any faunal data from settlement site contexts.

11.3.2. Middle Bronze Age Cultures of Outer Mongolia (ca. 1915–1350 BCE)

"...a geographic concentration of Mongolia's earliest monumental traditions (Afanasievo, Chemurchek and Munkhkhairkhan) to the western, southwestern and Altai regions of Mongolia. Combined with their shared flexed burial pattern and overlapping cultural boundaries, these results suggest shared cultural traditions for the people who built Mongolia's early Bronze Age burial monuments, as well as a likely entry of these traditions from western Eurasia." (Taylor et al. 2019)

There is not much that can be said about the Middle Bronze Age of Outer Mongolia. The very limited number of settlement sites from this period (two in total) precludes any in-depth analysis or reconstruction of the material culture, subsistence, social organization, or lifeways more broadly during this period. The two archaeological cultures associated with the Middle Bronze Age, the Munkhkhairkhan and the Ulaanzuukh, are known only by their burial features. Munkhkhairkan monuments are concentrated in the south and southwest, while the later Ulaanzukh monuments are concentrated in the south (Taylor et al. 2019). Grave goods found interred in these burials testify the continued practice of bronze metallurgy (in certain regions), manufacture of redware pottery, and the modification of natural materials (e.g. bone and shell) into tools and adornment. I will explore both the archaeology associated with the Munkhkhairkhan and the Ulaanzuukh below. I will discuss the only two settlement sites from the Middle Bronze Age of Outer Mongolia in Chapter 13.

<u>The Munkhkhairkhan (ca. 1860–1345 BCE)</u>

The Munkhkhairkhan (or Mönkhkhairkhan) archaeological cultural was so-named by archaeologists Alexey Kovalev and Diimaajav Erdenebaatar following their discovery and excavation of 13 Middle Bronze Age burials in Western and Central Mongolia, starting in 2003 (Kovalev & Erdenebaatar 2009). They derived the moniker from the Mönkhkhairkhan sum of Khovd aimag, though burials have also been found in Zavkhan aimag and Khövsgöl aimiag (Kovalev & Erdenebaatar 2009). The Munkhkhairkhan are known exclusively through their burial archaeology, having no known settlement sites in Outer Mongolia. Munkhkhairkhan barrows were constructed from stones heaped onto pits filled with stone slabs, grave goods, and the bodies of their dead (Kovalev & Erdenebaatar 2009). Grave goods included bronze tools and weapons, bone tools and jewelry, and shell disc ornaments (Kovalev & Erdenebaatar 2009). Uniquely, artistic arrangements of black shale and rose granite stones appear to form a bird's claw clutching the burial pit have been observed in at least one Munkhkhairkhan tomb (Kovalev

& Erdenebaatar 2009). As fascinating as Munkhkhairkhan burials have proven to be, virtually nothing can be said currently about the subsistence strategies and human-animal relationships of the Munkhkhairkhan archaeological culture.

The Ulaanzuukh (ca. 1470–1170 BCE)

Ulaanzuukh refers to an archaeological culture with a distinctive burial tradition that inhabited the Eastern and Central regions of Mongolia during the Middle and Late Bronze Ages (Dashtseveg et al. 2014; Wright et al. 2019). This archaeological complex was named after the Ulaanzuukh Valley were the 33 attributed burials were initially discovered, during fieldwork conducted from 2008 to 2012 (Dashtseveg et al. 2014). Ulaanzuukh burials have also been excavated in the valleys of Adgiin Gol and Bulgiin Ekh (Dashtseveg et al. 2014). By 2014, a total of 470 Ulaanzuukh burials had been discovered; 110 in the Ulaanzuukh Valley, 129 in the Adgiin Gol Valley, and 241 in the Bulgiin Ekh Valley (Dashtseveg et al. 2014). Unfortunately every single one of these graves had been looted to some extent, or otherwise disturbed, though redware ceramics, white beads, and a single stone object were recovered (Dashtseveg et al. 2014). Notably, no metal objects (bronze or otherwise) have been recovered from Ulaanzuukh-attributed burials (Dashtseveg et al. 2014; Wright et al. 2019) - though this may very well be a consequence of grave-robbing.

Equally unique, human individuals exhumed from Ulaanzuukh graves were found in prone positions and in general alignment with the Northeast direction (Dashtseveg et al. 2014). These burial positions are distinct from the flexed and supine burial positions of Afanasievo and Chemurchek individuals, for example. Although the Ulaanzuukh archaeological culture continued into the Late Bronze Age, as of yet no settlement sites or published faunal reports have been associated with them (see Honeychurch 2015). It has been speculated that the Ulaanzuukh represented a continuance of Epipaleolithic hunter-gatherer lifeways, possibly related to the Neolithic traditions of the Yellow River and Inner Mongolia, as opposed to the metallurgist-pastoralist lifeways that (presumably) unfolded during the Bronze Age in Mongolia (Wright et al. 2019). On the other hand, the Ulaanzuukh have also been suggested to have been mobile pastoralists reliant on domesticated animal husbandry (see Honeychurch 2015).

11.3.3. Late Bronze Age Cultures of Outer Mongolia (ca. 1350–950 BCE)

“Based on available evidence, the turn of the first millennium BCE saw the emergence of a highly mobile, multispecies pastoral economy characteristic of East Asian pastoralism, including ephemeral habitations and the use of domestic horses for meat and dairy.” (Taylor et al. 2021b)

The Late Bronze Age of Outer Mongolia is the Bronze Age period most associated with domesticated animal husbandry, mobile pastoralism, societal complexity, and horseback riding (Allard & Erdenebaatar 2005; Borjigin & Wang 2023; Burentogtokh 2017; Dashtseveg et al. 2014; Fitzhugh 2009; Honeychurch 2015; Houle 2014; Makarewicz et al. 2018; Taylor & Tuvshinjargal 2018; Taylor et al. 2017, 2020a,b; Wright 2007, 2021). Hunting has been suggested to have continued alongside herding, while evidence of agriculture is notably missing (and unsupported by stable isotopic analysis) (Honeychurch 2015; Houle 2014; Machicek 2011).

The ritual role of horses is emphasized in the archaeological record and art of this period (Honeychurch 2015; Houle 2014; Makarewicz et al. 2018; Taylor 2017; Taylor et al. 2017, 2020a), and has been connected to cultural and communal networking across vast swathes of land (Allard & Erdenebaatar 2005; Fitzhugh 2009; Honeychurch 2015) that horseback riding would have facilitated (Bemmann et al. 2024; Houle 2014; Taylor 2017). I will review and discuss Late Bronze Age human-horse relationships further into this dissertation.

The Late Bronze has, in general, been suggested by scholars to have represented a major shift in the social organization, subsistence strategies, ritual culture, range of mobility, and overall lifeways that had characterized Outer Mongolia more broadly during the Eneolithic, Early, and Middle Bronze Ages. Settlement sites seemingly became much more common during the Late Bronze Age (Honeychurch 2015; Houle 2014), or otherwise more resilient to the passage of time, though truly permanent residencies do not seem to have been constructed (Clark 2014; Honeychurch 2004; Houle 2010, 2014). A number of archaeological cultures have been associated with the Late Bronze Age of Outer Mongolia, including the Khirigsuur, Sagsai, Slab Burial, Deer Stone, and Baitag. I will outline each of the archaeological cultures below, and review all associated settlement site data and faunal reports.

The Sagsai (ca. 1330–1070 BCE)

Sagsai is another Late Bronze Age Mongolian archaeological culture that is known exclusively through burial features, so-named after the Sagsai region of Western Outer Mongolia. There is some contention amongst scholars regarding how to classify Sagsai burials, as can be seen in a very recent publication (Bemmann et al. 2024) disputing the accuracy of the attribution of certain burials to the Sagsai culture and their subsequent corporation into Taylor et al.'s (2019) radiocarbon study. In general, the burials associated with the Sagsai have been square-shaped and the individuals within them positioned either supine or on their side and in a northward alignment (Bemmann et al. 2024; Miyamoto et al. 2016, 2017, 2018, 2023). With so many overlapping burial traditions spanning the Late Bronze of Outer Mongolia, especially in the Western and Central regions, there is a risk of manufacturing problems and diluting the already limited archaeological evidence by adhering too rigidly to artificial groupings.

The bones of reportedly sacrificed horses and caprines were retrieved from the Sagsai graves of Emeelt Tolgoi (Miyamoto et al. 2018), and unidentified animal bones were discovered in the graves of Khyar Kharaach (Miyamoto et al. 2017). A faunal report published for the burial site of Avdalai khyasaa details highly fragmented finds that were determined through combined zooarchaeoogical and ZooMS analysis (one one specimen) to have belonged to a mixture of equids, cervids, and bovids including caprines (Miyamoto et al. 2023). However, individuals from the DSKC culture (discussed in the next subsection) are believed by some scholars to have looted Sagsai graves and subsequently deposited sacrificed animals in them (Miyamoto et al. 2023). Higher resolution taxonomic identification of animal bones recovered from Sagsai-affiliated graves would not necessarily clarify pre-DSKC subsistence strategies or human animal relationships. As there are no settlement sites currently associated with the

Sagsai archaeological culture, there is little more to be said about specifically Sagsai animal economies or subsistence practices.

The Deer Stone - Khirigsuur Complex (DSKC) (ca. 1350–755 BCE)

"Deer Stones" refer to the monumental stone stele engraved with stylized depictions of deer that have been found throughout a wide range of Outer & Inner Mongolia, Southern Siberia, the Transbaikal region, and Northwest China (Burentogtokh 2017; Esin et al. 2021; Honeychurch 2015) and radiocarbon dated to ca. 1165–755 BCE (Taylor et al. 2019). Deer stones also commonly feature engravings of faces, belts, weapons, and tools, and have been speculated to represent tattooed humans (Allard & Erdenebaatar 2005). Similarly, "khirigsuur" does not refer to a place, but to the monumental stone mounds scattered throughout Western and Central Mongolia (Allard & Erdenebaatar 2005; Burentogtokh 2017; Fitzhugh 2009; Honeychurch 2015; Wright 2007) that have been radiocarbon dated from ca. 1350 to 885 BCE (Taylor et al. 2019). Khirgisuurs are distinct from, but probably related to, the stone kurgans and burial mounds of Southern Siberia (see Chapter 10), Inner Mongolia, and Northwest China (Honeychurch 2015).

As deer stones and khirigsuur mounds are often found adjacent to one another in Western and Central Mongolia (Fitzhugh 2009; Honeychurch 2015), an archaeological cultural phenomenon deemed the The Deer Stone - Khirigsuur Complex (DSKC, or DSK) has been adopted by some modern scholars when referring to both, or either (e.g. Esin et al. 2021; Fitzhugh 2009, 2017; Jeong et al. 2018; Hsu et al. 2020; Lepetz et al. 2019; Lymer et al. 2014; Taylor 2017; Taylor & Tuvshinjargal 2018; Taylor et al. 2016, 2017, 2019, 2020a,b). I have chosen to do the same in my discussion of the archaeological complex associated with Outer Mongolian deer stones and khirigsuur mounds. No settlement sites have been found in relation to the DSKC tradition (Allard & Erdenebaatar 2005), which is more of a ceremonial (see Lepetz et al. 2019; Makarewicz et al. 2018) and arguably funerary (in the case of khirgisuurs in more Western regions; see Fitzhugh 2009; Honeychurch 2015) complex than anything else. Importantly, both deer stones and khirigsuur mounds commonly feature ritually deposited horse skulls at their base (Allard & Erdenebaatar 2005; Honeychurch 2015; Lepetz et al. 2019; Makarewicz et al. 2018), though less often in Western regions (Fitzhugh 2009), and these horses are now known to have been *domesticated* (Taylor 2017; Taylor et al. 2020b).

The discovery of securely identified domesticated horse bones in the contexts of Late Bronze Age Outer Mongolia is extremely significant. I will discuss the relevance and implications of these domesticated horse bone deposits further into this chapter, in the course of my overview of Late Bronze Age animal economies. The ritual emphasis on horses can be viewed as evidence for a mobile pastoralist economy (see Chapter 09, as well as Johannesson 2015), as can the presence of caprine remains interred in DSKC burials (Lepetz et al. 2019) should they prove to have come from domesticated animals. Scholars have suggested that DSKC-affiliated peoples would have been highly mobile pastoralists (Allard & Erdenebaatar 2005; Fitzhugh 2009; Wright 2007). This would be in keeping with the seeming lack of DSKC settlement sites preserved in the archaeological record, which would have consisted of temporary encampments.

The Slab Burial Culture (ca. 1170–395 BCE)

While Sagsai and DSKC burials are largely concentrated in the western and central regions of Outer Mongolia, the eastern (and central) regions feature Late Bronze Age slab graves, or slab burials, which have come to be associated with the Slab Burial Culture (Dashtseveg et al. 2014; Honeychurch 2015). Slab burials also extend into Southern Siberia and the Transbaikal region (Dashtseveg et al. 2014; Honeychurch 2015). The Slab Burial tradition chronologically overlapped with the DSKC tradition (Taylor et al. 2019), with the later being predominant in Western Mongolia and the former in Eastern Mongolia, and scholars have wondered whether relations between the two traditions were generally more harmonious or confrontational (Dashtseveg et al. 2014). Slab Burial grave goods such as horse harnesses and mouth bits (the earliest yet found in Mongolia) have been interpreted as signs of social stratification and complexity (Honeychurch 2015), which may have affected their relations with other groups.

More relevant to the topic of this dissertation, the presence of horse equipment alongside the bones of horse, cattle, and caprines interred inside of Slab Burial graves (Grishin 1975; Honeychurch 2015; Honeychurch et al. 2009; Navaan 1975; Tsybiktarov 1998) strongly suggest a reliance on animal husbandry and a mobile pastoralist economy. This suggestion is strengthened by the presence of domesticated horse bones in the graves of DSKC, with whom the peoples of the Slab Burial tradition coexisted. Scholars have subsequently suggested that the peoples of the Slab Burial Culture either witnessed or instigated a widespread intensification of mobile pastoralism (the early forms of which being introduced by the Afanasievo) that would sweep across the entirety of the Mongolian Plateau by the Iron Age (Borjigin & Wang 2023).

In all likelihood many of the animals (especially the horses) interred in Slab Burial graves *were* domesticated as reported (e.g. in Grishin 1975; Navaan 1975; Tsybiktarov 1998), but this has not yet been verified by robust zooarchaeological or biomolecular analysis. There is still every indication that the Slab Burial Culture, and the archaeological cultures of the Late Bronze Age in Outer Mongolia more broadly, were herding livestock and using horses for traction, riding, or both. That being said, the Slab Burial Culture, along with the Sagsai (and to a lesser extent the DSKC, as a ritual complex), are exclusively known as burial traditions. There are no Slab Burial settlement sites or animal assemblages from non-funerary contexts to comment upon.

The Baitag (ca. 1055–910 BCE)

Kovalev & Erdenebaatar (2009) excavated eight stone ring burials in Bulgan sum, Khovd aimag in the Baitag Bogd Mountain region of Southern Mongolia in 2005, which they subsequently attributed to a new “Baitag” archaeological culture (Kovalev & Erdenebaatar 2009). These burials were moundless and the bodies interred within them were positioned with flexed legs and oriented eastward; this has led to the Baitag culture to be compared to the Eneolithic archaeological cultures of the Western Eurasian Steppe (Kovalev & Erdenebaatar 2009). The small beads and bronze ornaments recovered from Baitag burials have also been compared to the grave goods of the Late Bronze Age Karasuk culture of Southern Siberia (see Chapter 10) (Kovalev & Erdenebaatar 2009). There are no published accounts or reports of any animal

bones having been recovered from Baitag contexts. In keeping with the rest of the Late Bronze Age archaeological cultures of Outer Mongolia, which might more appropriately be viewed as mortuary and ritual complexes, no settlement sites have been associated with the Baitag. The location of Baitag graves on the border of China might suggest a continuation of or a closer affiliation with more Eastern lifeways, but this is not necessarily the case.

11.4. Bronze Age Outer Mongolia (ca. 3170–910 BCE): Conclusion

“Although Mongolia's often-ephemeral archaeological deposits can make it challenging to do so, we need to strive to build data-driven models for the human-animal story in Inner Asia.” (Taylor 2021)

Several archaeological cultures have been associated with the Bronze Age of Outer Mongolia, though evidence for groups predating the Late Bronze Age (ca. 1350 BCE) is often limited to burial monuments. Settlement sites are few and far in between, as are faunal data. Valuable finds include horse harnessing equipment from Late Bronze Age contexts; these are complemented by the recovery of domesticated horse remains starting from this period. I will overview these remains alongside the rest of the faunal data currently available from the settlement site contexts of Outer Mongolia and Southern Siberia in the next three chapters of this dissertation. Each chapter will be dedicated to a subdivision of the Bronze Age (i.e. Eneolithic & Early Bronze Age, Middle Bronze Age, and Late Bronze Age), where I will outline the known settlement sites of both regions as well as the faunal reports that are attached to them. I will conclude these chapters with an overview of the Bronze Age economies of Outer Mongolia and Southern Siberia (Chapter 15), as can be inferred from these data.

12. Eneolithic & Early Bronze Age Sites

12.1. Southern Siberia (ca. 3000–1700 BCE)

Numerous Afanasievo-associated burial sites have been excavated (see Bokovenko & Legrand 2010; Bokovenko & Mityaev 2010; Bokovenko et al. 2021; Dashkovisky 2019; Honeychurch et al. 2021; Kirginekov 2010a, 2010b; Kiryushin et al. 2012; Kovalev & Erdenbaatar 2010; Kovaleva et al. 2010; Poliakov & Esin 2015; Qu et al. 2020; Shulga 2010; Stepanova 2010; Syvatko et al. 2017; Vadeka 2010). A more extensive list of Afanasievo burial features can be found in Vadetskaya et al. (2014). There are far fewer excavation reports for Afanasievo settlements (Alekhine et al. 1995; Tishkin et al. 2021), all of which are located near rivers and feature stone-lined hearths (Hermes et al. 2020; Honeychurch et al. 2021; Svyatko et al. 2017). Known habitation sites with excavation reports include Balyktyyul, Kara-Tenesh, Maliy Dugan, Nizhnyaya Sooru, Partizanskaya Katushka, Podsinushka, Tepsei-X, Toora Dash, Uznezya I, and Ust'-Biyke-I.

Okunevo-associated archaeological sites, as with Afanasievo ones, are largely limited to burial contexts (Outram et al. 2018). Okunevo-type burials excavated within the Minusinsk Basin include the kurgans of Bateni (Gryaznov 1953), Chernovaya VIII (Maksimenkov 1980), Karasuk III, Lebyazhye, Pristan I, Razliv X (Pshentitsya & Pyatkin 2006), Syda V, Tas Khazaa (Lipsky 1957), Uibat III and V (Lazartov 1997), Ust-Kindirla, Verhniy Askiz I, and Verkh-Askiz (Khavrin 1997) (see also Gryaznov 1969; Jacobsen-Tepfer 2015; Outram et al. 2018; Poliakov & Lazaretov 2020; Poliakov & Svyatko 2021; Syvatko et al. 2009). Information on Minusink settlements is far more limited and seemingly restricted to non-residential mountain complexes classified as "fortresses" such as Chebaki Sve (Gotlib 1999).

Beyond the Minusinsk Basin, the Okunevo-associated sites of Tuva are scarce and predominantly funerary in nature (e.g. Aymyrlyk XIII, Aymyrlyk XXVII, and Azas II; see Gokhman 1980; Semenov 1997). Cultural layers within Toora-Dash (Semenov 1992, 1997, 2018; Kilunovskaya & Semenov 2019) and the recently excavated settlement of Zhelvak V (Zhogova et al. 2023) provide rare exceptions. I review these settlement sites, their archaeological reports, and associated faunal data reviewed below, with the exception of Chebaki Sve. Due to the ongoing conflict between Russia and the Ukraine, I am not able to access the report for Chebaki Sve, which is only available from Russian distributors.

Balyktyyul (Балыктыюль) (Abdulganeev et al. 1982)

The Balyktyyul settlement site is located on the lower left bank of the Balyktyyul River, 300 meters east of the Balyktyyul village in the Ulagache district of the Altai Republic (Abdulganeev et al. 1982). The site was excavated by a team from Altai State University in 1980, which uncovered cultural layers at depths between 0.2 meters and 4 meters (Abdulganeev et al. 1982; Vadetskaia et al. 2014). The site chronology is not clarified in Abdulganeev's et al.'s (1982) report and neither is the stratigraphic distribution of finds within them. It is also unclear if the archaeological assemblages from Balyktyyul are mixed, as is the case for Maily Dugan and Kara-Tenesh (Kosintsev & Stepanova 2010; Pogožheva & Molodin 1978), or if there is a straight-forward stratigraphy.

Several ceramic finds and burnt faunal remains associated with hearths were recovered and though no stratigraphic faunal data was reported, Kalashnikova's overall taxonomic abundance counts from 1980 fortunately were (Abdulganeev et al. 1982) (Tbl.27). The faunal assemblage was initially interpreted as evidence of a primarily cattle-breeding based economy with a secondary reliance on the hunting of wild game (Abdulganeev et al. 1982). Russian archaeologists later erroneously credited the assemblage as proof that Afanasievo archaeological populations utilized domesticated horses (Alekhin et al. 1995), although it is unclear exactly which species of equid remains were retrieved.

Tbl.27 Table of published faunal data from Balyktyyul (Abdulganeev et al. 1982).

Taxon	NISP	MNI
Caprine	53	5
Horse	7	2
Cattle	7	2
Roe Deer	6	2
Elk	3	1
Beaver	1	1
Bird	2	1

Denisova Cave (Денисова Пещера), Layers 08B, 10-13 (Derevyanko & Molodin 1994)

Denisova Cave is a stratified site of extreme paleontological, paleoanthropological, and archaeological significance. The cave is located in the Soloneshensky district of Altai Krai, 6 km northwest of the village of Cherny Anui, on the right bank of the Anuya River (Derevyanko & Molodin 1994; Vadetskaya et al. 2014). Excavations at Denisova Cave began in 1977 under the direction of Nikolay Dmitrievich Ovodov (Derevyanko & Molodin 1994). The cave's location in the foothills of the Altai (Altai Krai) complicates its association with Southern Siberia; it might more appropriately be assigned to Western Siberia. Far more complicated, at first glance, is the characterization of any Afansievo context at Denisova Cave.

"Layers 11 and 12" have been linked to the Afanasievo in modern publications (e.g. Vadetskaya et al. 2014; Svyatko et al. 2017), without any further context. At the same time, the large-scale ZooMS identification of paleolithic fauna from the eleventh and twelfth layers in all three sections studied (the Main, Eastern, and Southern Chambers) revealed multiple Elephantids and Rhinoceretids (Brown et al. 2021b). Radiocarbon dating has also secured Paleolithic contexts for these same layers (e.g. Douka et al. 2019; Zavala et al. 2021). How, then, could Afansievo-attributed ceramics have come to share the same stratigraphic context as wooly rhino and mammoth bones? The answer lies in the disconnection between the Pleistocene and Bronze Age research of Denisova Cave.

Denisova Cave was separated into multiple areas by its excavators (Derevyanko & Molodin 1994). The aforementioned Southern Chamber, Eastern Chamber, and Main Chamber are thoroughly Pleistocene (Brown et al. 2021b; Douka et al. 2019; Zavala et al 2021). Holocene material is instead limited to the Entrance Area (Derevyanko & Molodin 1994), and so was not included in the paleolithic ZooMS study (i.e. Brown et al. 2021b). The scientist who collagen fingerprinted the paleolithic fauna, Samanatha Brown, has been very involved in the study of the Pleistocene faunal and hominin remains from Denisova Cave and was not aware of the Entrance Area or of any recovered Afansievo ceramics (pers.comm. Samantha Brown 2024).

The Entrance Area itself was excavated in multiple sections, including "Pre-entrance Area" and "Gallery", which revealed 21 complex and non-uniform stratigraphic layers (Derevyanko & Molodin 1994). A total of 13 cultural layers were found to contain archaeological materials attributed to the Eneolithic through the Medieval Periods (Derevyanko & Molodin 1994). The archaeologists who subsequently referred to the Bronze Age findings from these layers in the Entrance Area (i.e. Vadetskaya et al. 2014; Svyatko et al. 2017) were not concerned with the Pleistocene contexts of Denisova Cave, and so did not offer any further clarification.

Layer 8B was determined to have contained Afansievo pottery, as well as Bronze Age vessels, Iron Age ceramics, and an intact horse pelvis (Derevyanko & Molodin 1994). Layer 10 was determined to have fragments of Afanasievo vessels, deposited amongst Bronze and Iron Age pottery. Layers 11 and 12 were attributed entirely to the Afansievo archaeological culture (Derevyanko & Molodin 1994). Layer 11B was specifically attributed to Afansievo fencing and decomposing sheep coprolites, and to have been significantly damaged by "Scythian period

pits” (Derevyanko & Molodin 1994). A hearth containing Afanasievo-attributed pottery was also uncovered in Layer 11 (Derevyanko & Molodin 1994). Layer 13 contained material culture finds, including Afanasievo, all of which were considered to have been redeposited from the Eneolithic through Iron Ages (Derevyanko & Molodin 1994). All of the Holocene fauna from the Entrance Area of Denisova Cave was analyzed by Nikolay Dmitrievich Ovodov, with the assistance of I.E. Grebnev and S.V. Vasil'ev (Derevyanko & Molodin 1994). I have done my best to present their data in association with the Afanasievo cultural layers of Denisova Cave (Tbls.28–30).

Tbl.28 Table of faunal data from the Pre-entrance Area of Denisova Cave (Derevyanko & Molodin 1994).

	8B		10		11		12	
	NISP	**MNI**	**NISP**	**MNI**	**NISP**	**MNI**	**NISP**	**MNI**
Canis familiaris	3	1	1	1	4	2	0	0
Equus caballus	25	2	1	1	2	1	0	0
Sus scrofa	5	1	5	1	0	0	1	1
Bos taurus	23	2	0	0	7	1	2	1
Capra et Ovis	216	7	7	1	68	9	26	2
Tapia altaica	0	0	33	4	0	0	0	0
Sorex sp.	0	0	0	0	0	0	0	0
Lepus timidus	0	0	0	0	0	0	1	1
Lepus tolai	0	0	0	0	0	0	0	0
Ochotona sp.	0	0	0	0	0	0	0	0
Pterymos volans	1	1	0	0	0	0	0	0
Sciurus vulgaris	0	0	0	0	0	0	0	0
Tamia sibircus	0	0	0	0	0	0	0	0
Citellus sp.	0	0	1	1	0	0	0	0
Marmota baibacina	5	1	0	0	2	1	2	1
Castor fiber	7	2	0	0	2	1	0	0
Cricetus cricetus	1	1	3	1	8	2	0	0
Myospalax myospylax	6	2	0	0	1	1	0	0
Arvicola terrestis	0	0	1	1	0	0	0	0
Microtinae sp.	1	1	0	0	0	0	0	0
Canis lupus	11	1	0	0	0	0	0	0
Vulpes vulpes	2	1	0	0	0	0	0	0
Ursus arctos	5	2	0	0	2	1	0	0
Martes zibelina	0	0	2	1	1	1	0	0
Mustella altaica	0	0	0	0	0	0	0	0
Meles meles	0	0	1	1	0	0	0	0
Lutra lutra	2	1	0	0	0	0	0	0
Lynx lynx	0	0	0	0	0	0	0	0
Cervus elaphus sibericus	44	1	2	1	8	2	0	0
C. caprelous pygarus	210	8	34	1	34	2	12	1
Alces alces	1	1	0	0	0	0	0	0
Capra siberica	1		0	0	0	0	0	0
Pisces	0	0	0	0	2		0	0
Peptilia	0	0	0	0	0	0	0	0
Aves	26		3		18		1	
Indeterminate	3721		1141		2515		291	

**Table excludes Layer 13.*

Tbl.29 Table of published faunal data from the Entrance Area of Denisova Cave (Derevyanko & Molodin 1994).

	10		12		13	
	NISP	MNI	NISP	MNI	NISP	MNI
Canis familiaris	1	1	4	2	0	0
Equus caballus	1	1	2	1	0	0
Sus scrofa	5	1	1	1	1	1
Bos taurus	1	1	4	1	0	0
Capra et Ovis	7	1	11	3	2	1
Tapia altaica	37	5	108	13	26	2
Sorex sp.	0	0	0	0	0	0
Lepus timidus	0	0	0	0	0	0
Lepus tolai	0	0	0	0	1	1
Ochotona sp.	0	0	0	0	0	0
Pterymos volans	0	0	0	0	0	0
Sciurus vulgaris	0	0	0	0	0	0
Tamia sibircus	0	0	0	0	0	0
Citellus sp.	1	1	0	0	0	0
Marmota baibacina	0	0	2	1	0	0
Castor fiber	0	0	4	2	2	1
Cricetus cricetus	3	1	9	3	0	0
Myospalax myospylax	1	1	1	1	0	0
Arvicola terrestis	1	1	1	1	0	0
Microtinae sp.	0	0	0	0	0	0
Canis lupus	0	0	5	1	0	0
Vulpes vulpes	0	0	5	2	0	0
Ursus arctos	3	2	1	1	0	0
Martes zibelina	0	0	0	0	0	0
Mustella altaica	0	0	0	0	0	0
Meles meles	1	1	0	0	0	0
Lutra lutra	0	0	0	0	0	0
Lynx lynx	0	0	0	0	0	0
Cervus elaphus sibericus	2	1	18	4	0	0
C. caprelous pygarus	36	3	60	5	12	1
Alces alces	0	0	3	1	0	0
Capra siberica	0	0	0	0	0	0
Pisces	0	0	3		3	3
Peptilia	0	0	0	0	0	0
Aves	4		31		1	
Indeterminable	1157		2663		292	

**Table excludes Layers 8B and 11 .*

Layers 8B, 10, and 13 all present material culture redeposition or commingling, and so the faunal data from these layers should not be incorporated into any analysis or reconstruction of Afanasievo animal economies. I have created a table comparing the distributions of medium and large-sized mammals throughout the eleventh and twelfth layers of the Pre-Entrance and Entrance Areas (Tbl.30). Caprines and cervids appear in abundance, especially Siberian roe deer (*Capreolus capreolus pygarus*). No argali (*Ovis ammon*) or Siberian ibex (*Capra siberica*)

were recorded, though Siberian ibex were recorded in other layers of the cave (Derevyanko & Molodin 1994).

The presence of wild taxa could be the result of hunting or natural animal activity. The identification of *Equus caballus* in the Eneolithic layers is questionable, as domesticated horse remains have not yet been verified in Afanasievo contexts. These specimens would be excellent candidates for ZooMS with chymotrypsin (see Paladugu et al. 2023). Caballoid remains could be submitted for both aDNA analysis and AMS radiocarbon dating to help identify the earliest domesticated horse remains in Siberia. ZooMS could also prove very helpful for refining the caprine attributions (see Chapter 05).

Tbl.30 Table comparing the distributions of medium and large-sized mammal remains from Denisova Cave.

	Pre-Entrance Area				Entrance Area	
	Layer 11		Layer 12		Layer 12	
	NISP	MNI	NISP	MNI	NISP	MNI
Equus caballus	2	1	0	0	2	1
Bos taurus	7	1	2	1	4	1
Sus scrofa	0	0	1	1	1	1
Capra et Ovis	68	9	26	2	11	3
Capra siberica	0	0	0	0	0	0
Alces alces	0	0	0	0	3	1
Cervus elaphus sibericus	8	2	0	0	18	4
C. caprelous pygarus	34	2	12	1	60	5
Ursus arctos	2	1	0	0	1	1
Canis lupus	0	0	0	0	5	1
Canis familiaris	4	2	0	0	4	2
Vulpes vulpes	0	0	0	0	5	2

Kara-Tenesh (Кара-Тенеш), Layers 03-04 (Pogožheva & Molodin 1978)

The Kara-Tenesh settlement site is located on the left bank of the Nizhny Kuyus River, 19 km upstream from its confluence with the Katun River, in the Chemalsky District of the Altai Republic (86°17'58.20" E, 51°2'33.64" N) (Pogožheva & Kadikov 1979, Pogožheva & Molodin 1978; Slavinsky & Rybin 2015). Kara-Tenesh was excavated in 1976 after a student named Aidar Olonew discovered a polished stone axe in the area following a mudslide in 1972 (Pogožheva & Kadikov 1979). The stratified site was reported as being occupied from the Paleolithic through the Medieval period (Pogožheva & Molodin 1978). Sheep, goat, horse, cattle, deer, elk/moose, bear, bird, and water vole bones were identified by N.D. Ovodov (Pogožheva & Molodin 1978). The faunal data from Kara-Tenesh was presented in the initial report (Pogožheva & Molodin 1978) and again in Kostinov & Stepanov (2010) **(Tbl.31**).

Tbl.31 Table of published faunal data from Kara-Tenesh (Pogožheva & Molodin 1978).

Taxon	Layer 4	Layer 3
Cattle	30	3
Caprine	555	193
Horse	60	4
Dog	x	2
Cervus sp.	70	8
Gazelle	50	6

While AMS radiocarbon dating has verified an Eneolithic cultural component at this site (Hermes et al. 2021), a lack of clear stratigraphy, significant disturbances caused by previous excavations, and the inclusion of Iron Age pottery within the Eneolithic cultural layers (Pogožheva & Molodin 1978) strongly complicate any interpretation of archaeofauna recovered from this layer. Although the third and fourth layers have been attributed to the Afanasievo, Afanasievo- associated material cultural finds were distributed throughout multiple layers of the site (Pogožheva & Molodin 1978). No age-at-death estimation has been provided. Several scholars have used the faunal data from these layers (Tbl.31) in subsequent comparisons of Afanasievo-associated faunal profiles, including the mixed assemblage from Maily Dugan (e.g. Frachetti 2012; Honeychurch 2021; Kostinov & Stepanova 2010; Shulga 2010).

Maily Dugan (Малый Дуган) (Stepanova 1990)

The Maily Dugan settlement site is located on the right bank of the Kuyum River across from the Ust-Kuyum complex in the Chemalsky District of the Altai Republic (Kosintsev & Stepanova 2010; Kungurova 1992; Stepanova 1990). Maily Dugan was discovered and excavated by N.F. Stepanova in 1987, revealing several features including hearths and dwellings as well as ceramic, lithic, faunal, and metal artifact assemblages (Kosintsev & Stepanova 2010). Problematically, although the site is stratified, the cultural layer beyond the Neolithic layer is not, and finds have been *typologically* associated with Bronze Age, Iron Age, and Medieval contexts (Kosintsev & Stepanova 2010). Afanasievo-attributed ceramics were recovered from every layer above the Neolithic layer of Maily Dugan.

The mixed nature of these assemblages greatly obscures any faunal analysis, though a shift has been proposed from a primary reliance on elk/moose (*Alces alces*) during the Neolithic to a more mixed economy incorporating domestic ungulates (i.e. cattle, sheep, and goat) (Kosintsev & Stepanova 2010; Krasnienko 2010). Additional recovered fauna include horse, dog, gazelle, roe deer, red deer, red fox, badger, otter, bird, hamster, and brown bear (Kosintsev & Stepanova 2010) (Tbl.31). Although it is not specified in the faunal report, the slashes in the table presumably represent NISP versus MNI counts. No age-at-death data appear to have been estimated, precluding any attempts at comparing and contrasting culling profiles throughout the periods of cultural occupation at Maily Dugan.

Tbl.32 Table of published faunal data from Maily Dugan (Stepanova 1990).

Taxon	Layer 1	Layer 2	Layer 3	Layer 4	Layer 5	Layer 6
Bos taurus	1/1	134/8	19/3	35/3	-	-
Ovis aries / Capra hircus	6/2	440/12	69/8	77/6	-	-
Ovis aries	1/1	196/11	42/8	44/6	-	-
Capra hircus	-	2/1	-	-	-	-
Equus caballus	15/3	84/8	5/2	3/2	-	-
Canis familiaris	-	2/1	2/1	3/1	-	-
Alces alces	-	2/1	-	-		-
Cervus elaphus		63/3	-	4/2	2/1	1/1
Capreolus pygarus	2/2	274/7	20/2	16/2	143/3	35/2
Procapra guturossa	-	-	1/1	-	-	-
Canis lupus	-	2/1	-	-	-	-
Vulpes vulpes	-	-	2/1	1/1	-	-
Meles leucurus	-	2/1	-	-	-	-
Lutra lutra	-	2/1	-	-	-	-
Ursus arctos	-	1/1	-	1/1	-	-
Cricetus cricetus	-			1		
Mammalia sp.	77	9700	830	670	287	66
Aves sp.	-	-	-	-	-	1

Nizhnyaya Sooru (Нижняя Соору), Layer 05 (Larin et al. 1998)

The Nizhnyaya Sooru settlement site is situated in the Nizhnyaya Sooru Valley of the Ongudai region in the Altai Republic of Russia (Tishkin et al. 2021) (Fig.7). The inter-mountain valley along the Karakol River is known even today for its ideal winter cattle-grazing conditions (Tishkin et al. 2021). Nizhnaya Sooru was first excavated in 1998 by Altai archaeologists surveying erosion in the Nizhnyaya Sooru Valley of the Altai Mountains in South Siberia (Kosintsev 2005; Larin et al. 1998; Tishkin et al. 2021; Yelin & Larin 1998). The test-pit excavation revealed a stone hearth feature from which 33 lithic artifacts, 25 ceramic artifacts, and a few hundred animal bones were recovered (Tishkin et al. 2021). The faunal profile was determined to reflect a heavy reliance on sheep exploitation (Tbl.33) (Kosintsev 2005; Tishkin et al. 2021).

Tbl.33 Table of published faunal data from Nizhnyaya Sooru (Larin et al. 1998).

Taxon	NISP	MNI
Caprine (*Ovis aries / Capra hircus*)	229	19
Horse (*Equus caballus*)	4	2
Cattle (*Bos taurus*)	41	5
Red Deer (*Cervus elaphus*)	2	1
Fox (*Vulpes vulpes*)	1	1
Badger (*Meles anakuma*)	1	1
Mammalia sp.	198	(Blank)

The recovered materials were associated with Afanasievo culture, though they were not radiocarbon dated until the twenty-first century (Hermes et al. 2020b ;Larin et al. 1998; Tishkin et al. 2021). Further excavations planned for 2020 had to be delayed due to the covid pandemic and were continued by Alexey Tishkin in 2021, revealing seven stratigraphic layers associated with up to four prehistoric Altaic cultures (Tishkin et al. 2021). These excavations uncovered an abundance of animal bones (numbering in the thousands) which are currently undergoing zooarchaeological analysis. The faunal assemblage is characterized by heavy fragmentation and the bones of small, medium, and large sized animals that are not easily distinguished from one another, resulting in numerous unsecure and low-resolution taxonomic assignments.

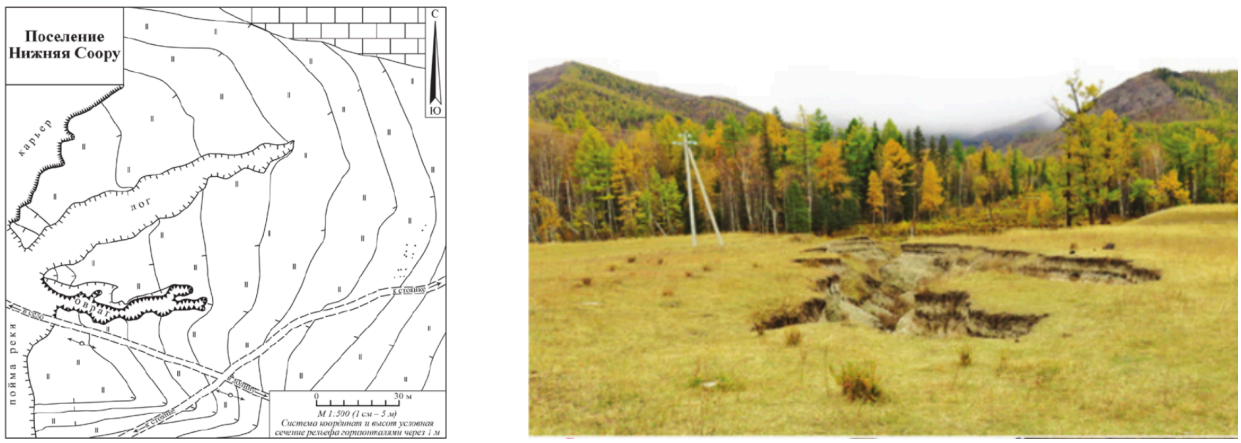


Fig.7 Illustration and picture of Nizhnyaya Sooru (Tishkin et al. 2021).

Partizanskaya Katushka (Партизанская Катушка), Layer 03 (Shulga 1998)

The Partizanskaya Katushka settlement was discovered by the P.I. Shulga in 1985 during a survey of the right bank of the Katun River, 1 km northwest of the village of Uznezya (Shulga 1998). The site was typologically associated with Eneolithic, Early Iron Age, and Medieval occupation based off of the ceramic assemblages (Shulga 1998). Without radiocarbon dating it is difficult to ascertain how secure the Afanasievo attribution to Layer 03 should be considered. The assemblage from the third layer is mixed at any rate, containing a significant number of Early Iron Age material culture finds (Shulga 1998). A number of animal bones (183) were recovered and recorded from Layer 03, of which 121 were identifiable to a taxon (Tbl.34). Percentages were reported in lieu of absolute counts, and these do not add up to 100% but 98.2%.

Tbl.34 Table of published faunal data from Partizanskaya Katushka (Shulga 1998).

Taxon	Cattle	Sheep/Goat	Sheep	Goat	Horse	Dog	Maral Deer	Roe Deer	Boar	Indeterm.
%	0.8%	21.4%	14%	7.4%	30.6%	0.8%	5.8%	15.7%	1.7%	?

Podsinushka (Подсинушка)((Grushin & Lyzhnikova 2009)

The Podsinushka settlement site is located near the Podsinushka village in the Northwestern foothills of the Altai Mountains (N 51 15.641, E 82 38.582) (Grushin & Lyzhnikova 2009; Grushin & Stepanova 2010). Podsinushka was initially discovered and excavated by S.P. Grushin and O.G. Lyzhnikova in 1993, and revisited by the same team again from 2005-2008 (Grushin & Lyzhnikova 2009; Grushin & Stepanova 2010). Although Afansievo-associated features such as hearths and dwellings containing an abundance of ceramics and stone tools were unearthed, virtually no faunal remains were preserved in the sediments (Grushin & Lyzhnikova 2009; Grushin & Stepanova 2010).

Tepsei-X (Тепсей X), Layer 11 (Gryaznov & Komarova 1979)

Uniquely, Tepsei-X is an Afanasievo-associated settlement site situated in the Minusinsk Basin as opposed to the Altai Mountains (Gryaznov & Komarova 1979; Vadetskaya et al. 2014). The site is located on the edge of a cliff overlooking the right bank of the Yenisei River and features eleven stratigraphic layers and two stone-lined hearths, all of which were excavated by M.N. Komarova in 1968 (Gryaznov & Komarova 1979; Vadetskaia et al. 2014). This site has since been described as a seasonal encampment (Vadetskaya et al. 2014). Stone tools, ceramics, and a small number of animal bones were recovered from the eleventh layer of Tepsei-X and associated with the Afanasievo (Gryaznov & Komarova 1979; Vadetskaia et al. 2014) (Tbl.35).

Tbl.35 Table of published faunal data from Tepsei-X (Gryaznov & Komarova 1979).

Taxon	**NISP**	**MNI**
Caprine	19	6
Horse	4	/
Cattle	1	/

Toora Dash (Тоора-Даш), Layers 06-07 (Semenov 1983)

Toora Dash was a stratified settlement situated on the right bank of the Yenisei River in the Ermakovsky district (Krasnoyarsk Territory) of Tuva (Semenov 1992, 1997, 2018; Kilunovskaya & Semenov 2019; Vadetskaya et al. 2014; Vasil'ev & Seminov 1993). Excavations led by V.A. Semenov from 1978–1984 revealed thirteen cultural layers spanning the Neolithic to the Medieval Periods (Semenov 1992, 1997, 2018; Kilunovskaya & Semenov 2019; Vadetskaya et al. 2014). The site of Toora Dash has, unfortunately, since been flooded and destroyed by the Sayano-Shushenskoye Reservoir following the construction of a hydroelectric power station (Semenov 1992, 1997, 2018; Kilunovskaya & Semenov 2019).

Layer 05 (covering 440 square meters) was determined to represent an Eneolithic stage above the Neolithic layers and associated with the Afanasevo, followed by an Okunevo occupation (Semenov 1992, 1997, 2018; Kilunovskaya & Semenov 2019; Vadetskaya et al. 2014). This layer contained a number of lithic and ceramic scatters as well as animal bones, most of which were found in association with stone hearths. Even outside of the Altai Mountains and the Minusinsk Basin, the archaeological site retains the typical aforementioned Eneolithic features of stone hearths constructed near a river.

The sixth and seventh layers which immediately follow the Afanasievo cultural layer have been attributed to an Okunevo occupation based upon the associated ceramic, stone, and metal artifact finds (Semenov 1992, 1997, 2018; Kilunovskaya & Semenov 2019). There does not seem to be any faunal data or report associated with any of these layers, though it has been noted that sheep limbs, bull and goat skulls, and fragmented animal bones were recovered from the seventh layer (Semenov 1997). These were later reported as “pits containing bulls’ and rams’ heads and smaller holes filled with the crushed bones of domestic animals.” (Kilunovskaya & Semenov 2019).

Ust’-Biyke-I (Усть-Бийке-I) (Semibratov & Majchikov 1997)

The Ust’-Biyke-I settlement site is located on the right bank of the mouth of the Biyke River, near the Yelanda village in the Chemalsky district of the Altai Republic (Semibratov & Majchikov 1997). Ust’-Biyke-I was initially discovered during a pedestrian survey in 1989 and excavated in 1996 by a team led by V.P. Semibratov (Hermes et al. 2021; Semibratov & Majchikov 1997). Six stratigraphic layers spanning the Mesolithic to the Eneolithic were uncovered, along with an abundance of ceramics, lithics, and some human remains (Hermes et al. 2021; Semibratov & Majchikov 1997). A combination of pottery analysis and AMS radiocarbon dating has been used to secure the Afanasievo site association (Hermes et al. 2021; Semibratov & Majchikov 1997). Although at least 45 “bone fragments” were found in the cultural layers (Semibratov & Majchikov 1997), it is not clear if any of them were determined to be non-human in origin. It appears that no information about faunal remains have been recorded from Ust’-Biyke-I, which was reported to be in critical condition by the end of the twentieth century (Semibratov & Majchikov 1997). Fishing tools recovered from the Afanasievo-associated layer (Semibratov & Majchikov 1997) suggest that fish exploitation formed a part of the Eneolithic subsistence strategy at Ust’-Biyke-I.

Uznezya-I (Узнезья-1), Layers 03-05 (Stepanova 1981, 1994)

The Uznezya-I settlement site is situated 1.5-2 km above the confluence of the Katun and Uznezya Rivers, on the left side of the river valley, in the Chemalsky District of the Altai Republic (Kungurov 2006; Stepanova 1981, 2012). Uznezya-I was discovered by N.F. Stepanova in 1980 (Stepanova 1981) and excavated by Stepanova and Kungurov between 1985 and 1989 (Kungurov 2006; Stepanova 1981, 2012). Uznezya-I was found to be a highly stratified site with occupation levels spanning the Eneolithic all the way to the Medieval period (Stepanov & Gorbunov 1994); unfortunately, the stratigraphy was reported as “broken” (Stepanova 2012) with ceramics from all periods distributed throughout (Stepanova 1981). The hearths from this layer were noted for their similarity to the hearths of Ust’-Biyke-I (Stepanova 1981).

Stepanova (1981, 2012) notes that of the few faunal remains recovered, roe deer were identified by A.V. Galchenko in an Afanasievo hearth context. Species counts of faunal remains from Uznezya-I were included in analysis of fauna from Nizhnyaya Sooru, without any stratigraphic context (Kostinev 2005) (Tbl.36). Kostinev (2005) also incorporated faunal data from Balyktyyul which matches the initial site report (Abdulganeev et al. 1982) perfectly (see Tbl.27 above), so it is likely that these data are accurate. Notably, Uznezya-I is the only Afanasievo site associated with yak remains. The faunal data recorded in Kostinev (2005) does not line up with Stepanova’s (1981, 2012) account of there being few (fragmented and poorly preserved) animal bones recovered in the Afanasievo-associated layers of Uznezya-I. Considering the mixed nature of the ceramic assemblages (which formed the basis for the initial Afansievo association of the third through fifth layers), it is likely that the archaeological fauna are also commingled.

Tbl.36 Table of published faunal data from Uznezya-I (Kostinev 2005).

Taxon	Caprine	Siberian Ibex	Yak	Horse	Kulan	Roe Deer	Bird
NISP	48	55	77	127	7	132	4

Zhelvak V (Желвак V), Layer 01 (Zhogova et al. 2023)

Zhelvak V is a stratified settlement site located 6 km north-west of Arzhan village in Tuva (Zhogova et al. 2023). The site was discovered during an extensive survey of the Kurtushibin range of the Sayan mountains and excavations began in 2017 (Zhogova et al. 2023). The excavations revealed evidence of Bronze Age to modern occupations, including by the Okunevo archaeological culture in the earliest layer, dated to ca. 2500–1700 BCE (Zhogova et al. 2023). The ceramic assemblage recovered from this layer was found to be similar to the Okunevo-associated ceramic assemblage from Toora Dash. Although the discovery of “a small pit containing bones of a young sheep” in the Okunevo-attributed layer and “a pit with lamb bones” in the subsequent Bronze Age layers were mentioned in the article detailing the site (Zhogova et al. 2023), the animal remains were not discussed and no faunal data were made available in the supplementary index. The other Bronze Age layers are not attributed to any

particular culture in the publication (i.e. Zhogova et al. 2023), such as the Andronovo or Karasuk archaeological cultures.

12.2. Outer Mongolia (ca. 3170–1915 BCE)

Although not currently associated with any particular archaeological cultures, the very recently excavated sites of Bagsagiin Bulan (see Taylor et al. 2020b), Biluut III (see Fitzhugh & Kortum 2011), and ZK513 (see Houle et al. 2022) represent the only three currently known Bronze Age archaeological settlement sites in Outer Mongolia with evidence of human occupation dating back to the Eneolithic and Early Bronze Age. Fortunately, the sites of Bagsagiin Bulan, Biluut, and ZK513 have all been excavated in keeping with modern excavation standards, have been securely dated with AMS radiocarbon dating, and feature faunal reports. I review these sites below, with an emphasis on their respective faunal data.

Bagsagiin Bulan (Багсагиин Булан) (Taylor et al. 2020b)

Bagsagiin Bulan is a stratified settlement site situated on a river terrace in the Darkhad Basin of Northern Mongolia (Taylor et al. 2020b). The site was initially surveyed by a team of archaeologists led by William Taylor, revealing a stone ring, central hearth, and post holes, and was subsequently excavated in 2017 (Taylor et al. 2020b). AMS radiocarbon dating of charcoal from Bagsagiin Bulan have demonstrated human occupation from the Early Bronze Age, with the oldest hearth charcoal sample dating to ca. 2500 BCE (concurrent with known Chemurchek occupation in Outer Mongolia more broadly) (Taylor et al. 2020b). A modest faunal assemblage was recovered from Bagsagiin Bulan, all of which were taxonomically identified with ZooMS. Unfortunately, all of the animal bones were radiocarbon dated to the Late Historical or Modern period, revealing nothing about the subsistence strategies of the Bronze Age occupants of Bagsagiin Bulan.

Biluut III (Билуут III) (Fitzhugh & Kortum 2011)

The non-stratified site of Biluut III in Tsengel sum (district) in Bayan Ulgii aimag (subdistrict) was initially excavated by a team of American and Mongolian archaeologists during the summer of 2012 (Fitzhugh & Kortum 2011). Although there may be additional archaeological features in the area of Biluut III which have not yet been excavated, charcoal from the central hearth feature has been AMS radiocarbon dated to ca. 2136–1907 BCE (Taylor et al. 2020b). This Early Bronze Age date coincides with the Chemurchek cultural phenomenon, though as with Bagsagiin Bulan, no archaeological culture has been associated with Biluut III. Other features of Biluut III include a double-walled stone structure and four stone-lined trough features (Fitzhugh & Kortum 2011; Taylor et al. 2020b). Over one thousand heavily fragmented and calcined mammal bones were recovered from the central hearth; those which retained diagnostic morphological characteristics were attributed to *Ovis* sp., *Capra* sp., and *Bos* sp. (Taylor et al. 2020b). Although ZooMS and bulk DNA metabarcoding was attempted on 25 specimens, they were unfortunately too poorly preserved for analysis. It remains unclear whether or not the caprines and cattle from Biluut III were domesticated or wild.

ZK513 (Trench ZK513-1) Layers 08, 11-12 (Houle et al. 2022)

ZK513 is a stratified archaeological habitation site situated in a modern pastoralist winter camp ca. 1.5 north of the Khar Usny Gol River in Zuunkhangai, Mongolia (Houle et al. 2022). ZK513 covers an area of approximately 70 × 40 meters and is positioned in an open steppe environment, surrounded by both prehistoric and historical monuments from the Bronze Age, Iron Age, and Turk-Uyghur periods (Houle et al. 2022). Surface finds of lithics and ceramics led to the discovery of ZK513 in 2017, and the site was subsequently excavated in 2018 by a team led by Jean-Luc Houle (Houle et al. 2022). Shovel probe tests, test excavations, and geoarchaeological sampling revealed two separate archaeological contexts in the middle and upper parts of ZK513 (Houle et al. 2022). Two units were selected for excavation; ZK5131-1, a 3 x 1 meter trench in the upper part of the site, and ZK513-2, a 2 x 2 trench in the middle of the site (Houle et al. 2022) (Fig.8).

The excavation of the ZK513-1 trench revealed 13 stratigraphic layers reaching 4000 years back into the archaeological record (Houle et al. 2022). Uniquely, ZK513-1 is the most deeply stratified pastoralist site of its kind to have been discovered in Mongolia (Houle et al. 2022). Evidence for human occupation is strongest in layers 1-8 and 11-12 and consists of lithic, ceramic, botanical, and faunal assemblages (Houle et al. 2022). AMS radiocarbon dating of dental enamel has secured an Eneolithic & Early Bronze Age context for Layers 11-12, while charcoal from Layer 08 has also been dated to this period (Houle et al. 2022) (Tbl.37). The AMS radiocarbon dates for these layers do not line up perfectly with the periodization model adapted for this dissertation (Tbl.38), and there is a notable disordering of the stratigraphic radiocarbon dates recorded for Layers 8-10 (Houle et al. 2022). The reason for this radiocarbon dating reversal is currently unclear, but may be related to shifts in the depositional process and the incorporation of windblown sediments from more arid regions (Houle et al. 2022).

Tbl.37 Table of radiocarbon dates of samples from Trench ZK513-1 (Houle et al. 2022).

Layer	Material	Lab Code	Date
Layer 08	Charcoal	D-AMS034378	2020 - 1780 BCE
Layer 09	Charcoal	D-AMS034379	1890 - 1690 BCE
Layer 10	Charcoal	D-AMS034380	1410 - 1230 BCE
Layer 11	Enamel	AA11276381	2010 - 1770 BC
Layer 12	Enamel	AA112764	2030 - 1880 BCE

**All radiocarbon dates are calibrated.*

Tbl.38 Table of Bronze Age chronologies for ZK513.

Date	Period (Houle 2014)	Period (Houle et al. 2022)	Period (this dissertation)
2020 - 1780 BCE	Early / Middle Bronze Age	Early Bronze Age	Eneolithic & Early Bronze Age – Middle Bronze Age
1890 - 1690 BCE	Early / Middle Bronze Age	Middle Bronze Age	Middle Bronze Age
1410 - 1230 BCE	Late Bronze Age	Late Bronze Age	Middle Bronze Age –Late Bronze Age
2010 - 1770 BCE	Early / Middle Bronze Age	Early Bronze Age	Eneolithic & Early Bronze Age –Middle Bronze Age
2030 - 1880 BCE	Early / Middle Bronze Age	Early Bronze Age	Eneolithic & Early Bronze Age –Middle Bronze Age

Thousands of bone and bone fragments were excavated from the deep stratigraphic layers of ZK513-1 (n=2735), possibly including some of the oldest domesticated animal remains to have yet been found in Mongolia (Houle et al. 2022). Butchery marks were recorded on eleven of the bones, the oldest being a haphazardly disarticulated caprine astragalus from Layer 12 and the most recent being a more carefully disarticulated caprine pelvis from Layer 7 (Houle et al. 2022). This has been interpreted as a refinement of butchery practices over time from the Eneolithic and Early Bronze Age to the Iron Age, possibly in relation to pastoralist emergence and development (Houle et al. 2022).

Three hundred and twenty-two bone fragments were recovered from the undisturbed Eneolithic and Early Bronze Age Layers (11-12), though only 13 of them were morphologically identifiable (Tbl.39). From the reversed layer (Layer 08), only 4 specimens out of 447 could be morphologically identified. Species identified from Layers 08, 11, and 12 include *Ovis* sp., *Capra* sp., *Bos* sp., and *Equus* sp.. Upcoming ZooMS analysis of this assemblage, and my own preliminary ZooMS analysis, will hopefully help to clarify the taxonomic composition of the Eneolithic and Early Bronze Age fauna from ZK513-1. Though, aDNA analysis will still be necessary to establish which taxa were wild and which were domesticated (see Chapters 04–06).

Tbl.39 Table of published faunal data from Trench ZK513-1 (Houle et al. 2022).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Layer 08	0	0	4	1	0	0	447
Layer 11	0	0	1	1	0	1	127
Layer 12	3	1	5	0	0	1	195

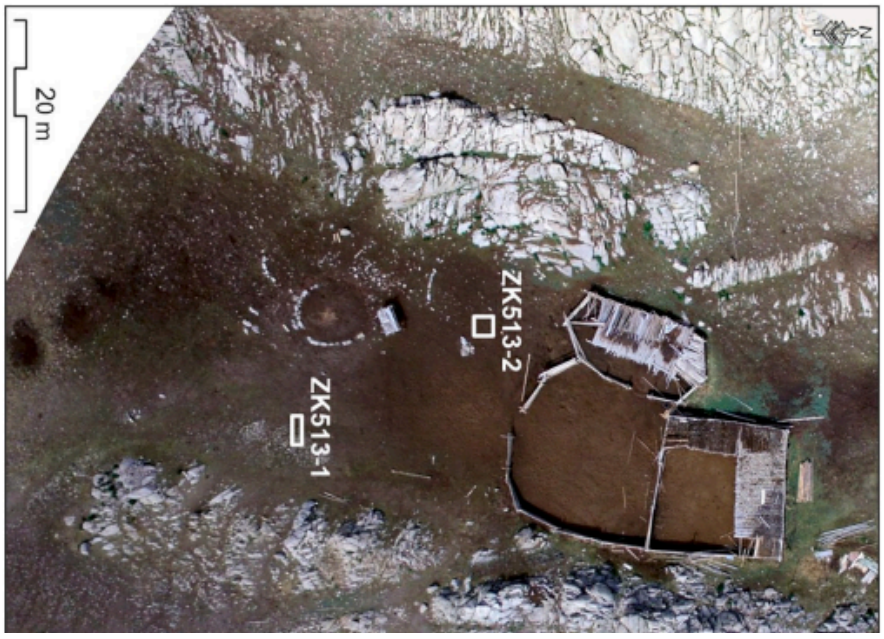


Fig.8 Photograph of ZK513 including Trench ZK513-1 (Houle et al. 2022).

13. Middle Bronze Age Sites

13.1. Southern Siberia (ca. 1700–1500 BCE)

The burial monuments associated with the Andronovo (Fedorovo) are much better understood than their settlement sites in Southern Siberia (see Legrand 2006 for a detailed overview). The Minusinsk Basin tombs which archaeologists have rediscovered are all located near bodies of water and were originally enclosed by circles or rectangles of local stones (Gryzanov 1969; Legrand 2006). Lacking a large stone source, any such tombs that might have been constructed in the Altai region are presumed to have been earthworks that did not preserve in the archaeological record (Gryzanov 1969). As with the Afanasievo, Okunevo, Karakol, and Yelunino archaeological cultures of the Eneolithic and Early Bronze Age, settlement sites of the the Middle Bronze Age Andronovo (Fedorovo) archaeological cultural complex are far less common than burial sites in Southern Siberia (Legrand 2006; Svatko et al. 2013). In the literature, it is written that the only archaeological site which has been securely identified as a settlement (and was possibly a livestock enclosure) was discovered at Klyuchi near the Kamchatka River in the Yenisei Valley (Gryzanov 1969; Legrand 2006).

Although Gryzanov (1969) commented that a number of animal bones (and little else) were recovered from the Klyuchi site, he did not cite any sources. Legrand (2006) connects this site to Maksimenkov (1978) and elaborates that domesticated cattle, caprine, and horse bones were recorded in Maksimenkov's (1978) report (as were roe deer). I will go further in-depth about the site excavation and faunal remains recovered below. This same report (Maksimenkov 1978) also mentions an Andronovo settlement of the Yenisei in Central Siberia named "Obyul" situated on the right bank of the Obyul River, 1 km away from the village of Ivanovka. Obyul was excavated by N.L. Chlenova in 1957, though no report from Chlenova is listed in Maksimenkov's (1978) review of the site. Chlenova reportedly identified over 100 ceramics and casting molds that he associated with the Andronovo, Tagar, and Kulaiskaya (Fominsky stage) archaeological cultures (Maksimenkov 1978). It is unclear if the site was stratified, though four open hearths were identified. Animal bones are mentioned, but no faunal data are provided (Maksimenkov 1978).

Klyuchi (Maksimenkov 1978)

Klyuchi is a non-stratified settlement site located in a basin off of the Northwestern bank of the Chernovava River Valley (Maksimenkov 1978). Maksimenkov excavated this site in 1967, revealing a Southeastern and a Northwestern structure, as well as a poorly-preserved third structure (Maksimenkov 1978). Only a single cultural layer was identified in the turf, containing 130 ceramic fragments and 34 taxonomically attributable animal bones (Tbl.40) that were associated with the Andronovo archaeological culture; the majority of these were recovered from the Southwestern structure (Maksimenkov 1978). Maksimenkov (1978) notes that fragmented animal bones were also found scattered throughout the structure, severely complicating MNI estimates. No NISP is provided.

Tbl.40 Table of published faunal data from Klyuchi (Maksimenkov 1978).

Bones	Cow	Horse	Sheep	Roe Deer
Pelvis	1	3	3	0
Scapula	0	3	2	3
Heel Bone	0	1	0	0
Astragalus	0	1	1	0
Patella	0	1	0	0
Vertebra	0	4	0	3
Rib	2	0	0	8
Teeth	2	0	1	0
Humerus	0	0	1	3
Femur	0	0	2	2
Tibia	0	0	1	0
Radius / Ulna	0	0	0	1
Phalanges	0	0	1	0
Skull	0	0	0	1
Metapodial	0	0	0	1
Total	5	13	12	4

13.2. Outer Mongolia (ca. 1915–1350 BCE)

Two settlement sites in Outer Mongolia have been dated to the Middle Bronze Age– Tsagaan Asga (see Taylor et al. 2020b; Taylor 2024) and ZK513 (see Houle et al. 2022). Both sites were only recently excavated and have been securely dated with AMS radiocarbon dating, though a faunal report has only been published for ZK513. I review the archaeology of Tsagaan Asga and ZK513 below, as well as the Middle Bronze Age zooarchaeology of the ZK513-1 Trench from ZK513.

Tsagaan Asga (Тсараан Асга) (Taylor et al. 2020b)

Tsagaan Asga is a non-stratified settlement site with ritual features situated in the eastern quarter of the Altai Tavan Bogd National Park near Dayan Nuur (Taylor et al. 2020b). It was discovered during a series of archaeological surveys by a team led by William Taylor (Taylor et al. 2020b) and subsequently excavated in 2017 (pers.comm. Will Taylor 2024). Sheep bones recovered from Tsagaan Asga have been AMS radiocarbon dated to ca. 1626–1530 BCE (Taylor et al. 2020b), coinciding with the Munkhkhairkhan cultural phenomenon (though, the site has not been attributed to any archaeological culture). The results of the ZooMS analysis of 33 of the recovered fauna has been published (Tbl.41), establishing the presence of *Ovis* sp., *Bos* sp., and possibly wild ungulates (e.g. *Cervus* sp.) at the site (Taylor et al. 2020b). It has been suggested that either most or all of these taxa were domesticated, and that Tsagaan Asga was a Middle Bronze Age pastoralist encampment (Taylor et al. 2020b).

Tbl.41 Table of published Middle Bronze Age faunal data from Tsagaan Asga (Taylor et al. 2020b).

Ovis sp.	*Bos* sp.	*Ovis / Capra / Capreolus / Cervus / Saiga / Gazella* sp.
16	4	13

ZK513 (Trench ZK513-1) Layer 09 (Houle et al. 2022)

The excavation and Bronze Age chronology of the stratified settlement site of ZK513 has already been introduced, and discussed in its Eneolithic and Early Bronze Age context (see section “12.4.1.”). The Middle Bronze Age (ca. 1915–1350 BCE; Tbl.42) layers of the site are arguably limited to Layer 09, though there is some overlap with Layers 08 and 10-12. For simplicity and fluidity, only Layer 09 of ZK513-1 will be attributed to the Middle Bronze Age and overviewed here. Although this chapter has segmented ZK513 by its radiocarbon-dated chronological contexts for consistency, a more useful approach would be to discuss the site as a whole. I will do so further into this dissertation when discussing the results of my ZooMS analysis of selected samples from the ZK513-1 faunal assemblage (see Chapter 21).

Tbl.42 Table of radiocarbon dates from Trench ZK513-1 (Houle et al. 2022).

Layer	Material	Lab code	Date	Period (Houle et al. 2022)	Period (this dissertation)
Layer 8	Charcoal	D-AMS034378	2020 - 1780 BCE	Early Bronze Age	Eneolithic & Early Bronze Age–Middle Bronze Age
Layer 9	Charcoal	D-AMS034379	1890 - 1690 BCE	Middle Bronze Age	Middle Bronze Age
Layer 10	Charcoal	D-AMS034380	1410 - 1230 BCE	Late Bronze Age	Middle Bronze Age–Late Bronze Age
Layer 11	Tooth Enamel	AA11276381	2010 - 1770 BCE	Early Bronze Age	Eneolithic & Early Bronze Age–Middle Bronze Age
Layer 12	Tooth Enamel	AA112764	2030 - 1880 BCE	Early Bronze Age	Eneolithic & Early Bronze Age–Middle Bronze Age

**All radiocarbon dates are calibrated.*

A very modest number of animal bone finds (22 in total) were recovered from Middle Bronze Age Layer 09, only two of which could be morphologically identified to a taxonomic grouping (Houle et al. 2022) (Tbl.43). One sample was identified as caprine (*Ovis* sp. or *Capra* sp.) and another as cattle (*Bos* sp.). While the very low sample number (n=2) precludes any reconstruction or interpretation of Middle Bronze Age animal management strategies (see Chapter 07–09), the biomolecular verification of the presence of domesticated cattle, sheep, or goat, would be valuable. The ZooMS results from my own analysis of a small sample of specimens from Layer 09 will be discussed in the results section of this dissertation.

Tbl.43 Table of published Middle Bronze Age faunal data from Trench ZK513-1 (Houle et al. 2022).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Layer 09	0	0	1	0	0	0	20

14. Late Bronze Age Sites

14.1. Southern Siberia (1500–900 BCE)

Thousands of ancient graves entombed within hundreds of cemeteries have been associated with the Karasuk archaeological culture complex inside the Minusinsk Basin alone (Gryzanov 1969; Legrand 2006). Less than a quarter of these graves contained animal bones (Jettmar 1950). Karasuk-associated tombs are very similar to those attributed to the Andronovo (Fyodorovka) complex, though presenting more complexity and variety in their stone assembly (Gryzanov 1969; Legrand 2006). Karasuk settlement sites in Southern Siberia were instead constructed partially beneath ground from wooden posts solidified with wattle-and-daub (i.e. clay and branches) (Legrand 2006; see also Honeychurch 2014). Gryzanov (1969) notes only the settlement of Kammeny (or Kamenniy) Log I in the Yenisei Valley.

Legrand (2006) attributes seven settlement sites to the Karasuk, though only three are actually named: Tunchuch (Sebas'tjanova 1977), Kopenskoe (cited as Savinov 1996), and Torgazhak (Savinov 1996). Kamenniy Log I might be the fourth. Kopenskoe and Toragazhak are also noted as Karasuk settlement sites by Honeychurch (2014), along with Kamenniy Log I. There seems to be a miscitation regarding Kopenskoe, so I will not discuss it further. I was also unable to locate an original report for Kamenniy Log I. Drawing from the literature and reports that I was able to find, I discuss the settlement sites and associated faunal data of Toragazhak (Sebas'tjanova 1977) and (Savinov 1996) Tunchuch below.

Tunchuch (Тунчуч) (Sebas'tjanova 1977)

Tunchuch is a 45,000 square meter settlement site located 6km away from Askiz station, beneath the mountain it was named for (i.e. Tunchuch) in Khakassia (Sebas'tjanova 1977). The site consists of log, clay, and stone slab dwellings heavily damaged by years of plowing (Sebas'tjanova 1977). A single cultural layer was identified, from which ceramic fragments, a stone pendant, a bone buckle, and animal bones were recovered (Sebas'tjanova 1977). There is no faunal report for this site, though a cluster of ram jaws is mentioned (Sebas'tjanova 1977).

Torgazhak (Торгажак), Layers 01-07 (Savinov 1996)

Torgazhak (or Torgajak) is a stratified settlement site in the southern Minusinsk Basin that was excavated by D.G. Savinov from 1988-1990 (Savinov 1996) (Fig.9). The site is considered to have belonged entirely to the Late Bronze Age, and to the Karasuk archaeological culture specifically (Savinov 1996). Savinov (1996) associated the site with the 10th and 11th centuries BC, which would place it securely within the Karasuk period of Southern Siberia (following Poliakov & Svyatko 2021), though these dates have not been confirmed with any radiocarbon measurements that I am aware of. Torgazhak spans more than 1300 meters, containing seven individual dwellings from which several archaeological assemblages were recovered (Savinov 1996).

The ceramic assemblage itself is estimated to have equaled some 300-400 vessels, 202 of which were reconstructed by archaeologists (Savinov 1996). Other finds included bronze sickles, arrow heads, horse harness paraphernalia, pebbles with geometric designs, and artistic expressions of horses in sculpted stone and tiles (Savinov 1996). Hundreds of animal bones were also recovered (Savinov 1996), and the faunal report from Torgazhak (Tbl.44) is thorough. The report (Savinov 1996) contains clear NISP and MNI counts for each cultural layer as well as a total MNI count. Select faunal remains are illustrated in the back of the report (Savinov 1996) (Fig.10).

The peoples of Torgazhak clearly engaged in domesticated horse husbandry, as evidenced by the recovery of horse harnesses and the prominent depiction of horses in sculpture and tiles (Savinov 1996). Higher degrees of mobility and intensified horseback riding as practiced amongst the Karasuk archaeological culture have been both argued for (Legrand 2006; Savinov 1996) and disputed against (Honeychurch 2014) using this same material and stylistic evidence from Torgazhak. At any rate, domesticated horse husbandry in general at Torgazhak is further supported by the recorded identification of at least 26 “horses” (no scientific nomenclature), though how many of these actually represent domesticated horses is not currently known.

There is little reason to doubt that domesticated horses, cattle, sheep, and goats were present in a Late Bronze Age site that also presents evidence of cereal cultivation. It is very likely that the occupants of Torgazhak were either mostly-sedentary or semi-sedentary agropastoralists who also hunted wild boar, cervids, and small game, and fished. Savinov (1996) remarks upon the surprising lack of fishbones recovered from the site (which is near to a river) and concludes that fishing was unlikely even a secondary economic activity. Savinov (1996) interprets the site, overall, to have been a seasonal summer encampment. It should be noted that Savinov’s (1996) narrative that Torgazhak was a summer encampment site, and the general idea that Karasuk peoples constructed seasonal dwellings, has since been challenged by other scholars (e.g. Honeychurch 2014; Legrand 2006).

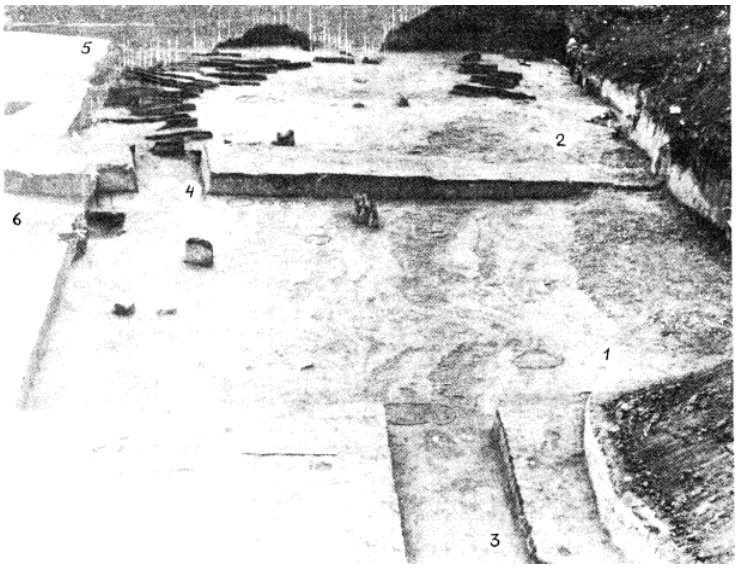
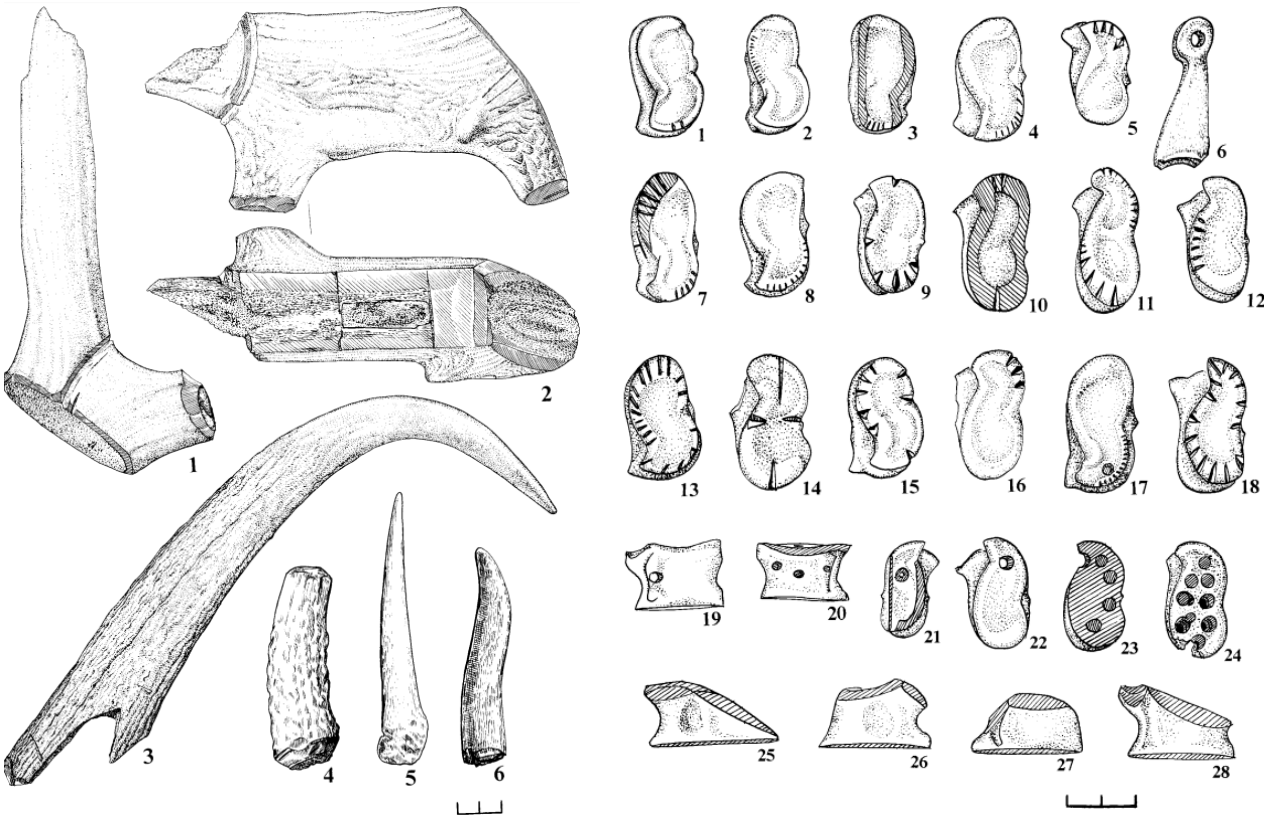


Fig.9 Photo of the excavation of Torgazhak (Savinov 1996).

Tbl.44 Table of published faunal data from Torgazhak (Savinov 1996).

	Layer 01		Layer 02		Layer 03		Layer 04		Layer 05		Layer 06		Layer 07		Ямы (Pits)	
Taxa	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI
Sheep	377	25	51	11	58	6	57	11	55	13	102	5	62	5	11	3
Goat	35	4	3	1	13	3	6	2	5	1	8	2	17	4	2	1
Cattle	251	17	20	3	55	2	37	2	31	3	117	5	114	3	11	2
Horse	145	11	21	3	37	2	11	2	27	2	51	3	36	2	5	1
Dog	2	1	1	1	1	1	0	0	0	0	1	1	1	1	0	0
Roe deer	80	8	18	4	14	5	6	3	14	5	20	5	6	3	0	0
Saiga	14	2	8	1	9	2	3	2	9	1	2	1	7	1	0	0
Maral	0	0	3	1	3	1	1	1	0	0	1	1	4	2	0	0
Argali	18	3	0	0	0	0	0	0	0	0	0	0	3	2	0	0
Moose	9	2	0	0	0	0	0	0	0	0	0	0	2	1	0	0
Bear	2	?	0	1	1	0	0	0	0	0	0	0	0	0	1	1
Boar	16	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fox	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hare	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ibex	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Wolf	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Badger	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
Bird	3	?	0	0	0	0	0	0	0	0	2	1	0	0	0	0
Fish	3	?	1	1	0	0	2	1	1	1	0	0	2	?	0	0

Fig.10 Illustrations of faunal remains recovered from Torgazhak (Savinov 1996).



14.2. Outer Mongolia (ca. 1350–910 BCE)

"...what is known of the actual subsistence economy of Late Bronze Age Mongolia is, not surprisingly, very little. But this is to be expected of a type of archaeology that has been mainly interested in burials, ritual sites and objects of fine craftsmanship. Botanical remains and animal bones have not been given the same attention—especially those from domestic contexts. As a result, interpretations regarding the nature of Late Bronze Age subsistence practices has to date remained speculative." (Houle 2010)

Although Late Bronze Age settlement sites are reported as being more abundant than earlier Bronze Age sites in Outer Mongolia (Honeychurch 2015; Houle 2014), there is a noticeable paucity of publications overviewing them. The exception to this is the reporting of the settlement sites excavated in the Khanuy River Valley (Houle 2010), as well as the previously discussed stratified ZK513 site in the Khan Khökhii Mountains (Houle et al. 2022), all of which fall under the broader region of the Khangai Mountains in Central-Northwestern Outer Mongolia (Fig.11). A total of fourteen sites excavated in the Khanuy River Valley were determined to have been occupied during the Late Bronze Age (Houle 2010). I overview their excavation and associated faunal remains below, alongside the Late Bronze Age layer (Layer 10; Houle et al. 2022) of the ZK513-1 Trench.

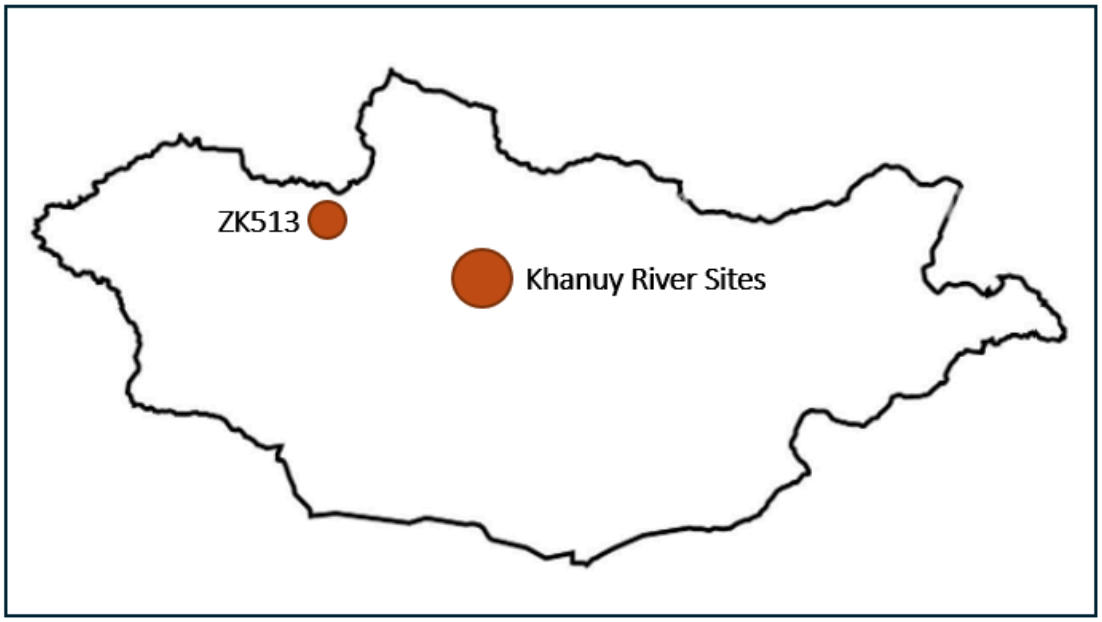


Fig.11 Distribution of Late Bronze Age settlement sites across Outer Mongolia.

SP22E-BMK (Houle 2010)

SP22E-BMK is situated within a flat, grassy valley by the western foothills of the Khanuy River Valley (Houle 2010). It is the largest of the settlement sites excavated, covering ca. 20 hectares (Houle 2010). A seasonal stream runs through the stratified site, which in modern times is the site of two or three winter encampments (Houle 2010). SP22E-BMK is surrounded by 17 burials and was occupied during the Late Bronze Age, the Iron Age, and possibly into the Turkic Period (Houle 2010). Excavations at the site went approximately 20 cm into the ground while archaeological finds were concentrated 10 - 15 cm deep (Houle 2010). The ceramic assemblage recovered from SP22E-BMK consisted of 112 pottery sherds, only 36 of which were associated with the Late Bronze Age (Houle 2010). Although 157 animal bone fragments were retrieved from the Late Bronze Age contexts of SP22E-BMK, only 2 of them could be identified to a genus level resolution (i.e. *Bos* sp., *Equus* sp.) (Houle 2010) (Tbl.45).

Tbl.45 Table of published faunal data from SP22E-BMK (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	1	0	1	0	0	0	0	1	154	0	157

Although Houle (2010) wrote that *"notably faunal remains associated with all four main domesticates for this period of time [The Late Bronze Age], that is, sheep, goat, horse and cattle"*, there are no actual identifications of sheep or goat. There were, however, 154 animal bones that were determined to have belonged to "medium mammals"; these could have just as easily come from cervids such as musk deer (*Moschus* sp.) or other wild game such as argali (*Ovis ammon*) or ibex (*Capra siberica*).

SP26E-WFA (Houle 2010)

SP26E-WFA is a stratified settlement site on a grassy slope divided by a seasonal stream in the western foothills of the Khanguy Valley (Houle 2010). The site is southwest of almost a dozen burials, and in modern times is the location of two winter encampments (Houle 2010). Excavations at SP26E-WFA reached ca. 15-20 cm depth, with the majority of archaeological materials being concentrated at depths between 10 and 15 cm (Houle 2010). The finds included a ceramic assemblage of 112 pottery sherds and a faunal assemblage (Houle 2010). Fifty-six of the pottery sherds were attributed to the Late Bronze Age, as well as a total of 134 animal bone fragments (Tbl.46). Only 18 of these fragments were morphologically identifiable to genus, and were reported by Houle (2010) as having come from domesticated sheep, goat, cattle, and horse. No deer or wild game were mentioned.

Tbl.46 Table of published faunal data from SP26E-WFA (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	4	0	2	9	1	2	0	28	79	9	134

SP26E-MAC (Houle 2010)

SP26E-MAC is a stratified settlement site situated on a high terrace with largely unfavorable habitation conditions (Houle 2010). There is no water or and little shelter available, and the area is no longer occupied in modern times (Houle 2010). This has led Houle (2010) to speculate that SP26E-MAC could have held a ritual and social significance that outweighed the poor living conditions it offered (e.g. constant wind exposure), possibly by proxy of it being located in the overall Khanuy River Valley settlement pattern. There are six burials near to SP26E-MAC, which is one of the smallest settlement sites unearthed by Houle (Houle 2010). Despite this, a large number of ceramic sherds and faunal remains were recovered from this site. Reaching 25 cm deep, but concentrated largely between 10 and 20 cm, a total of 496 pieces of pottery were recovered (Houle 2010). The ceramic assemblage was determined to be Late Bronze Age (no. 61) and Iron Age (no. 435) in origin (Houle 2010). Unfortunately only 5 animal bone fragments were associated with a Late Bronze Age context, none of which could be attributed to genus (Tbl.47).

Tbl.47 Table of published faunal data from SP26E-MAC (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	0	0	0	0	0	0	0	2	1	2	5

SP31E-JUL (Houle 2010)

Of all the sites excavated by Houle in the Khanuy River Valley, the settlement site named SP31E-JUL situated in the western foothills housed the largest number of people throughout its Bronze and Iron Age periods of occupation (Houle 2010). In modern times, only one winter campsite is known to be maintained in the grassy terrain (Houle 2010). Surprisingly, only a single burial was discovered in the vicinity of SP31E-JUL (Houle 2010). Excavations reaching a depth of between 15 - 30 cm revealed hundreds of ceramic sherds and animal bones, with the majority of these finds being recovered from depths between 10-15 cm (Houle 2010). One hundred forty-nine pottery sherds were determined to have been manufactured during the Late Bronze Age, and 111 animal remains were associated with the same period (Tbl.48). Although none of the bone fragments could be determined to a taxon, they were nonetheless reported as having belonged to domesticated animals; the large mammals (n=10) were unofficially attributed to horse or cow, and the medium mammals (n=52) were unofficially attributed to sheep and goat. 49 specimens could not be assigned a higher resolution than “mammal”.

Tbl.48 Table of published faunal data from SP31E-JUL (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	0	0	0	0	0	0	0	10	52	49	111

SP31E-QUE (Houle 2010)

SP31E-QUE is a settlement site situated in a grassy stretch of the western foothills of the Khanuy River Valley and vivisected by a seasonal stream (Houle 2010). Spanning roughly a dozen hectares, the site was estimated to have featured the second highest prehistoric population density (after SP31E-JUL) in the Khanuy River Valley settlement pattern, though only two burials have been located in the area and in modern times only a single winter camp is maintained (Houle 2010). SP31E-QUE was excavated to maximum depths ranging between 15 and 25 cm, revealing ceramic and faunal assemblages concentrated in depths between 10 and 15 cm (Houle 2010). The assemblages were determined to be Late Bronze Age and Iron Age in origin, with 166 out of 354 pottery sherds being attributed the Late Bronze Age (Houle 2010). Fifty-nine animal bone fragments were also associated with the Late Bronze Age, though only 10 could be assigned a genus-level resolution via morphological analysis (Houle 2010) (Tbl.49). Equids, large bovids, and caprines were all reported, as well as medium and large-sized mammals.

Tbl.49 Table of published faunal data from SP31E-QUE (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	2	2	2	4	0	0	0	15	34	0	59

SP27E-MTC (Houle 2010)

SP27E-MTC is a stratified settlement site situated within 100 meters of the Khanuy River (Houle 2010). The site spans less than 1 hectare of land characterized by grassy and feather-like vegetation and is located at the exact spot as a summer encampment that is maintained in modern times (Houle 2010). There are no known burials onsite or in the immediate surrounding area (Houle 2010). Excavations at SP27E-MTC reached depths of 15 cm and the bulk of ceramic and faunal finds were recovered from depths of between 5 and 10 cm (Houle 2010). Both assemblages were quite modest with the ceramic assemblage consisting of only 29 sherds, 20 of which were attributed to the Iron Age and the remainder attributed to the Late Bronze Age (Houle 2010). Although only 13 animal bone fragments from SP27E-MTC were determined to be Late Bronze Age in origin, this assemblage is one out of only two from sites in the Khanuy River Valley excavations led by Houle which includes specimens identified as wild game (i.e. *Moschus* sp.) (Houle 2010) (Tbl.50). Although the faunal table lists only "*Moschus* sp.", Houle identifies the fragment as "*Moschus moschiferus"* in his overview of SP27E-MTC (Houle 2010). Two equids were also identified at the site, along with 1 large mammal and 7 medium mammals.

Tbl.50 Table of published faunal data from SP27E-MTC (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	0	0	2	1	0	0	i	1	7	1	13

SP32E-MAB (Houle 2010)

SP32E-MAB is a stratified settlement site situated on a flat, grassy plain approximately 200m away from the Khanuy River Channel (Houle 2010). In modern times, a single campsite is generally maintained in this small area (ca. 1 hectare) throughout the summer (Houle 2010). Significantly, the only bronze arrowhead found in the courses of these Khanuy River Valley excavations was found at SP32E-MAB (Houle 2010), which might have been used for hunting wild game. Some of the shallowest excavations of the series were conducted here, digging only as far as 15 cm (except for one unit which reached 30cm deep), with the abundance of archaeological finds being recovered from between 5 and 10 cm deep (Houle 2010). Two hundred thirty-two pottery sherds were unearthed and 111 were attributed to the Late Bronze Age, as were 66 animal bones (Houle 2010) (Tbl.51). The overwhelming majority of these were not morphologically identifiable to a taxonomic group and were instead assigned size-based classifications, though 2 equids and 1 caprine were identified through morphological analysis.

Tbl.51 Table of published faunal data from SP32E-MAB (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	0	0	2	1	0	0	0	4	36	11	54

SP32E-SHA (Houle 2010)

SP32E-SHA is a settlement site situated on a flat and grassy expanse of land (less than 1 hectare), approximately 100 meters away from the Khanuy River (Houle 2010). There are no burials near to the site, which in modern times hosts a large summer campsite (Houle 2010). SP32E-SHA was excavated as deep as 25 cm, though the majority of archaeological materials were recovered from depths between 10 and 15 cm (Houle 2010). The ceramic assemblage uncovered totalled 159 pottery sherds, 40 of which were attributed to the Late Bronze Age; the remainder were assigned Iron Age contexts (Houle 2010). A substantial faunal assemblage was also unearthed and a total of 101 animal bones were determined to have been Late Bronze Age in origin (Houle 2010) (Tbl.52).

Tbl.52 Table of published faunal data from SP32E-SHA (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	0	0	0	6	6	2	2	5	70	10	101

Nearly two-thirds of the animal bones could only be morphologically identified to a size-based taxonomic determination, with 70 being reported as “medium mammals”. Two bone specimens were identified as musk deer, and as with the deer bone fragments from SP27E-MTC, they were recorded as *Moschus* sp.in the faunal table of Houle’s (2010) report, but written about as being “*Moschus moschiferus”*. The presence of wild game and the large number of unidentified medium-sized mammals at SP27E-MTC raises questions about hunting reliance and the prevalence of herding in the Khanuy River Valley during its Late Bronze Age occupation,

especially considering the presence of arrowheads and stone tools recovered from SP32E-MAB and SP11W-SAL, respectively.

SP07E-HUN (Houle 2010)

SP07E-HUN is a stratified settlement site situated with a deep, grassy, and slightly-sloping valley adjacent a now dried-up tributary (Houle 2010). The site covers approximately 2.3 hectares, is not located in the proximity of any burials, and in the present-day is home to a single winter campsite (Houle 2010). SP07E-HUN was excavated to depths between 20 and 30 cm throughout the various units, with the majority of the finds being recovered from depths between 10 and 15 cm (Houle 2010). Twenty-seven of the 69 ceramic sherds recovered from SP07E-HUN were attributed to the Late Bronze Age while the remainder were determined to belong to Iron Age contexts (Houle 2010). Five animal bone fragments were also attributed to the Late Bronze Age, only one of which was morphology diagnostic enough to even be designated a size-classification; the other four were reported as indeterminable mammals (Houle 2010) (Tbl.53).

Tbl.53 Table of published faunal data from SP07E-HUN (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	0	0	0	0	0	0	0	0	1	4	5

SP07E-SOV (Houle 2010)

SP07E-SOV is a stratified settlement site situated within a flat, grassy, and eastward-facing valley falling within Zone B of the Khanuy River Valley excavations (Houle 2010). Although the site measures just under 5 hectares it is in modern times occupied by only a single winter encampment (Houle 2010). SP07E-SOV is not surrounded by or in the proximity of any known burials. The settlement site was excavated to depths between 10 and 20 cm (40 cm in one unit), revealing archaeological finds scattered throughout most of the strata deeper than 5 cm (Houle 2010). Some of the finds within the deepest contexts have been considered to have been disturbed and redeposited by rodents (Houle 2010). The bulk of the ceramic assemblage was determined to have originated from the Late Bronze Age (133 pottery sherds out of 187 in total), with a secondary Iron Age context. No faunal remains were recovered from SP07E-SOV, despite the sizable ceramic assemblage uncovered.

SP10E-TOP (Houle 2010)

SP10E-TOP is a settlement site covering roughly 7.4 hectares in Zone B of Houle's excavations in the Khanuy Valley (Houle 2010). It is one of only two sites discovered in Zone B that are situated adjacent to slope burials (Houle 2010). SPI10E-TOP is characterized by grassy vegetation and does not seem to have been recently occupied, with all cultural finds being associated with the Late Bronze and Iron Ages (Houle 2010). The site was excavated to a depth of ca. 15 cm, with the bulk of the ceramic and faunal assemblages being recovered at a depth of

between 5–10 cm. Out of the 145 recovered ceramic sherds, only 23 were attributed to the Late Bronze Age (Houle 2010). Additionally, only 19 animal bone fragments were attributed to the Late Bronze Age, including remains from *Equus* sp. and *Ovis* sp. / *Capra* sp. (Tbl.54).

Tbl.54 Table of published faunal data from SP10E-TOP (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	0	0	2	4	0	0	0	1	12	0	19

SP11W-SAL (Houle 2010)

SP11W-SAL is a settlement site situated in a grassy stretch of land spanning 6.7 hectares adjacent to a khirigsuur mound, a deer stone complex, and 11 sloping burials (Houle 2010). SP11W-SAL is not occupied in modern times, though a substantial winter encampment is maintained a couple hundred meters north of the site (Houle 2010). Houle and his team excavated to a maximum depth of 20 cm, unearthing Late Bronze Age and Iron archaeological assemblages that were concentrated between 5 and 15 cm deep (Houle 2010). The ceramic sherds were determined to be both Late Bronze Age (no. 32) and Iron Age (no. 34) in origin (Houle 2010). An impressive lithic assemblage was also recovered, representing the largest number of stone tool finds from the Khnauy River Valley settlement site excavations (Houle 2010). Houle has speculated that the high number of lithics recovered from this site may represent a specialist economy, where stone tools might have been manufactured in exchange for food (Houle 2010). Unfortunately very few animal bones were recovered from SP11W-SAL and none of them were attributed to the Late Bronze Age (Houle 2010).

SP08E-GER (Houle 2010)

The stratified settlement site named SP08E-GER is the second site (the first being SP10E-TOP) that was discovered in Zone B of the Khanguy River Valley excavations (Houle 2010). SP08E-GER covers only 0.2 hectares and is the site of a modern day summer encampment, which slightly complicated excavation efforts (Houle 2010). The depth of the excavation was approximately 15 cm, revealing ceramic sherds and minimal faunal remains (mostly from between 5-10 cm) (Houle et al. 2010). Although the pottery assemblage was found to contain both Late Bronze Age and Iron Age ceramics, none of the faunal assemblage was determined to have been Late Bronze Age in origin (Houle 2010). Occupation at SP10E-TOP was seemingly more prevalent in the Iron Age period than the Late Bronze Age (Houle et al. 2010).

SP11E-HOA (Houle 2010)

SP11E-HOA is a stratified settlement site situated along the grassy floodplain of Zone B in the Khanguy River Valley excavations (Houle 2010). The site covers approximately 1.7 hectares and has not been associated with any burials (Houle 2010). In modern times the immediate SP11E-HOA area is host to between 1 and 2 summer encampments (Houle 2010). Excavating to depths only of 10 cm, Houle and his team uncovered a ceramic assemblage and a modest

faunal assemblage (Houle 2010). The vast majority of the finds from SP11E-HOA were attributed to Late Iron Age occupation, though there was some Late Bronze Age and meager Turkik Period representation as well (Houle 2010). In the context of the Late Bronze Age, 79 pottery sherds and 9 animal bone fragments (Tbl.55) were recovered (all from the second unit of excavation) (Houle 2010). A single equid specimen was identified, as was a single sheep; the remaining 7 fragments could be attributed to a size group or reported as indeterminable.

Tbl.55 Table of published faunal data from SP11E-HOA (Houle 2010).

Taxon	*Bos* sp.	*Bos* / *Equus* sp.	*Equus* sp.	*Ovis* / *Capra* sp.	*Capra* sp.	*Ovis* sp.	*Moschus* sp.	Large Mammal	Medium Mammal	Ind. Mammal	Total
No.	0	0	1	0	0	1	0	2	4	1	9

ZK513, Trench ZK513-1 Layer 10 (Houle et al. 2022)

The Late Bronze Age stratigraphy of ZK513, Trench ZK513-1 is limited to Layer 10 (Tbl.56), which was radiocarbon dated to ca. 1410 - 1230 BC (charcoal sample D-AMS034380; see Houle et al. 2022). Only 20 animal bone fragments were recovered from Layer 10, and not a single specimen could be attributed to a taxonomic classification via morphological analysis (Tbl.57). The data are thus very limited and there is little that can be extrapolated from the faunal report about the animal economies or subsistence practices that would have characterized Late Bronze Age occupation at ZK513. My own preliminary ZooMS analysis does help to clarify a sub-section of the faunal composition for the Late Bronze Age context of this site, which I will discuss in-depth in the “Results” chapter of this dissertation (see Chapter 21).

Tbl.56 Radiocarbon dates from Trench ZK513-1, Layer 10 (Houle et al. 2022).

Layer	Material	Lab code	Date	Period (Houle et al. 2022)	Period (this dissertation)
Layer 10	Charcoal	D-AMS034380	ca. 1410–1230 BC	Late Bronze Age	Middle Bronze Age - Late Bronze Age

**All radiocarbon dates are calibrated.*

Tbl.57 Table of published faunal data from Trench ZK513-1, Layer 10 (Houle et al. 2022).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis sp.* / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Layer 10	0	0	0	0	0	0	16

15. Bronze Age Animal Economies

15.1. Introduction

"Preventing a coherent understanding of animal domestication and dispersal in the region are two fundamentally intertwined challenges – an absence of simple empirical criteria for identifying domestication in the prehistoric record, and a striking lack of accessible and relevant archaeological data from archaeological sites across the region" (Taylor et al. 2020c)

In the last three chapters I provided an overview of the archaeological settlement sites and associated faunal data that has been associated with Afansievo, Okunevo, Karakol, Yelunino, Andronovo (Fedorovo), and Karasuk occupation in Southern Siberian as well as with Afanasievo, Chemurchek, Munkhkhairkhan, Ulaanzuukh, Sagsai, Khirigsuur, Deer Stone, and Baitag occupation in Outer Mongolia. Here I will explore what can and has been inferred from these data regarding the Bronze Age animal economies of both Southern Siberia and Outer Mongolia. My discussion will consist of overviews of what can be inferred about the animal economies of each individual archaeological culture as well as the animal economies of each major archaeological period within the Bronze Age, i.e. the Eneolithic & Early Bronze Age, the Middle Bronze Age, and the Late Bronze Age.

15.2. Eneolithic & Early Bronze Age Animal Economies

Multiple archaeological cultures are known to have inhabited Southern Siberia during the Eneolithic and Early Bronze Age periods. The Afanasievo migrated into the region from the Western Steppe, bringing their domesticated animals (namely sheep, goat, and cattle) with them. Whether or not local populations were already practicing animal husbandry or pastoralism in Southern Siberia is unknown. Whether or not Afanasievo peoples domesticated horses also remains a somewhat open question, though if they did, these horses would not have been the ancestors of modern domesticated horses. It is also unclear whether shifts in Afanasievo reliance on hunting versus herding followed a diachronic trend, or occurred in different regions (i.e. in the Altai Mountains versus Minusinsk Basin). The faunal data currently available from Afanasievo settlement sites can do little to clarify any of these questions, due to poor stratigraphic contextualization, assemblage commingling, uncertainty of taxonomic attributions, and lackluster reporting. The upcoming analysis of the archaeological animal remains from Nizhnyaya Sooru will ideally provide much needed insight into Afanasievo animal economies.

Although Afanasievo peoples were genetically distinct from Okunevo peoples, aspects of their material culture was shared (including their artistic depiction of animals) and they inhabited the Minusinsk Basin together for at least a century. There is very limited faunal data available from Okunevo settlement sites, and so it is not currently possible to comment upon any differences in Okunevo versus Afansievo (or Eneolithic versus Early Bronze Age) animal economies, subsistence strategies, or human-animal relationships. This is unfortunately also the case in the Altai Mountains, where animal remains from Karakol and Yelunino settlement site contexts are virtually undocumented. It is reasonable to imagine that all of these archaeological groups were

herding sheep and goat, and possibly cattle, while also hunting and fishing; however, there is not nearly enough faunal data to support or refute this narrative. The animal economies of Eneolithic and Early Bronze Age Southern Siberia will remain elusive until more evidence comes to light.

As is the case for Southern Siberia, very little can be said about the animal economies of the Eneolithic and Early Bronze Age peoples of Outer Mongolia. Faunal remains from Afanasievo or Chemurchek settlement contexts have yet to be identified, by virtue of there being no known archaeological settlement sites which can be attributed to them, though sheep and horse have been identified in occasional burial and ritual contexts. It remains unclear whether these were wild or domesticated specimens. Only three settlement sites have been securely radiocarbon dated to the Eneolithic and Early Bronze Age– none of which have been associated with any particular archaeological culture and only two of which are associated with an Eneolithic and Early Bronze Age faunal assemblage. The faunal assemblage from Biluut III is significant but too poorly preserved for biomolecular analysis, while the faunal assemblage from ZK513 is substantial and currently undergoing taxonomic identification. Morphological analysis has identified only 13 of the 322 animal bone fragments, and these identifications are limited to the genus level (Tbl.58). Ongoing ZooMS analysis should clarify the taxonomic composition of the Eneolithic and Early Bronze Age faunal assemblage from ZK513, though aDNA analysis would be necessary for any higher resolution identifications that can help resolve questions surrounding domesticated versus wild animal exploitation.

Tbl.58 Table of NISP counts of Eneolithic & EBA fauna recovered from Trench ZK513-1 (Houle et al. 2022).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Layer 08	0	0	4	1	0	0	447
Layer 11	0	0	1	1	0	1	127
Layer 12	3	1	5	0	0	1	195

**MNI counts are not available for ZK513-1 fauna.*

15.2.1. Afanasievo Animal Economies

Limited research on settlement sites dating to the Eneolithic period in the Altai Mountains has led to a poor understanding of Afanasievo animal economies and the initial spread of pastoralist subsistence to Inner Asia (Alekhine et al. 1995; Tishkin et al. 2021; Stepanov 2012). Caprine, bovine, equid, cervid, and suid remains have been recovered from Afanasievo faunal assemblages (Alekhin et al. 1995; Derevyanko & Molodin 1994; Frachetti 2012; Galchenko 1994; Gryaznov & Komarova 1979; Kostinev 2005; Hermes et al. 2020b; Honeychurch et al. 2021; Krasnienko 2010; Shulga 1988, 2012; Svyatko et al. 2017; Vadetskaya et al. 2014), though the accuracy of the wild versus domestic status attributions to these taxa in faunal reports is not clear. A lack of robust and reliable criteria for distinguishing equids (Chuang & Bonhomme 2019; Geigl & Grange 2012; Payne 1991; Twiss et al. 2017) has likely contributed to the description of archaeological equids from the Afanasievo sites of Kara-Tenesh and

Balykhutul as both domesticated (Frachetti 2012) and possibly wild horses (Honeychurch et al. 2021).

The association of sheep and goat domestication with Afansievo populations is more secure. A recent mitochondrial study has confirmed the presence of domesticated sheep at Nizhnyaya Sooru (Hermes et al. 2020b), securing at least some degree of Afanasievo reliance on caprine husbandry. However, the morphological distinction of domesticated sheep (*Ovis aries*) and goat (*Capra hircus*) remains is notoriously difficult (Bartosiewicz 1999; Boessneck 1969; Halstead et al. 2002; Lloveras et al. 2022; Payne 1973, 1985; Reitz & Wing 2008), as is the discrimination of wild caprines (e.g. *Ovis ammon, Capra siberica*) from domesticated ones (i.e. *Ovis aries, Capra hircus*) (Clutton-Brock et al. 1990; Helmer 2000; Halstead et al. 2002). The morphological identifications of domesticated caprines at Afanasievo sites are questionable, but not unreasonable. Domesticated pigs (*Sus scrofa domesticus*) were not managed during the Eneolithic and Early Bronze Age periods of Southern Siberia, and all suid remains recovered from Afanasievo contexts should be considered to have been wildstock.

The role of hunting in Afanasievo communities is also poorly understood, as wild game remains are rarely recovered from Afanasievo sites (Syvatko 2010; Syvatko et al. 2017). It has been speculated that hunting initially played a minor role in Afanasievo economies but became increasingly significant as an adaptation to life in the Altai Mountains (Kosintsev & Stepanova 2010; Krasnienko 2010). High occurrences of dental calculus alongside the absence of caries in Afanasievo individuals buried in Altai and Middle Yensei kurgans suggest a high protein and comparatively low carbohydrate diet, supporting a heavy reliance on animal husbandry and / or hunting supplemented with barley and cereals (Svyatko 2014; Tour 2010). Stable nitrogen, carbon, and sulfur isotope analyses of Afanasievo skeletal remains also indicate a heavy reliance on meat, with Altai individuals consuming more mammalian protein and Yensei individuals consuming more freshwater fish (Syvatko et al. 2017). Higher resolution taxonomic attributions of reliably radiocarbon dated animal remains from settlement contexts are necessary to clarify Afanasievo animal husbandry and reliance on herding versus hunting.

AMS radiocarbon dates would also be extremely valuable because stratigraphic context for faunal remains recovered from Afansievo settlement sites is not always available, e.g. for Balyktyyul (Abdulganeev et al. 1982) or Tepsei-X (Gryaznov & Komarova 1979). The Afanasievo settlement sites of Maily Dugan, Kara-Tenesh, Uznezya-I, and sections of Denisova Cave are characterized by stratigraphic disarray and assemblage commingling (Derevyanko & Molodin 1994; Kosintsev & Stepanova 2010; Pogožheva & Molodin 1978; Stepanova 2012). Fortunately, the stratigraphy of the multi-period occupation site of Nizhnyaya Sooru appears to be straightforward and unbroken (Larin et al. 1998; Kosintsev 2005; Tishkin et al. 2021; Yelin & Larin 1998). The Eneolithic context attributed to Nizhnyaya Sooru has also been confirmed with direct AMS radiocarbon dating of faunal remains; this is also true of Kara-Tenesh and Ust'-Biyke-I (Hermes et al. 2021). The Eneolithic contexts of the remaining Afanasievo settlements sites have not been verified with AMS radiocarbon dating.

The faunal data that has been published for Afanasievo settlement site contexts is both sparse and often compromised, but still extremely valuable (Tbls.59–60). The inclusion of this data into archaeological studies and publications should be done so with transparency as to its context and limitations. New methodologies have evolved which can be used to examine older lines of evidence and they should be tactfully applied to faunal samples from Afanasievo contexts where possible. For example, zooarchaeology by mass spectrometry (ZooMS) could be used to discern sheep (*Ovis* sp.) from goat (*Capra* sp.) remains (see Buckley et al. 2009, 2010). Neither ZooMS nor zooarchaeology, combined or individually, are able to confidently discriminate between domesticated and wild remains, but could be used to screen for samples to submit for higher-resolution genetic studies (e.g. Hermes et al. 2021; Pan et al. 2024). The inclusion of biomolecular techniques does not erase the immense importance of earlier zooarchaeological analysis, but can be used to fill in gaps and the data and provide new insights.

Tbl.59 Table of NISP counts of Eneolithic & EBA fauna from Afanasievo-associated settlement sites.

Site	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Balyktyyul	0	0	53	7	9	7	?
Denisova Cave	0	0	105	13	42	4	?
Nizhnyaya Sooru	0	0	229	41	2	4	?
Tepsei-X	0	0	19	1	0	4	?

**See Chapter 12 for source publications.*

Tbl.60 Table of MNI counts of Eneolithic & EBA fauna recovered from Afanasievo-associated settlement sites.

Site	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Balyktyyul	0	0	5	2	3	2	?
Denisova Cave	0	0	14	3	8	2	?
Nizhnyaya Sooru	0	0	19	5	1	2	?
Tepsei-X	0	0	6	/	0	/	?

**See Chapter 12 for source publications.*

15.2.2. Okunevo Animal Economies

There are very limited faunal data from Okunevo settlement contexts in Southern Siberia to reconstruct or analyze. Insights from stable isotopic studies are also limited, suggesting only that Okunevo-associated peoples may have consumed more freshwater fish than Andronovo-associated individuals (Svyatko et al. 2013). Any forthcoming faunal analysis from Zhelvak V could provide crucial insight into what are otherwise the very poorly understood animal economies of the Okunevo archaeological culture. A biomolecular reevaluation of the fauna from Toora Dash which could confirm whether the animals were wild or domesticated would also go a long way to elucidate Okunevo subsistence strategies.

15.3. Middle Bronze Age Animal Economies

Klyuchi is the only settlement site in Southern Siberia connected with the Andronovo (Fedorovo) complex, which is the only archaeological “culture” connected with the Middle Bronze Age in the region. The faunal sample is small, consisting of only 34 animal bones (Tbl.61). The site preserves roe deer, suggesting hunting still played a role. The presence of horse and sheep could suggest mobile pastoralism, especially with the secondary counts of cattle. Stable isotopic studies suggest only that (Fedorovo) Andronovo-associated peoples may have consumed less freshwater fish than Afanasievo and Okunevo-associated peoples (Svyatko et al. 2013).

Tbl.61 Table of MNI counts of MBA fauna recovered from Klyuchi (Maksimenkov 1978).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Klyuchi	12	0	0	5	4	13	?

**NISP counts are not available for Klyuchi fauna.*

The Middle Bronze Age presumably witnessed both a continuance of hunter-gatherer lifeways in Eastern Outer Mongolia that stemmed from the traditions of the Neolithic peoples of Inner Mongolia and China, as well as the intensification of pastoralist-metallurgance lifeways introduced into Western Outer Mongolia by Afanasievo peoples migrating into Inner Asia from the Western Eurasian Steppe. With such limited archaeological evidence, it is difficult to make a solid case either in support or refutation of this idea. The sparse faunal data from the only two Middle Bronze Age settlement sites that have been discovered in Western Outer Mongolia, i.e. Tsagaan Asga and ZK513, clearly establish the presence and exploitation of caprines and cattle (Tbl.62). It is unclear when looking at the available fauna data whether sheep, goat, and cattle were also present in Eastern Outer Mongolia during the Middle Bronze Age, though it seems likely considering the presence of livestock in both Western and Inner Mongolia during this time (see Chapter 13).

Tbl.62 Table of NISP counts of fauna from MBA settlement sites (Houle et al. 2022; Taylor et al. 2020b).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Tsagaan Asga	16	0	0	4	0	0	?
ZK513-1	0	0	1	0	0	1	20

**MNI counts are not available for Tsagaan Asga or ZK513-1 fauna.*

15.4. Late Bronze Age Animal Economies

The Late Bronze Age of Southern Siberia has been consistently linked with mobile pastoralism in archaeological and historical literature (e.g. Blyakharchuk et al. 2013; Jettmar 1950, 1970; Legrand 2006; Gryzanov 1969; Savinov 1996). Horse domestication and riding in Southern Siberia have been reported as the “first-time innovations” of the Karasuk archaeological culture populations (Blyakharchuk & Chernova 2013), though this has yet to be confirmed. The seasonal transhumance initially attributed to the Karasuk by Savinov (1996) and perpetuated by

Blyakharchuk & Chernova (2013) has been disputed (Legrand 2006; Honey church 2014). Stable isotopic evidence also suggests that the Karasuk peoples of the Minusinsk Basin were also consuming freshwater fish (Svatko et al. 2013), and a modest number of fish bones were recovered from Torgazhak (Savinov 1996). The Late Bronze Age in Southern Siberia probably involved a mixture of hunting and domesticated animal husbandry, and arguably fishing as well (Tbls.63–64).

Tbl.63 Table of NISP counts of fauna from Torgazhak (Savinov 1996).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Layer 01	395	42	437	251	94	145	?
Layer 02	51	3	54	20	29	21	?
Layer 03	58	13	71	55	26	37	?
Layer 04	57	6	63	37	10	11	?
Layer 05	55	5	60	31	25	27	?
Layer 06	102	8	110	117	23	51	?
Layer 07	65	17	82	114	17	36	?
Pits	11	2	13	11	0	5	?
TOTAL	794	96	890	636	224	333	?

**Boar remains were only recovered from Layer 01 at Torgazhak (NISP=16). "Ovis sp. / Capra sp." were calculated by combining Ovis sp. and Capra sp. Counts; they are not a unique category of ambiguous caprines from the original report.*

Tbl.64 Table of MNI counts of fauna from Torgazhak (Savinov 1996).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
Layer 01	28	4	0	17	12	11	?
Layer 02	11	1	0	3	6	3	?
Layer 03	6	3	0	2	8	2	?
Layer 04	11	2	0	2	6	2	?
Layer 05	13	1	0	3	6	2	?
Layer 06	5	2	0	5	6	3	?
Layer 07	7	4	0	3	7	2	?
Pits	3	1	0	2	0	1	?
TOTAL	79	18	0	35	52	26	?

**Boar remains were only recovered from Layer 01 at Torgazhak (MNI=2). "Ovis sp. / Capra sp." were calculated by combining Ovis sp. and Capra sp. Counts; they are not a unique category of ambiguous caprines from the original report.*

Although the Late Bronze Age has been credited as the period in which mobile pastoralism came to dominate Outer Mongolian subsistence strategies, there is very little faunal evidence available to address these claims. Domesticated animal bones have been reported at over a dozen Late Bronze Age settlement sites excavated in the Khanuy River Valley (Houle 2010) (Fig.12), but sample sizes are small and the actual ratio of wildstock to livestock remains virtually unknown. What can be inferred about the Late Bronze Age animal economies of Outer Mongolia is limited to the Western region, suggesting a preference for caprines followed by equids and cattle, and lastly antelopes and cervids (Tbl.65). The majority of bone fragments recovered have not been identified to a taxonomic group.

Tbl.65 Table of NISP counts of fauna from the Khanuy River Valley sites (Houle 2010).

Layer	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	Antilopinae / Cervidae	*Equus* sp.	Unknown
SP07E-HUN	0	0	0	0	0	0	5
SP10E-TOP	0	0	4	0	0	2	13
SP11E-HOA	1	0	0	0	0	1	7
SP22E-BMK	0	0	0	1	0	1	155
SP26E-MAC	0	0	0	0	0	0	5
SP26E-WFA	2	1	9	4	0	2	116
SP27E-MTC	0	0	1	0	1	2	9
SP31E-JUL	0	0	0	0	0	0	111
SP31E-QUE	0	0	4	2	0	2	51
SP32E-MAB	0	0	1	0	0	2	51
SP32E-SHA	2	6	6	0	2	0	85
ZK513-1	0	0	0	0	0	0	16
TOTAL	**5**	**7**	**25**	**7**	**3**	**12**	**624**

**MNI counts are not available for fauna from any of the Khanuy River Valley sites reported in Houle 2010.*

The faunal data from the Khanuy River Valley sites are insightful while giving rise to a number of questions surrounding animal exploitation strategies. It is unclear whether the recovered sheep bone fragments are the result of herders managing domesticated sheep, hunters pursuing argali, or a mixture of both. Similarly, the medium mammal remains could have come from domesticated caprines or wild game, and the ratio of these groups is unclear. The lack of cattle remains outside of the largest valley draws is also interesting, if this is reflective of actual cattle management strategies in the Khanuy River Valley during the Late Bronze Age. Finally, if the equid remains represent domesticated horses as opposed to wild hunted equids, were they being ridden? A lack of horse harnessing gear recovered from the site would suggest otherwise, though a paleopathological review of their vertebrae and teeth might suggest otherwise (see Chapter 02). Unfortunately the adjacent, limited faunal remains from Sagsai, DSKC, Slab Burial, and Baitag mortuary and ritual contexts do not provide much clarification. A notable exception to this is the securely established presence of domesticated horse remains in DSKC contexts and the inclusion of both horse bones and horse harnessing equipment in Slab Burials.

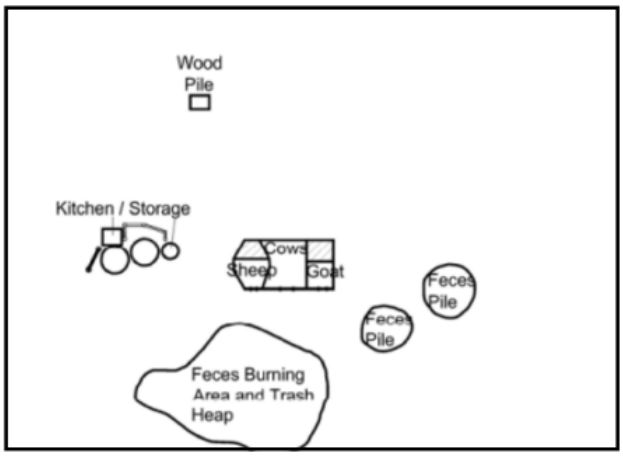


Fig.12 Modern winter campsite in the Khanuy River Valley (Houle 2010)

15.5. Bronze Age Animal Economies: Conclusion

"...what is known of the actual subsistence economy of Late Bronze Age Mongolia is, not surprisingly, very little. But this is to be expected of a type of archaeology that has been mainly interested in burials, ritual sites and objects of fine craftsmanship. Botanical remains and animal bones have not been given the same attention—especially those from domestic contexts. As a result, interpretations regarding the nature of Late Bronze Age subsistence practices has to date remained speculative." (Houle 2010)

The Southern Siberian Bronze Age can be roughly divided into the Eneolithic and Early Bronze Age, the Middle Bronze Age, and the Late Bronze Age. The Afanasievo and Okunevo archaeological cultures inhabited the Minusinsk Basin during the Eneolithic and Early Bronze Age, and the Afanasievo very likely introduced domesticated animal husbandry into the area. Faunal evidence is rare, which makes definitive conclusions difficult. Hunting and fishing likely remained prevalent economic strategies during the Eneolithic and Early Bronze Age, evidenced by stable isotopic studies indicative of fresh-water fish consumption that waned with the onset of the Middle Bronze Age. The Middle Bronze Age has in turn been associated with the Andronovo culture conglomerate. In the context of Southern Siberia, the Andronovo (Fedorovo) variety has been associated with the settlement site of Klyuchi. Less than 35 bones were reported from this site, tentatively suggesting both hunting and livestock rearing.

It is possible that an intensification of both cereal agriculture and pastoralism took place during the Middle Bronze Age, leading to an overall decrease in fishing and / or hunting, but there are not nearly enough data to affirm or support this. The Late Bronze Age of Southern Siberia remains equally enigmatic, with limited evidence from a single Karasuk settlement site (Torgazhak) suggesting an intensified human-horse relationship and reliance on both domesticated livestock and hunting. The role of fishing at Torgazhak, and during the Late Bronze of Southern Siberia in general, remains unclear. The continued AMS radiocarbon dating, alongside new initiatives in the verification of old taxonomic attributions with biomolecular methods such as ZooMS and aDNA analysis, would go a long way to clarify the human-animal relationships and subsistence strategies of the Southern Siberian Bronze Age.

The Outer Mongolian Bronze Age is elusive, from archaeological and especially zooarchaeological perspectives. The Eneolithic and Early Bronze Age periods (ca. 3170–1915 BCE) have come to be associated with the Afanasievo and Chemurchek cultural phenomena and while equid and caprine remains have reportedly been discovered in their tombs, there are no settlement sites attributed to them to offer glimpses into the realities of their daily subsistence. The recently excavated sites of Bagsagiin Bulan, Biluut III, and ZK513 have provided clear evidence of Eneolithic and Early Bronze Age human occupation. Animal bone assemblages were recovered from Biluut III and ZK513 (Trench ZK513-1), though poor preservation has complicated the interpretation of the faunal data from Biluut III. Caprine, cattle, and equid remains were morphologically identified in the Eneolithic and Early Bronze Age Layers of ZK513, and ongoing ZooMS analysis is refining these taxonomic attributions. I will discuss this analysis in the "Results" chapter of my dissertation (see Chapter 21).

The body of faunal evidence for the Eneolithic and Early Bronze Age period is very limited, both in mortuary and domestic contexts. The evidence we do have could represent the hunting of wild animals, the husbandry of domesticated ones, or a mixture of both. Higher-resolution

biomolecular studies, wherever possible, will be necessary to refine our understanding. The attempted ZooMS analysis of fauna from Biluut III (Taylor et al. 2020b) was a solid step towards this direction that was unfortunately undermined by poor collagen preservation. Between soil acidity, calcination, and the general taphonomic loss that occurs in the course of thousands of years, poor preservation will continue to present a challenge when attempting biomolecular analysis on animal bones this ancient. The site of ZK513 presents a mixed case of poor preservation in some layers, and exceptional preservation in others, as I will revisit in Chapter 21.

Progressing into the Middle Bronze Age of Outer Mongolia (ca. 1915–1350 BCE), the same questions about hunting and herding persist, as do the challenges distinguishing domesticated fauna from wild game in a limited number of assemblages, especially in the context of settlement sites. The archaeological cultures associated with this period, the Munkhkhairkhan and Ulaanzuukh, are known only from their burials. No faunal remains have been recovered from the tombs of either, at least not that have been published, strongly limiting the reconstruction of their subsistence activities. The seeming absence of metal objects in Ulaanzuukh grave goods has been used to argue for a continuation of earlier Neolithic hunter-gatherer lifeways (e.g. Wright et al. 2019), though other scholars have suggested an economic preference for pastoralism (e.g. Honeychurch 2015). There is currently little evidence available to support either claim, or to reconstruct the subsistence strategies associated with Munkhkhairkhan or Ulaanzuukh mortuary complexes.

Two settlement sites, Tsagaan Asga and ZK513, have been securely radiocarbon dated to this period and both caprine and cattle bones have been biomolecularly identified at both. Due to the limitations of ZooMS, it remains unclear if these specimens represent domesticated animals or predated aurochs (*Bos primigenius*) or even wild yak (*Bos mutus*), ibex (*Capra sibirica*), and argali (*Ovis ammon*). If domesticated, would they have been the result of an initial introduction of animal husbandry into Outer Mongolia by Western Eurasian Steppe herders (e.g. the Afanasievo), or reflective of an older, local pastoralist tradition? An overall lack of pig or chicken remains in contexts where archaeofauna have been excavated suggests that domesticated animals were not previously introduced from East Asia (pers.comm. Will Taylor 2024). The introduction of domesticated sheep and goat into Mongolia from Central Asia is also unlikely (pers.comm. Will Taylor 2024). There is not enough archaeological data available at this time to definitively state that domesticated animals were introduced into Outer Mongolia by Afanasievo peoples, though this does seem to be the most likely scenario.

Finally, the Late Bronze Age of Outer Mongolia (ca. 1350–910 BCE) has been associated with the terminal Ulaanzukh and the DSKC, Sagsai, Slab Burial, and Baitag cultural phenomena. Significantly, domesticated horse remains have been identified in DSKC and Slab Burial contexts, along with horse harnesses and associated paraphernalia. A comparative abundance of settlement sites, 15 in total, have also been associated with the Late Bronze Age. Bovines, equids, caprines, and cervids have all been identified; it is very likely that some of these animals were domesticated. Stone tools and cervid remains suggest continued hunting, though whether this was a primary or secondary economic activity is unclear. Although archaeologists have

recovered hundreds of animal bones from Late Bronze Age settlement site contexts, very few of them proved to be morphologically diagnostic.

Future ZooMS analysis of the abundance of remains from the Khanuy River Valley settlements has the potential to clarify whether or not pastoralist intensification was taking place in the Khangai Mountain region of Western Mongolia. The presence of domesticated horse remains in DSKC and Slab Burial contexts strongly suggests that this is the case. ZK513 perhaps provides the best opportunity to reconstruct Bronze Age subsistence transitions, as the stratified site has been secured with AMS radiocarbon dating and has given up a massive faunal assemblage of thousands of bones. The future discovery of similar sites and the continued combination of ZooMS and zooarchaeological analysis of faunal assemblages will be crucial to reconstructing subsistence transitions and the story of animal husbandry in Outer Mongolia. Having reviewed the limited evidence that has been published so far, I will now move on towards the history, settlement archaeology, and zooarchaeology of Ancient Transoxiana.

16. Unraveling the Silk Road

16.1. Introduction

"Much has been said and written about "The Silk Road" since Ferdinand Freiherr von Richthofen coined the phrase in 1877…Yet, it is never quite clear what exactly the Silk Road concept really entails." (Selbitschka 2018)

In the previous six chapters of this dissertation I focused on the emergence of domesticated animal husbandry in Eneolithic and Bronze Age Southern Siberia and Mongolia, as well the complexities of reconstructing human subsistence strategies (e.g. pastoralism) from the archaeological record of Inner Asia in prehistoric contexts. In this chapter I will bring the discussion forward to the diffusion of animal husbandry and animal-driven technologies throughout Eurasia. I will explore how economic activities such as pastoralism and the exploitation of animals for traction and transportation contributed to the formation of the Trans-Eurasian exchange networks commonly referred to as "the Silk Road", as well as the role of these networks in facilitating subsequent cultural and technological exchange. My historical and archaeological review of this complex process will contextualize my reconstruction of animal economies from Medieval archaeological contexts of Inner Asia, which I will provide further into this dissertation.

16.2. Trans-Eurasian Exchange Networks

"As Western explorers moved East during the 19th century, they began to think about Asia as exotic, mysterious, foreign, and dangerous, but most importantly Asia was also deemed to be savage, primitive, and monstrous compared to Europe." (Curtis 2023)

The subject matter of this chapter, "Unraveling the Silk Road", is likely to conjure images of medieval caravans traversing the Silk Road, their camels dripping with silks and laden with incense, tea, and spices. Palm tree oases and oceans of desert sands might come to mind, as well as romanticized adventures of Marco Polo and the mythicized military campaigns of Alexander the Great. These fantastic tales of cities of delight contained within the landscapes of imagination have little to do with the reality of Trans-Eurasian trade routes, which in the context of Central Asia would have involved rows of poplar trees and fruit orchards as opposed to palm groves (Wood 2002).

The nineteenth century European conception of the Silk Road as a singular ancient highway connecting Rome and China continues to fascinate the minds of the public at large (see Andrea 2014; Honeychurch 2014a), but is a distortion and oversimplification of the complex networks of commerce which gradually emerged after thousands of years of human innovation, interaction, conflict, and exchange (see Barsitz 2017; Francfort 2023; Graf 2018; Honeychurch 2014a; Kuzmina 2008; Mishra 2020; Paroń 2021; Selbitschka 2018; Spengler 2019; see also Rosén 2009 for Silk Road trade in Korea and Japan). This "exotic othering" is not only historically inaccurate, but also carries a dangerous legacy of eurocentricizing and sinocentricizing history,

diminishing Central and Southern Asian cultures, and legitimizing colonialism (see Curtis 2023; Mishra 2020).

An upcoming portion of this dissertation is dedicated to the review of the archaeological settlement sites and faunal data from the Medieval period of Transoxiana, with an emphasis on the sites situated in modern day Uzbekistan. My usage of the term “Medieval” is essentially an effort to communicate a post-Antiquity and pre-Modern period historical context. I occasionally use the term “Silk Road” in keeping with convention for chronological orientation, as it contains within it what could be called the Medieval period of Transoxiana in my review (see Chapter 17). The pitfalls of the continued application of outdated and obscure chronological models devised by historians and archaeologists of a different generation continues to complicate my discussions of Inner Asian animal economies, such as with my tentative use of the terms “Eneolithic” and “Bronze Age” in previous chapters (see Chapters 10–12, 15).

In order to avoid perpetuating Orientalist narratives and the commandeering of history, I will very briefly overview the emergence of Trans-Eurasian exchange networks from an archaeological perspective where possible. While an extensive overview of the archaeological and ecological findings related to the “proto-Silk Road” is beyond the scope of this dissertation, references are provided for more in-depth reading. I will begin with the innovations of the Neolithic and Bronze Age in Eurasia, segway into the Central Eurasian empires of the Iron Age and Antiquity, and conclude with the emergence of the Silk Road Period in Central Asia.

16.3. Neolithic Wheels & Bronze Age Chariots

“It is the use of wheeled transports that provided quick colonization by Indo-Europeans and establishment of the broadest cultural ties between Scandinavia and China, the Eurasian steppes and India.” (Elena Kuzmina in Novozhenov 1987)

The invention of the wheel was one of the most significant revolutions in human history, resulting in increased mobility, improved modes of transportation, and the transformation of human-animal relationships. The Neolithic innovation of the wheel initially facilitated new methods of material culture production (e.g. pottery manufacture) that, combined with advancements in metallurgy and the emergence of agriculture, would lead to food surpluses, extensive trade, and social stratification (Barsitz 2017; Bondár 2018; Jacobson-Topfer 2015; Kuzmina 2008; Novozhenov 1987). The subsequent invention of wheeled vehicles in the Bronze Age led to the yoking of domesticated cattle and yak to carts for traction, broadening not only human lifeways but the roles and perceptions of draught animals within them (Bondár 2018; Jacobson-Topfer 2015; Piggott 1968). This resulted in diversified animal husbandry strategies and differential livestock culling patterns (Bondár 2018; Taylor 2024; see also Chapter 08). The Bronze Age domestication of the horse (see Chapter 01, 06, 15) further deepened social stratification related to unequal wealth and power distributions, enhanced military capabilities, and the transmission of a shared ritual culture throughout Eurasia (Barsitz 2017; Bondár 2018; Frachetti & Rouse 2012; Jacobson-Topfer 2015; Kuzmina 2008; Novozhenov 1987; Taylor et al. 2015).

It is still not entirely clear if the invention of the wheel was a singular event that subsequently diffused throughout Eurasia and Africa, or if a series of independent invention events occurred (Bondár 2018). The initial joining of the wheel to an axle and frame to form carts and chariots is also an event that remains poorly understood and some questions remain as to whether or not the horse came before the cart, i.e. whether horses were initially ridden before or after they were first hitched to wheeled vehicles (Novozhenov 1987; Taylor & Tuvshinjargal 2018). I have already addressed the questions surrounding horse and cattle domestication (see Chapters 06, 09–15). In all likelihood, chariots provided a safer way to manage various equids across Eurasia before the advent of horse domestication and horseback riding (Taylor 2024).

What is clear is that the wheel was a part of many of the Neolithic lifeways of Eurasia and that domesticated horses and chariots were central to the Bronze Age, most especially in Central Eurasia (Barsitz 2017; Bayarsaikhan et al. 2024; Frachetti & Rouse 2012; Jacobson-Topfer 2015; Kuzmina 2008; McNeill 1987; Novozhenov 1987; Piggott 1968; Taylor 2024). The transmission of the wheel, the chariot, and domesticated plants and animals across Eurasia facilitated vast Bronze Age networks of cultural interaction and exchange (see Possehl 2007; Frachetti & Rouse 2012; Smith 2016) that would eventually culminate in what is now known as the Silk Road (see Spengler 2019; Taylor 2024; Taylor et al. 2018; Zhou et al. 2021). These Trans-Eurasian pathways would come to be solidified in part by the rise of nomadic steppe confederacies, as I will discuss below.

16.4. Iron Age Nomadic Confederacies

“Goods produced by sedentary civilizations most in need by nomads typically were farming products (e.g., grain), textiles (cloth), and manufactured metal products (notwithstanding steppe dwellers’ knowledge of metallurgy). Settled populations’ demand for nomadic products often focused on horses, meat, milk, and wool (although oasis inhabitants also engaged in limited stockbreeding).” (Barsitz 2017)

The technological and economic advancements of the Bronze Age, coupled with climatic changes related to glacial advances, gave rise to the formation and expansion of complex mobile herding communities across Central Eurasia around the onset of the Iron Age (ca. 1000 BCE) (Barsitz 2017; Bayarsaikhan et al. 2024; Che & Lan 2021; Khazanov 2015; Taylor 2024; Zhou et al. 2021). One of the primary economic activities of Iron Age nomadic steppe polities was livestock rearing, which often took the form of seasonal transhumance (see Chapter 09) and involved long distance migrations that facilitated regular contact with the more sedentary agriculturalists and agro-pastoralists of Inner Asia (Barsitz 2017). It would be a mistake to reduce all of Iron Age Inner Asia down to two modes of subsistence, or to suggest that either of these modes were uniform in practice (see Chapters 02, 09; also Brite et al. 2017; Chang et al 2023; Spengler et al. 2021).

At the same time, the emergence of mobile pastoralism as the predominant subsistence strategy of certain Central Eurasian communities and the regular interactions of these nomadic confederacies with more sedentary peoples transformed the sociopolitical and economic landscape of Inner Asia. The two nomadic confederations which probably had the most impact

on the Trans-East Eurasian relations of the Iron Age were the Scythians and the Xiongnu, whose legacies I will briefly discuss individually in turn below. It should first be noted that climate change itself may have played a role in the early formation of Trans-Eurasian trade routes, beyond being an attributing factor to the formation of nomadic steppe polities (see Tan et al. 2021).

16.4.1. The Scythians (ca. 900–300 BCE)

"The Scythians are frequently presented…as highly mobile warrior nomads…Here, we analyse…isotope data from human tooth enamel samples…Our multi-isotopic approach…supports economic diversity of urban locales and complex trading networks, rather than a homogeneous nomadic population.." (Ventresca Miller et al. 2021)

Before entering into a discussion about the role of Scythian populations in the development of Trans-Eurasian trade routes, it is necessary to clarify what "Scythian" even means. Scythian has been used somewhat indiscriminately as both a generic term for ancient Eurasian steppe and desert nomads as well as a specific Iron Age archaeological culture originating in Central Eurasia (Khazanov 2015). I am referring to the latter definition in my use of the term "Scythian", with the understanding that many different Iron Age communities have been roped under a singular and oversimplified Scythian cultural descriptor. An extensive overview of Scythian population origins, migrations, and dynamics are beyond the scope of this dissertation; an abundance of published craniometric, genetic, and genomic studies of Scythian populations are available for the interested reader (e.g. Gnecchi-Ruscone et al. 2021; Järve et al. 2019; Juras et al. 2017; Kozintsev 2007; Krzewińska et al. 2018; Mary et al. 2019; Movsesian & Bakholdina 2017; Unterländer et al. 2017).

The longstanding narrative of Scythians as bands of hierarchical warrior nomads sweeping across Iron Age Eurasia on horseback and dominating vast swathes of the landscape (e.g. Pankova 2017; Wendelken 2000) has faced criticism in the past decade, and has been challenged by scholars who have reevaluated the older sources and examined new lines of evidence (e.g. Aryamanesh & Khorashadi 2021; Barsitz 2017; Meyer 2024; Ventresca Miller et al. 2021; Spengler et al. 2021). Many of the aforementioned genetic studies have confirmed that Scythian groups established multiple genetically diverse populations across Eurasia (Krzewińska et al. 2018; Järve et al. 2019; Mary et al. 2019; Unterländer et al. 2017), while isotopic evidence suggests that Scythian communities were not uniformly mobile and did engage in agriculture (Ventresca Miller et al. 2021).

It is certain that some groups now referred to as Scythian were interacting with Anatolian and Greek communities by 700 BCE and that material goods were flowing back and forth between them (Alekseev et al. 2017; Barsitz 2017; Phillips 1972). Scythian objects, which are admired to this day for their stylized depictions of large game, wild beasts, birds of prey, and mythical creatures (see Jacobson-Tepfer 2015), seemingly enchanted the ancient world as well. The Scythian "animal art style" was adopted by Greek goldsmiths as well as Central Asian mobile pastoralist groups (Alekseev et al. 2017; Barsitz et al. 2017; Phillips 1972). Many reviews of archaeological investigations into the origins of the Scythian animal art style have been

published (e.g. Artamonov 1970; Il'Inskaia 1982; Sher 1988) as well as the influences of Scythian, Persian, Thracian, and Greek art upon one another (e.g. Brentjes 2000; Farkas 1977; Jacobson 1995).

Scythian population migrations expanded far beyond the reaches of Central Asia, with certain groups interacting with the communities of both West Asia (including modern day Syria, Palestine, Armenia, and Turkey; see Barsitz 2017; Phillips 1972; Sulimirski 1954) and East Asia (including modern day China and possibly the Korean peninsula; see Cambon 2008). Chinese silk and bronze mirrors have even been recovered from Scythian burials dated to the sixth century BCE in the Altai Mountains (Juping 2009). While a more in-depth review of Scythian lifeways is beyond the scope of this dissertation, it should be evident that Scythian population migrations and material culture exchanges strongly contributed to the extensive multicultural ties that would later solidify Trans-Eurasian exchange routes.

16.4.2. The Xiongnu (ca. 300 BCE–100 CE)

"The large quantities of silk…provided by the Chinese…were traded across the Xiongnu-held lands with their neighbors to the west, all the way to Rome…this re-export is likely to have taken place via the trade routes running through the north and the south of the Tarim Basin, then across the Tienshan, Pamir, and Karakorum mountains in western and southern directions (to Persia and India)...the trade connections of the Tarim Basin acquired strategic importance." (Barsitz 2017)

"Xiongnu" was a political term used by Chinese scribes to detail their accounts of the nomadic confederations which dominated stretches of the Mongolian Plateau (and beyond) during the Late Iron Age and into Antiquity (Brosseder 2016; Psarras 1995). As with the term "Scythian", "Xiongnu" cannot be said to refer to any singular group, but is also less easily related to any distinct archaeological culture (Brosseder 2016). My use of the term Xiongnu should thus be interpreted as a political contextualization as opposed to an indication of ethnicity (though for craniometric and genetic Xiongnu studies see Keyser et al. 2021 & Schmidt & Seguchi 2016, both of which support high population diversity; see also Psarras 1995 for arguments regarding the inseparability of Xiongnu ethnicity and politics).

Xiongnu grave goods have revealed socially stratified but largely homogeneous ceramics and weapons assemblages (Brosseder 2016; but see Psarras 1995 for contradictory commentary on the preservation of multiple local indigenous forms and burial traditions leading to diverse items in Xiongnu tombs). The more ornate grave goods originating from China, Central Asia, and Western Eurasia have been found in the tombs of high status individuals, testifying to Xiongnu participation in expansive trade and tribute networks (Brosseder 2016; Taylor 2024). Diplomatic tribute paid to the Xiongnu by the Han Dynasty regularly included parcels of silk as well as gold, rice, and wine, though scholars disagree about the role these tributes did (Barsitz 2017; Tu 2022) or did not (Selbitschka 2018) play in the formation of the Silk Road trade routes.

Scholars have also disagreed about the degree to which the Xiongu practiced and relied upon mobile pastoralism as well as, partially by extension, their dependency on trade with sedentary communities to meet their economic needs (see Kradin et al. 2021; Wright et al. 2009). I will not

examine questions of Xiongnu subsistence strategies or diplomatic relations in-depth or attempt to resolve them here. Suffice to say, the very real military threat that the Xiongnu confederation posed to the Han Dynasty resulted in their receipt of regular gifts of tribute from China (Barsitz 2017; Brosseder 2016; Liu 2010; Psarras 1995; Selbitschka 2018; Tu 2022). The luxury goods which were not reserved for high status individuals and fixed displays of wealth were subsequently traded across the Tarim Basin, occasionally reaching destinations as distant as the Mediterranean (Barsitz 2017; Liu 2010). The emergence of Trans-Eurasian trade networks was clearly facilitated, at least in part, by the economic and political activities of the nomadic confederacies which emerged in the late prehistory of Central Eurasia.

16.5. Camels & Caravans

"In India and Central Asia…wheels had to compete with caravans, because…technological advances in the management of camels…made wheels obsolete after about 300 A.D…until the eighteenth century." (McNeil 1987)

I have discussed how the domestication of the horse, the invention of the wheel and the wheeled vehicle, and the development of equestrianism eventually led to the formation of powerful steppe polities and the widespread adaptation of pastoralism across Inner Asia (see also Taylor 2024). However, it was the domestication of the camel and the conception of caravans that facilitated the long-distance transmission of material goods and cultural contact across South and Southwest-Central Asia in Early Antiquity (Kuzmina 2008; McNeil 1987). There are two species of domesticated camel; the Dromedary (*Camelus dromedarius*) and the Bactrian (*Camelus bactrianus*) (see Chapter 06). Both species were domesticated in Asia (Western and Southwest-Central, respectively) and exploited for transportation by the third millennium BCE (Anjum 2006; Sala 2017).

Camels are extraordinarily resilient animals and are especially well-suited for traversing the most arid regions of Asia, such as the Arabian, Cholistan, Gobi, Karakum, Kharan, Kyzylkum, Lop, Ordos, Registan, Taklamakan, Thal, and Thar deserts (Bornstein 1990; Barsitz 2017; see also Chapter 07). Domesticated camels were saddled and hybridized by the first millennium BCE for use as pack animals carrying tents and goods across Asian caravan routes, as well as cavalry animals aiding in the military control of desert territories (Anjum 2006; Sala 2017). The history and geography of caravan routes connecting wide regions of continental Asia could constitute a book in itself and will not be covered in any detail here (see instead Codrignton 1944; Franklin & Boak 2021; McLaughlin 2010; Parker 2019; Wilson & Bowman 2018; Wood 2002).

What I have sought instead to emphasize is the role of camels in facilitating long distance trade and even warfare across otherwise environmentally hostile regions, enabling the formation of caravan routes which would later be woven into Silk Road trade networks. At the same time, it is not my intention to draw a line in the sand between two camps of "camels, caravans, and deserts" on one side and "horses, chariots, and grasslands" on the other. Camels and horses have absolutely been managed (separately and together) in herds throughout various biotopes

in Eurasia and Inner Asia specifically (see Chapter 08). Horses have been used for transport, trade, socialization, and warfare without having been hitched to wheeled vehicles (see Chapters 08, 15). Camels have been fastened to wheeled caravan vehicles as well as to trains of humans and animals ferrying goods (Sala 2017).

The adaptability of domesticated horses and camels to difficult terrain, with or without wheeled vehicles trailing behind them, created a wide array of options related to mobility, transportation, and warfare that was previously unknown in ancient Eurasia. The ability to accommodate economic needs and social aspirations by loading domesticated animals and wheeled vehicles with materials goods and weapons was integral to the continued emergence of social stratification, political complexity, product manufacture and commerce, warfare and diplomacy, and cross-cultural interactions that would germinate into Trans-Eurasian exchange networks (i.e. the Silk Road).

16.6. The Empires of Antiquity (ca. 550 BCE–250 CE)

"It was the imperial initiative–though frequently oppressive and brutal..that created the most extensive long-distance connections from the Mediterranean to Central and Eastern Asia yet seen in the ancient world, laying the foundations of what is today known as the Silk Road." (Abbott 2022)

I have endeavored so far to establish the major innovations and mechanisms which expanded and transformed social, cultural, political, and economic relationships in ancient Eurasia. I will now briefly explore how these relationships culminated and expressed themselves in the empires of Central Eurasia during the period of Antiquity, and the relevance of these empires to the formation of Trans-Eurasian exchange networks that solidified during the Silk Road period. My use of the term "Antiquity" here loosely refers to the period following the Iron Age and preceding the Medieval Period, without any chronological relation to the cultural histories of Mediterranean civilizations (e.g. "classical antiquity"). The actual chronology of the Silk Road period will be outlined in the next chapter of this dissertation.

The empires that I will discuss are the Achaemenid Empire of Persia (i.e. modern day Iran) (ca. 550–330 BCE), the empire established by Alexander the Great of Macedonia (i.e. modern day Greece) (ca. 334–323 BCE), the Seleucid Empire (ca. 312–64 BCE), and the Graeco-Bactrian Kingdom (ca. 256–120 BCE). Importantly, the majority of evidence that has survived for many of these empires is literary and often unreliable or fragmentary (Morris 2019a,b; see for example Jakobsson 2020), which should be kept in mind when reading my brief overview. Excavated settlement sites from the Antiquity period of Central Asia are especially lacking (see Kidd & Stark 2019). For a thorough overview of the nature of the literary, numismatic, and archaeological data available to contextualize the Central Asian empires of Antiquity, see Morris (2019b). A brief summary of the situation can be found in Morris's (2019b) concluding statement:

"Information conveyed by Graeco-Roman and Chinese transmitted texts sheds light on many aspects of the economy and its development. An enormous body of numismatic data is available to be exploited,

although the perennial lack of contextual data shapes the questions we may ask of it...Archaeological data relevant to the…Kingdoms…were produced between disparate intellectual traditions with different research interests, and much of the published data still have major problems and biases in coverage that make it difficult to define and analyze economic macro-processes from an imperial perspective."

16.6.1. The Achaemenid Empire (ca. 550–330 BCE)

"...the Achaemenid Empire, for over two centuries the most important player from the Aegean to the Indus...affected the social and economic landscape of Central Asia even after the demise of the Empire itself, thus considerably shaping the world of the Silk Road(s)…Central Asia was fully integrated into the imperial framework and deeply entangled with networks reaching far and wide beyond it…on both sides of the borderlands, local societies interacted with the Empire and mutual gains resulted from the connectivity generated by its needs for products, peoples, and a wide array of resources." (Ferrario 2022)

Before beginning my discussion I should note that although I have assigned the Achaemenid Empire to the early period of Antiquity, many archaeologists familiar with Achaemenid material culture typology and radiocarbon dates would argue instead for an Iron Age attribution in the context of Central Asian chronology (e.g. Baumer & Novák 2019; Lhuillier 2018; Wu et al. 2015) (Tbl.66). Under Lhuillier's (2018) schematic, the expansion of the Achaemenid Empire beyond Persia would correspond with the Late Iron Age of Central Asia. The prehistoric chronological models of Central Asia (excluding Mongolia) and their intersection with the chronological models of West Asia are beyond the scope of my dissertation (see instead Baumer & Novák 2019).

However, I would be remiss to not make mention of these chronological discrepancies in a chapter about Central Asian archaeology, especially in a subsection that openly aspires to examine the formation of Trans-Eurasian exchange networks from an archaeological perspective. I have also associated the Xiongnu (ca. 300 BCE–100 CE) who nearly overlapped with Acheamenids (ca. 550–330 BCE) with the Late Iron Age and Antiquity periods. I will continue to use the term Antiquity when discussing the Achaemenid Empire, both in keeping with some convention (e.g. Barsitz 2017; Kidd & Stark 2019) and to maintain the flow of this dissertation. I will not discuss the origins of the Achaemenid Empire or its history before 550 BCE, which may be found in Henkelman (2012).

Tbl.66 Table of an Iron Age Achaemenid Empire chronology (Lhuillier 2018).

Archaeological Age	Material Culture Phase	Estimated Dates
Early Iron Age	Yaz I Phase	ca. 1500-1000 BCE
Middle Iron Age	Yaz II Phase	ca. 1000-540 BCE
Late Iron Age	Yaz III Phase	ca. 550-330 BCE

In the second half of the fifth century BCE, the Achaemenid King Cyrus II of Persia executed a series of military campaigns across Eurasia which resulted in the subjugation of several West Asian territories (Barsitz 2017; Ferrario 2022; Khatchadourian 2012; Morris 2019a). Cyrus II's son and successor Cambyses II continued the Achaemenid invasion, bringing parts of North Africa, the Indus Valley, and the Ferghana Basin under Achaemenid rule and extending the Northeastern boundary of the Empire to the Karakum Desert (Barsitz 2017; Khatchadourian

2012). Darius I (who had usurped Cambyses II's brother Bardiya) pushed further into the Indus Valley and the Central Asian Steppe, as well as into Macedonia, Thrace, and Greece (Barsitz 2017; Ferrario 2022; Khatchadourian 2012; Morris 2019a).

By the second half of the fifth century BCE, twenty administrative provinces, or *satrapies* (a later Greek term), had been established across Eurasia and Africa under Achaemenid authority (Barsitz 2017; Ferrario 2022; Khatchadourian 2012; Wu 2020). Four of these satrapies were located in Central Asia, i.e. Margiana, Bactria, Sogdia, and Khorezm, and they were required to pay heavy taxes to the Empire while subjugated steppe peoples were drafted into the army (Barsitz 2017; Morris 2019a). The taxes levied from satrapies were in part used to construct roads connecting Persia, Central Asia, and India, as well as widespread irrigation, strategic fortresses, and a royal postal system (Barsitz 2017; Ferrario 2022; Khatchadourian 2012).

The Achaemenid Empire instigated long distance trade on a hitherto unprecedented scale, accumulating substantial wealth and transforming both Margiana and Sogdia into commercial hubs which minted their own local coins (Barsitz 2017; Ferrario 2022). And yet, Achhaemenid wealth was largely reserved for royals and elites who spent it maintaining a military presence at the Empire's borders, deploying the military in expeditions to annex new territories (which were not always victorious), and sending soldiers to quell the civil unrest (which often led to property damage) that arose from brutal taxation and labor conscription (Barsitz 2017). The governors, or *satraps*, and officiating regents of the satrapies themselves often resorted to over-taxing incoming merchants to meet their tribute quotas while also filling their own coffers (Ferrario 2022).

By the time Alexander III (i.e. Alexander the Great) arrived in Central Asia the Achaemenid Empire had lost several satrapies (including Sogdia and Khorezm) to revolt and, while stable, was on the edge of decline (the extent of this decline was likely exaggerated by Greek historians; see Brosius 2003; Sherwin-White & Kuhrt 1993). However, the investments that Achaemenid rulers had made into infrastructure such as long-distance roads, irrigation systems, postal service, fortified strongholds, and even bureaucracy were instrumental in the development of trans-Eurasian exchange networks (Barsitz 2017; Juping 2009; Ferrario 2022). Far from being an uncultivated wasteland, Central Asia was one of the greatest commercial and cultural crossroads of ancient Eurasia.

16.6.2. The Macedonian Empire of Alexander III (ca. 334–323 BCE)

"Even though the channels of communication were open in the Persian Empire, in the 4th century BCE other civilizations in Eurasia, such as Rome, India and China, had not established contact with one another…There was as yet no link connecting the two ends of Eurasia. Forging such a link was the task fulfilled by Alexander the Great and Han Wudi…"(Juping 2009)

Alexander III ascended to the Macedonian throne after his father, Phillip II, was assassinated by his own bodyguard in 336 BCE (Gilley 2016). Alexander III aspired to achieve his father's goal of conquering the Achaemenid Empire (then ruled by Darius III) in retaliation for the invasions of Darius I, and successfully invaded Persia in 334 BCE (Gilley 2016). Alexander III and his army

arrived in Central Asia in 329 BCE (Gilley 2016; Morris 2019a) and razed Samarkand to the ground (Barsitz 2017). By 327 BCE the Achaemenid satrapies of Margiana and Bactria, as well as the independent Kingdom of Sogdia (formerly a satrapy), had been assimilated into Alexander III's empire (Barsitz 2017; Morris 2019a).

Alexander III did not manage to conquer the independent Kingdom of Khorezm nor the remainder of Persia, which neither he nor the Graeco-Macedonian world at large were likely to have known the full extent of (Barsitz 2017; Brosius 2003; Morris 2019a). Alexander III subsequently granted the deposed Darius III a dignified funeral, married into royal Persian bloodlines, began to dress like a royal Persian, and introduced royal Persian customs to his court (Abbott 2022; Barsitz 2017; Gillez 2016). He appointed local regents to positions of power in South, West, and Central Asia and began recruiting soldiers from these regions into his own army (Gillez 2016). Alexander III also continued the Achaemenid practice of levying taxes from satrapies, and even had his own coinage minted for distribution throughout his new empire (Abbott 2022; Barsitz 2017; Gillez 2016).

Alexander III's forced hybridization of Mediterranean and Asian culture dismayed his army to the point of mutiny (twice), but successfully appeased the populations he had invaded (Gillez 2016). He founded dozens of new colonies and cities, including in Central Asia, many of which were strategically situated along long distance trade routes and populated by ethnically diverse settlers from across Eurasia (Barsitz 2017). Archaeological excavations in Uzbekistan suggest that pre-existing urban centers swiftly declined while new cities in agricultural areas benefited from irrigation works (Pugachenkova 1996). Urban growth of this scale had never before been seen in Central Asia (Abbott 2022). Under Alexander III's rule, the trade routes and networks which had been fostered by the Achaemenid Empire were further developed within the context of a new Trans-Eurasian empire (Abbott 2022). Alexander III's full ambitions were never fully realized, being cut short by his sudden death in 323 BCE; his short-lived empire, in many ways, died with him (Barsitz 2017; Gillez 2016; Moore 2018).

The finer details of Alexander III's military campaigns, political machinations, life and death, and long-standing legacy, while fascinating, are not relevant to the subject matter of this dissertation (extensive overviews may be found instead in Freeman 2011; Moore 2018; Roisman 2002). His instigation of Hellenistic rule in Asia is very relevant, as it forever transformed the cultural landscape of Eurasia. Alexander III's reign led to the intensification of cross-cultural contact, settlement, and commerce across the long-distance networks that became more and more ingrained into Eurasian lifeways. The Macedonian Empire of Alexander III brought Asia and Europe closer together than they had ever been, in a series of connections which withstood the fracturing of the empire itself.

16.6.3. The Seleucid Empire (ca. 312–64 BCE)

"…before the campaigns of Alexander, the Greeks viewed Central Asia and India as near-mythical lands at the edge of the world…in the decades after the campaigns of Alexander, we find evidence that this worldview had been drastically altered…The edge of the world had been found to continue on, and the worlds of Central

and East Asia would, as a result, become more connected to the Mediterranean and Western Asian worlds than ever before." (Abbott 2022)

Three empires were carved out of the Macedonian Empire of Alexander III following his death and the ensuing power struggle (i.e. the Wars of the Diadochi) - the Ptolemaic Empire of Egypt, the Antigonid Empire of Macedonia, and the Seleucid Empire of Asia (Abbott 2022; Barsitz 2017; Sherwin-White & Kuhrt 1993). The Seleucid Empire was the largest of the three and was first ruled by Seleucos I Nicator, a general who had served under Alexander III and been mythologized as a son of Apollo (much as Alexander III himself had been proclaimed a son of Zeus-Ammon) (Abbott 2022; Moore 2018; Sherwin-White & Kuhrt 1993; Strootman 2012). The Seleucid Empire encompassed vast and diverse territories of West, South, and Central Asia, including Sogdia, Bactria, and Margiana (Abbott 2022; Bernard 1994; Strootman 2012). Though predominantly Macedonian in culture and ethnicity, Asian bloodlines were woven into the Seleucid Dynasty through Seleukos I's son Antiochus I, whose mother Apama was Sogdian nobility (Abbott 2022; Moore 2018; Strootman 2012).

Social elites embraced multiculturalism in order to signal their loyalty to the empire (Strootman 2012). Greek language and coinage soon gained wider prominence in Sogdia and Bactria, which entered into a new period of Hellenisation under Seleucid rule (Moore 2018; Strootman 2012). The Seleucid Dynasty continued to exact tribute from the Central Asian satrapies, just as Alexander the Great and the Achaemenid Kings before him had done for the past several centuries (Barsitz 2017; Strootman 2012). Intensified trade across three major routes (northward to South Asia, westward across the Iranian Plateau to the Levant, and southward to the Persian Gulf) led to increased immigration and the importation of viticulture, Buddhism, and Brahmanism into Central Asia (Barsitz 2017). Artisan industries flourished, military colonies developed into cities, entirely new cities were founded, and cities that had suffered or been demolished under siege were restored (Abbott 2022; Barsitz 2017; Strootman 2012).

The South and Central Asian territories however were on the periphery of the Seleucid Empire, whose concerns had turned to consolidating land and power in West Asia (i.e. modern day Syria and Iraq) (Mairs 2022; Strootman 2012). Conflict broke out with the Ptolemaic Empire of Egypt during the reign of Antiochus II in the second half of the third century BCE, which would spill into a series of wars (Abbott 2022; Mairs 2022; Strootman 2012). Revolts across Bactria-Sogdiana and Central Asian colonies populated by Greek soldiers and mercenaries who had been forced to settle amongst local people who did not want them there had already begun as early as the fourth century BCE, while Alexander III was still alive and king (though believed to have died in India) (Mairs 2022). Civil unrest finally manifested in Graeco-Bactrian independence while the Seleucid Dynasty struggled with infighting between Seleucus II and his brother Antiochus Hierax (Juping 2009; Strootman 2012).

Antiochus III was unsuccessful in his attempts to reconquer Bactria (Abbott 2022), and subsequent revolts in Greece and West Asia further diverted Seleucid attention and resources from Central Asia (Bernard 1994; Mairs 2022). The Seleucid Empire suffered severe losses to the rising powers of Rome and Parthia (modern day Iran), and after a series of failed attempts to reconquer West Asia the dynasty eventually succumbed to infighting (Abbott 2022; Barsitz

2017; Strootman 2012). The Graeco-Bactrian Kingdom arose from the power vacuum as the Seleucid Dynasty faded into obscurity. However, it was the initiatives of the Seleucid Kings who had constructed new, multicultural, prosperous cities spanning South, Central, and West Asia as well as the Mediterranean under a single empire that facilitated Trans-Eurasian trade on a scale that would later bring together East Asia and Europe (Abbott 2022).

16.6.4. The Graeco-Bactrian Kingdom (ca. 256–120 BCE)

"...under the rule of Greeks, the number of cities and towns…so increased that Bactria was called "a state of one thousand cities." Parthians adopted the calendar of the Seleucid dynasty and issued Greek-style coins…The Indo-Greeks were influenced much more by Indian culture…It was against such a political and cultural background that Zhang Qian arrived in…Bactria…it was Zhang Qian who brought information about Hellenistic culture into central China and...marked the opening of the whole Silk Road" (Juping 2009)

After the death of Seleucid King Antioch II in the mid-third century BCE, the satrap of Bactria (Diodotos I) declared Bactrian independence (Abbott 2022; Barsitz 2017; Bernard 1994; Moore 2018; see also Jakobsson 2020). The former satrapy of Bactria was the heart of a new Graeco-Bactrian Kingdom which stretched as far east as the Syr Darya River, touched the Hindu Kush Mountains, and encompassed the multicultural epicenters of Sogdia, Margiana, and Aria (Bernard 1994; Moore 2018). The fruits of Bactrian agriculture greatly enriched the Graeco-Bactrian Kingdom (Abbott 2022; Moore 2018), and the resultant economic expansion is believed to have been strategically managed under Euthydemus I during the assaults of Antiochus III (see section "16.6.3.") (Bernard 1994). After defeating the military advances of the Seleucid Empire, the kings of the Graeco-Bactrian Kingdom began invading South Asia and had reached the Arabian Sea by 180 BCE (Barsitz 2017; Bernard 1994; Moore 2018). The expansion of the Graeco-Bactrian Kingdom into South Asia resulted not only in intensified Trans-Eurasian commerce but also in the fusion of Hellenistic and Indian art, philosophy, and religion (Barsitz 2017; Bernard 1994; Halkias 2014; Marlow 1954; Stoneman 2019).

This Indo-Greek fusion was expressed in the emergence of Greco-Buddhist art (Bernard 1994; Stoneman 2019), the issue of Greek coins depicting Indian deities (Gardner 1886; Glenn 2020), the incorporation of Vedic philosophy into Pyrrhonist Skepticism (Halkias 2014; Stonemen 2019), possible Greek influences on Indian theater and Indian influences on Greek astronomy (Bernard 1994), and possibly the fusion of Greek and Indian art motifs at Ai-Khanoum and the Pillars of Ashoka (Boardman 1998; Ghosh 2020; Lecuyot 2020). The extent of Mediterranean influence on Bactrian pottery since the reign of Alexander III has been called into question by archaeologists who argue for a uniquely Bactrian ceramic tradition until the onset of the Greco-Bactrian Kingdom and intensified Hellenisation, especially at Ai-Khanoum (Junker 2021). The merging of Greek and Indian culture in Asia found its strongest initial expression during the Graeco-Bactrian Empire, beginning with the founding of the Indo-Greek Empire by King Demetrius I ca. 186 BCE (Jakobsson 2009; for a discussion of whether or not the Graeco-Bactrian Kingdom and the Indo-Greek Empire should truly be considered empires, see Hoo & Wiesehöfer 2022; for an overview of Greco-Bactrian archaeology, see Sanahuja 2020).

Graeco-Bactrian expansion into South Asia also considerably weakened the northern border of the Kingdom (Bernard 1994). Ai-Khanoum was abandoned ca. 145 BCE, most likely due to the death of King Eucratides and the arrival of a diasporic group known as the Yuezhi (who had been forced out of their territory by the Xiongnu ca. 162 BCE) (Barsitz 2017; Benjamin et al. 2004; Bernard 1994). The unstable internal dynamics of Graeco-Bactria could not withstand invasions from both the Yuezhi and the Parthians, and the empire collapsed ca. 120 BCE (Barsitz 2017; Jakobsson 2009; Moore 2018). The Chinese ambassador Zhang Qian arrived in Bactria only a decade later, and his reports back to Emperor Han Wudi of a rich but broken land directly facilitated Chinese exchange with Central Asia and officiated the beginning of the Silk Road period (Bernard 1994; Jumping 2009).

16.7. Unraveling the Silk Road: Conclusion

“In an increasingly globalized world that emerged from the 1st millennium BCE…emerging imbalances drove the first formalization of the Silk Road…” (Taylor 2024)

Here I have briefly reviewed how the emergence of Trans-Eurasian exchange networks was facilitated by technological innovation and evolving human-animal relationships in the Neolithic and Bronze Ages, intensified commerce, diplomacy, and warfare in the Iron Age, and the investments of many empires into civil infrastructure and services during Antiquity. All of these events contributed to and culminated in the rise of the so-called Silk Road. In the next chapter I will outline a chronology of the Silk Road period with a focus on Transoxiana, i.e. the region which once encompassed Sogdia (and arguably Bactria and Khorezm) (Bosworth 998; Erkoc 2023; Gregoratti 2023; Rhie 2007; Simpson 2014; Zeimal 1983; Zhabagin et al. 2017). Transoxiana is the setting of Tashbulak, i.e. the third archaeological settlement that I have collagen fingerprinted fauna from for my doctoral research, and will thus be the focus of not just the following chapter but the next two chapters of this dissertation.

17. Ancient Transoxiana

17.1. Introduction

“In reconstructing the political history of Transoxiana...it is necessary to take into account not only the fragmentary character of the information at our disposal, but also the point of view from which Transoxiana is being mentioned or described.” (Ziemal 1983)

In this chapter I will define and briefly discuss the history of ancient Transoxiana, one of the major crossroads of Silk Road period cultural and commercial exchange. I will provide and outline a chronology of the Silk Road period in Transoxiana as well as explore the challenges involved in doing so. I will then discuss the political, economic, and cultural backdrops of Transoxiana leading up to Qarakhanid rule in order to contextualize the research questions relevant to my overview of the archaeological settlement sites and faunal assemblages of Medieval Transoxiana (provided in Chapters 18–19) as a region at the fringe of the wider Islamic world. I will not address actual Qarakhanid era trade and diplomacy until the next chapter. My discussion here will instead focus on the shaping of Turko-Islamic identities and diets before and after Arab conquest in Transoxiana, as well as the logistics of woolen textile production in the Transoxian region of Ustrushna.

17.2. Defining Transoxiana

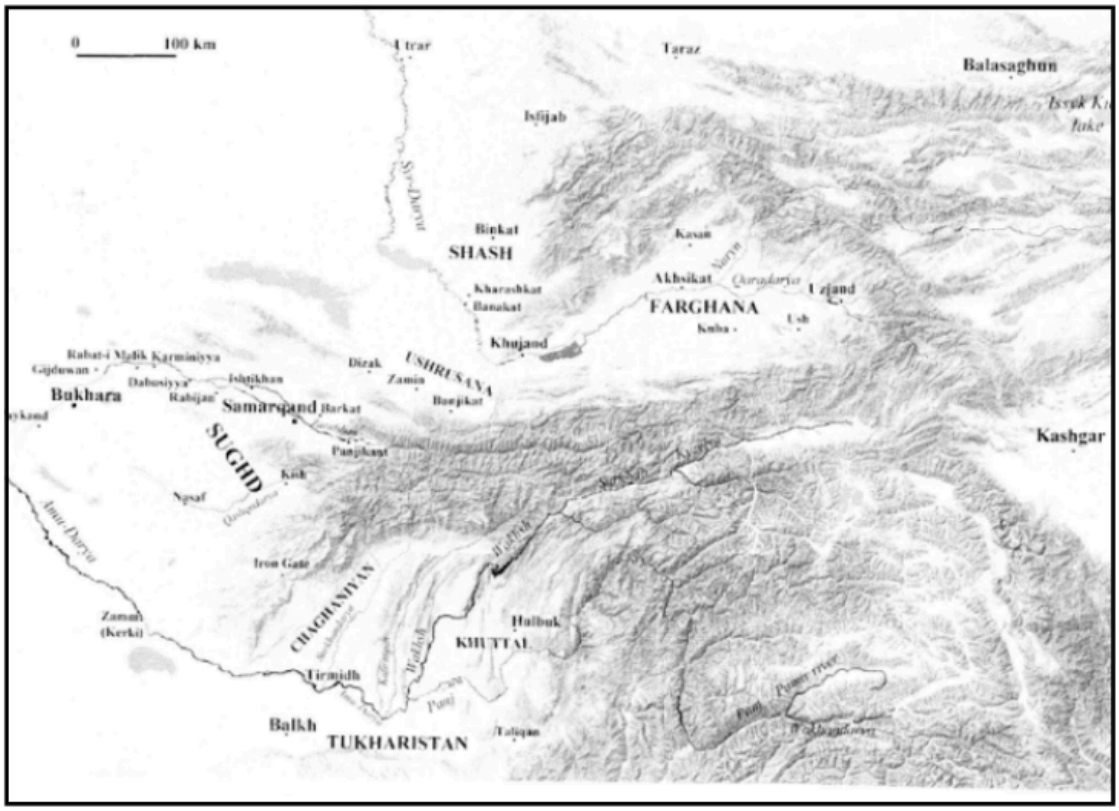
“Cities in Transoxiana were divided into five regions, with the most important center being Soghdia, where Samarqand and Bukhara are located. It included Khwarazm in the west, Sağaniyan in the southeast, Ushrusana on the east side of Samarqand, and Ferghana and Shash in the far east…These regions were followed by numerous populous cities, villages, and agricultural areas…” (Erkoc 2023)

“Transoxiana” is a Latin term meaning “across the Oxus (River)”. The Arabic equivalent, “Ma wara' al-nahr”, means “land beyond the river”. Both refer to a region of Central Asia that was once situated between the Oxus River (Amu Darya) and the Jaxartes River (Syr Darya) (Rhie 2007). Historians and scholars have not always been consistent in their descriptions of the countries, provinces, and cities that comprised Transoxiana. Uzbekistan, Tajikistan, and Kazakhstan are listed in every definition of Transoxiana that I have come across, while Kyrgyzstan and Turkmenistan are only sometimes included (e.g. Azarpay 1977; Zhabagin et al. 2017). Bactria (or Bactriana) is generally equated with modern day Afghanistan, a country not included in definitions of Transoxiana, yet is also identified (exclusively) with Uzbekistan (e.g. Pugachenkova 1996). Bactria has also been included in the list of Transoxian regions (e.g. Rhie 2007) and excluded from it (e.g. Erkoc 2023; Gregoratti 2023; Simpson 2014; Zeimal 1983). The same is true of Khorezem, also spelled as Khawarzm and Chorasmia (included in Rhie 2007 and Erkoc 2023, yet excluded in Bosworth 1998).

Further complications arise from the fact that as empires rise and fall, borders shift and so do seats of municipal governance. Provinces can be absorbed into one another or temporarily incorporated into eachother’s jurisdictions (see Zeimal 1983). Fortunately, narrowing down a

precise definition of Transoxiana is not terribly important for this dissertation. My decision to focus on Transoxiana is related to the need to align within an appropriate scale of research (see Orser Jr. 2010) as opposed to aligning with specific geographical borders. I have included a map of Transoxiana from Karev (2013) below (Fig.13). For the purposes of this dissertation, Bactria and Khorezem will not be considered a part of Transoxiana. My decision to exclude them is not about drawing decisive boundaries and holding them as fact, but about facilitating a meaningful discussion about Medieval (and thus historical) subsistence strategies and animal economies in a defined time and place.

Fig.13 Map of Transoxiana (Karev 2013).



17.3. The Silk Road Period Chronology of Transoxiana

"With the close of the Hellenistic period and the outset of the Common Era, a handful of…Kingdoms…laid claims to the lands previously held and developed in Central Asia and India by the Achaemenids, Alexander, the Seleucids, and the Greco-Bactrians…The subsequent centuries would see long-distance Silk Roads trade continue in new forms, characterized by the involvement of many different states." (Abbott 2022)

The chronology of the Silk Road period as it unfolded in Transoxiana is extensive, reflecting the complex and at times brutal regime changes that characterized the sociopolitical landscapes of Eurasia. Transoxania was conquered by various Central Asian, Iranian, Turkic, Arab, and Mongolian empires and political complexes in a series of regime turnovers that can be roughly divided into five phases (Tbl.67). Many of the associated dates have ultimately been derived from very old literary sources that have been shown to contradict one another; some historical

literary sources have been excluded altogether by scholars after they have been shown to be categorically false (see for example Davidovich 1989). The chronology below should not be viewed as completely fixed, especially considering regional and cultural variation and overlap, and seemingly endless warfare.

Tbl.67 Table of a Silk Road Period chronology for Transoxiana devised for this dissertation.

Silk Road Period	Regime	Approximate Dates	Reference
Early Period (1st – 3rd Century CE)	Kushan Empire	ca. 50–225 CE	Benjamin 2020
Middle Period (4th–10th Century CE)	Sassanid Empire	ca. 230–365 CE	Daryaee & Rezakhani 2018
	Kidara Huns	ca. 335–370 CE	Neelis 2010
	Alchon Huns	ca. 370–450 CE	Neelis 2010
	Hephthalite Khanate	ca. 500–600 CE	Kurbanov 2016
	Göktürk Khaganate	ca. 600–800 CE	Grousset 1970
	Umayyad Caliphate	ca. 674–748 CE	Bosworth & Bolshakov 1998
	Abbasid Caliphate	ca. 748–819 CE	Bosworth & Bolshakov 1998
	Samanid Empire	ca. 819–999 CE	Kia 2015
High Period (10th–14th Century CE)	Ghaznavid Empire	ca. 977–1186 CE	Golden 1990
	Qarakhanid Khanate	ca. 999–1200 CE	Golden 1990
	Seljuk Empire	ca. 1037–1194 CE	Golden 1990
	Khwarezmian Empire	ca. 1077–1231 CE	Grousset 1970
	Qara Khitai	ca. 1124–1218 CE	Biran 2020
	Chagatai Khanate	ca. 1227–1363 CE	Biran 2023
Late Period (14th–16th Century CE)	Timurid Empire	ca. 1370–1501 CE	Biran 2023
	Shaybanid Dynasty	ca. 1500–1600 CE	Kılıç 1999
Period of Decline (16th–19th Century CE)	Bukhara Khanate	ca. 1540–1702 CE	Burton 2020
	Khiva Khanate	ca. 1511–1920 CE	Wood 2019
	Kokand Khanate	ca. 1709–1876 CE	Tagayev 2019

The challenges of trying to delineate discrete chronological categories related to power struggles between sedentary empires and their offshoots (e.g. the Sassanid Empire and the Kushano-Sassanids) as well as nomadic confederacies with somewhat fluid identities (e.g. the Kidara Huns, the Alchon Huns, and the Hephthalite Khanate) carving out different territories of regions with shifting borders cannot be understated. I have included the approximate timelines of regimes that arose in regions adjacent to Transoxiana in an attempt to capture the broader

contexts of the Silk Road period. I am also, imperfectly, equating the term “Medieval” with the Middle, High, and Late Silk Road periods for the purposes of this dissertation. “Medieval” as a term was initially conceived in the context of European history, and there is no real equivalent for Central Asia.

17.4. Turko-Islamic Identities in Transoxiana

“Archaeologists increasingly understand identities as produced through the negotiation of power relations in distinct sociohistorical settings rather than as fixed identities…The ways in which the identities are expressed—materially, socially, visually, and ideologically—depend on the spatiotemporal environment...the analysis of temporal and spatial variables necessarily includes a consideration of analytical scale.” (Orser Jr. 2010)

Turkic peoples had been living in the areas of Transoxiana that coincided with Turkistan since at least ca. 200 BCE, long before the arrival of the Turko-Islamic Qarakhanid Khanate ca. 999 CE (Erkoc 2023; see Tbl.67). The substantial presence of Turkic populations across wide areas of Transoxiana can be traced back to at least ca. 600 CE, when the Göktürk Khaganate overthrew the Hephthalite Khanate (see Tbl.67). The Göktürk Khaganate was a confederation of mobile pastoralists from the Ashina clan (Yang et al. 2023a) which were the first group to refer to themselves as (“Celestial”) Turks, and also the first to develop an alphabet for Turkic languages (Yüksel 2024). Cattle-breeding was central to nomadic Turkic lifeways and though meat consumption was prevalent, dairying was even more essential, and hunting was preferred to the slaughtering of livestock (Yesil 2023). Grain-based foods, animal blood, and alcoholic beverages were also prominent in Turkic pastoralist diets (Yesil 2023).

The religious beliefs of the Göktürk Khaganate remain poorly understood, though they were likely rooted in Tengrism (Talgat & Ayman 2015). Funeral rites may have involved the inclusion of horses into human burials, in keeping with the reconstructed Turkic traditions of Central Asia from ancient through Medieval times (Kaldybayev 2023; see also Chapter 11 for parallels in ancient Mongolian burial customs). The Turkic peoples of Transoxiana were often referred to as “pagans” during the seventh century Arab expansion into Central Asia (Erkoc 2023; Negmatov 1998). The Arab conquest of Transoxiana did not make a significant impact on the genetic landscape (Zhabagin et al. 2017; see Rahmati 2018 for a non-molecular review of the demographic change), though it certainly had a lasting impact on the religious one (Zhabagin et al. 2017).

Although the Turkic peoples of Transoxiana were initially involved in military efforts to repel the invading forces of the Rashidun and Umayyad Caliphates (Erkoc 2023), the decline of the Göktürk Khaganate resulted in the rise of Islamic rule in the seventh century and its solidification in the eighth (Golden 1990; see Tbl.67). The subsequent fall of the Uyghur Khaganate in the ninth century led to mass migrations of Turkic peoples towards Islamic cities in Central Asia (Duturaeva 2022d), including those in Transoxiana. Muslim merchants also began immigrating into Transoxiana, lured by its lucrative trading prospects (Golden 1990), and established settlements in the (largely Turkic) steppe zone (McClary 2020).

Importantly, not all Turkic peoples in Transoxiana were mobile pastoralists; many were farmers, merchants, soldiers, bureaucrats, and governing officials (Erkoc 2023). Turkic peoples who did not convert to Islam were still welcome in the marketplace and the military, but forbidden under *dhimma* (the law for non-Muslims) from entering the religious and administrative spaces which fell under “Daru’l-Islam” (the abode of Islam) (Erkoc 2023). The emerging association of civilization, community, and status with Islam is believed to have made a strong impression on the Turkic peoples of Transoxiana (Golden 1990). The widespread conversion of Turkic peoples to Islam presumably resulted in decreased alcohol and animal blood consumption, as well as a decrease in hunting (which was prohibited by the Abyssid Caliphate) (Yesil 2023).

Nearly two centuries of Arab rule over Transoxiana came to an end when the local Samanid emirs of Sogdia declared independence from the Abbasid Caliphate in the early ninth century (Kia 2015; Shahrian & Seyyed 2023; see Tbl.67). The Samanids were the descendants of a prominent Persian landowner (Saman Khuda) who had converted from either Buddhism or Zoroastrianism (see Kamoliddin 2006) to Islam in the eighth century (Frye 1944; Golden 1990; Meirison & Harir Muzakki 2021; Negmatov 1998). Persian peoples had been living in Sogdia and Transoxiana more broadly at least since the onset of the Achaemenid Empire ca. 550 BCE. Sassanian King Khosrow I later tactically settled Persian peoples enmasse amongst Turkic peoples in Ferghana, Shash, Ushrusana, and Ilek in the sixth century (Erkoc 2023). The Samanids had come to power in eighth century Sogdia for helping to subdue rebellion against the Abbasid Caliphate (Meirison & Harir Muzakki 2021; Negmatov 1988).

The caliphate initially welcomed Samanid independence as a tactical way to buffer Baghdad from the assaults of Turkic nomads while still receiving tribute and exercising control in Central Asia (Bashiri 1997). The Samanid emirs continued encouraging the peoples of Transoxiana to convert to Islam, including settled Turkic peoples and Turkic mobile pastoralists in the mountain and steppe regions (Bullion et al. 2022; Golden 1990; McClary 2020). They were largely unsuccessful in the latter (Bullion et al. 2022), and non-Muslim Turkic peoples continued to be forbidden from entering Daru’l-Islam (Erkoc 2023). Nonetheless, Transoxiana (and Khorasan, i.e. modern day Iran) under Samanid rule has been said to have constituted “the heart of the Sunni Islamic world” (Tor 2015).

Transoxiana-Khorasan grew extraordinarily wealthy from Persian control of the Trans-Eurasian slave trade, and the Samanids reinvested much of this wealth into the patronage of Persian language, arts, music, philosophy, scholarship, science, architecture, and culture (Meirison & Harir Muzakki 2021; Tor 2015) as opposed to paying tribute to Baghdad (Bashiri 1997). The “Persian Renaissance” ushered in by the Samanids flowered in Transoxiana as an intensified Turco-Persian identity, which was Sunni Muslim in religious expression and led certain Turkic groups (e.g. the Oghuz, but not all of them; see Tor 2015) to abandon their own language for Middle Persian (Erkoc 2023).

Turkic peoples in Samanid Transoxiana did not, however, live under the same law as Iranian peoples, and were treated more harshly under *dhimma* (Meirison & Harir Muzakki 2021). At the

same time, the Samanids relied on Turkic *Mamluks* (i.e. enslaved Turkic soldiers) to bolster their military (Bosworth 1988; Meirison & Harir Muzakki 2021). This ultimately led to the downfall of the Samanid Empire, for the economic and cultural expansion of the Persians in Transoxiana (and the degree of independence they maintained) had far exceeded Arab expectation and intention (Bashiri 1997). The resentment of Turkic peoples was easily stoked by the Abbaysid Caliphate, which incited rebellion through Turkic administrators in Baghdad and Central Asia (Bashiri 1997).

The Samanid Empire, which was already struggling with internal conflict and against the political and military advances of a Turkic tribal confederacy from modern day Kyrgyzstan, was subsequently dismantled by their own Turkic military forces in the tenth century (Bosworth 1988; Davidovich 1998; Meirison & Harir Muzakki 2021). The Turkic Mamluk usurpers did not fall under Abyssid authority as the caliphate had envisioned, but instead seized Khorasan for themselves and formed the Ghaznavid Empire (Bashiri 1997; Bosworth 1988; Meirison & Harir Muzakki 2021). Transoxania was seized by the invading Turkic tribal confederacy ca. 999 CE with the help of local Transoxian land owners, who then formed the Qarakhanid Khanate (Davidovich 1998; Golden 1990).

The Qarakhanids had converted to Islam shortly before seizing Transoxiana, but maintained much of their Turkic identity (Davidovich 1998). They attached Muslim honorifics to hierarchical Turkish titles (mostly taken from the names of predatory animals) and had begun referring to themselves as sultans even before their conquest of Transoxiana (Davidovich 1998; Golden 1990). Transoxiana had slipped out of the grasp of the Islamic Persian dynasties and remained at the edge of the Islamic Arab world, and was now under the authority of Islamic Turkic rule. What, then, did Transoxian lifeways look like under the rule of a formerly nomadic Turko-Islamic khanate?

The peoples of Transoxiana were now a mix of ethnically diverse but culturally Persianized city dwellers, agropastoralists, and mobile pastoralists in mountain and steppe zones- the latter of which were increasingly integrating Muslim traditions and beliefs into their own religious and spiritual frameworks (Bullion et al. 2022; Golden 1990). Transoxiana had for centuries been a sanctuary for many religions, including Zoroastrianism, Buddhism, Judaism, Christianity, and Manicheism (Golden 1990; Şirin 2010). Did adherence to Islamic ideology and tenants regarding diet and burial customs vary by landscape, region, ethnicity, social strata, degree of mobility, or predominant subsistence strategy?

A genetic analysis of Central Asian populations has determined that landscape had little to no influence on the genetic makeup of Transoxiana, while agricultural versus pastoralist lifeways strongly contributed to haplogroup distribution (Zhabagin et al. 2017; though, this raises serious questions about the relationship between landscape and subsistence, or alternatively the design of the study). How did the Islamification of Medieval Transoxian peoples manifest in relation to the geographic and cultural landscapes, and how did this intersect with the expression of Turkic identities? These are some of the questions that I will attempt to address with this dissertation.

17.5. Woolen Textile Production in Transoxiana

"...bones also do not help us with understanding…wool– for that we need to look at archaeological textiles made of wool… however, wool is invisible archaeologically…Our evidence for ancient wool trade is hence fragmentary and often indirect. The sources of information include written texts and archaeological textiles made of wool." (Gleba 2014)

The innovation of spinning fibers into thread and wool into yarn was arguably as revolutionary for humans in Eurasia as the innovation of the wheel (Barber 1994). Wool subsequently became nearly indispensable to pre-modern Eurasian lifeways, being utilized for clothing, textiles, housing, and trade (Gleba 2014). Woolen textiles and twills characterized the non-silk fiber industries of Uzbekistan and Central Asia both prior to and during the Silk Road period (Dupuy et al. 2018). At least since the Silk Road period, the peoples of Jizzakh (Dizak) in the Malguzar mountains of Ustrushna specialized in the production of woolen textiles (Abduraimov 2022). The textile production centers of Jizzakh are written about as having been fixed (Abduraimov 2022), though it is currently unclear whether wool-producing animals were managed on site or if wool was outsourced from either sedentary farmers, agropastoralists, or mobile herders. It is also unclear whether sheep, goat, or camel were favored for woolen textile production.

Reconstructing wool economies is a challenging endeavor. In lieu of written records, animal bone and tool assemblages can provide insight- but without the textiles themselves, the archaeological evidence can be insubstantial (see Gleba 2014). For example, archaeologists have argued that caprine taxonomic distributions (verified with ZooMS) and mortality profiles suggest an emphasis on wool production at Chap I in the Tien Shan Mountains during the Bronze and Iron Ages (Ananyevskaya et al. 2021). However, compositions dominated by caprines are almost a defining characteristic of Central Asian herds (see Chapters 08, 15), and culling templates adapted from West Asian and European animal economies are not necessarily suitable for Central Asian economies (see Chapters 02, 09).

The presence of stone tools which the authors admit may or may not have been used for shearing and whorling (Ananyevskaya et al. 2021) offers some support for a wool economy. At the same time, pre-modern Eurasian households commonly kept sheep and created their own textiles (Barber 1994; Gleba 2014), so the presence of wool-working implements does not need to indicate large-scale production. Stronger evidence for woolen textile production at Chap I would be extremely valuable, as it would support the idea that the mortality profile being used to argue for this specialization could confidently be applied to faunal assemblages from other Central Asian sites (in combination with other lines of evidence).

Unfortunately, I cannot say what stronger evidence would look like, and it is difficult to conceive of other ways to reconstruct prehistoric wool economies in Central Asia without actual textiles. Even in the Medieval period, there does not appear to be an abundance of records available–though, it may be the case that such records do exist, but have not been published or translated into English. I have not been able to find any information about the logistics of woolen textile production in Silk Road period Central Asia, and the Uzbek archaeologists that I have asked (e.g. Farhod Maksudov and Sherzod Pardaev) have been unable to provide any insight.

Spindle whorls and needles were recovered from the Bactrian city of Termez (Portero et al. 2022), though it is unclear whether they were being used to produce textiles for trade or for household use. The logistics of woolen textile production pipelines in Transoxiana remain poorly understood, and can likely only be approached with ethnography and modern analogs until more written records and textile production sites come to light.

17.6. Ancient Transoxiana: Conclusion

"In addition to the active commerce of Transoxiana and traffic of different merchants to here, the enthusiasm for participating in the religious operations of Ghaza and preaching Islamic religion also attracted many Muslims…this led to the basic transformation of the political structure and ethnic-racial change of Transoxiana." (Rahmati 2018)

The emergence of Transoxiana as a distinct entity is poorly understood, but has been traced back to at least ca. 300 BCE, with a solid political structure arising ca. 700 CE. Sovereignty in Transoxiana was transferred through dozens of Central Asian, Iranian, Turkic, Arab, and Mongolian regimes, leading to complex populations and lifeways. The Arab conquest dramatically impacted Transoxian identities and resulted in the widespread yet non-uniform adaptation of Islamic practices. While it is easy to assume that this involved an adherence to a Muslim diet, the reality of how Arab expansion and subsequent Islamification impacted subsistence practices in Transoxiana is unclear, especially after the collapse of Samanid authority. The logistics of secondary animal product economies, especially wool production, are also shrouded in uncertainty. In the next chapter I will discuss specifically the Qarakhanid era Transoxiana with an emphasis on the impact of intensified Trans-Eurasian trade on settlement sites, as well as the faunal data currently available for these sites.

18. Qarakhanid Transoxiana (ca. 999–1200 CE)

18.1. Introduction

“With direct access to the trade along the Silk Roads...the Qarakhanids shaped the largest nomadic polity before the Mongols, stretching their political and economic power from Western China to the north of Iran. Conversely, diplomacy, trade, and cultural exchange in...the period of the Qarakhanids, is less well-documented, and…remains one of the least studied stages of Silk Road history.” (Duturaeva 2022d)

In this chapter I will examine the settlement archaeology and faunal data of Medieval Transoxiana. Although Transoxiana spanned multiple modern day countries of Central Asia, my own work is centered upon the ZooMS analysis of a Medieval complex situated in modern day Uzbekistan. I have structured this chapter accordingly, with an emphasis on Uzbek archaeology. I will begin with a discussion of the history of archaeology and zooarchaeology in Uzbekistan, which I will discuss briefly below. I will then discuss Trans-Eurasian commerce and diplomacy in Transoxiana under Qarakhanid rule as well as urbanization in Transoxiana as reflected in civic infrastructure up to the Qarakhanid period. Finally, I will provide a list of these settlements currently known to archaeologists as well as an overview of their excavation and any associated faunal data.

18.2. Archaeology in Uzbekistan

“Archeology is one of the youngest scientific disciplines in Uzbekistan…It is known that until the second half of the twentieth century, archeological data…were almost non-existent…it is necessary to mention the interaction of Russian archeology with the archeology of Uzbekistan” (Ahmedjonov 2021)

The history of archaeological practice in Uzbekistan has been traced back to the nineteenth century, with some memory of the antiquarians and geographers that first began exploring (and plundering) the remnants of ancient Uzbek monuments (Ahmedjonov 2021). Uzbek archaeology can be divided into three phases: Russian colonial archaeology, Soviet archaeology, and Independence era archaeology (Ahmedjonov 2021; Mavlonberdi 2022). Uzbek archaeology is truly the child of Russian archaeology, from the first Russian-led excavations of the archaeological monuments of the Khiva Khanate in 1819 (see Ahmedjonov 2021) to the archaeological theory currently underpinning the scholarship of Uzbek academics in the modern post-Independence period. Russian archaeologists greatly shaped the Uzbek perception and understanding of their country’s past, dominating the discipline to the point that there were no actual Uzbek archaeologists until Yahyo Gulomov (1908 - 1977) in the mid-twentieth century (Ahmedjonov 2021; Qizi 2022).

Gulomov remains beloved nearly to the point of being a culture hero amongst Uzbek archaeologists and historians (see Ahmedjonov 2021; Mavlonberdi 2022; Qizi 2022; Sheraliyevich 2024; Rakhmon 2021; Saiyora 2021). His prolific legacy includes research into ancient systems of water irrigation and the “origin of primitive culture” in Uzbekistan, as well as the organization of several archaeological expeditions and the training of a generation of Uzbek

archaeologists in alignment with the Soviet school of archaeology (Ahmedjonov 2021; Kanimkulov 2022; Qizi 2022) (see Chapter 09–10). At least some of Gulomov's work was published in Russian first and Uzbek only second (Sheraliyevich 2024). Archaeology itself continues to be described by Uzbek scholars as a historical science centered upon the study of "the tools of labor" and "the primitive" (Ahmedjonov 2021; Qizi 2022; Rakhmon 2021; Saiyora 2021; Togaev 2020), strongly echoing Soviet era and Marxist perspectives (see Chapter 09–10). The continued emphasis on the archaeology of labor systems and social evolution has impacted the collection of faunal data in Uzbek archaeology, as I will explore below.

18.2.1. Uzbek Zooarchaeology

Zooarchaeological practice in Uzbekistan has only recently been viewed as important, drawing particular interest in Samarkand, Termez, and Tashkent (pers.comm. Delphine Decruyenaere 2024). To this day, it is common for Uzbek archaeologists to forgo collecting animal bones from archaeological sites, or to deem them unimportant and throw them away (pers.comm. Delphine Decruyenaere 2024; pers.comm. Robert Spengler 2024). There is currently only one practicing Uzbek zooarchaeologist who also teaches, at least in Samarkand (pers.comm. Delphine Decruyenaere 2024). Zoorchaeology is not taught as an isolated subject, but is typically considered a branch of veterinary science (pers.comm. Delphine Decruyenaere 2024). Faunal analysis is more typically conducted by non-Uzbek archaeologists as part of international collaborations (pers.comm. Delphine Decruyenaere 2024). A zooarchaeological reference collection currently consisting of chicken and caprine bones is also being curated in Samarkand (Delphine Decruyenaere 2024). Furthermore, there are currently plans to bring some 20 students from Uzbekistan to China to receive specialist zooarchaeological training (Delphine Decruyenaere 2024).

18.2.2. Chronology & Radiocarbon Dating in Uzbek Archaeology

The skeletal remains of individuals recovered from archaeological Uzbek contexts were radiocarbon dated for the first time in the early twenty-first century, using AMS radiocarbon dating (Blau & Yogodin 2005). Prior to this point relative dating using material culture typology and numismatics were used to contextualize prehistoric archaeological sites in Uzbekistan (Blau & Yogodin 2005; Frye 1949; Pugachenkova 1996; Teufer 2005; see also Schreiber 2022). Historical monuments such as Medieval fortresses were understood largely through the lens of written records, coins, and local folklore, with some superficial archaeological studies being conducted during the Soviet phase of Uzbek archaeology (Mavlonberdi 2022). Historical archaeology in Uzbekistan has blossomed in its Indepence phase (Ahmedjonov 2021; Mavlonberdi 2022) and AMS radiocarbon dating is being employed alongside typological material culture analysis to more accurately secure chronological contexts (e.g. Betts 2016; Kot 2022; Krakhmal 2015; Krivoshapkin et al. 2010; Mantellini 2018a; Nishiaki et al. 2022; Stark 2024).

18.3. The (Historical) Archaeology of Medieval Transoxiana

"Issues of scale in historical archaeology have been embedded in the field since its inception, and considerations of scale will always be pertinent in archaeological thinking…historical archaeologists face serious conceptual and practical issues when attempting to move beyond the community and the city and into the wider world." (Orser Jr. 2010)

So far in this chapter I have briefly discussed archaeological theory and practice in Uzbekistan, including faunal analysis and radiocarbon dating. I will soon provide a list of archaeological sites and associated faunal assemblages that have been excavated in the former region of Transoxiana and attributed to the Qarakhanid period (ca. 999–1200 CE). An archaeological review of the entire Silk Road period, or even the High Silk Road period, of Transoxiana would be a book in itself. I will only be reviewing the phase of the High Silk Road period which contextualizes the archaeological site that I have done preliminary ZooMS for - i.e. Tashbulak (see Maksudov et al. 2019). Before overviewing the settlement archaeology, zooarchaeology, and animal economies of Qarakhanid Transoxiana, it is necessary to discuss the research questions attached to them.

Historical archaeology is very different from prehistoric archaeology, due to differences in complexity that result in very different research questions. The structure of this chapter will not mirror that of the previous chapters which focused on investigating early animal husbandry and the timing of horse domestication in prehistoric Inner Asia (see Chapters 10–15). A systematic overview of all the settlement sites and faunal data associated with Medieval Uzbekistan is unlikely to be as useful as it was for Bronze Age Southern Siberia and Mongolia, as questions regarding the timing of pastoralist emergence are no longer relevant.

Any attempt to list every settlement site associated with the Medieval period would quickly turn into an overwhelming architectural catalog, complimented with scant faunal data. Archaeological sites exhibit far more diversity (and social stratification) in historical contexts and can no longer be neatly separated into burial versus habitation sites. Cities can also be highly stratified and preserve the archaeological evidence of dozens of imperial regime changes. Imperial regimes are different from archaeological cultures, and the very act of defining cultural horizons not by populations (e.g. Afanasievo) but by their rulers (e.g. Qarakhanid) speaks to a remarkable intensification of social stratification. I have thus adapted the structure and flow of this chapter to reflect the complexity of Medieval Transoxiana.

My focus here will still be on faunal assemblages and reports from archaeological sites and the reconstruction of the animal economies which characterized them. This will facilitate my discussion of Medieval animal economies in the next chapter, which will in turn be incorporated into my analysis of my ZooMS results from Tashbulak in the Results chapter (see Chapter 21). However, my interest will shift from what herd compositions can reveal about the onset of animal husbandry to what they can reveal about identity, modes of pastoralism, secondary product manufacture, and Silk Road trade on the periphery of the Medieval Islamic world. I will also examine the role of camels in urban contexts and discuss the surprising lack of camel remains that have been discovered in Silk Road period animal assemblages.

18.4. Qarakhanid Era Trade

"Two branches of the Silk Road passed through the Transoxiana region…The strategic location of Transoxiana ensured its contact with the peoples of eastern Central Asia, Afghanistan, Gandhara, Iran and other areas to the west, and the nomadic tribes of the north." (Rhie 2007)

I have already discussed the human innovations and interactions of the Neolithic, Bronze Age, Iron Age, and Antiquity periods that led to the emergence of the Trans-Eurasian exchange networks, with an emphasis on Central Asia (see Chapter 16). I have also discussed the influx of merchants into Transoxiana and the stimulation of trade that partially resulted from Arab expansion and the Persian Renaissance in the early Medieval Period (see Chapter 17). The Qarakhanid Khanate which came into power after the fall of the Samanid Empire played a crucial role in the trade and cultural exchanges that developed between East Asia and West Asia during the tenth to twelfth centuries (Biran 2015; Duturaeva 2022a, 2022b, 2022c, 2022d). The Qarakhanid Khanate established diplomatic trade relations and exchanged valuable commodities such as musk with neighboring Islamic states (Duturaeva 2016).

The Qarakhanids also liaised with the Liao and Song dynasties of China and facilitated the trade of Islamic artifacts, Chinese porcelain, jade, silk, kingfisher feathers, tea, and precious stones amongst Han, Khitan, Tangut, and Jurchen peoples (Biran 2001, 2015; Duturaeva 2022a, 2022b, 2022c). The Qarakhanids, along with the Uyghurs and Tibetans, effectively acted as intermediaries in the trade between the Turko-Islamic and Sino-Tibetan worlds (Biran 2015). Qarakhanid trade eventually connected Eastern and Western Eurasia, enabling commerce with India, Khurasan, Iraq, and Egypt (Biran 2015). Their connections extended even into Europe, placing them at the center of a complex trade network of frankincense, amber, and horses that connected Scandinavia, the Islamic world, and China (Duturaeva 2016, 2022c; see also Taylor 2024). The Qarakhanid export of fine textiles and import of rarities and spices along Trans-Eurasian exchange routes greatly contributed to the political and economic landscape of Medieval Eurasia, as was reflected in urban spaces.

18.5. Qarakhanid Era Urbanization

"The urban history of the Karakhanid state is…derived from…lowland urban centres…" (Maksudov et al. 2019)

Urbanized areas in Central Asia often emerged from ancient settlements and colonies that had been established near water sources, such as rivers and oases, and trade routes. I have already discussed how Achaemenid investment into irrigation, long-distance roads, postal service, and trans-Eurasian trade transformed Transoxian provinces such as Sogdia into urbanized culture capitals and major economic centers (see Chapters 16–17). The Hellenistic period resulted in the decline of some of these centers, the restoration of others, and the emergence of dozens of new cities that benefited from intensified irrigation and the expansion of trade routes (see Chapter 16). For a review of a selection of urban settlements from the Antiquity period of Central Asia, see Kidd & Stark (2019). Temples, markets, schools, bathouses, palaces, houses, and more characterized the early Medieval urban landscapes of

Transoxiana (see Dawkes & Jorayev 2015; Smagulov & Yatsenko 2008), which were organized around available water sources (Kidd & Stark 2019; Rante 2018). Hospitals ("bimaristans") were probably introduced during Arab conquest and expansion (see Latif 2019), when architecture was Islamified (see Şirin 2010).

The Samanids and Qarakhanids further developed and refined urban centers, building minarets and mausoleums (see Markova 2023; McClary 2020; Mir-Makhamad et al. 2021) Cities and settlements strategically located along important trade routes, such as the road connecting Samarkand and Bukhara, effectively served as commercial and administrative centers during these periods (Decruyenaere et al. 2024; Mir-Makhamad et al. 2021). Although the organization of civil infrastructure around large-scale trade precedes Qarakhanid rule, the presence of features such as *sharestans* (fortified urban areas) and *rabats* (complex suburban commerce centers and roadside inns for strangers; pers.comm. Basir Mir-Makhamad 2024) at Qarakhanid sites such as Paykend (Mir-Makhamad et al. 2021) is a testament to the economic importance of Silk Road period exchange at these sites. The fact that certain sharestans and rabats likely continued to be maintained under Qarakhanid rule even after administrative centers were abandoned following aridification (Mir-Makhamad et al. 2021) further emphasizes the role of commerce at certain settlement sites. The impact of Silk Road trade on the animal economies of these settlements is not as clear, nor is the relationship between this trade and Islamification outside of lowland trading hubs. I will provide an overview of the available archaeological data below.

18.6. Qarakhanid Settlement Sites of Transoxiana

"The archaeological analysis of urban space is complex…cities are vast archaeological sites…'Historic cores'...tend to be relatively small, but they are still among the most complex of all archaeological sites...the extensive settled areas that stretch out beyond such 'historic cores' are also of interest, and…have complex histories…almost all cities…that were founded in more ancient times but were still flourishing in the sixteenth century are…living places today…the most recent layers of the record are most often…disturbed…because they are 'high up' in the stratigraphy." (O'Keefe & Yamin 2006)

Although the Qarakhanids were traditionally nomadic, they gradually settled into suburban dwellings and eventually urban palaces and citadels in Bukhara and Samarkand (Karev 2013; McClary 2020). The Qarakhanids also oversaw the construction (and reconstruction) of architectural and irrigation works in Transoxiana, especially under Khagan Ali Aslan Khan (McClary 2020; Mir-Makhamad et al. 2021). Scholars have argued that urban expansion under the Qarakhanids was oriented towards integrating traditionally mobile people more firmly into the empire (Maksudov et al. 2019; McClary 2020). As far as I am aware, the only residential sites that have been excavated and associated with the Qarakhanid Khanate are Afrasiab (Mantellini 2017), Iskijkat (Rante 2019), Kafir Kala (Mantellini & Berdimuadov 2005), Mailykhotan (Frachetti & Maksudov 2014), Mingtepa (Akhunbabaev 1983), Paykend (Omelchenko & Mirzaakhmedov 2024), Tashbulak (Frachetti & Maksudov 2014; Maksudov et al. 2019), and Ulukdush (Frachetti & Maksudov 2014). I will detail each of these sites and their excavation below, as well as any associated faunal data that has been published.

Afrasiab (Samarkand Oasis, Sogdia) (ca. 600 BCE–1200 CE)

Afrasaib refers to a former urban settlement and administrative center of ancient Samarkand that was (possibly) founded in the Early Antiquity period (ca. 600–500 BCE), and spanned nearly 220 hectares (Karev 2013; Mir-Makhamad et al. 2024; Shihskina 1994). Soviet excavations at Afrasiab date back to the nineteenth century, while the French-Uzbek archaeological mission led a series of excavations in the twentieth century (Karev 2013). The collection and analysis of archaeobotanicals from Afrasiab has been published very recently by Basira Mir-Makhamad, alongside radiocarbon dating (see Mir-Makhamad et al. 2024). The results this study indicated that cotton had been introduced to Afrasiab (and the Zarafshan Basin) before Arab expansion, while fig, mulberry, and pomegranate remains have yet to have been recovered from Pre-Islamic contexts (Mir-Makhamad et al. 2024).

Urban expansion at Afrasiab can in general be traced back to the Islamic rule, including under the Abyassid Caliphate and the Samanid Empire (as traditionally acknowledged) as well as the Qarakhanid Khanate (as demonstrated more recently; see Karev 2013; Mir-Makhamad et al. 2024). Although Afrasaib was an important center of culture and commerce during the reign of the Qarakhanids, no faunal remains have been published or even mentioned in any archaeological literature that I have come across. I contacted Saidov Muminkhon, the director of the Samarkand Archaeological Institute who oversees all excavations at Afrasaib, but unfortunately did not hear back from him. It is very unlikely that there were not any animal bones recovered from such a vast and ancient site (pers.comm. Robert Spengler 2024), but as of the time of this dissertation, there is no information available.

Iskijkat (Bukhara Oasis, Sogdia) (ca. 300 BCE–1500 CE)

Iskijkat is an archaeological settlement that has been referred to as both a town (Decruyenaere et al. 2024) and a city (Rante 2019). Situated on the bank of a southwestern branch of the Zerafshan River in the Bukhara Oasis, Iskijkat would have been en route to the cities of Samarkhand and Bukhara (Decruyenaere et al. 2024; Rante 2019). Archaeological features at Iskijkat include a citadel and adjacent housing, and material finds recovered from these features have been typologically dated from Late Antiquity (ca. 300 BCE) to the Late Silk Road Period (ca.1500 CE) (Decruyenaere et al. 2024; Rante 2019). The period of occupation associated with the Qarakhanid period has also been associated with a market and commercial production center (Rante 2019), though no wool-working implements have been recovered (pers.comm. Delphine Decruyenaere 2024). An abundance of faunal remains (n=2,154) were recovered from Iskijkat, from both the citadel and especially from the surrounding residential features (Decruyenaere et al. 2024).

Zooarchaeological analysis at Iskijkat is ongoing (Decruyenaere et al. 2022 [abstract], 2024). The bulk of the remains date back to the Early Silk Road Period (ca. 100 CE) and have not been recovered from residential contexts dated beyond the fall of the Samanid Empire (ca. 999 CE) (Decruyenaere et al. 2024). Only faunal remains from the Iskijkat citadel have been attributed to the Qarakhanid period, and these number less than 50 (Decruyenaere et al. 2024).

The overwhelming majority of the animal bones recovered from all stratigraphic contexts of Iskijkat have been attributed to domesticated livestock (ca. 90%), with caprines dominating the assemblage (Decruyenaere et al. 2024). ZooMS is currently being employed to distinguish *Ovis* sp. from *Capra* sp. (pers.comm. Delphine Decruyenaere 2024). Cattle remains were the second most common, and were recovered with notable butchery marks (Decruyenaere et al. 2024). Pig (no. 25) and chicken remains were also recorded, as well as camel (n=10) (Decruyenaere et al. 2024). Wild taxa included gazelle, roe deer, and possibly saiga (Decruyenaere et al. 2024).

The large number of faunal remains recovered as well as the robust nature of their study (including taphonomical analysis and mortality profile reconstruction) represents a very exciting step forward for the subsistence archaeology of Medieval Transoxiana and Central Asia. Additionally, the currently ongoing use of ZooMS to refine taxonomic attributions (especially caprine), stable isotope analysis to investigate diet, and genomic analysis to retrace Karakul sheep breed origins and dispersal (pers.comm. Delphine Decruyenaere 2024) will all combine to recreate a nuanced picture of Iskijkat lifeways throughout centuries of occupation. The zooarchaeological, biomolecular, and stable isotopic research of the archaeological fauna from Iskijkat represents one of the most promising endeavors in the reconstruction of ancient through pre-modern human-animal relationships in Central Asian oases.

Kafir Kala (Samarkand Oasis, Sogdia) (ca. 650–1100 CE)

Kafir Kala is a citadel situated in the alluvial flats of the Zeravshan Valley in the Samarkand Oasis, which once safeguarded the agricultural outskirts of Transoxiana south of Afrasiab (Mantellini & Berdimuadov 2005; Serrone et al. 2007). Kafir Kala has been superficially excavated off-and-on again since the beginning of the Soviet era, with systematic excavations finally commencing in 2001 under the Uzbek-Italian “Samarkand and Its Territory" archaeological initiative (Mantellini & Berdimuadov 2005; Serrone et al. 2007). Material finds from Kafir Kala were typologically analyzed and attributed to the mid-seventh through twelfth century (ca. 650–1100 CE), which has been divided into the “Pre-Islamic” and “Islamic” periods (Mantellini & Berdimuadov 2005; Serrone et al. 2007). As far as I am aware, no archaeological materials from Kafir Kala have been radiocarbon dated.

A detailed faunal report has been published for Kafir Kala, including not only taxonomic distributions (see Tbl.68) but also age-at-death data and taphonomic analysis (Serrone et al, 2007). Although ibex and roe deer (presumably *Capra siberica* and *Capreolus pygargus*) were mentioned in the report, they are not represented in the table of taxonomic attributions and counts. Seronne et al. (2007) determined that Islamification did not have any great impact on the animal economy of Kafir Kala, which was largely centered upon the rearing and exploitation of caprines. Uniquely, camel remains were recovered from Kafir Kala, as were horses, asses, cattle, suids, dogs, cats, birds, foxes, and wild ungulates. Butchery marks were recorded on cattle, caprine, and fox bones, and one caprid astragalus had even been fitted with a metal ring to create finger jewelry (Serrone et al. 2007). Culling profiles were reconstructed for caprines attributed to the Pre-Islamic and Islamic period; they do not diverge greatly, and the authors

(Serrone et al. 2007) offer no further comments about mortality profiles or their relation to primary and secondary animal products.

Tbl.68 Faunal data from the Islamic period of Kafir Kala (ca. 750–1100 CE) (Serrone et al. 2007).

Taxonomic Group	NISP	NISP%	MNI	MNI%
Caprines	1001	65.7%	72	45%
Ovis aries	111	7.3%	25	15.6%
Capra hircus	39	2.6%	10	6.3%
Bos taurus	189	12.4%	22	13.8%
Equus sp.	14	0.9%	3	1.9%
Equus caballus	17	1.1%	6	3.8%
Equus asinus	6	0.4%	2	1.3%
Sus scrofa domesticus	7	0.5%	5	3.1%
Sus scrofa	4	0.3%	2	1.3%
Camelus sp.	3	0.2%	2	1.3%
Cervus elaphus	2	0.1%	1	0.6%
Small-medium wild ungulates	3	0.2%	2	1.3%
Canis familiaris	7	0.5%	3	1.9%
Vulpes vulpes	22	1.4%	3	1.9%
Felid	1	0.1%	1	0.6%
Felis catus	3	0.2%	1	0.6%
Aves	88	5.8%	N.A.	N.A.
Micromammal	6	0.4%	N.A.	N.A.
TOTAL	1523	100	160	100

Mailykhotan (Jizzakh, Ustrushna) (ca. 2021 BCE–1200 CE)

Mailykhotan (SITE 3021) is a stratified settlement site situated on an alluvial terrace in the foothills of the Malguzar Mountains in Uzbekistan (Frachetti & Maksudov 2014). The site was excavated by a team of archaeologists as a part of the Malguzar Uzbek-American Archaeological Research Project (MALGUZAAR), who concluded that it was a pastoralist encampment (Frachetti & Maksudov 2014). Charcoal and bone samples from the deepest layer of the site were radiocarbon dated to ca. 2021–1935 BCE, securing a Bronze Age context for the oldest phase of occupation at Mailykhotan (Frachetti & Maksudov 2014). Two other occupation phases were identified, the oldest of which was attributed to the Late Medieval period through typological analysis of ceramic finds (Frachetti & Maksudov 2014). If spindle whorls, needles, or shears were recovered, these finds were not reported. A faunal report has yet to be published for Mailykhotan, though over a dozen boxes of animal bones were recovered from the site.

Mingtepa (Samarkand Oasis, Sogdia) (ca. 500 CE– 1000 CE)

There are two archaeological sites in Uzbekistan named Mingtepa. One is situated in the Samarkand Oasis in Sogdia (see Akhunbabaev 1983; Bergmatov et al. 2021, 2022; Rakhmonov et. al. 2021) and the other in Andijan in the Ferghana Valley (see Gorbunova 1986;

Turdikhujaeva 2021), both of which fall under Transoxiana. The Mingtepa site in Andijan has been dated to ca. 300 BCE–400 CE, and as of yet no associated faunal data has been published (pers.comm. Basira Mir-Makhamad 2024). I will thus not discuss the Mingtepa site located in Ferghana any further, and any mention I make of Mingtepa should be understood to be in reference to the site in Sogdia. Mingtepa is located approximately 20 km northeast of Samarkand in the northwest part of the Qoramöyin village, Jomboy district (Akhunbabaev 1983; Bergmatov et al. 2021, 2022; Rakhmonov et. al. 2021).

The site spans ca. 35 hectares and includes a citadel, a defensive wall, and urban housing that have been undergoing excavation since the late twentieth century (Akhunbabaev 1983; Bergmatov et al. 2021, 2022; Rakhmonov et. al. 2021). Archaeological materials such as ceramics and coins have been typologically dated to sixth through eleventh centuries (Akhunbabaev 1983; Bergmatov et al. 2021, 2022; Rakhmonov et. al. 2021). Zooarchaeological analysis is currently ongoing (Delphine Decruyenaere et al. 2022). Archaeological eggshells collected from Mingtepa have been identified as chicken with peptide mass fingerprinting (Peters et al. 2024). Wool-working implements, on the other hand, were not recovered (pers.comm. Delphine Decruyenaere 2024). I am unable to further comment about the animal economies of Mingtepa.

Paykend (Bukhara Oasis, Sogdia) (ca. 500 BCE–1200 CE)

Paykend, like Afrasiab, was a major urban center of Sogdiana during the Silk Road period of Transoxiana (Mir-Makhamad et al. 2021; Omelchenko & Mirzaakhmedov 2024). Excavations at Paykend date back to the late twentieth century and are currently still ongoing (see Omelchenko & Mirzaakhmedov 2024). Situated on the edge of the Kyzyl–Kum Desert in the Bukhara Oasis, Paykend was originally a fortified Iron Age site that expanded into a city between the Late Antiquity and Early Silk Road periods (Mir-Makhamad et al. 2021). The extensive archaeological features at Paykend include a citadel (with both Islamic and Zoarastrian religious spaces), residential buildings in two sharestans, a bazaar, a number of rabats and streets, and water works (Mir-Makhamad et al. 2021; Omelchenko & Mirzaakhmedov 2024). Basira Mir-Makhamad's recent analysis (including AMS radiocarbon dating) of archaeobotanicals recovered from the rabats and sharestans has demonstrated that dryland agriculture was prevalent during the Qarakhanid period of Paykend (Mir-Makhamad et al. 2021). Cultivated crops included chickpeas, lentils, barley, wheat, and millet, with rice and fruits having likely been imported (Mir-Makhamad et al. 2021).

As with Afrasiab, no faunal remains have been reported from Paykend. Paykend was eventually reduced to a commercial center and subsequently abandoned following the onset of the Medieval Climate Anomaly (Mir-Makhamad et al. 2021; see also Misa et al. 2023); it is unclear how this impacted local animal management strategies. I have been told that approximately 20 camel bones were recovered (pers.comm. Delphine Decruyenaere 2024), though these findings have not yet been published. Although one publication states that an abundance of domesticated and wild animal bones, including of wild boar, were recovered from Paykend (Omelchenko & Mirzaakhmedov 2024), no data are provided and the publication cited

(Omelchenko 2013) does not include any mention of faunal remains. The specific page referenced (page 108) refers instead to coins, daggers, and ritual objects. More thorough reporting on the presence or absence of animal bones recovered from urban centers along Trans-Eurasian exchange routes would be essential for the investigation of animal economies and urban agropastoralism in Medieval Transoxiana.

Tashbulak (Jizzakh, Ustrushna) (ca. 800–1100 CE)

Tashbulak (Site 3409) is a settlement site spanning 12-15 hectares in the Malguzar Mountains of the Jizzakh Province in Eastern Uzbekistan (Maksudov et al. 2019). Tashbulak, like Mailykhotan, was surveyed by a team of archaeologists as a part of the MALGUZAAR project (Frachetti & Maksudov 2014). Tashbulak was subsequently excavated as a part of the Archaeological Research of the Qarakhanids (ARQ) project (Spengler et al. 2018; Maksudov et al. 2019). Some 20 archaeological features were identified, including a citadel, military barracks, metallurgical workshops, a defensive tower, and a necropolis (Frachetti & Maksudov 2014; Maksudov et al. 2019). The application of VHR Lidar has very recently revealed approximately a hundred habitation dwellings at Tashbulak, which was previously reported as spanning only 7 hectares (Frachetti et al. 2024). The archaeological material finds from Tashbulak have been typologically associated with at least the tenth century CE (Bullion et al. 2022; Maksudov et al. 2019; Spengler et al. 2018). Notably, the reported date range for occupation at Tashbulak varies by publication, probably due to the overall complexity of the site (see Tbl.69).

Tbl.69 Table of published dates for Tashbulak.

Publication	Reported Date Range	Reformatted Range
Bullion et al. 2022	“from the early to mid-eighth century to the mid-eleventh century”	ca. 710–1050 CE
Greer & Bullion 2021	“between the mid-8th and 11th century CE”	ca. 750–1000 CE
Hermes et al. 2018	“9th–11th c.”	ca. 800–1000 CE
Maksudov et al. 2019	“late 10th and early 11th century CE”	ca. 990–1000 CE
Spengler et al. 2018	“800–1100 A.D.”	ca. 800–1100 CE

Although radiocarbon dating is mentioned in Bullion et al. 2022, with a supporting citation of Maksudov (2019), no radiocarbon sample numbers or dates are provided in any publication (including Maksudov 2019). What all the aforementioned publications do agree on is the Qarakhanid occupation and urban expansion of Tashbulak. The urban planning of Tashbulak has led scholars to argue that the settlement represented Qarakhanid attempts to integrate nomadic principles and populations into highland complexes, though analysis is still ongoing (Maksudov et al. 2019).

The osteoarchaeological and funerary analysis of individuals in the necropolis has demonstrated that the community members interred at Tashbulak observed Islamic burial customs, such as being positioned in alignment with Mecca and without personal possessions (Bullion et al. 2022; Bullion 2024; Greer & Bullion 2021). Grape seeds were identified at Tashbulak (Spengler et al. 2018), raising questions as to whether or not wine was being produced and consumed at a Medieval urban complex that was practicing Muslim funerary rites.

Residue analysis of vessels from Tashbulak could possibly help to clarify questions about viticulture and wine drinking at Tashbulak (see Chapter 02).

Cattle, sheep, and goat were tentatively identified at Tashbulak by a non-specialist (Maksudov et al. 2019) and subsequently submitted for professional analysis. The results of this faunal analysis have not yet been published. Although no spindle whorls, shears, or needles were reported from Tashbulak (Maksudov et al. 2019), at least spindle whorls were recovered (pers. comm. Fahrod Maksudov 2024). Whether or not wool was being shorn or worked at Tashbulak remains an open question, though pottery is believed to have been made on site (pers.comm. Fahrod Maksudov 2024).

Ulukdush (Jizzakh, Ustrushna) (ca. 1100 BCE–1200 CE)

Ulukdush (Site 3029) is a stratified archaeological encampment situated in a deep valley in the Malguzar Mountains of Uzbekistan (Frachetti & Maksudov 2014). The archaeological features of Ulukdush, limited to fire pits and a clay floor, were excavated by a team of archaeologists as a part of the MALGUZAAR project (Frachetti & Maksudov 2014). The ceramic assemblage from Ulukdush was typologically analyzed and charcoal samples were radiocarbon dated, suggesting that occupation spanned ca. 1100 BCE–1200 CE (Frachetti & Maksudov 2014). Although pottery and pottery sherds were recovered, there was no mention of faunal remains in the report.

18.7. Qarakhanid Transoxiana: Conclusion

“The Qarakhanids (999-1212) were the first Turkic dynasty after the Arab conquest to come from the steppe and take control of the old urban centres of Transoxania.” (Karev 2013)

Archaeology and zooarchaeology in Uzbekistan was initially shaped by Soviet theory and practice but has since developed into their own unique fields. Zooarchaeology is not practiced or understood as widely as archaeology, though collaborations with other countries such as China are resulting in more widespread training. Although faunal data collection has not been historically been prioritized there is a faunal report available for the important Qarkhanid era settlement site of Kafir Kala, and the analysis of animal bones assemblages from sites such as Iskijkat, Mingtepa, Tashbulak, and Mailykhotan is underway. Available archaeological data point to Transoxian settlement sites along important Trans-Eurasian exchange routes functioning primarily as important economic centers as opposed to agricultural centers, at least during the Qarakhanid period of rule. In the next chapter I will discuss animal economies during the Medieval period of Transoxiana in depth, including outside of lowland urban centers, including available evidence of Islamification in different contexts.

19. The Medieval Animal Economies of Transoxiana

19.1. Introduction

"According to Islamic geographers, the cities along the Jaxartes River…stood out due to their abundant natural resources…the quality of vegetables and fruits was such that the people could meet all their needs…Ibn Hawqal mentioned that the most fertile lands on earth were created in this region by Allah, and he praised the abundance of vegetable production and rich pastures for grazing animals." (Erkoc 2023)

In this chapter I will discuss what can currently be inferred from published faunal data, and my own ZooMS results, about the Medieval animal economies of Transoxiana. I will preface this discussion by briefly overviewing the prehistoric animal economies of Inner Asia as well as herd compositions and faunal assemblages recorded from Neolithic through historical Transoxian contexts. I will focus on the management of key livestock species, ie. cattle (*Bos* sp.), equids (*Equus* sp.), caprines (*Ovis*. sp., *Capra* sp.), camels (*Camelus* sp.), and suids (Sus sp.), as well as the exploitation of various bird, reptile, and amphibian species. Finally, I will explore the modes of pastoralism that may have been practiced in Medieval Transoxiana, based not only upon zooarchaeological data but also archaeobotanical remains and material culture finds.

19.2. The Prehistoric Animal Economies of Transoxiana

"The last few years have seen an increase in bioarchaeological research in southern Central Asia...The least documented area is probably the subsistence economies in the urban centres established in the oases along the major routes of the Silk Road during the historical periods.." (Decruyenaere et al. 2024)

A discussion of the Medieval animal economies of Transoxiana should perhaps first be contextualized with the local prehistoric and Antiquity period animal economies which preceded them, especially in relation to the introduction of domesticated animals. There are very limited archaeological data from the Neolithic period of Uzbekistan in general, though a detailed discussion about this is beyond the scope of my dissertation. Faunal data are available from the rock shelter of Kaynar Kamar in Bactria, which was inhabited from the Early Neolithic through the Iron Age (Nishiaki et al. 2022; see Tbl.70). The data are provided in NISP counts which convey a clear prevalence of caprines throughout all periods of occupation after the Late Neolithic. It is currently unclear whether any of the caprines from Neolithic Kaynar Kamar were domesticated, though it is certainly possible (see Taylor et al. 2021a). The Early and Middle Neolithic periods were characterized by birds and reptiles, though how many of these animals were being economically exploited and how many were accumulating naturally is unclear.

Tbl.70 Table of faunal data (NISP) from the Bactrian rock shelter of Kaynar Kamar (Nishiaki et al. 2022).

Archaeological Period	Estimated Dates	Caprines	Cattle	Equids	Camelids	Cervids	Canids	Suids	Reptiles	Birds
Early Neolithic	ca. 9200–8700 BCE	61	0	0	0	0	1	2	24	51
Middle Neolithic	ca. 7700–6600 BCE	81	0	0	0	0	2	4	15	34
Late Neolithic	ca. 5600–5300 BCE	151	7	0	0	1	1	7	10	20
Bronze Age	ca. 4200–2900 BCE	170	0	0	0	2	0	0	15	20
Iron Age–Early Antiquity	ca. 1200 BCE–300 CE	53	0	0	0	2	0	0	3	12

**Archaeological ages were partially determined following Novák & Baumer 2019, and certain taxonomic categories from Nishiaki et al. 2022 were combined to form categories in this table (.e.g. "Caprines" and "Canids").*

19.3. Transoxian Faunal Assemblages & Herd Compositions Through Time

"One way to ease the problem of small sample sizes is to approach zooarchaeological analysis using large scale analysis…Large and not so large datasets can be combined or…compared, to identify regional patterns…we must be careful not to over-interpret our evidence. Regional analysis is…an essential part of our work…there is a constant interplay between researches carried out at different scales…however, outliers can be more easily identified when a regional pattern is reconstructed." (Albarella 2018)

What can be said about the animal economies of Transoxiana more generally is that faunal assemblage composition remained relatively unchanged from the Late Neolithic onwards, at least that we can infer with the available zooarchaeological data. Caprines dominated, cattle and equids were secondary, while suids and camels were only minimally exploited (Fig.14; Tbls.71–72).

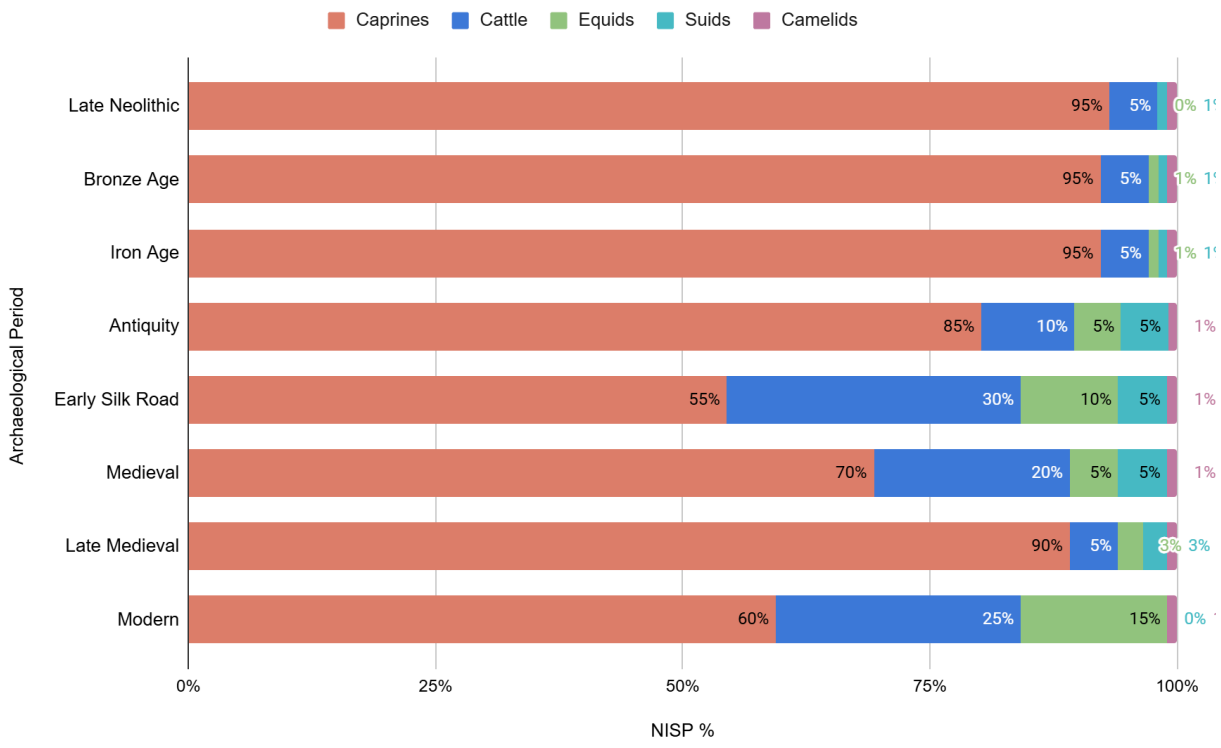


Fig.14 Bar graph of approximate estimations of taxonomic ratios in Uzbek herds though time, roughly calculated from Brite et al. 2017, Krader 1955, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.

Tbl.71 Table of published faunal data for Transoxian assemblages (absolute counts).

Estimated Dates	Site	Caprines		Cattle		Equids		Suids		Camelids	
		NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI
ca. 9200– 8700 BCE	Kaynar Kamar	61	?	0	?	0	?	2	?	0	0
ca. 7700– 6600 BCE	Kaynar Kamar	81	?	0	?	0	?	4	?	0	0
ca. 5600– 5300 BCE	Kaynar Kamar	151	?	7	?	0	?	7	?	0	0
ca. 4200– 2900 BCE	Kaynar Kamar	170	?	0	?	0	?	0	?	0	0
ca. 1200 BCE– 300 CE	Kaynar Kamar	53	?	0	?	0	?	0	?	0	0
ca. 910– 460 BCE	Kyzyltepa	1329	?	329	?	127	?	44	?	4	?
ca. 400– 100 BCE	Kojtepa	91	15	9	4	4	1	1	1	0	0
ca. 300 BCE– 50 CE	Termez	201	16	18	3	9	5	5	2	0	0
ca. 200 BCE–200 CE	Kojtepa	19	4	0	0	0	0	0	0	0	0
ca. 100– 300 CE	Kara-Tepe	8	?	6	?	2	2	1	1	0	0
ca. 100– 400 CE	Kojtepa	140	13	51	7	6	4	20	6	0	0
ca. 150– 350 CE	Termez	102	16	13	2	9	3	18	3	0	0
ca. 300– 400 CE	Kara-Tepe	38	?	5	?	5	?	1	1	0	0
ca. 350– 600 CE	Termez	297	17	75	4	28	4	28	2	1	1
ca. 650– 750 CE	Kafir Kala	460	37	73	8	13	6	3	1	2	1
ca. 750– 1100 CE	Kafir Kala	1151	107	189	22	37	11	7	5	3	2
ca. 800– 1400 CE	Termez	310	17	5	1	2	2	3	2	0	0

**The faunal data in this table were taken directly from Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

Tbl.72 Table of published faunal data for Transoxian assemblages (relative percentages).

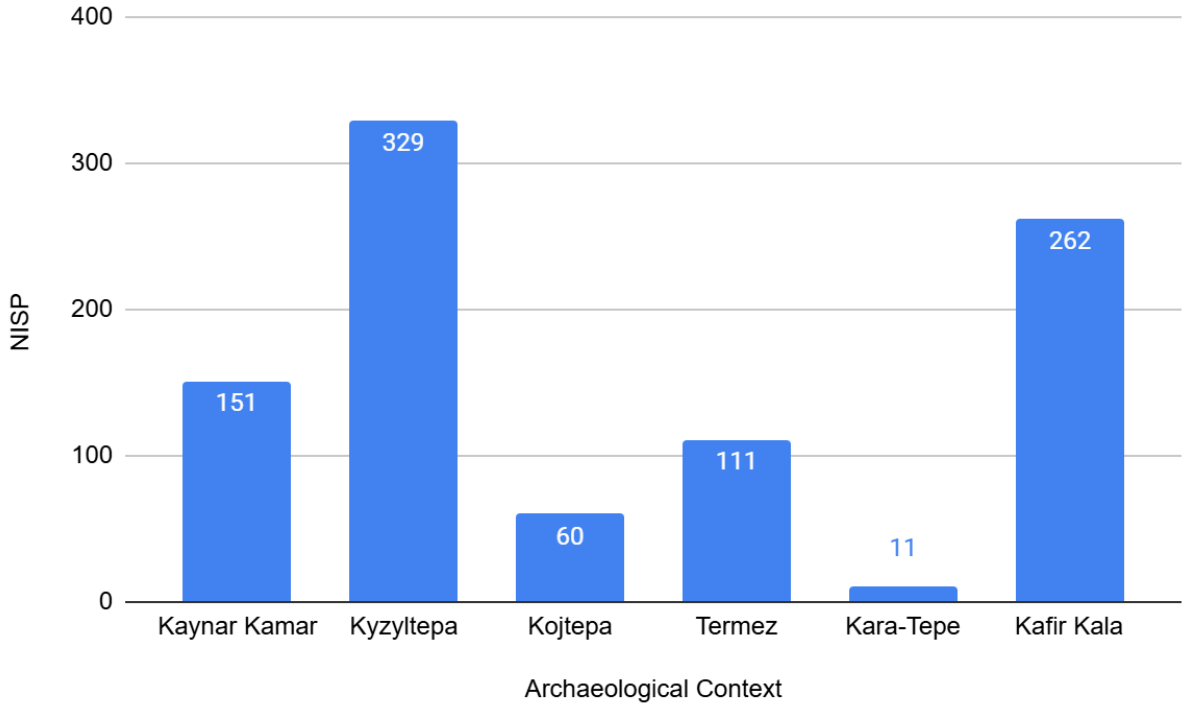
Estimated Dates	Site	Caprines		Cattle		Equids		Suids		Camelids	
		NISP%	MNI%	NISP%	MNI%	NISP%	MNI%	NISP%	MNI%	NISP%	MNI%
ca. 9200– 8700 BCE	Kaynar Kamar	28.6%	?	0%	?	0%	?	0.1%	?	0%	0%
ca. 7700– 6600 BCE	Kaynar Kamar	36.2%	?	0%	?	0%	?	0.2%	?	0%	0%
ca. 5600– 5300 BCE	Kaynar Kamar	68%	?	2.3%	?	0%	?	0.3%	?	0%	0%
ca. 4200– 2900 BCE	Kaynar Kamar	74.2%	?	0.4%	?	0%	?	0%	?	0%	0%
ca. 1200 BCE– 300 CE	Kaynar Kamar	60.9%	?	2.3%	?	0%	?	0%	?	0%	0%
ca. 910– 460 BCE	Kyzyltepa	46%	?	11.4%	?	1%	?	1.5%	?	0.1%	?
ca. 400– 100 BCE	Kojtepa	65.2%	63.9%	5.7%	11.1%	2.5%	2.8%	0.6%	2.8%	0%	0%
ca. 300 BCE– 50 CE	Termez	76.7%	51.6%	7.4%	7.8%	3.7%	10.3%	2%	5.1%	0%	0%
ca. 200 BCE–200 CE	Kojtepa	64%	55.8%	0%	0%	0%	0%	0%	0%	0%	0%
ca. 100– 300 CE	Kara-Tepe	38.1%	?	28.6%	?	9.5%	?	4.8%	14%	0%	0%
ca. 100– 400 CE	Kojtepa	62.4%	45.2%	21.1%	16.7%	2.5%	9.5%	8.3%	14.3%	0%	0%
ca. 150– 350 CE	Termez	65%	46%	8.3%	5.7%	5.8%	8.6%	11.5%	8.6%	0%	0%
ca. 300– 400 CE	Kara-Tepe	63.3%	?	8.3%	?	8.3%	?	1.2%	7.1%	0%	0%
ca. 350– 600 CE	Termez	65.7%	39%	16.6%	9.1%	6.2%	9.1%	6.2%	6.2%	0.2%	2.3%
ca. 650– 750 CE	Kafir Kala	74.6%	63.8%	11.8%	15.1%	2.1%	11.3%	1.7%	0.5%	0.3%	1.7%
ca. 750– 1100 CE	Kafir Kala	75.6%	71.3%	12.4%	14.7%	2.4%	7.3%	3.1%	0.5%	0.2%	1.3%
ca. 800– 1400 CE	Termez	93.9%	50%	1.5%	2.9%	0.6%	0.6%	0.9%	0.1%	0%	0%

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

19.3.1. Cattle Representation

Cattle are known to have been present in the animal economies of Uzbekistan from the Late Neolithic period onwards, having been recovered from archaeological contexts dating as far back as ca. 5600– 5300 BCE (Fig.15; Tbl.73). Their management is seemingly always secondary to the management of caprines, although there seems to have been an intensification of cattle husbandry around the Early Silk Road period (Tbl.73). Cattle appear to have been managed in similar numbers in cities and towns as well as at fortresses and outposts (Tbl.74), which is likely a reflection of the ecological needs of cattle and their association with more sedentary lifeways (see Chapter 07).

Fig.15 Bar graph of NISP data available for *Bos* sp. from archaeological sites in Uzbekistan (Brite et al. 2017, Maini & Serrone 2020, Portero et al. 2022, Serrone et al. 2007, Wu et al. 2015).



Tbl.73 Table of published NISP & NISP% counts for cattle (*Bos* sp.) recovered from Transoxian sites.

Period	Dates	Region	Site	Site Context	Cattle (NISP)	Cattle (NISP%)
Early Neolithic	ca. 9200–8700 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Middle Neolithic	ca. 7700–6600 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Late Neolithic	ca. 5600–5300 BCE	Bactria	Kaynar Kamar	Rock Shelter	7	2.3%
Bronze Age	ca. 4200–2900 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0.4%
Iron Age–Early Antiquity	ca. 1200 BCE–300 CE	Bactria	Kaynar Kamar	Rock Shelter	0	2.3%
Late Iron Age–Early Antiquity	ca. 910–460 BCE	Bactria	Kyzyltepa	Town	329	11.4%
Iron Age	ca. 400–100 BCE	Sogdia	Kojtepa	Fortress	9	5.7%
Antiquity	ca. 300 BCE–50 CE	Bactria	Termez	City	18	7.4%
Antiquity–Early Silk Road	ca. 200 BCE–200 CE	Sogdia	Kojtepa	Fortress	0	0%
Early Silk Road–Middle Silk Road	ca. 100–300 CE	Khorezm	Kara-Tepe	Fortress	6	28.6%
Early Silk Road– Middle Silk Road	ca. 100–400 CE	Sogdia	Kojtepa	Fortress	51	21.1%
Early Silk Road– Middle Silk Road	ca. 150–350 CE	Bactria	Termez	City	13	8.3%
Middle Silk Road	ca. 300–400 CE	Khorezm	Kara-Tepe	Fortress	5	8.3%
Middle Silk Road	ca. 350–600 CE	Bactria	Termez	City	75	16.6%
Middle Silk Road	ca. 650–750 CE	Sogdia	Kafir Kala	Fortress	73	11.8%
Middle Silk Road–Late Silk Road	ca. 750–1100 CE	Sogdia	Kafir Kala	Fortress	189	12.4%
Middle Silk Road– Late Silk Road	ca. 800–1400 CE	Bactria	Termez	City	5	1.5%

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

Tbl.74 Table of published faunal data for cattle (*Bos* sp.) from Transoxian fortresses and cities.

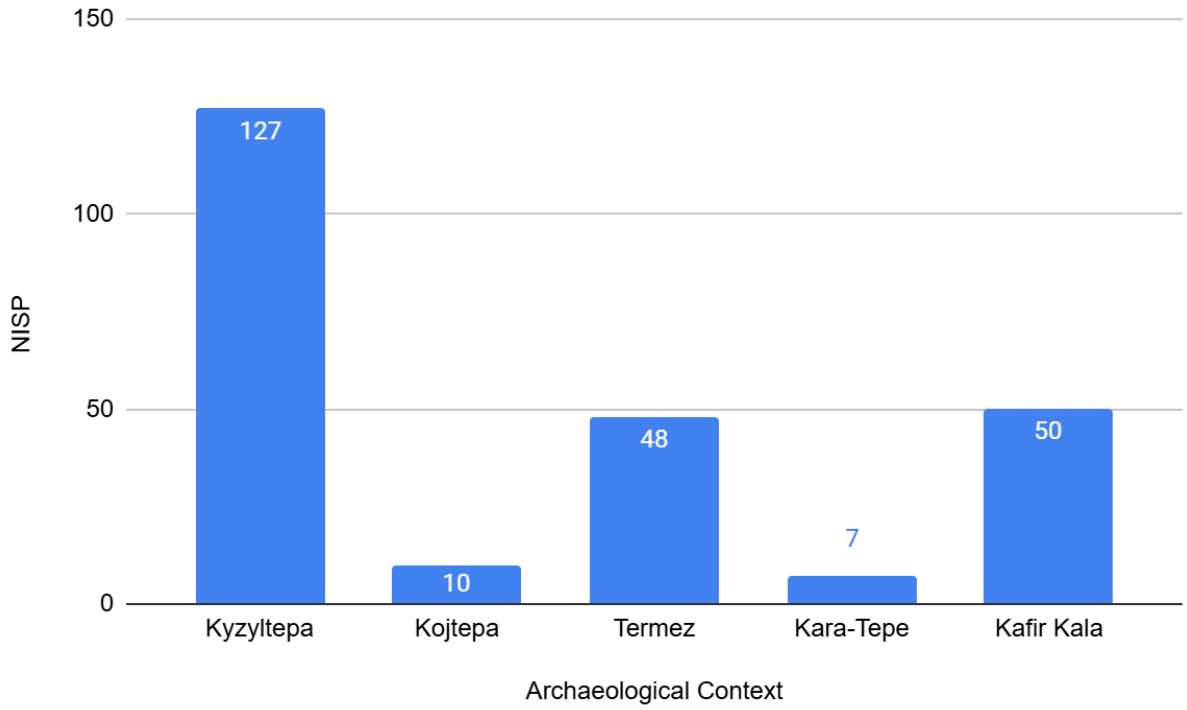
Fortresses & Outposts					Cities & Towns				
Site Context	*Bos* sp.				Site Context	*Bos* sp.			
	NISP	NISP%	MNI	MNI%		NISP	NISP%	MNI	MNI%
Kafir Kala (Sogdia) ca. 650–750 CE	73	11.8%	8	15.1%	Kyzyltepa (Bactria) ca. 910–460 BCE	329	11.4%	?	?
Kafir Kala (Sogdia) ca. 750–1100 CE	189	12.4%	22	14.7%	Termez (Bactria) ca. 300 BCE–50 CE	18	7.4%	3	7.8%
Kojtepa (Sogdia) ca. 400–100 BCE	9	5.7%	4	11.1%	Termez (Bactria) ca. 150–350 CE	13	8.3%	2	5.7%
Kojtepa (Sogdia) ca. 100–400 CE	51	21.1%	7	16.7%	Termez (Bactria) ca. 350–600 CE	75	16.6%	4	9.1%
Kara-Tepe (Khorezm) ca. 100–300 CE	6	28.6%	?	?	Termez (Bactria) ca. 800–1400 CE	5	1.5%	1	2.9%
Kara-Tepe (Khorezm) ca. 300–400 CE	5	8.3%	?	?					

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

19.3.2. Equid Representation

Neither wild nor domesticated equids appear in the data compiled here until the Iron Age (Fig.16; Tbls.75–76), as opposed to the Bronze Age intensification witnessed in other areas of Inner Asia such as Mongolia (see Chapter 15). Equids most likely were being managed and exploited in Bronze Age Transoxiana, but on a small enough scale that their remains are not prevalent in the scarce assemblages recovered by archaeologists. The intensification of equid management in Transoxiana does not appear to have occurred until the Early Silk Road period, perhaps due to intensified Trans-Eurasian trade, warfare, and diplomacy, and seems to peak in the Early Medieval Period.

Fig.16 Bar graph of NISP data available for *Equus* sp. from archaeological sites in Uzbekistan (Brite et al. 2017, Maini & Serrone 2020, Portero et al. 2022, Serrone et al. 2007, Wu et al. 2015).



Tbl.75 Table of published NISP & NISP% counts for equids (*Equus* sp.) recovered from Transoxian sites.

Period	Dates	Region	Site	Site Context	Equids (NISP)	Equids (NISP%)
Early Neolithic	ca. 9200–8700 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Middle Neolithic	ca. 7700–6600 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Late Neolithic	ca. 5600–5300 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Bronze Age	ca. 4200–2900 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Iron Age–Early Antiquity	ca. 1200 BCE–300 CE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Late Iron Age–Early Antiquity	ca. 910–460 BCE	Bactria	Kyzyltepa	Town	127	1%
Iron Age	ca. 400–100 BCE	Sogdia	Kojtepa	Fortress	4	2.5%
Antiquity	ca. 300 BCE–50 CE	Bactria	Termez	City	9	3.7%
Antiquity–Early Silk Road	ca. 200 BCE–200 CE	Sogdia	Kojtepa	Fortress	0	0%
Early Silk Road–Middle Silk Road	ca. 100–300 CE	Khorezm	Kara-Tepe	Fortress	2	9.5%
Early Silk Road– Middle Silk Road	ca. 100–400 CE	Sogdia	Kojtepa	Fortress	6	2.5%
Early Silk Road– Middle Silk Road	ca. 150–350 CE	Bactria	Termez	City	9	5.8%
Middle Silk Road	ca. 300–400 CE	Khorezm	Kara-Tepe	Fortress	5	8.3%
Middle Silk Road	ca. 350–600 CE	Bactria	Termez	City	28	6.2%
Middle Silk Road	ca. 650–750 CE	Sogdia	Kafir Kala	Fortress	13	2.1%
Middle Silk Road–Late Silk Road	ca. 750–1100 CE	Sogdia	Kafir Kala	Fortress	37	2.4%
Middle Silk Road– Late Silk Road	ca. 800–1400 CE	Bactria	Termez	City	2	0.6%

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

Tbl.76 Table of published faunal data for equids (*Equus* sp.) from Transoxian fortresses and cities.

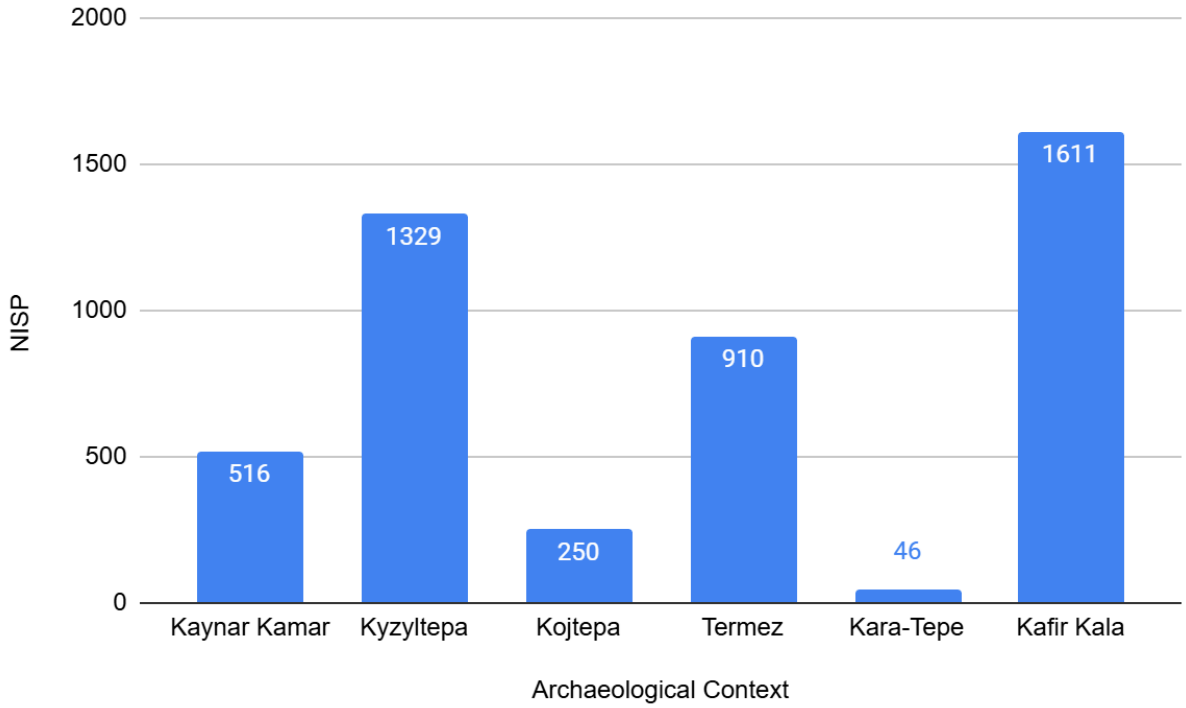
Fortresses & Outposts					Cities & Towns				
Site Context	*Equus* sp.				Site Context	*Equus* sp.			
	NISP	NISP%	MNI	MNI%		NISP	NISP%	MNI	MNI%
Kafir Kala (Sogdia) ca. 650–750 CE	13	2.1%	6	11.3%	Kyzyltepa (Bactria) ca. 910–460 BCE	127	1%	?	?
Kafir Kala (Sogdia) ca. 750–1100 CE	37	2.4%	11	7.3%	Termez (Bactria) ca. 300 BCE–50 CE	9	3.7%	5	10.3%
Kojtepa (Sogdia) ca. 400–100 BCE	4	2.5%	1	2.8%	Termez (Bactria) ca. 150–350 CE	9	5.8%	3	8.6%
Kojtepa (Sogdia) ca. 100–400 CE	6	2.5%	4	9.5%	Termez (Bactria) ca. 350–600 CE	28	6.2%	4	9.1%
Kara-Tepe (Khorezm) ca. 100–300 CE	2	9.5%	2	?	Termez (Bactria) ca. 800–1400 CE	2	0.6%	2	0.6%
Kara-Tepe (Khorezm) ca. 300–400 CE	5	8.3%	?	?					

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

19.3.3. Caprine Representation

Caprine representation is ubiquitous from the Neolithic period, and caprine predominance could almost be considered diagnostic of most Uzbek and Inner Asian herds regardless of regional or temporal context (see Chapters 08, 18). I have compiled two tables of faunal data from the sites discussed throughout this chapter (Fig.17) to demonstrate this point (Tbls.77–78); importantly, these tables do not take into account domesticated versus wild taxa. They also include data from Bactria, which may or may not be considered a part of Transoxiana or Uzbekistan (see Chapter 17), but is certainly culturally adjacent. These tables also suffer from many of the biases I pointed out in the corpus of faunal data available for Southern Siberia and Mongolia (see Chapters 12–15), i.e. not all sites and strata have been securely dated with radiocarbon dating, and the accuracy of the taxonomic attributions is unknown. Taphonomic, sampling, reporting, and methodological biases undoubtedly play a role in shaping this data as well (see Chapter 02).

Fig.17 Bar graph of NISP data available for *Ovis* sp. / *Capra* sp. from archaeological sites in Uzbekistan (Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, Wu et al. 2015).



The tables below (Tbls.77–78) highlight the domineering role of caprines in Uzbek herds throughout prehistory and Antiquity without trying to compare ratios of livestock to wild game.If this table is a reasonable indication of herd composition, it should be clear that caprine reliance has been a fixture of subsistence lifeways throughout ancient Uzbekistan and Bactria. Moving into the Silk Road / Medieval period and incorporating some data from Khorezm (outside of Transoxiana or Uzbekistan), a similar pattern continues (Tbl.77). The noticeable decline in

caprine representation at Kara-Tepe during the Early Silk Road period is likely a product of very low sample representation.

Tbl.77 Table of published NISP & NISP% counts for *Ovis* sp. / *Capra* sp. recovered from Transoxian sites.

Period	Dates	Region	Site	Site Context	Caprines (NISP)	Caprines (NISP%)
Early Neolithic	ca. 9200–8700 BCE	Bactria	Kaynar Kamar	Rock Shelter	61	28.6%
Middle Neolithic	ca. 7700–6600 BCE	Bactria	Kaynar Kamar	Rock Shelter	81	36.2%
Late Neolithic	ca. 5600–5300 BCE	Bactria	Kaynar Kamar	Rock Shelter	151	68%
Bronze Age	ca. 4200–2900 BCE	Bactria	Kaynar Kamar	Rock Shelter	170	74.2%
Iron Age–Early Antiquity	ca. 1200 BCE–300 CE	Bactria	Kaynar Kamar	Rock Shelter	53	60.9%
Late Iron Age–Early Antiquity	ca. 910–460 BCE	Bactria	Kyzyltepa	Town	1329	46%
Iron Age	ca. 400–100 BCE	Sogdia	Kojtepa	Fortress	91	65.2%
Antiquity	ca. 300 BCE–50 CE	Bactria	Termez	City	201	76.7%
Antiquity–Early Silk Road	ca. 200 BCE–200 CE	Sogdia	Kojtepa	Fortress	19	64%
Early Silk Road–Middle Silk Road	ca. 100–300 CE	Khorezm	Kara-Tepe	Fortress	8	38.1%
Early Silk Road– Middle Silk Road	ca. 100–400 CE	Sogdia	Kojtepa	Fortress	140	62.4%
Early Silk Road– Middle Silk Road	ca. 150–350 CE	Bactria	Termez	City	102	65%
Middle Silk Road	ca. 300–400 CE	Khorezm	Kara-Tepe	Fortress	38	63.3%
Middle Silk Road	ca. 350–600 CE	Bactria	Termez	City	297	65.7%
Middle Silk Road	ca. 650–750 CE	Sogdia	Kafir Kala	Fortress	460	74.6%
Middle Silk Road–Late Silk Road	ca. 750–1100 CE	Sogdia	Kafir Kala	Fortress	1151	75.6%
Middle Silk Road– Late Silk Road	ca. 800–1400 CE	Bactria	Termez	City	310	93.9%

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015. The MNI% of total caprines recorded for the Middle Silk Road (Pre-Islamic) period was calculated incorrectly as "69.8%" in Serrone et al. 2007, and has been modified in this table.*

Tbl.78 Table of published faunal data for *Ovis* sp. / *Capra* sp. from Transoxian fortresses and cities.

Fortresses & Outposts					Cities & Towns				
Site Context	*Ovis* sp. / *Capra* sp.				Site Context	*Ovis* sp. / *Capra* sp.			
	NISP	NISP%	MNI	MNI%		NISP	NISP%	MNI	MNI%
Kafir Kala (Sogdia) ca. 650–750 CE	460	74.6%	37	63.8%	Kyzyltepa (Bactria) ca. 910–460 BCE	1329	46%	?	?
Kafir Kala (Sogdia) ca. 750–1100 CE	1151	75.6%	107	71.3%	Termez (Bactria) ca. 300 BCE–50 CE	201	76.7%	16	51.6%
Kojtepa (Sogdia) ca. 400–100 BCE	91	65.2%	15	63.9%	Termez (Bactria) ca. 150–350 CE	102	65%	16	46%
Kojtepa (Sogdia) ca. 200 BCE–200 CE	19	64%	4	55.8%	Termez (Bactria) ca. 350–600 CE	297	65.7%	17	39%
Kojtepa (Sogdia) ca. 300– 400 CE	140	62.4%	13	45.2%	Termez (Bactria) ca. 800–1400 CE	310	93.9%	17	50%
Kara-Tepe (Khorezm) ca. 100–300 CE	8	38.1%	?	?					
Kara-Tepe (Khorezm) ca. 300–400 CE	38	63.3%	?	?					

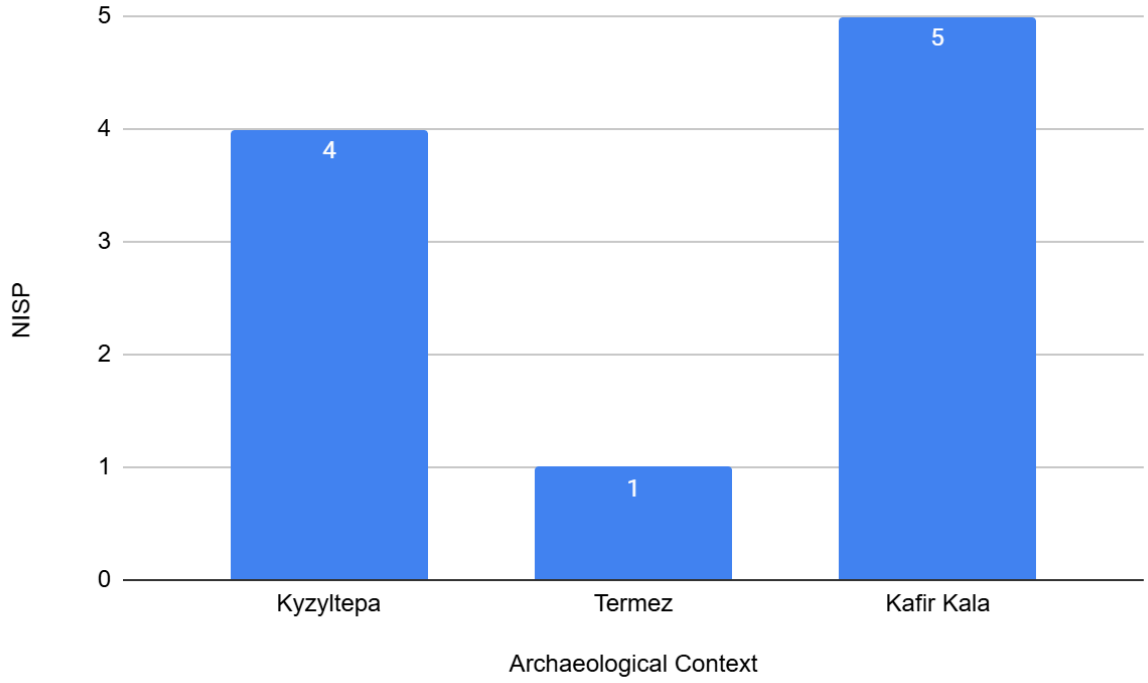
**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015. The MNI% of total caprines recorded for the Middle Silk Road (Pre-Islamic) period was calculated incorrectly as "69.8%" in Serrone et al. 2007, and has been modified in this table.*

Less clear are the ratios of sheep versus goats in archaeological herds or how these vary by time, region, context, and animal product specialization throughout Transoxiana, Uzbekistan, and Central Asia. ZooMS analysis would be an ideal method to discern strategies and expressions of sheep versus goat exploitation throughout prehistory and Antiquity. Researchers could subsequently investigate whether or not these ratios were impacted by intensified Trans-Eurasian exchange and / or Islamification. There is a significant gap in faunal data available for Medieval and especially Late Silk Road settlement sites; my own review of six Qarakhanid sites involved only a single faunal report from the Sogdian fortress of Kafir Kala (Tbl.77).

19.3.4. Camel Representation

Looking beyond the rise of Islamic empires and the impacts of widespread religious conversion on patterns of subsistence and exploitation, questions of camel management in Transoxiana remain unresolved. No camel remains were reported from Kaynar Kamar (see Nishiaki et al. 2022) Kojtepa (see Maini & Serrone 2020), or Kara-Tepe (see Brite et al. 2017). Instead of examining camel representation in faunal assemblages through time, it may be more useful to examine camel representation in different spatial contexts. Unfortunately the restraints of the available data prevent any meaningful comparison (Fig.18). This approach will likely prove useful in the future, when more zooarchaeological reports have been published and when more ZooMS analyses have refined taxonomic attributions. What could be tentatively inferred is that neither region (i.e. Bactria, Sogdia, Khorezm) nor scale of urbanization were particularly relevant to camel management (Tbl.79), which remain nearly absent from the temporal or spatial archaeological contexts of Transoxiana and adjacent regions.

Fig.18 Bar graph of NISP data available for *Camelus* sp. from archaeological sites in Uzbekistan (Portero et al. 2022, Serrone et al. 2007, Wu et al. 2015).



Tbl.79 Table of published NISP & NISP% counts for camels (*Camelus* sp.) recovered from Transoxian sites.

Period	Dates	Region	Site	Site Context	Camels (NISP)	Camels (NISP%)
Early Neolithic	ca. 9200–8700 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0
Middle Neolithic	ca. 7700–6600 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0
Late Neolithic	ca. 5600–5300 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0
Bronze Age	ca. 4200–2900 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0
Iron Age–Early Antiquity	ca. 1200 BCE–300 CE	Bactria	Kaynar Kamar	Rock Shelter	0	0
Late Iron Age–Early Antiquity	ca. 910–460 BCE	Bactria	Kyzyltepa	Town	4	0.1%
Iron Age	ca. 400–100 BCE	Sogdia	Kojtepa	Fortress	0	0
Antiquity	ca. 300 BCE–50 CE	Bactria	Termez	City	0	0
Antiquity–Early Silk Road	ca. 200 BCE–200 CE	Sogdia	Kojtepa	Fortress	0	0
Early Silk Road–Middle Silk Road	ca. 100–300 CE	Khorezm	Kara-Tepe	Fortress	0	0
Early Silk Road– Middle Silk Road	ca. 100–400 CE	Sogdia	Kojtepa	Fortress	0	0
Early Silk Road– Middle Silk Road	ca. 150–350 CE	Bactria	Termez	City	0	0
Middle Silk Road	ca. 300–400 CE	Khorezm	Kara-Tepe	Fortress	0	0
Middle Silk Road	ca. 350–600 CE	Bactria	Termez	City	1	0.2%
Middle Silk Road	ca. 650–750 CE	Sogdia	Kafir Kala	Fortress	2	0.3%
Middle Silk Road–Late Silk Road	ca. 750–1100 CE	Sogdia	Kafir Kala	Fortress	3	0.2%
Middle Silk Road– Late Silk Road	ca. 800–1400 CE	Bactria	Termez	City	0	0

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

Tbl.80 Table of published faunal data for camels (*Camelus* sp.) from Transoxian fortresses and cities.

Fortresses & Outposts					Cities & Towns				
Site Context	Camels				Site Context	Camels			
	NISP	NISP%	MNI	MNI%		NISP	NISP%	MNI	MNI%
Kafir Kala (Sogdia) ca. 650–750 CE	2	0.3%	1	1.7%	Kyzyltepa (Bactria) ca. 910–460 BCE	4	0.1%	0	?
Kafir Kala (Sogdia) ca. 750–1100 CE	3	0.2%	2	1.3%	Termez (Bactria) ca. 300 BCE–50 CE	0	0%	0	0%
Kojtepa (Sogdia) ca. 400 BCE–400 CE	0	0%	0	0%	Termez (Bactria) ca. 150–350 CE	0	0%	0	0%
Kara-Tepe (Khorezm) ca. 100–400 CE	0	0%	0	0%	Termez (Bactria) ca. 350–600 CE	1	0.2%	1	2.3%
					Termez (Bactria) ca. 800–1400 CE	0	0%	0	0%

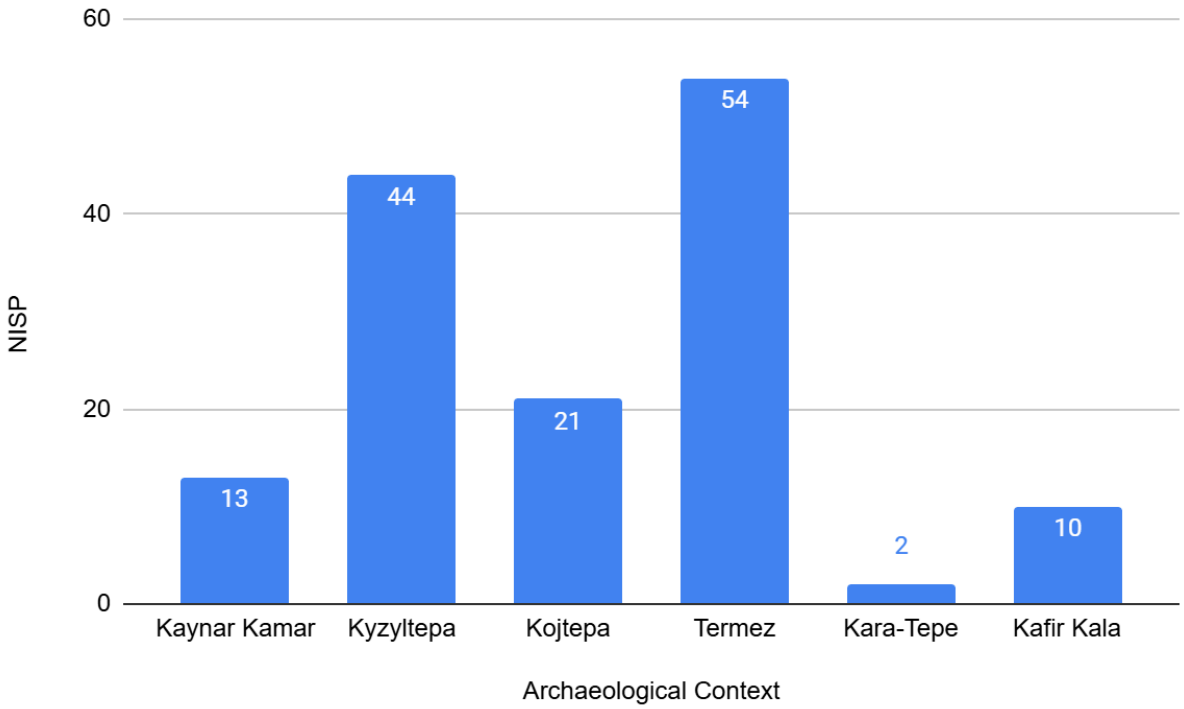
**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

19.3.5. Suid Representation

There does not appear to be any evidence that either wild boar hunting or domesticated pig rearing were primary economic activities that contributed substantially to ancient Transoxian lifeways and diets. Suid remains most often constituted less than 1% of the selected faunal assemblages recovered from the Neolithic through Early Antiquity periods (Fig.19; Tbl.81). There is some indication that suid consumption intensified significantly after the onset of the Hellenistic period (while still paling in comparison to caprine exploitation), but began to taper off around the Middle Silk Road period (Fig.19; Tbl.81). The Arab conquest does appear to have impacted Transoxian subsistence strategies, with a notable decrease in suid consumption seeming to coincide with the Ummayyid conquest ca. 674 CE (and the seizing of Samarkand ca. 712 CE) when Termez and Kara-Tepe are compared in tandem (Fig.19; Tbl.81).

Subsequent Islamification may be responsible for a reduction of suid consumption in cities that does not appear to have been as significant as in fortresses (Tbl.82), though more faunal data would be necessary to make a stronger argument for this. The overall lack of faunal reports from Medieval settlement sites (especially after the seventh century) complicates comparisons of Pre-Islamic and Islamic contexts, which are useful oversimplifications in themselves. A larger body of faunal data, ideally from a wide range of contexts (urban, rural, highland, lowland, etc.), would be necessary for a more robust analysis and reconstruction of Pre-Islamic and Islamic animal economies in Transoxiana and adjacent regions.

Fig.19 Bar graph of NISP data available for *Sus* sp. from archaeological sites in Uzbekistan (Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015).



Tbl.81 Table of published NISP & NISP% counts for suids (*Sus* sp.) recovered from Transoxian sites.

Period	Dates	Region	Site	Site Context	Suids (NISP)	Suids (NISP%)
Early Neolithic	ca. 9200–8700 BCE	Bactria	Kaynar Kamar	Rock Shelter	2	0.1%
Middle Neolithic	ca. 7700–6600 BCE	Bactria	Kaynar Kamar	Rock Shelter	4	0.2%
Late Neolithic	ca. 5600–5300 BCE	Bactria	Kaynar Kamar	Rock Shelter	7	0.3%
Bronze Age	ca. 4200–2900 BCE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Iron Age–Early Antiquity	ca. 1200 BCE–300 CE	Bactria	Kaynar Kamar	Rock Shelter	0	0%
Late Iron Age–Early Antiquity	ca. 910–460 BCE	Bactria	Kyzyltepa	Town	44	1.5%
Iron Age	ca. 400–100 BCE	Sogdia	Kojtepa	Fortress	1	0.6%
Antiquity	ca. 300 BCE–50 CE	Bactria	Termez	City	5	2%
Antiquity–Early Silk Road	ca. 200 BCE–200 CE	Sogdia	Kojtepa	Fortress	0	0%
Early Silk Road–Middle Silk Road	ca. 100–300 CE	Khorezm	Kara-Tepe	Fortress	1	4.8%
Early Silk Road– Middle Silk Road	ca. 100–400 CE	Sogdia	Kojtepa	Fortress	20	8.3%
Early Silk Road– Middle Silk Road	ca. 150–350 CE	Bactria	Termez	City	18	11.5%
Middle Silk Road	ca. 300–400 CE	Khorezm	Kara-Tepe	Fortress	1	1.2%
Middle Silk Road	ca. 350–600 CE	Bactria	Termez	City	28	6.2%
Middle Silk Road	ca. 650–750 CE	Sogdia	Kafir Kala	Fortress	3	1.7%
Middle Silk Road–Late Silk Road	ca. 750–1100 CE	Sogdia	Kafir Kala	Fortress	7	3.1%
Middle Silk Road– Late Silk Road	ca. 800–1400 CE	Bactria	Termez	City	3	0.9%

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Nishiaki et al. 2022, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

Tbl.82 Table of published faunal data for suids (*Sus* sp.) from Transoxian fortresses and cities.

Fortresses & Outposts					Cities & Towns				
Site Context	Suids				Site Context	Suids			
	NISP	NISP%	MNI	MNI%		NISP	NISP%	MNI	MNI%
Kafir Kala (Sogdia) ca. 650–750 CE	3	1.7%	1	0.5%	Kyzyltepa (Bactria) ca. 910–460 BCE	44	1.5%	?	?
Kafir Kala (Sogdia) ca. 750–1100 CE	7	3.1%	5	0.5%	Termez (Bactria) ca. 300 BCE–50 CE	5	2%	2	5.1%
Kojtepa (Sogdia) ca. 400–100 BCE	1	0.6%	1	2.8%	Termez (Bactria) ca. 150–350 CE	18	11.5%	3	8.6%
Kojtepa (Sogdia) ca. 200 BCE–200 CE	0	0%	0	0%	Termez (Bactria) ca. 350–600 CE	28	6.2%	2	6.2%
Kojtepa (Sogdia) ca. 300– 400 CE	20	8.3%	6	14.3%	Termez (Bactria) ca. 800–1400 CE	3	0.9%	2	0.1%
Kara-Tepe (Khorezm) ca. 100–300 CE	1	4.8%	1	14%					
Kara-Tepe (Khorezm) ca. 300– 400 CE	1	1.2%	1	7.1%					

**The faunal data in this table were either taken directly from or calculated from Brite et al. 2017, Maini & Serrone 2020, Portero et al. 2022, Serrone et al. 2007, and Wu et al. 2015.*

19.3.6. Bird, Reptile, & Amphibian Representation

Reliance on birds, reptiles, and amphibians appears to have declined after the Neolithic (unsurprisingly), though it did not disappear entirely– at least not in relation to birds such as chickens (Tbls.83–84). It is possible that chicken rearing was more prevalent in cities than at fortresses (Tbl.84; see also Peters et al. 2024). Here even more caution is necessary, for bird, reptile, and amphibian bones are smaller and less dense than the bones of livestock and most wild game, and do not preserve as well in the archaeological record (see Chapter 02). They also may accumulate naturally, as opposed to through human behaviour. Chicken eggshells recovered from Transoxian cities such as Mingtepa (Peters et al. 2024) are much stronger markers of intentional management. In the Medieval period, reliance on chickens and other birds could be said to be roughly as common as suid reliance, and rearing chickens was seemingly more common than rearing camels.

Tbl.83 Table of published NISP% counts for fauna recovered from Transoxian sites.

Period	Site	Birds	Reptiles / Amphibians	Mammals
ca. 9200– 8700 BCE	Kaynar Kamar	23.9%	11.7%	64.4%
ca. 7700– 6600 BCE	Kaynar Kamar	15.2%	10.3%	74.5%
ca. 5600– 5300 BCE	Kaynar Kamar	9.1%	4.5%	86.4%
ca. 4200– 2900 BCE	Kaynar Kamar	8.7%	7.9%	83.4%
ca. 1200 BCE– 300 CE	Kaynar Kamar	13.8%	4.6%	81.6%
ca. 910– 460 BCE	Kyzyltepa	0.9%	0%	99.1%
ca. 400– 100 BCE	Kojtepa	1.3%	10.8%	87.9%
ca. 300 BCE– 50 CE	Termez	2.5%	0%	97.5%
ca. 200 BCE–200 CE	Kojtepa	1.2%	7.2%	91.6%
ca. 100– 300 CE	Kara-Tepe	9.5%	0%	90.5%
ca. 100– 400 CE	Kojtepa	4.8%	7.1%	88.1%
ca. 150– 350 CE	Termez	3.2%	0%	96.8%
ca. 300– 400 CE	Kara-Tepe	1.7%	1.7%	96.6%
ca. 350– 600 CE	Termez	2.4%	0%	97.6%
ca. 650– 750 CE	Kafir Kala	5.7%	0%	94.3%
ca. 750– 1100 CE	Kafir Kala	5.8%	0%	94.2%
ca. 800– 1400 CE	Termez	2.4%	0%	97.6%

Tbl.84 Table of published faunal data for chickens (*Gallus gallus*) from Transoxian fortresses and cities.

Fortresses & Outposts					Cities & Towns				
Site Context	Chickens				Site Context	Chickens			
	NISP	NISP%	MNI	MNI%		NISP	NISP%	MNI	MNI%
Kafir Kala (Sogdia) ca. 650–1100 CE	0%	0%	0%	0%	Kyzyltepa (Bactria) ca. 910–460 BCE	12	0.4%	?	?
Kojtepa (Sogdia) ca. 400 BCE–400 CE	0%	0%	0%	0%	Termez (Bactria) ca. 300 BCE–50 CE	6	2.5%	5	2%
Kara-Tepe (Khorezm) ca. 100–400 CE	0%	0%	0%	0%	Termez (Bactria) ca. 150–350 CE	5	3.2%	1	2.9%
					Termez (Bactria) ca. 350–600 CE	11	2.4%	2	4.6%
					Termez (Bactria) ca. 800–1400 CE	6	1.8%	1	2.9%

19.4. Modes of Pastoralism in Transoxiana

"According to Islamic geographers, the cities along the Jaxartes River…stood out due to their abundant natural resources…the quality of vegetables and fruits was such that the people could meet all their needs…Ibn Hawqal mentioned that the most fertile lands on earth were created in this region by Allah, and he praised the abundance of vegetable production and rich pastures for grazing animals." (Erkoc 2023)

I have already written at length about the archaeological markers and modes of pastoralism, as well as the ecological niches of key livestock species and their management within the context of Inner Asia (see Chapters 08–09). Subsistence strategies and animal husbandry practices are fluid, exist on a spectrum as opposed to a polarity (e.g. sedentary versus mobile), and can be adapted to suit unique (micro-) environments and conditions (see Brite 2017; Chang et al. 2023; Chapterss 02, 11). Transoxiana was characterized by a diversity of terrain including deserts, steppes, oases, river basins, foothills, and mountains (Bullion et al. 2023; Mir-Makhamad et al. 2021; Zhabagin et al. 2017). Medieval Transoxian peoples lived in cities, villages, agricultural dwellings, and highland dwellings (Erkoc 2023; Maksudov 2016). In this subsection, I will briefly explore how different modes of pastoralism developed throughout the Medieval period up until the emergence of the Qarakhanaid Khanate, with an emphasis on the role of the Medieval Climate Anomaly in shaping Transoxian subsistence practices (see Misa et al. 2023).

19.4.1. Urban Agropastoralism

"...existing studies focus almost exclusively on steppe communities and…the Bronze Age…still missing are studies that take this new perspective and apply it to…the oases and later periods…the oases were critical nexuses where Central Eurasia's agricultural and pastoral communities came together…" (Brite et al. 2017)

There are a number of ways that agro-pastoralist strategies could have manifested in the diverse urban contexts of Medieval Transoxiana (see Chapter 18). People living in cities and villages could have cultivated gardens and patches of crops. They also could have managed livestock as a community, or negotiated with pastoralists to manage them on their behalf. Small herds (and chicken clutches) could have been managed inside more densely settled and built up areas, while moderate herds could have been managed on the outskirts. Livestock could have been exchanged between settled and mobile peoples, perhaps at fortified trading outposts. Small herds may have been managed at these fortified trading outposts as well.

Defensive fortresses in oases and rural regions, such as Kafir Kala, Kojtepa, and Qarshovul Tepa, were often characterized by a mix of commerce and agriculture and are believed to have been spaces where farmers, pastoralists, and merchants could come together in a protected setting (Abdullaev & Genito 2014; Genito 2018; Mantellini 2018b; Mir-Makhamad et al. 2021; Sheyko et al. 2019; see also Negmatov 1998). Landowners (*dhiqans*) lived in castles overlooking their fields and orchards, which were tended to by independent workers (as opposed to serfs) (Şirin 2010). Palaces such as Vardāna in Sogdia also functioned as defensive outposts on the oasis borderlands (Pozzi et al. 2016).

The faunal report from Kojtepa fortress (Antiquity–Early Silk Road period Samarkand) suggests that caprines were the most abundant source of livestock (Maini & Serrone 2020; Tbl.85). More

interesting is the fact that caprine representation drops significantly after the Hellenistic period, while suids spike substantially (and equids as well, though less so). These abundances seem to level out entirely by the Early Silk Road period, with caprines not only dominating assemblages but also seeming to be the only livestock animals represented. A deeper reflection on these subsistence transitions is beyond the scope of my dissertation, but they do help to present a window into a pattern of subsistence through time in the urban contexts of Transoxiana, at least in Sogdian fortresses. I will revisit this data later, in my concluding discussion of Medieval animal economies in Transoxiana.

Tbl.85 Table of published faunal data (MNI%) from the Sogdian fortress of Kojtepa (Maini & Serrone 2020).

Period	Estimated Dates	Caprines	Cattle	Equids	Suids	Reptiles	Birds
Hellenistic (Antiquity)	ca. 400–100 BCE	63.9%	11.1%	2.8%	2.8%	5.6%	5.6%
Antiquity–Early Silk Road	ca. 200 BCE–200 CE	70%	0%	0%	0%	10%	10%
Early Silk Road–Middle Silk Road	ca. 100–400 CE	45.2%	16.7%	9.5%	14.3%	7.1%	4.8%

**Table does not discriminate between wild and domesticated fauna, and does not include the more ambiguous taxonomic groupings (e.g. "small mammals") from the original report.*

A detailed faunal report is also available from Kara-Tepe, a Middle Silk Road / Early Medieval period settlement site in nearby Khorezm (Brite et al. 2017; Tbl.86). It is again unclear why some cells contain fractions and others whole numbers, even in the case of "1" and "1/1" (see Chapter 12, e.g. Tbl.32). I have conferred with zooarchaeological colleagues, including the esteemed Umberto Albrella, and have not been able to clarify what seems to be convention in the reporting of faunal data from Inner Asia. Regardless from the Hellenistic–Early Silk Road period subsistence at Kojtepa fortress in rural Sogdia to the Middle Silk Road period fortress of Kara-Tepe in Khorezm (adjacent to Transoxiana), caprines continue to dominate, though little more can be said with such low sample numbers.

Table of published faunal data (NISP / MNI) from the Khorezm fortress of Kara-Tepe (Brite et al. 2017).

Period	Estimated Dates	Caprines	Sheep	Goats	Cattle	Horses	Ass / Mule	Suids	Red Deer
Early Silk Road	ca. 100–300 CE	5 / 1	1	2	6 / 1	1 / 1	1	1 / 1	0
Middle Silk Road	ca. 300–400 CE	26 / 7	12	0	5 / 1	2 / 1	3	1 / 1	4 / 1

Faunal reports from Kafir Kala (also in rural Sogdia, in the Samarkand oasis) suggest that suid consumption was a very minor contribution to Pre-Islamic subsistence at the fortress, which increased after the Arab conquest. The Islamic period assemblage also expanded to include both domesticated pig (*Sus scrofa domestictus*) and wild boar (*Sus scrofa*) (Serrone et al. 2007; Tbls.87–88). However, this increase was minor and likely indicates that suid consumption at Kafa Kalir, which was not prevalent to begin with, was not strongly affected by the initial onset of Islamification. Birds and reptiles, which were once fairly prevalent in the Sogdian fortresses of the Hellenistic through Early Silk Road periods (see Tbl.86), seemingly lose all representation by the Middle Silk Road period. This may simply be the result of taphonomic / sampling bias

(see Chapter 02), or may reflect an actual subsistence transition. It could also be the case that the reptiles and birds of Kojtepa accumulated naturally and were not incorporated into human diets. Additionally, domesticated canid and felid remains do not appear until the Islamic period.

Tbl.87 Table of published faunal data (MNI%) from the Sogdian fortress of Kafir Kala (Serrone et al. 2007).

Period	Sheep / Goat	Sheep	Goat	Cattle	Horse	Ass / Mule	*Equus* sp.	Camel	Pig	Wild Game
Pre-Islamic (ca. 650–750 CE)	44.8%	13.8%	5.2%	13.8%	3.4%	1.7%	5.2%	1.7%	1.7%	8.5%
Islamic (ca. 750–1100 CE)	45%	15.6%	6.3%	13.8%	3.8%	1.3%	1.9%	1.3%	3.1%	3.8%

**Table merges certain taxonomic categories from the original report into "Wild Game".*

Tbl.88 Table of published faunal data (MNI%) from the Sogdian fortress of Kafir Kala (Serrone et al. 2007).

Period	Caprines	Cattle	Equids	Camelids	Suids	Cervids	Canids	Felids
Pre-Islamic	69.8%	15.1%	11.3%	1.9%	1.9%	1.7%	3.4%	0%
Islamic	71.3%	14.7%	7.3%	1.3%	3.3%	0.6%	3.8%	1.2%

**Table does not discriminate between wild and domesticated fauna, and does not include the more ambiguous taxonomic groupings (e.g. "small-medium wild ungulates") from the original report.*

The faunal data suggest that hunting at Kafir Kala was more common than pig rearing, though both were strongly overshadowed by livestock consumption, especially of caprines. Herd composition also does not appear to have drastically changed at Kafir Kala following Arab expansion, although hunting became less prevalent. It is unclear if hunting at fortresses and outposts was less prevalent during the Qarakhanid period as well. It is interesting that the greatest shift in suid consumption (in fortresses at least) seems to coincide not with the widespread conversion to a religion that forbids eating pork, but with events dating back to Antiquity (see Tbls.89–90). Reptile and bird consumption is also poorly understood, including the role of chickens in fortress and outpost economies, or the role of chickens in households and farmsteads.

Domesticated chicken remains were reported from the fortified Bactrian town of Kyzyltepa during Antiquity (Wu et al. 2015; Tbl.89), as well as throughout Antiquity and Medieval (including Islamic) occupations in the Bactrian city of Termez (Portero et al. 2022; Tbl.90). The recent peptide mass fingerprinting of archaeological eggshells has also confirmed that chicken rearing was widespread throughout Medieval Central Asia (Peters et al. 2024). Suid remains were also reported from all periods of occupation at Termez, including the periods that coincided with Islamic rule in Central Asia. Notably, suid representation at Termez does appear to decrease drastically after Arab conquest, though sample numbers are quite low.

Domesticated dogs are reported from Termez before the Islamic period, including a butchered specimen from the Antiquity period (Portero et al. 2022), contrary to the fortresses of Transoxiana. Camel remains are notably scarce, a theme that will be revisited later in this chapter (see section "V.V.IV."). The lack of reptile remains at Termez could be related to

recovery biases (pers.comm. Robert Spengler 2024), or possibly to differences in fortress versus city subsistence.

Tbl.89 Table of published faunal data (NISP) from the fortified Bactrian town of Kyzyltepa (Wu et al. 2015).

Archaeological Period	Estimated Dates	Caprines	Cattle	Equids	Camelids	Gazelle	Cervids	Suids	Canids	Felids	Chickens
Late Iron Age & Early Antiquity	ca. 910–460 BCE	1332	329	128	4	13	0	44	21	1	12

**Table does not discriminate between wild and domesticated fauna nor include all taxonomic groupings from the original report, some of which have been merged (e.g. certain domesticated and wild animals have been combined to form one broad category).*

Tbl.90 Table of published faunal data from the Bactrian city of Termez (Portero et al. 2022).

Species	Antiquity (ca. 300 BCE–50 CE)		Early Silk Road–Middle Silk Road (ca. 150–350 CE)		Middle Silk Road (ca. 350–600 CE)		Middle Silk Road – Late Silk Road (ca. 800–1400 CE)	
	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI
Bos taurus	18	3	13	2	75	4	5	1
Ovis aries	31	6	16	5	22	3	52	5
Capra hircus	11	3	18	1	52	3	13	2
Caprinae	159	7	68	10	223	11	245	10
Gazella subgutturosa	2	1	2	1	3	1	1	1
Sus scrofa	5	2	18	3	28	2	3	2
Equus caballus	7	2	6	1	11	2	1	1
Equus asinus	1	1	1	1	5	1	1	1
Equus sp.	1	1	2	1	12	1	0	0
Saiga tatarica	1	1	0	0	0	0	0	0
Camelidae	0	0	0	0	1	1	0	0
Vulpes corsac	0	0	0	0	1	1	0	0
Cervus elaphus	1	1	6	1	5	1	0	0
Canis familiaris	1	1	1	1	2	1	1	1
Gallus domesticus	6	2	5	1	11	2	4	1
Leporidae	0	0	0	0	1	1	0	0

**Table does not include all taxonomic groupings (e.g. "small size mammal") from the original report.*

ZooMS could help to clarify the actual faunal profile of each phase by taxonomically identifying a select number of the thousands specimens which were not morphological diagnostic. The faunal profile from Medieval Termez, as far as it has been identified, is largely parsimonious with the profiles from Medieval Transoxian fortresses (see Tbls.85–89). It is likely that herd compositions in the Medieval cities of Transoxian also have ranged from fifty to seventy five percent caprine (ca. 3:1 sheep to goat ratio), with the remainder of livestock being composed of equids, cattle, or camels (see Chapter 18). How dependent would these compositions have been on region, landscape, or wool and woolen textile industries, and how similar would they have been to the twentieth century herds of Uzbekistan (Tbl.91), is unclear.

Tbl.91 Table of twentieth century Uzbek herd composition data (Krader 1955).

Country	Sheep	Goat	Cattle	Horse	Ass/Mule	Camel
Uzbekistan	44%	17%	26%	9%	6%	2%

**Absolute counts are not available in the census data (Krader 1955).*

There does not seem to have occurred any deviation from caprine herd dominance in any of the urban archaeological contexts of Transoxiana, Khorezm, or Bactria discussed so far. A more interesting question then, would be if ratios of sheep to goat fluctuated or remained consistent. Here again, ZooMS would be an optimal method to help refine taxonomic attributions (see Chapter 05). Moving beyond questions exclusive to animal husbandry, how would urban agro-pastoralism have been modified in response to climate change and aridification (see Brisset al. 2023; Misa et al. 2023) leading up to Qarakhanid rule? These are some of the major questions surrounding mixed subsistence modes in the Medieval urban contexts of Transoxiana.

19.4.2. Highland Agropastoralism

"...pastoral transhumance and agropastoralism were interchangeable economic strategies used by peoples …through Medieval periods in mountain-river valleys…These economic strategies combined the pasturing of sheep, goats, cattle, and horses with the cultivation of cereals in a system that was adapted to different vegetational zones along a vertical gradient…" (Chang et al. 2023)

A discussion of highland agropastoralism warrants a pivot from architecture to physical geography (i.e. topography), though one still defined by traditional geography (i.e. region) in this case. Elevation becomes more relevant than population density and highland (or upland) landscapes are characterized by foothills, mountain slopes, and mountain summits (see Garcia-Molsosa 2023) instead of farmhouses, villages, cities, fortresses, and palaces. Transoxiana contains the Nuratau, Hissar, and Malguzar mountain ranges. The Malguzar range is an extension of the Turkestan range, which is a part of the Tien Shan range. Combined genetic, ZooMS, and cementum analyses have confirmed the presence of domesticated sheep at the Neolithic site of Obishir V in the Ferghana Valley, suggesting that humans have been herding sheep in the Tien Shan Mountains for over 8000 years (Taylor et al. 2021; see also Chapter 09 for theories on the relationship between Central Asian mountain corridors and pastoralist emergence).

Although mountains and foothills are typically associated with highly mobile pastoralism in Central Asia (see Frachetti & Maskudov 2014), recent archaeological reconstructions of Bronze Age through Medieval subsistence models have challenged the uniformity of this narrative (e.g. Chang et al. 2023; Misa et al. 2023; Motuzaite-Matuzeviciute et al. 2020; Spengler et al. 2013; for related discussions see also Bullion et al. 2022; Rouse et al. 2022; Spengler et al. 2021). Faunal assemblages recovered in association with cereals and agricultural tools from sites in the Tien Shan Mountains suggest a mixed economic strategy where livestock manured cereal fields and wild game were hunted as a secondary activity (Chang et al. 2023; Motuzaite Matuzeviciute et al. 2020; Spengler et al. 2013).

In the the Malguzar range of Transoxiana, the rich archaeobotanical assemblage recovered from the Qarakhanid settlement of Tashbulak suggests that fruits, nuts, grains, and legumes were being cultivated in the foothills (Spengler et al. 2018). The faunal assemblage from Tashbulak suggests a herding economy centered around caprines and cattle (Maksudov et al. 2019). Uniquely, Tashbulak is both a highland and an urban site with a published faunal report

that has been attributed to the Qarakhanid Khanate, providing a window into Qarakhanid expansion in both contexts.

The questions surrounding highland agropastoralism in Medieval Transoxiana are similar to those surrounding urban agropastoralism. The prevalence of pig and boar consumption (as well as hunting versus herding in general) in relation to Islamic regimes and identities, the relationships between herd composition and elevation, biotype, and time period, and the absence or presence of chicken husbandry are all currently poorly understood. Additional questions include whether or not faunal assemblages support the idea that aridification drove economic adaptations in the highlands during the Qarakhanaid period. Was highland agropastoralism a predominant strategy since the Bronze and Iron Ages, as in the Tien Shan Mountains, or a later adaptation in Transoxiana? The latter question would require the examination and analysis of faunal, archaeobotanical, and tool assemblages from prehistoric and Early Medieval sites in the Nuratau, Hissar, and Malguzar mountain ranges.

19.5. The Medieval Animal Economies of Transoxiana: Conclusion

The overall lack of archaeological animal remains, especially from Medieval contexts, precludes inferring too much from any of the data that I have provided here. A good amount of the data are derived from the archaeological sites of Bactria, as opposed to more “classically Transoxian” regions. The faunal data collated from the sites of Bactria and Khorezm are also not exhaustive. I have no doubt that the data as I have tabulated it is somewhat misleading, and could be refined not only by more thorough faunal analysis, but also by case-by-case studies of complex Medieval spaces. The animal economies of Qarakhanid Transoxiana, though difficult to reconstruct, could be said to have been dominated by caprines, primarily supplemented by cattle and horses, and secondarily supplemented by birds (mostly chickens but also geese, duck, and corvids), suids, cervids, gazelle, and small game.

Whether or not this signature of subsistence, which I have tentatively reconstructed from cities and fortresses, holds up in highland complexes and pastoralist encampments is currently beyond investigation in lieu of faunal data from these contexts (e.g. Mailykhotan, Tashbulak, and Ulukdush). The role of wool and woolen textile production in herd composition, and the relationship between these industries and elevation, region, and social organization, is difficult to reconstruct with the archaeological data that is currently available. It is also difficult to say what the culling patterns which characterized wool-working economies in Transoxian contexts would have looked like. Future faunal analyses will help to expand the faunal data available and refine our understanding of Medieval animal economies in Transoxiana and Central Asia more broadly.

20. Materials & Methods

I have already discussed ZooMS as an application of PMF to the proteinaceous remains of archaeological animals in pursuit of taxonomic identification (see Chapters 04–06). Although ZooMS was initially developed as a form of archaeological collagen PMF, the method is no longer limited to the analysis of collagen (see Chapters 04–05). My own application of ZooMS is strictly collagen-based. I have also explained how sample extracts are spotted onto steel ground plates with matrix solution and left to dry before being loaded onto a MALDI-TOF mass spectrometer (see Chapter 04). I further explained how MALDI-TOF instruments measure the masses of ionized peptides with a mass detector and record them as *m/z* ratios on a MS1 spectrum, or TOF spectrum (see Chapter 05). Here I will explain the sample preparation protocols I used, as well as my approach to MALDI-TOF MS data conversion and analysis.

20.1. Sample Pretreatment Protocols

Although I noted that a number of sample pretreatment protocols have been developed for ZooMS (see Chapter 05), I did not explore any of them in detail. Here I will overview the three protocols that I used in the course of my own ZooMS analysis, i.e. the acid soluble, acid insoluble, and AmBic protocols. Although these three protocols differ in extraction method, with the acid soluble and insoluble protocols being acid-based and the AmBic protocol being buffer-based, they are all used to extract collagen from archaeological animal bone samples. For each protocol, all samples should be weighed (~10-20 mg for archaeological; ~10 mg modern) and deposited into individually labeled microcentrifuge tubes. Extraction blanks should also be prepared for quality control.

Acid Soluble Protocol (Buckley et al. 2009; Brown et al. 2020; Welker et al. 2015)

All samples should be deposited into individually labeled microcentrifuge tubes with 500 µL of 0.6 M HCl at 4 °C (or enough HCl to cover the whole sample). All samples and extraction blanks should be left at 4 °C until acid demineralization is complete, i.e. when the bone or tooth becomes spongy and all bubbling has ceased. The samples and blanks should then be centrifuged for one minute at high speed (20000 rpm) before the acid supernatants are eluted into new tubes individually labeled “AC” (acid). For buffer exchange, 250 µL of acid supernatant from each sample should be eluted into an individual 30 kDa ultrafilter placed into an individually labeled tube. The acid supernatants of poorly preserved samples can instead be eluted through 3 kDA or 10 kDA ultrafilters. All tubes with ultrafilters should then be centrifuged 3700 rpm for between 5 and 30 minutes, until the acid supernatant has been pushed through the ultrafilters.

All flow through should then be discarded and 500 µL of 50mM AmBic added to each tube with an ultrafilter. These samples should then be centrifuged again at 3700 rpm for between 5 and 30 minutes, until the AmBic has been pushed through the ultrafilters. The flow through should again be discarded. Another 100 µL of 50 mM AmBic should be added to each ultrafilter and

mixed by being gently pipetted up and down repeatedly. For each sample and blank, 50 µL of each AmBic supernatant should be transferred into new tubes labeled “EXT” (extract); the remaining 50 µL of AmBic supernatant transferred into new tubes labeled “SE” (second extract). The collagen extracts should then be digested by adding1 µL of 0.4 µg/µl trypsin solution to each EXT tube. The EXT tubes should then be incubated at 37 °C for between 12 and 18 hours. All samples and blanks should then be centrifuged at high speed (20000 rpm) before adding 1 µL of 5 % (v/v) TFA to stop the trypsin digestion. Before being purified using C18 ZipTip, the samples and blanks may optionally be stored at -20 °C.

The samples and blanks should then be ziptipped. Each individual ZipTip should be washed twice with 100 µL of conditioning solution and discarded, then twice again with 100 µL of wash solution and discarded. The sample (EXT tube) should then be resuspended at least 5 times back and forth over the ZipTip to bind the peptides. The tip should then be washed twice with 100 µL of wash solution and discarded. Finally, the collagen peptides should be eluted into new tubes individually labeled “COL” (collagen) with 50 µL of conditioning solution that the ZipTip has been passed through at least 5 times. All samples and blanks may either be spotted with a crystallizing matrix (after being diluted with a conditioning solution, if desired) on a ground steel MALDI plate, or stored at -20 °C.

Acid Insoluble Protocol (Buckley et al. 2009; Brown et al. 2020; Welker et al. 2015)

All samples should be demineralized in 0.6 M HCl at 4 °C in accordance with the ZooMS acid soluble protocol above (Buckley et al. 2009; Brown et al. 2020; Welker et al. 2015). However, instead of extracting collagen from the acid supernatant, collagen should be extracted from the collagen bone shadow. After demineralization and centrifugation, the acid supernatants may either be discarded or saved and stored at -20 °C for subsequent insoluble extraction. The samples themselves should be washed by pipetting 200 µL of 50 mM AmBic over them and then centrifuging them for one minute at high speed (20000 rpm). Delicate samples may instead be centrifuged at a slower speed. In either case, all flow through should be discarded. Each sample and blank should be washed in this way 3 times to neutralize pH.

All samples and blanks should then be washed with NaOH to remove humic acids and other contaminants. 200 µL of 0.1 M NaOH should be pipetted up and down into each tube before being centrifuged for one minute at high speed (20000 rpm), or at a slower speed for more delicate samples. After flow-through is discarded, the samples and blanks should be washed 2 more times– or less for smaller and more collagen-poor samples. This step can also sometimes be skipped altogether, as NaOH washes can damage collagen. All samples and blanks should then be washed three more times with 50 mM AmBic in the same way they were before being washed with NaOH; this step may skipped if the samples were not washed with NaOH, as there would be no need to neutralize the pH again after the first 3 AmBic washes.

The samples and blanks are then gelatinized, digested, purified with C18 ZipTips, optionally diluted with conditioning solution, and spotted with a crystalizing matrix on a steel ground plate

in the same was as with the ZooMS acid soluble protocol above (Buckley et al. 2009; Brown et al. 2020; Welker et al. 2015).

AmBic Protocol (Buckley et al. 2009; van Doorn et al. 2011; Brown et al. 2020)

All samples should be deposited into individually labeled microcentrifuge tubes with 100 µL of 50 mM AmBic (or enough AmBic to cover the whole sample). All samples and extraction blanks should be left overnight (or up to a week) at room temperature. The samples and blanks should then be centrifuged for one minute at high speed (20000 rpm), though delicate samples may be centrifuged at a slower speed. The supernatants should then be discarded and an additional 100 µL of 50 mM AmBic added to each sample, which should be gelatinized by being incubated for one hour at 65 °C. The samples and blanks should then be centrifuged at high speed (20000 rpm). Delicate samples may alternatively be suspended in only 50 µL of AmBic and centrifuged at a lower speed; these samples will not have enough AmBic supernatant for backup tubes.

Samples gelatinized in 100 µL of 50mM AmBic should have half of the AmBic supernatant transferred into new tubes labeled “EXT” (extract) and the remaining 50 µL of AmBic supernatant transferred into new tubes labeled “SE” (second extract). SE tubes should be stored at -20 °C, and the leftover bone may be dried by leaving the tubes open at room temperature and re-stored. For digestion, a single µL of 0.4 µg/µl trypsin solution should then be added to each EXT tube, which should then be incubated at 37 °C for between 12 and 18 hours. The digested samples and blanks should then be centrifuged at high speed (20000 rpm) and 1 µL of 5 % (v/v) TFA added to stop the trypsin. Before being purified using C18 ZipTip, the samples and blanks may optionally be stored at -20 °C.

For ziptipping, each individual ZipTip should be washed twice with 100 µL of conditioning solution and discarded, then twice again with 100 µL of wash solution and discarded. The sample (EXT tube) should then be resuspended at least 5 times back and forth over the ZipTip to bind the peptides. The tip should then be washed twice with 100 µL of wash solution and discarded. Finally, the collagen peptides should be eluted into new tubes individually labeled “COL” (collagen) with 50 µL of conditioning solution that the ZipTip has been passed through at least 5 times. All samples and blanks may either be spotted with a crystallizing matrix (after being diluted with a conditioning solution, if desired) on a ground steel MALDI plate, or stored at -20 °C.

20.2. Peptide Marker Screening (MALDI-TOF)

I traveled to the University of Tübingen in December 2023 and selected eight reference samples of goitered gazelle (*Gazella subgutturosa*) and sika deer (*Cervus nippon*) (Tbl.92) from the zooarchaeological collection at the Institute for Archaeological Sciences. I conducted all subsequent sampling and analysis at the University of Tübingen. I used a dremel drill to subsample ca. 5 mg from each sample, all of which were weighed and given new lab sample numbers (Tbl.92).

Tbl.92 Table of reference collection species, sample numbers, lab codes, and weights.

Species	Collections Sample No.	Lab Sample No.	Lab Sample Weight
Gazella subgutturosa	CE74	EH01	6.42 mg
Gazella subgutturosa	CE75	EH02	4.88 mg
Gazella subgutturosa	CE76	EH03	5.44 mg
Gazella subgutturosa	AT2	EH04	11.35 mg
Gazella subgutturosa	A32	EH05	5.6 mg
Cervus nippon	AT38	EH06	8.04 mg
Cervus nippon	AT44	EH07	6.08 mg
Cervus nippon	AT194	EH08	7.4 mg

I extracted collagen from all modern and archaeological reference samples (*Gazella subgutturosa, Cervus nippon*) in the ZooMS Lab at the University of Tübingen following the AmbBic protocol (Buckley et al. 2009; Brown et al. 2020). I created three blanks for quality control. I spotted all samples and blanks in duplicate on a ground steel plate which was run on the MALDI-TOF instrument at Tübingen University in June 2024.

20.3. Nizhnaya Sooru, Southern Siberia

This study required samples that could not be morphologically identified to a single taxon, with special consideration for caprines and fragments associated with Afanaievo occupation. I selected 171 bone and tooth samples total from six out of the seven stratigraphic layers of the Nizhnyaya Sooru faunal assemblage (Tbl.93) at the Max Planck Institute for Evolutionary Anthropology in Leipzig, DE and sub-sampled ca. 5-10 mg from each at the Pharmapark Labs in Jena, DE in February 2022. I then hand-carried the subsamples to Harvard University and subsampled them again in the Archaeological Multiplex User Labs (AMUL) in March 2022.

Tbl.93 Table of stratigraphic information for samples selected from Nizhnyaya Sooru.

Layer	Period	Associated Archaeological Culture	Sample No.
Layer 1	Historical / Modern	N.A.	0
Layer 2	Early Iron Age	Scythian	6
Layer 3	Mid-Late Bronze Age	Andronovo	3
Layer 4	Early Bronze Age	Elunino / Karakol	17
Layer C	Eneolithic	Afanasievo	33
Layer 5A/5B	Eneolithic	Afanasievo	112

I extracted collagen from all 171 samples using the acid insoluble protocol at AMUL. I created extraction blanks to check for lab contamination and ensure quality control. I then spotted the collagen extracts and extraction blanks 1:1 with CHCA matrix in duplicate on a ground steel plate. All samples were measured on a MALDI-TOF in the Bauer Core Facility at Harvard University. Collagen yield cannot be quantified in advance and I needed to dilute several samples with conditioning solution and/or re-extract them using the acid soluble protocol; these samples were measured with the MALDI multiple times. Samples NZS058.A, NZS064.A, NZS103.A, NZS130.A, NZS138.A, NZS155.A, NZS161.A, and NZS186.A did not retain enough collagen for ZooMS and failed to produce suitable spectra. Additionally, 13 samples that were

extracted and measured with MALDI (NZS049.A, NZS065.A, NZS066.A, NZS083.A, NZS090.A, NZS122.A, NZS140.A, NZS173–174.A, NZS202.A, NZS216.A, NZS226.A, NZS234.A) were ultimately excluded due to unclear sample contexts.

20.4. ZKG513, Outer Mongolia

Four hundred twenty-seven animal bones samples were selected by Mongolian archaeologists in the National Museum of Mongolia and exported to MPI-EVA. One hundred forty-three medium mammal bone fragments, large mammal bone fragments, and unidentifiable bone fragments were preselected from the assemblage for ZooMS (Figs.20–22). These 143 samples were specifically selected in hopes of identifying domesticated mammal specimens which could then be submitted for genomic analysis, as part of the ERC DairyCultures investigation into the dispersal of domesticated animals throughout Central Eurasia. Collagen had initially been extracted from all 143 samples by another researcher in the Archaeological Multi-User Lab (AMUL) at Harvard University in 2021, following the acid insoluble protocol. I subsequently re-extracted collagen from 41 of the samples which did not contain enough collagen for secure taxonomic identification at AMUL in 2022, following the acid soluble protocol. I elected to use the acid soluble protocol instead of the acid insoluble protocol because less well-preserved bones have begin to break down and release collagen outside of the bone inorganic matrix, which can be recovered in the acid soluble fractions (Wang et al. 2021). I spotted all samples and a single extraction blank with a crystalizing matrix (CHCA) on ground steel plates, which were run on a MALDI-TOF instrument at the Harvard University Bauer Core Facility. Sample ZKG065.A was determined to be a rock, and thus excluded from my study.

Fig.20 Bar graph of numbers of faunal samples recovered from Trench ZK513-1 strata (Houle et al. 2022).

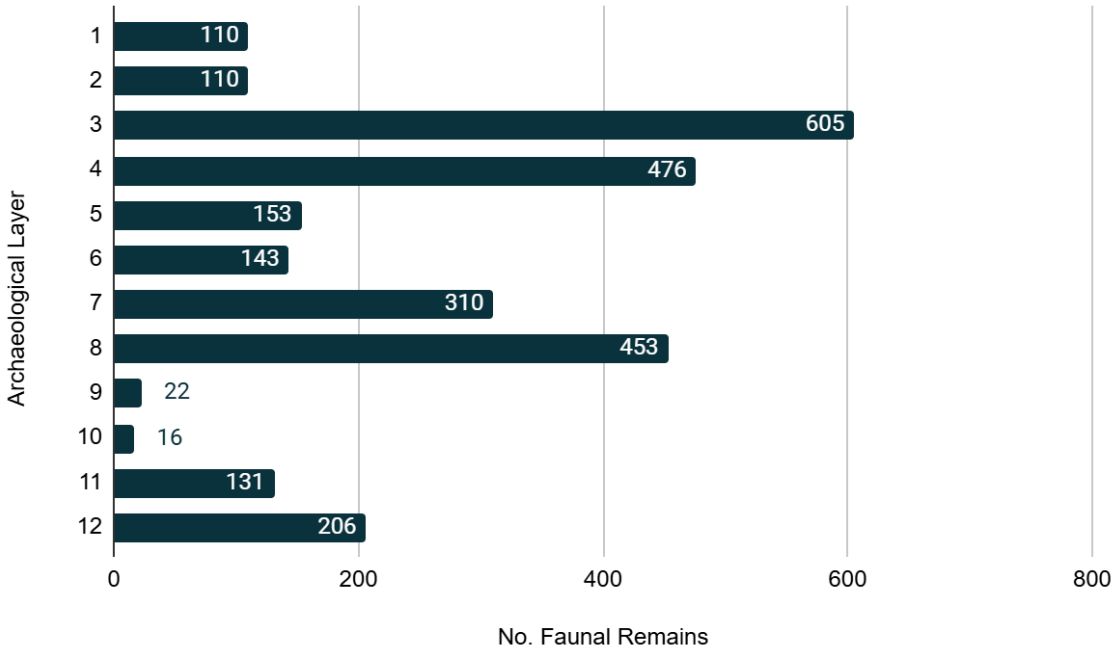


Fig.21 Bar graph of numbers of size-based classes morphologically attributed to faunal remains recovered from Trench ZK513-1 strata (Houle et al. 2022).

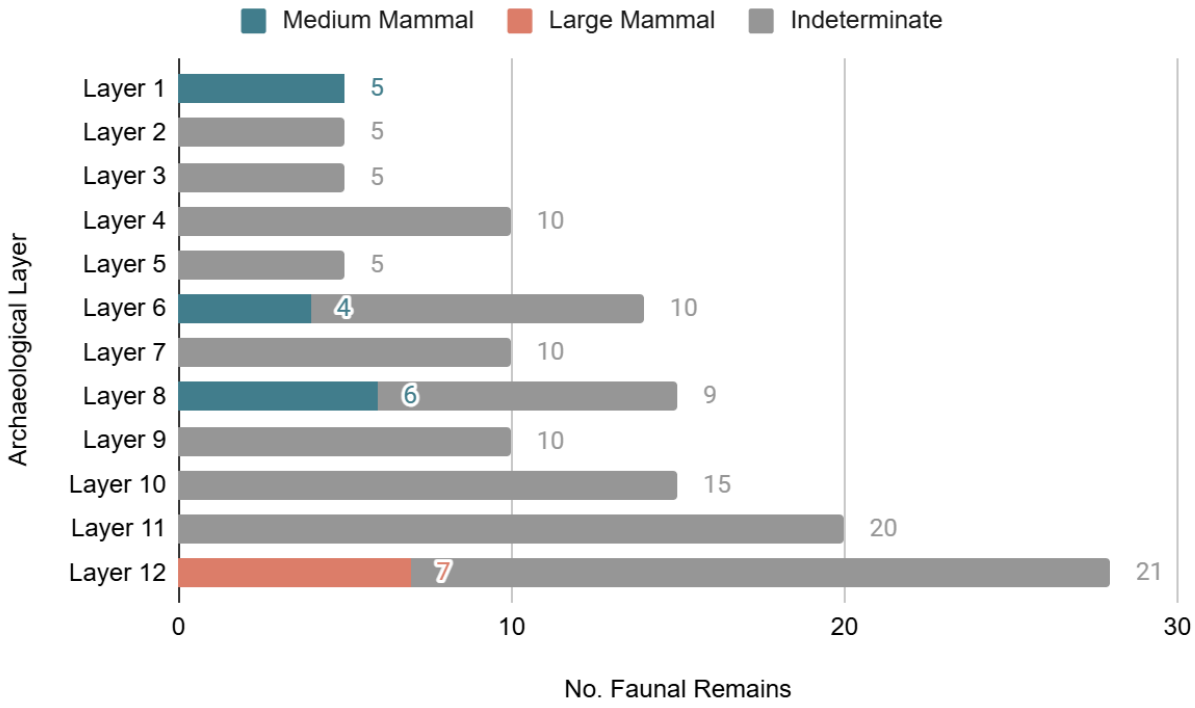
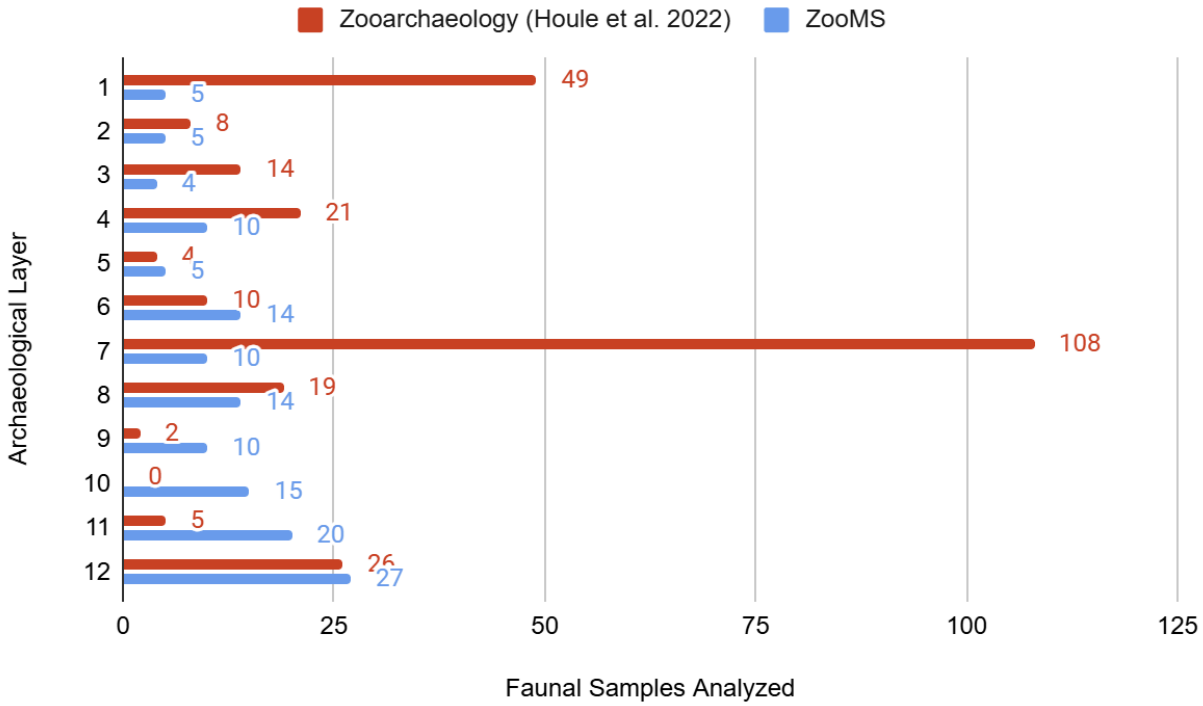


Fig.22 Bar graph comparing the number of faunal remains from Trench ZK513-1 strata and analyzed by a zooarchaeologist (Houle et al. 2022) with the number selected for this ZooMS study, by strata.



20.5. Tashbulak, Uzbekistan

This targeted study was designed to refine the morphological identifications of samples that could not be identified to a single taxon, or were too fragmented to be identified at all. I selected 340 bone and tooth samples from Tashbulak at the Max Planck Institute for Evolutionary Anthropology in Leipzig and sub-sampled ca. 5-10 mg from 338 of them at the Pharmapark Labs in Jena in February 2022. I then hand-carried the subsamples to Harvard University in Cambridge, MA and subsampled them again in the Archaeological Multiplex User Labs (AMUL) at Harvard in March 2022. I took two intact astragali (TBK339.A & TBK340.A) from MPI-EVA / MPI-SHH whole (i.e. without subsampling) and sampled them in AMUL with a drill in May 2022, after photographing and 3D-scanning them at Harvard University. Sample TBK015.A was destroyed when the eppendorf tube containing it opened due to third-party handling during transit, and so I was not able to extract collagen from this sample.

I used the acid insoluble to extract collagen from 331 samples from the Tasbulak faunal assemblage in AMUL in Apr 2022. I created eight blanks. I used the acid soluble protocol to extract collagen from 8 samples that looked less well-preserved, and created one clean blank (NZS BLANK 1.1) for this batch of samples (which included samples from Nizhnyaya Sooru). I diluted all collagen extracts and extraction blanks 1:10 with a conditioning solution and spotted them 1:1 with CHCA matrix in duplicate on ground steel plates. Eighty-three of these samples were re-spotted in August 2022 when it became clear that high humidity conditions at AMUL had compromised the drying of some of the samples I had spotted. All samples were then measured with MALDI-TOF in the Bauer Core Facility at Harvard University between May 2022 and August 2022. Seven samples (TBK033.A, TBK109.A, TBK195.A, TBK197.A, TBK235.A, TBK241.A, TBK247.A) were ultimately excluded from my analysis due to unclear sample contexts, while sample TBK294.A was extracted but never spotted.

20.6. MALDI-TOF MS Data Analysis

For all sites, I converted the RAW files generated by MALDI-TOF to mzML files. I then used the free mass spectrometry software “mMass” (Strohalm et al. 2008; Niedermeyer & Strohalm 2012) to identify the samples to a taxon, following the data analysis protocol provided by Brown (2021). I kept the default parameters for smoothing (Savitzky-Golay method, window size offset 0.3 *m/z*, 2 cycles). For peak picking, I set a signal-to-noise (*s/n*) threshold of 3.5 to differentiate between the baseline and peptide markers. I compared the *m/z* ratios of all peptide markers with the published collagen peptide marker mass values reported in the online York University ZooMS marker database (no DOI available). I also analyzed all samples from ZK513-1 that were previously extracted and measured in 2021 by a different researcher. I entered all of the *m/z* ratios I used to taxonomically identify all samples in excel sheets (see Appendix 03), using the peptide marker notation recommended by Brown et al (2021a) (see also Chapter 05, Tbl.1).

York University ZooMS Marker Database:
https://docs.google.com/spreadsheets/d/1ipm9fFFyha8IEzRO2F5zVXIk0ldwYiWgX5pGqETzBco/edit?gid=1005946405#gid=1005946405

20.7. MALDI-TOF MS Data Availability

I uploaded all ZooMS spectra as mzML files and spreadsheets to the online data repository Zenodo. I have created individual links for data for samples from Nizhnyaya Sooru, ZK513-1, Tashbulak, and my collagen peptide marker screening study. DOI's are available for each (see Appendix 03), though some data has been embargoed pending publication.

21. Results

21.1. Quality Control

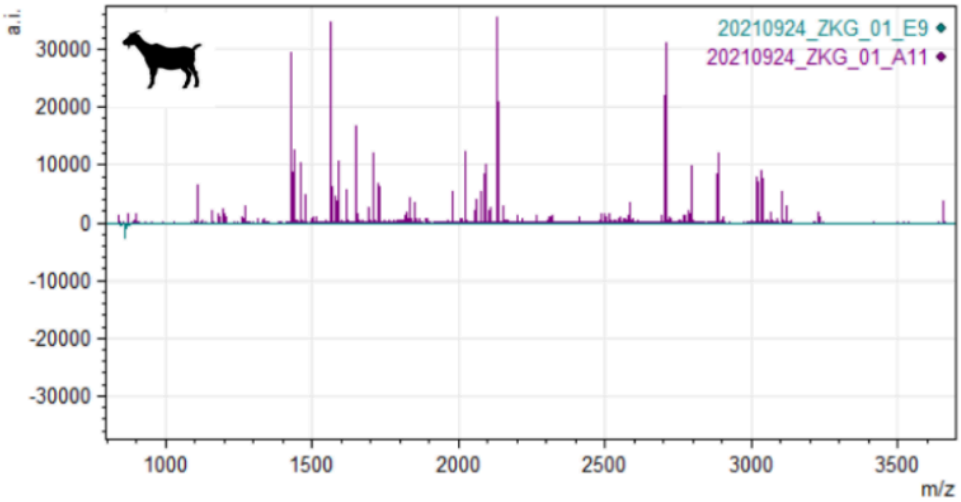
Extraction blanks from my MALDI-screening study of antilopine and cervid collagen as well as my ZooMS analysis of fauna from Nizhnyaya Sooru, ZK513-1, and Tashbulak showed negligible levels of background contamination, with only trypsin peaks consistently observed (see Appendix 03). Three extraction blanks from my Tashbulak ZooMS study (Blank 6.1, Blank 8.1, Blank 9.1) were completely devoid of protein and produced no MALDI spectra. The results confirm that there was no lab contamination.

21.2. Collagen Preservation

Preservation of the samples selected from the Nizhnyaya Sooru faunal assemblage was excellent, and 96% of all samples (n=156) retained enough collagen to produce taxonomically diagnostic spectra (Fig.24; Tbl.94; see Appendix 03).

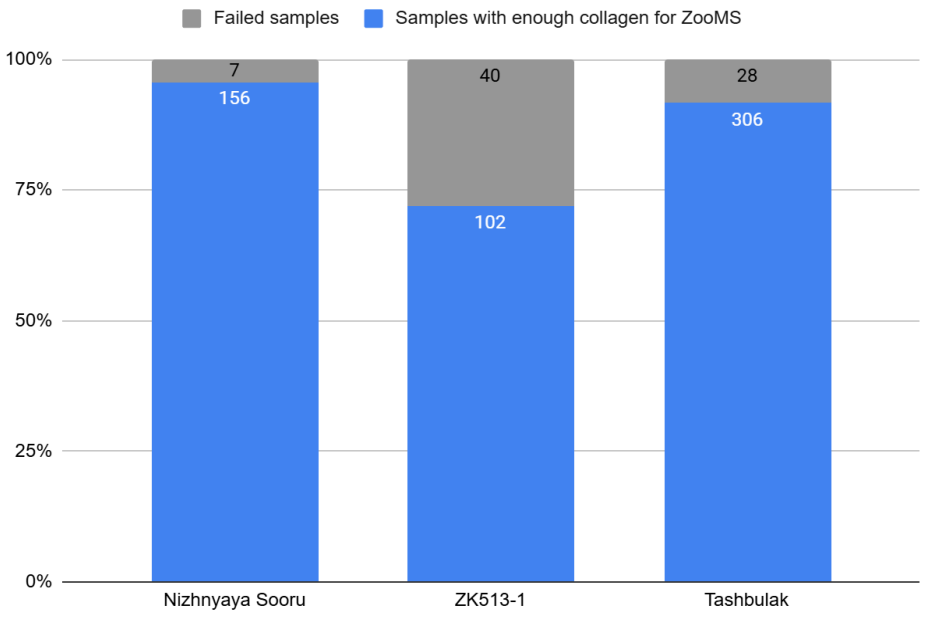
Of the 143 samples from the ZK513-1 Habitation Site that were submitted for ZooMS analyses, 102 yielded MALDI-TOF spectra with sufficient collagen preservation to be taxonomically assigned (Figs.23–24; see Appendix 03). Significant calcination of animal bone fragments from Layer 08 led to poor collagen preservation in many samples (n=12) in this layer, and these samples could not be taxonomically identified with ZooMS (Tbl.94). Sample ZKG065.A was initially categorized as a failed sample, but was determined to be a rock as opposed to a bone, and is thus not included in the failed sample count.

Fig.23 Mirrored spectra of successful (top) and failed (bottom) MALDI spectra from ZK513-1.



The collagen preservation of the samples selected from the Tashbulak faunal assemblage was exceptional, and >92% of all samples (n=306) retained enough collagen to produce MS spectra that were taxonomically diagnostic (Fig.24; Tbl.94; see Appendix 03).

Fig.24 Bar graph contrasting the number of failed ZooMS samples with successful samples from Nizhnyaya Sooru, ZK513-1, and Tashbulak.



Tbl.94 Morphologically identified samples from TBK that could not be taxonomically identified with ZooMS.

Zooarch ID	NZS	ZK513-1	TBK
Ovis sp. / *Capra* sp.	3	0	7
Ovis sp. / *Capra* sp. ?	1	0	1
Ovis sp. / *Capra* sp. / *Gazella* sp.	0	0	1
Ovis sp.?	1	0	0
Bos sp. / *Cervus* sp.	1	0	0
Bos sp.	0	0	1
"Wildy McWildface"	0	0	1
Vulpes sp. / *Canis* sp.	1	0	0
Large Mammal	0	0	13
Medium Mammal	0	7	4
Indeterminate	0	4	1

**Twenty-eight of the samples from Tashbulak failed, and one sample (TBK235.A) could not be identified based upon retained peptide markers. Sample NZS065.A was determined to be a rock.*

Of the comparative collection samples of goitered gazelle (*Gazella subgutturosa*) and sika deer (*Cervus nippon*) that I selected to screen with MALDI, all but one sample (EH03) retained enough collagen to produce spectra (Tbl.95; see Appendix 03).

Tbl.95 Table contrasting failed ZooMS samples with successful samples from the reference collection.

Species	No. successful samples	No. failed samples	No. samples in total
Gazella subgutturosa	5	0	5
Cervus nippon	2	1	3

21.3. Proteomic Taxonomic Identification (Archaeological Sites)

21.3.1. Nizhnyaya Sooru

Using the York Online Marker Database (see Chapter 20), I identified all samples with sufficient collagen preservation (n=156) as *Ovis* sp., *Capra* sp., *Ovis sp. / Capra sp.*, *Bos* sp. / *Bison* sp., *Canis* sp. / *Vulpes* sp., *Equus* sp., *Cervus* sp / *Gazella* sp. / *Saiga* sp., or *Lepus* sp. (Fig.25; Tbl.96; see Appendix 03). I identified the majority of samples as *Ovis* sp., with *Bos* sp. as the second most common identification (Fig.25; Tbl.96). Notably, I could not technically identify large bovine samples beyond "*Bos* sp. */ Bison* sp.". These samples could not have been *Bison* sp., as most bison are endemic to North America and the European bison (*Bison bonasus*) is not believed to have inhabited Southern Siberia. Thus, I have determined all bovine samples to be *Bos* sp. (Tbl.96).

Not all collagen peptide markers are equally conserved through time, and in some cases even samples that produced high-quality spectra with many clear isotopic peak distributions did not retain the markers necessary for genus-level taxonomic identification. I was not always able to use MALDI spectra distinguish *Ovis* sp. from *Capra* sp., even in samples with high collagen yield, due to the loss of the diagnostic α2 757 peptide marker. In total, I was unable to distinguish 22 samples beyond "*Ovis* sp. / *Capra* sp." (Tbl.98). I identified 2 wild ungulates that could not be *Capreolus* sp., again based upon the α2 757 peptide marker, but could not further distinguish them beyond "*Cervus* sp. */ Gazelle* sp. */ Saiga* sp." (Tbl.97).

Tbl.96 Table of ZooMS-based identifications of samples selected from Nizhnyaya Sooru.

ZooMS-Based ID	Inferred Taxon	No. Samples
Bos sp.	Cattle	26
Capra sp.	Goats / Ibex	1
Cervus sp. */ Gazella* sp. */ Saiga* sp.	Antelopes / Deer	2
Canis sp. */ Vulpes* sp.	Canids	6
Equus sp.	Equids	4
Lepus sp.	Hares	1
Ovis sp.	Sheep	101
Ovis sp. / *Capra* sp.	Caprines	22
Aves	Bird	1
Failed		7
TOTAL		163

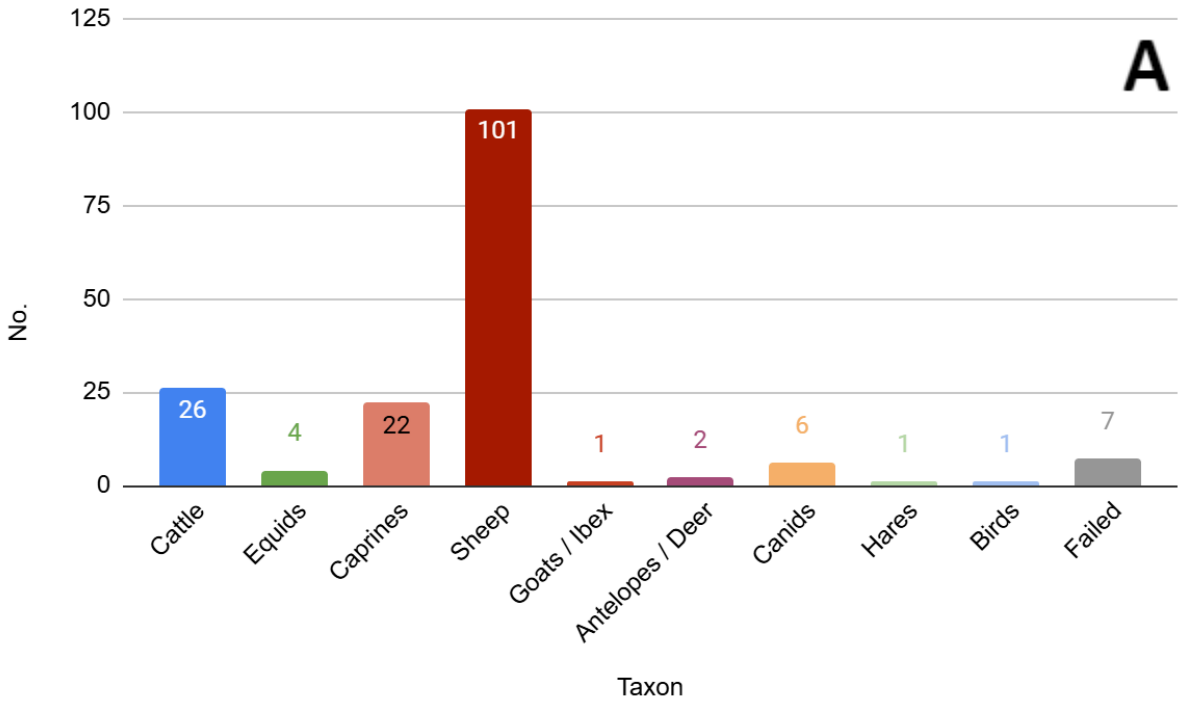
Tbl.97 Table of tryptic masses identified in antilopine / cervid samples from Nizhnyaya Sooru.

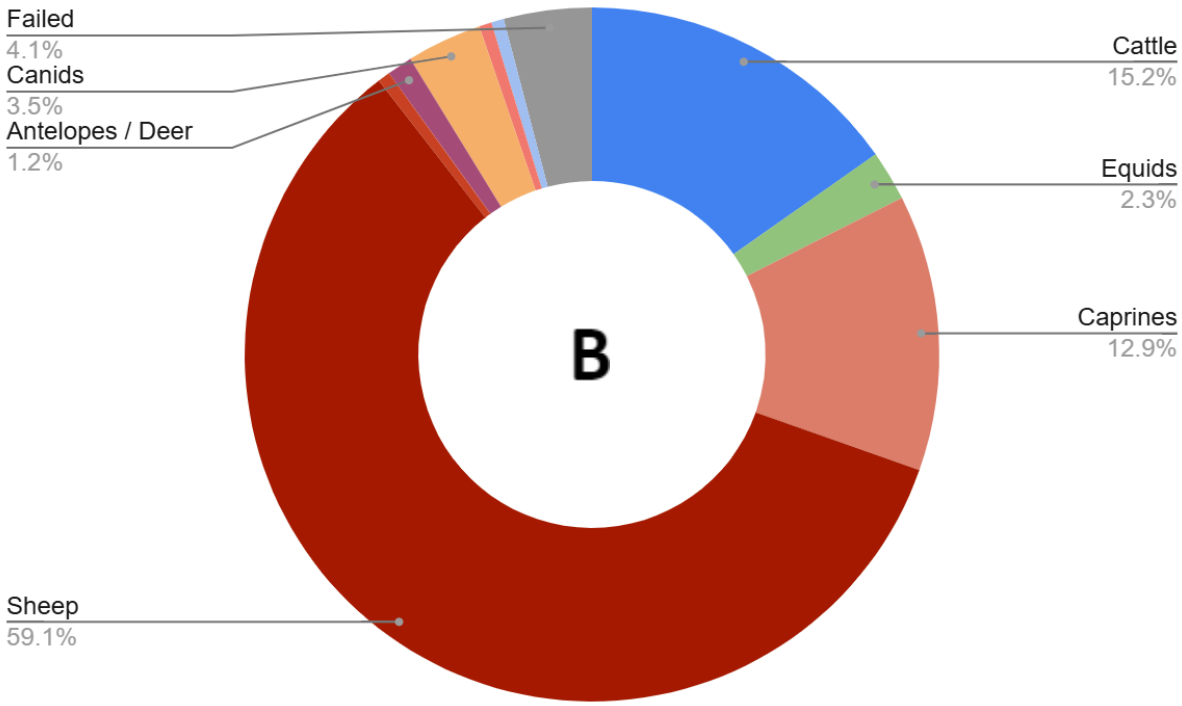
Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS228.A	1105.6	1180.7	1196.7	1427.8	1550.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.4	x
NZS231.A	1105.6	x	1196.7	1427.8	1550.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.4	x

Tbl.98 Table of tryptic masses identified in ambiguous caprine samples from Nizhnyaya Sooru.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS095.A	1105.6	1180.7	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	x	3017.5	x
NZS122.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	x
NZS139.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2793.4	2883.5	x	3017.4	x
NZS142.A	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.3	2882.	2899.4	3017.5	x
NZS153.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.5	2883.6	2899.6	3017.6	x
NZS158.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS160.A	1106.2	1181.3	1197.3	1428.5	1581.6	1649.7	2131.1	2791.2	2882	2900.8	3018.8	x
NZS162.A	1105.6	1180.6	1196.6	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.4	x
NZS183.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.1	x	2883.6	2899.6	3017.6	x
NZS187.A	1105.6	x	1196.6	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	x
NZS188.A	1105.6	1180.6	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS192.A	1105.6	1180.7	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS198.A	1105.6	1180.6	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS202.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.2	2792.5	2883.6	2899.6	3017.6	x
NZS203.A	1105.6	1180.7	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS208.A	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2898.4	3017.4	x
NZS212.A	1105.6	x	1196.7	1427.8	1580.8	1648.9	2131.1	x	2883.5	2899.5	3017.5	x
NZS214.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.2	2792.5	2883.6	2899.6	3017.6	x
NZS223.A	1105.6	1180.7	1196.6	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	x
NZS225.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS233.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.5	2883.6	2899.5	3017.5	x
NZS236.A	1106.1	x	x	1428.4	x	1649.6	2132	2793.4	2884.6	2900.6	3018.5	x

Fig.25 A) Bar graph of absolute ZooMS-based taxonomic determinations of faunal remains from Nizhnyaya Sooru & B) Pie chart of relative ZooMS-based taxonomic determinations of faunal remains from Nizhnyaya Sooru.





21.3.2. ZKG513-1

For all archaeological layers, I was able to use ZooMS to taxonomically identify ZK513-1 samples with sufficient collagen preservation (n=102) (Fig.26; Tbl.99; see Appendix 03). My ZooMS analysis of the ZK513-1 fauna found *Ovis* sp. to be the dominant taxa of the samples selected, in contrast with the "*Ovis aries / Capra hircus*" dominance reflected in the respective zooarchaeological analysis (Fig.26; Tbl.98). I was not able to use ZooMS to distinguish 6 samples beyond "*Ovis* sp. / *Capra* sp.", do to the loss of the α2 757 (+16) peptide marker (Tbl.100). As *Saiga* sp. and *Bison* sp. are not known to be present in the faunal ecology of Zuunkhangai, I used the consensus taxonomic groupings "*Cervus* sp. */ Gazella* sp." and "*Bos* sp." in place of "*Cervus* sp. */ Gazella* sp. */ Saiga* sp." and "*Bos* sp. / *Bison* sp." (respectively). My results are in general agreement with the faunal report in the published manuscript (i.e. Houle et al. 2022), even though they are representative of only a subselection of animal bone fragments that could not be identified to a high-resolution taxonomic group.

Tbl.99 Table of ZooMS-based identifications of samples selected from Trench ZK513-1.

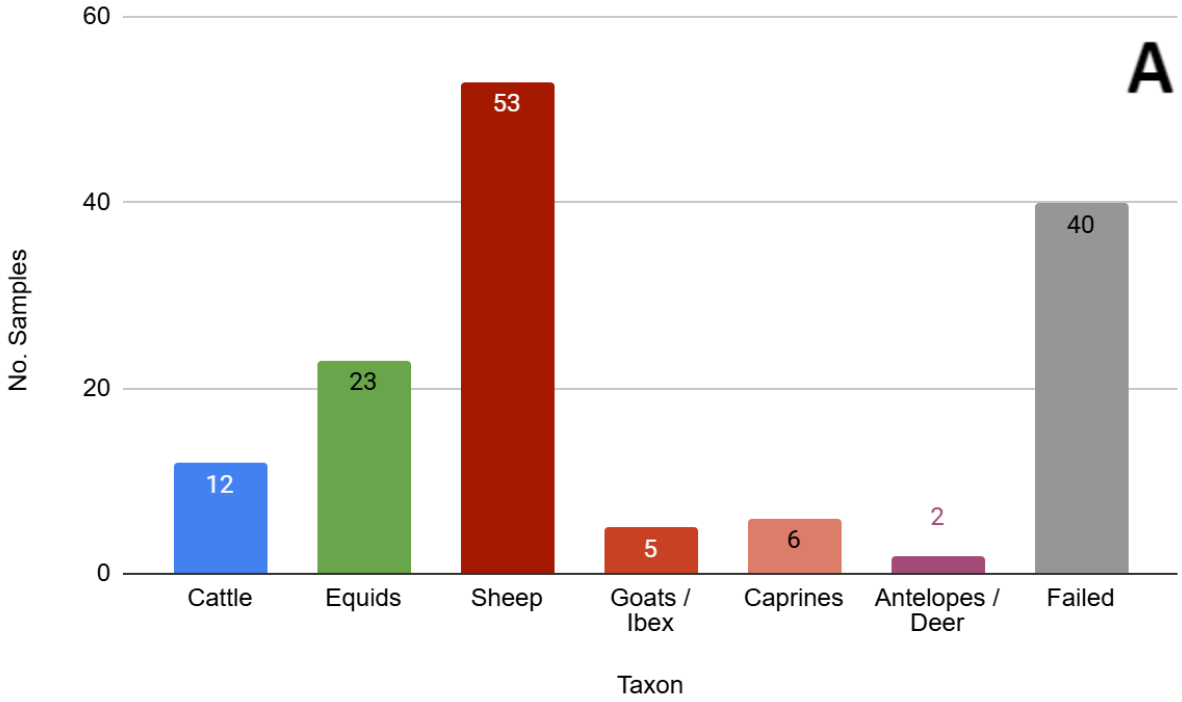
ZooMS-Based ID	Inferred Taxon	No. Samples
Bos sp.	Cattle	12
Capra sp.	Goats / Ibex	5
Cervus sp. */ Gazella* sp.	Antelopes / Deer	2
Equus sp.	Equids	23
Ovis sp.	Sheep	53
Ovis sp. / *Capra* sp.	Caprines	6
Failed		40
TOTAL		142

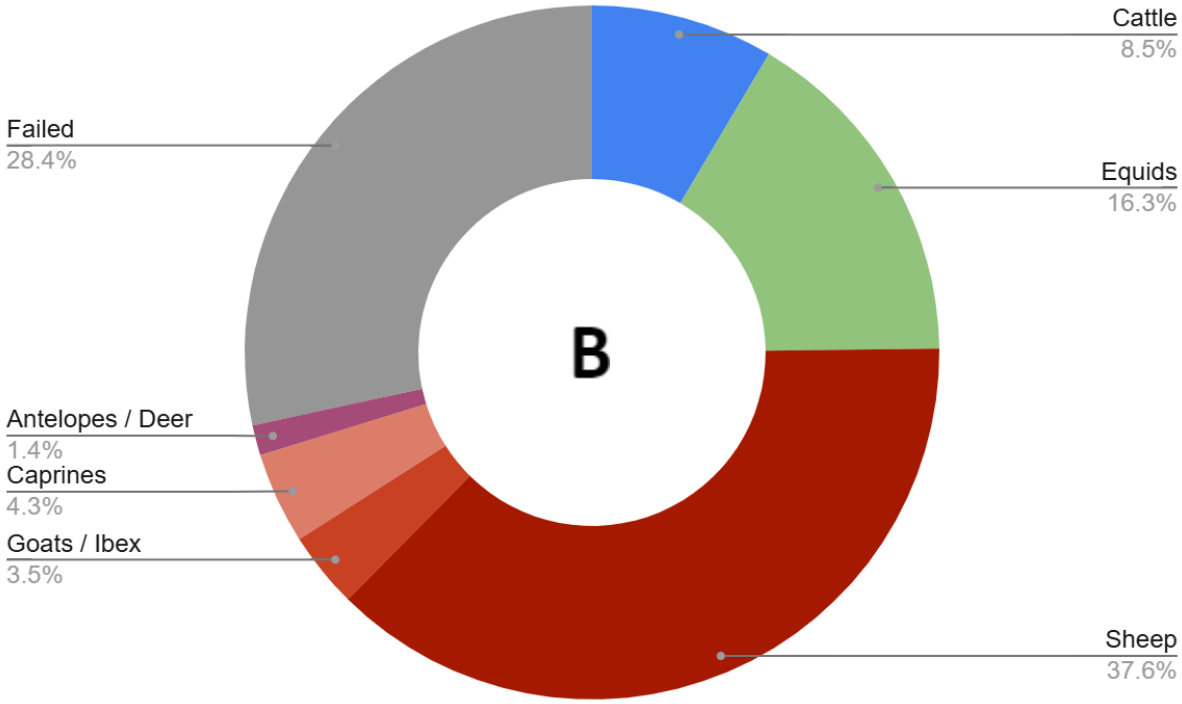
**Sample ZKG065.A was determined to be a rock and is thus not included in the sample count.*

Tbl.100 Table of tryptic masses identified in ambiguous caprine samples from Trench ZK513-1.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
ZKG021	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.3	2883.4	2899.4	3017.4	x
ZKG030	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	x
ZKG045	1105.6	1180.7	x	1427.8	1580.9	1648.9	2131.2	2792.4	x	x	3018.5	x
ZKG046	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.4	x
ZKG094	1105.7	1180.7	1196.7	1427.9	1580.9	1649	x	x	2883.7	2899.7	3017.7	x
ZKG137	1105.6	1180.6	1196.7	1427.8	1580.8	1648.9	x	2792.4	2883.5	2899.5	3018.4	x

Fig.26 A) Bar graph of absolute ZooMS-based taxonomic determinations of faunal remains from ZK513-1 & B) Pie chart of relative ZooMS-based taxonomic determinations of faunal remains from ZK513-1.





21.3.3. Tashbulak

My ZooMS-based taxonomic identifications of the selected Tashbulak samples (n=331) included *Ovis* sp., *Capra* sp., *Ovis sp. / Capra sp.*, *Bos* sp. / *Bison* sp., *Equus* sp., *Camelus* sp., *Cervus* sp / *Gazella* sp. / *Saiga* sp., *Canis* sp. / *Vulpes* sp., and *Testudo* sp. (Tbl.101, Fig.27; see Appendix 03). Bison are not known to have been present in Central Asia (see Chapters 02, 06), so all samples whose MS spectra are diagnostic of *Bos* sp. / *Bison* sp. should be considered to be *Bos* sp. (either *Bos taurus* or *Bos grunniens*; aurochsen were extinct by the Medieval period). I was unable to discern the genus of 10 caprine samples (out of 162) which did not retain the diagnostic α2 757 peptide marker, and could only identify them as *Ovis* sp. / *Capra* sp. (Tbl.102). I identified a single specimen that could not be *Caprelous* sp. due to the tryptic mass of its α2 757 peptide marker that could be either *Cervus* sp., *Gazelle* sp., or *Saiga* sp. (Tbl.101).

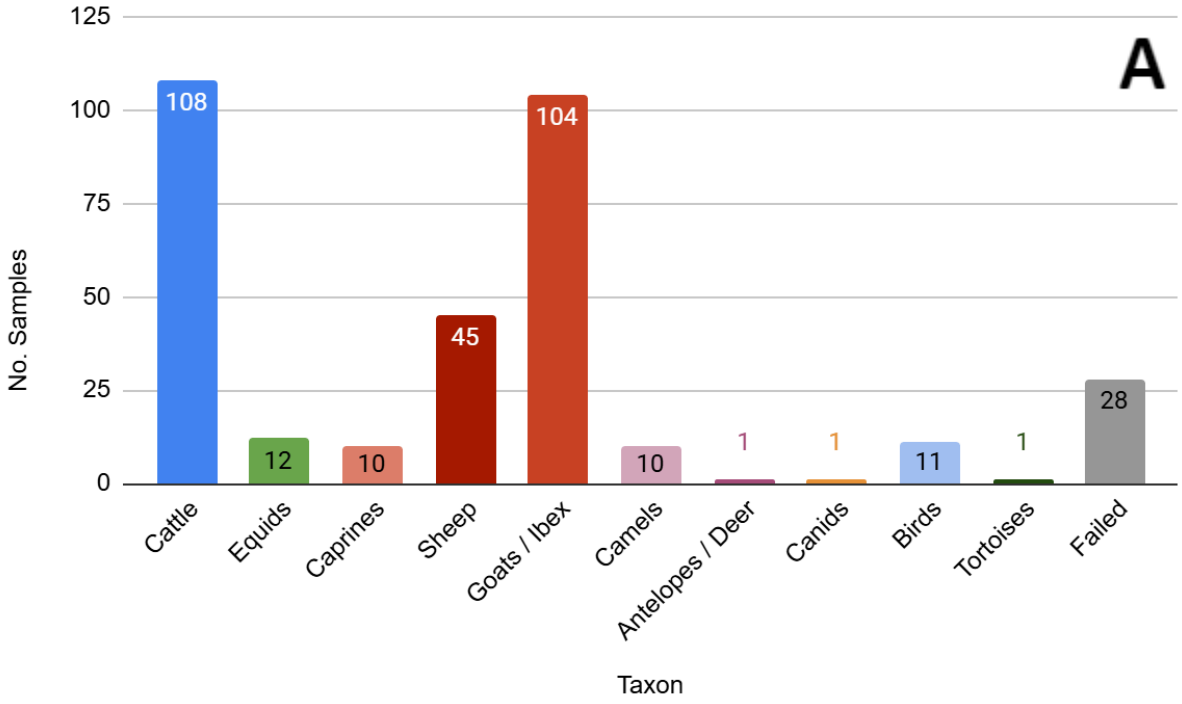
Tbl.101 Table of ZooMS-based identifications of samples selected from Tashbulak.

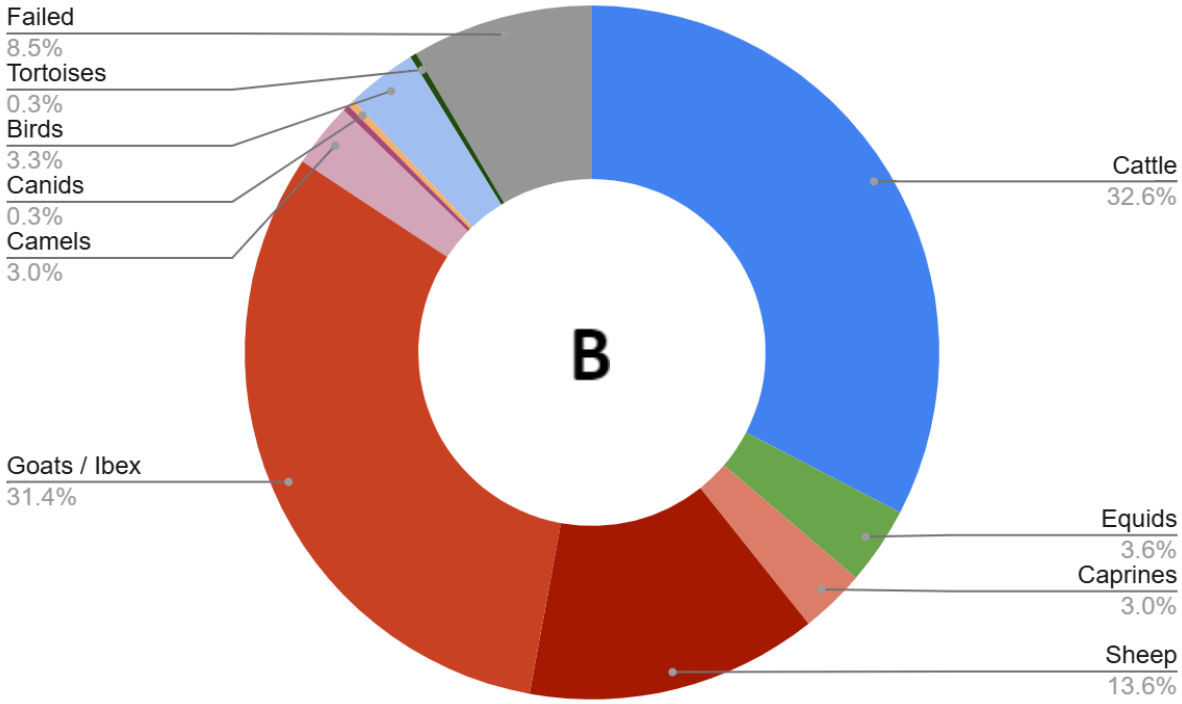
ZooMS-Based ID	Inferred Taxon	No. Samples
Bos sp.	Cattle	108
Equus sp.	Equids	12
Ovis sp. / *Capra* sp.	Caprines	10
Ovis sp.	Sheep	45
Capra sp.	Goats / Ibex	104
Camelus sp.	Camels	10
Canis sp. / *Vulpes* sp.	Canids	1
Cervus sp. / *Gazella* sp. / *Saiga* sp.	Antelopes / Deer	1
Testudo sp.	Tortoises	1
Aves sp.	Birds	11
Failed		28
TOTAL		331

Tbl.102 Table of tryptic masses identified in ambiguous caprine samples from Tashbulak.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
TBK043.A	1105.6	1180.6	1196.7	1427.8	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	x
TBK093.A	1105.6	1180.7	1196.7	1427.9	1581	1649	x	2792	2883	2899	3017.8	x
TBK137.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.8	2131.1	2792.3	2883.5	2899.5	3017.4	x
TBK166.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	x
TBK186.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	x
TBK199.A	1105.6	x	1196.7	1427.7	1580.8	1648.8	2131.1	x	2883.4	x	3017.4	x
TBK206.A	1105.6	1180.6	1196.7	1427.8	1580.8	1648.9	x	2792.3	2883.4	2899.4	3017.3	x
TBK207.A	1105.6	1180.6	1196.7	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.3	x
TBK283.A	1105.6	x	1197	1428.2	1581.3	1649.3	2131.7	2793.1	2884.2	2900.2	3018.2	x
TBK339.A	1106.1	1180.1	1197.2	1428.3	1581.4	1649.5	2131.9	2793.3	x	2900.4	3018.4	x

Fig.27 A) Bar graph of absolute ZooMS-based taxonomic determinations of faunal remains from Tashbulak & B) Pie chart of relative ZooMS-based taxonomic determinations of faunal remains from Tashbulak.



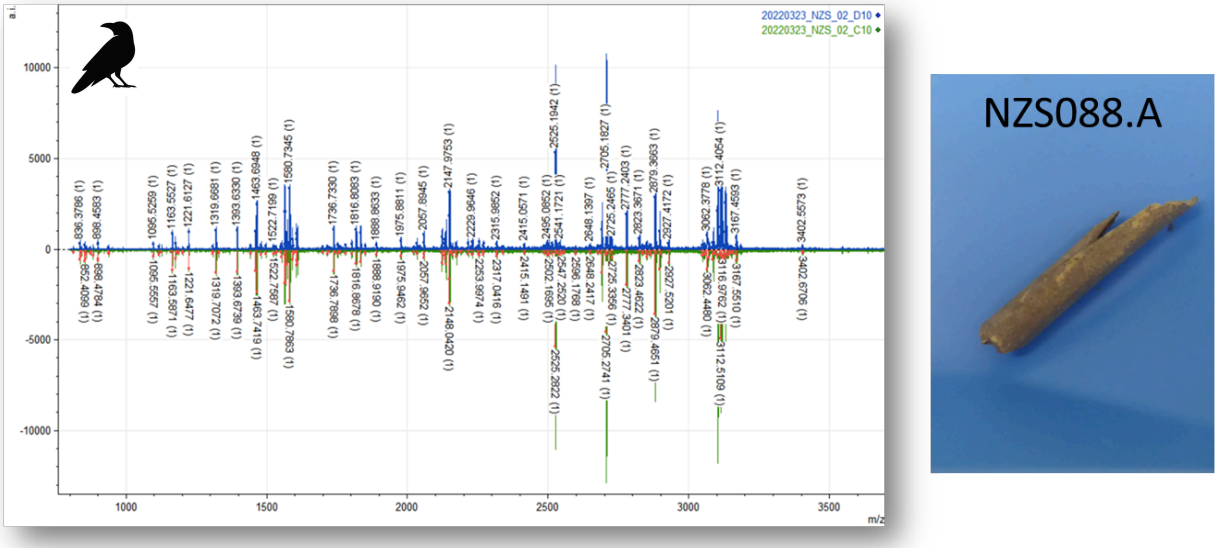


21.4. Proteomic Taxonomic Identification (Less Common Taxa)

21.4.1. Avifauna

Sample NZS088.A from Nizhnyaya Sooru was morphologically identified as “Aves” and although this sample produced a high quality MALDI spectrum (Fig.28; see Appendix 03), there are currently no published Eurasian bird markers to compare it with. Based on the peptide markers that have been developed for North American avian collagen (Codlin et al. 2022), the collagen signature is indicative of a corvid (Tbl.103)– possibly raven (*Corvus corax*), rook (*Corvus frugilegus*), carrion crow (*Corvus corone*), or Eurasian jackdaw (*Coloeus monedula*). Ten samples from Tashbulak (TBK236.A– 246.A, TBK248.A) were also morphologically identified as broadly avian, and these identifications were confirmed by my ZooMS results (Tbl.104; see Appendix 03). I identified 9 galliformes from Tashbulak which are likely chicken (*Gallus gallus*), considering the presence of chicken eggshells at the site (Peters et al. 2024), but could also be partridge (*Perdix perdix*, *Alectoris chukar, Perdix dauurica*), quail (*Coturnix coturnix*), grouse (*Lyrurus tetrix, Tetrastes bonaisia*), or pheasant (*Phasianus colchicus*) (Fig.29). I also identified a single gruiform (TBK237.A) amongst the Tashbulak samples, possibly a common moorhen (*Gallinula chloropus*) or Siberian crane (*Leucogeranus leucogeranus*) (Tbl.104; Fig.30).

Fig.28 Mirrored MALDI spectra of avian, likely corvid, collagen (NZS088.A) from Nizhnyaya Sooru.

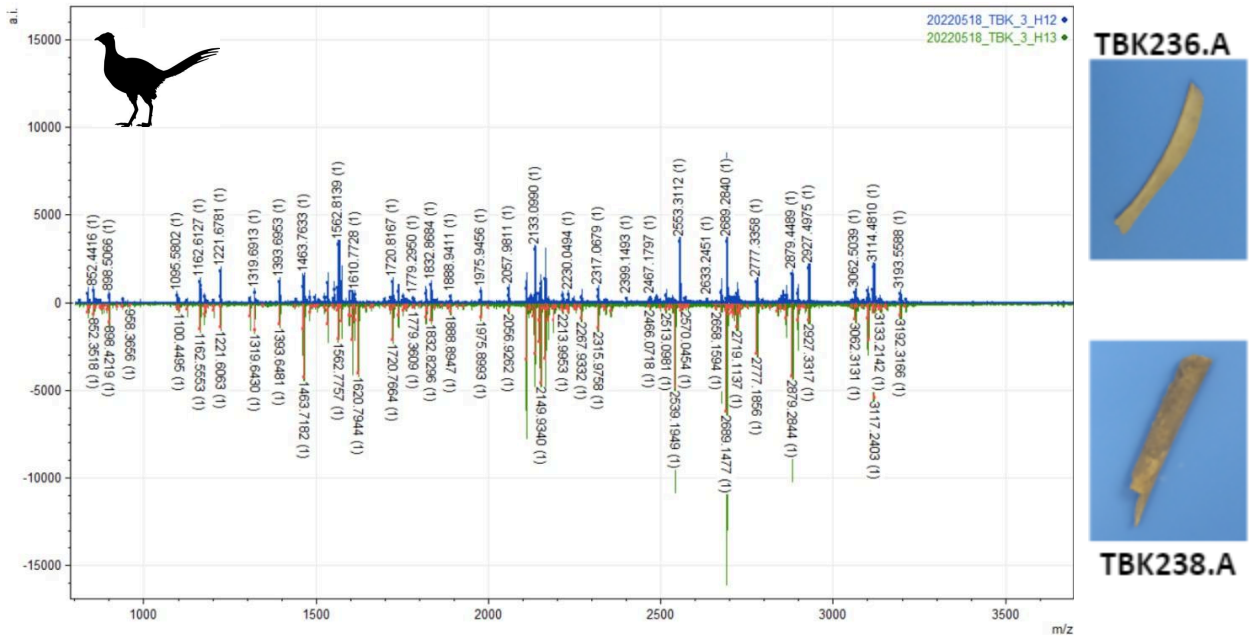


Tbl.103 Table of tryptic masses of raven, chicken, and common gallinule (Codlin et al. 2022; Eda et al. 2020).

Species	α2 978	α2 604	α2 502	α2 889	α2 889 (+16)	α2 175	α2 292	α2 625	α2 625	α2 658	α2 454	α1 586	α2 10	α2 10 (+16)	α2 520	α2 520 (+16)
Corvus corvax	1220.6	1221.6	1552.8	x	1580.8	1603.8	1608.8	2135	2493.2	2525.3	3166.5	2927.5	3111.4	3127.4	3166.5	3182.4
Gallus gallus	1220.6	1221.6	1594.8	1604.8	1620.8	1603.8	1609.7	2108	x	2539.3	2777.3	2927.5	3097.4	3113.4	3192.5	3208.5
Gallinula galeata	1220.6	1221.6	1578.8	1578.8	1594.8	1589.8	1609.7	2108	2466.2	2497.2	2804.3	2985.5	3097.4	3113.4	3152.4	3168.4

**Marker α2 625 is represented twice in the York ZooMS Marker Database and the original publications; m/z 1578.8 is listed twice for two separate markers in Gallinula galeata in the York ZooMS Marker Database and the original publications.*

Fig.29 Mirrored MALDI spectra of galliform samples (TBK236.A & TBK238.A) from Tashbulak.

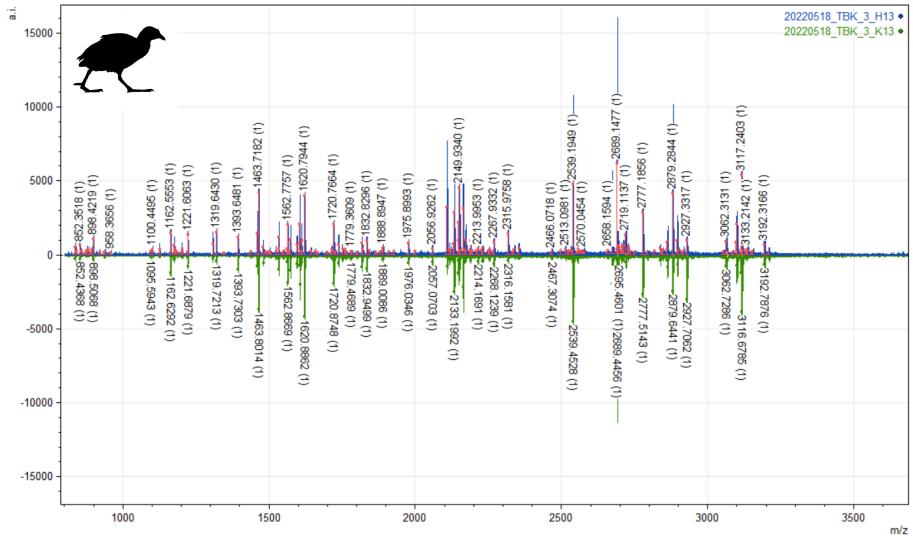


Tbl.104 Table of tryptic masses identified in avifauna samples from Nizhnyaya Sooru and Tashbulak.

Sample No.	α2 978	α2 604	α2 502	α2 889	α2 889 (+16)	α2 175	α2 292	α2 625	α2 625	α2 658	α2 454	α1 586	α2 10	α2 10 (+16)	α2 520	α2 520 (+16)
NZS088.A	1220.6	1221.6	1552.7	x	1580.7	1603.8	1608.7	2135.9	2494.1	2525.2	2777.2	2927.4	3111.4	3127.4	3166.5	3183.4
TBK236.A	1220.7	1221.7	1594.8	1604.8	x	1603.9	1609.8	2108	x	x	2777.4	2927.5	3097.5	3113.5	3192.6	3209.6
TBK237.A	1220.6	1221.6	1594.8	1604.8	1620.8	1603.8	1609.8	2108	x	2539.2	2777.2	2927.3	3097.3	3113,5	3192.3	3208.3
TBK238.A	1220.7	1221.6	1578.9	1578.9	x	x	x	2108	2466.2	2497.2	2804.3	x	3097.4	3113.4	x	x
TBK239.A	1220.7	1221.7	1594.8	1604.8	x	1603.8	1609.8	2108	x	x	2777.3	2927.5	3097.5	3113.4	3192.5	3208.5
TBK240.A	1220.7	1221.7	1594.9	1604.9	x	1603.9	1609.8	2108	x	x	2777.3	x	3097.5	3113.5	3192.6	3208.6
TBK241.A	1220.7	1221.6	1594.8	1604.8	x	1603.8	1609.8	2108	2466.1	2497.2	2777.3	2927.5	3097.5	3113.5	3192.5	3208.5
TBK242.A	1220.6	1201.6	1594.9	1604.9	x	1603.9	1609.8	2108.1	2466.2	2497.3	2777.4	2927.7	3097.7	3113.6	3192.7	3290.7
TBK243.A	1220.7	1221.7	1594.9	1604.9	x	1603.9	1609.8	2108.1	2466.2	2497.3	2777.4	2927.6	3097.7	3113.6	3192.7	3209.7
TBK244.A	1220.7	1221.6	1549.8	1604.8	1620.8	1603.8	1609.7	2108	2466.1	2497.2	2777.3	2927.5	3097.5	3113.5	3192.6	3209.6
TBK245.A	1220.7	1221.7	1549.8	1604.9	x	1603.9	1609.8	2108	2466.2	2497.2	2777.4	2927.6	3097.5	3113.6	3192.6	3208.6
TBK246.A	1220.7	1221.7	1549.8	1604.9	x	1603.8	1609.8	2108	x	x	2777.3	2927.5	3097.4	3114.4	3192.5	x
TBK248.A	1220.6	1221.6	1549.8	1604.8	1620.8	1603.8	1609.8	2108	2466.1	2496.2	2777.2	2927.4	3097.3	3113.4	3192.4	3208.4

**Marker α2 625 is represented twice in the York ZooMS Marker Database and the original publications.*

Fig.30 Mirrored MALDI spectra of gruiform sample (TBK237.A) from Tashbulak.



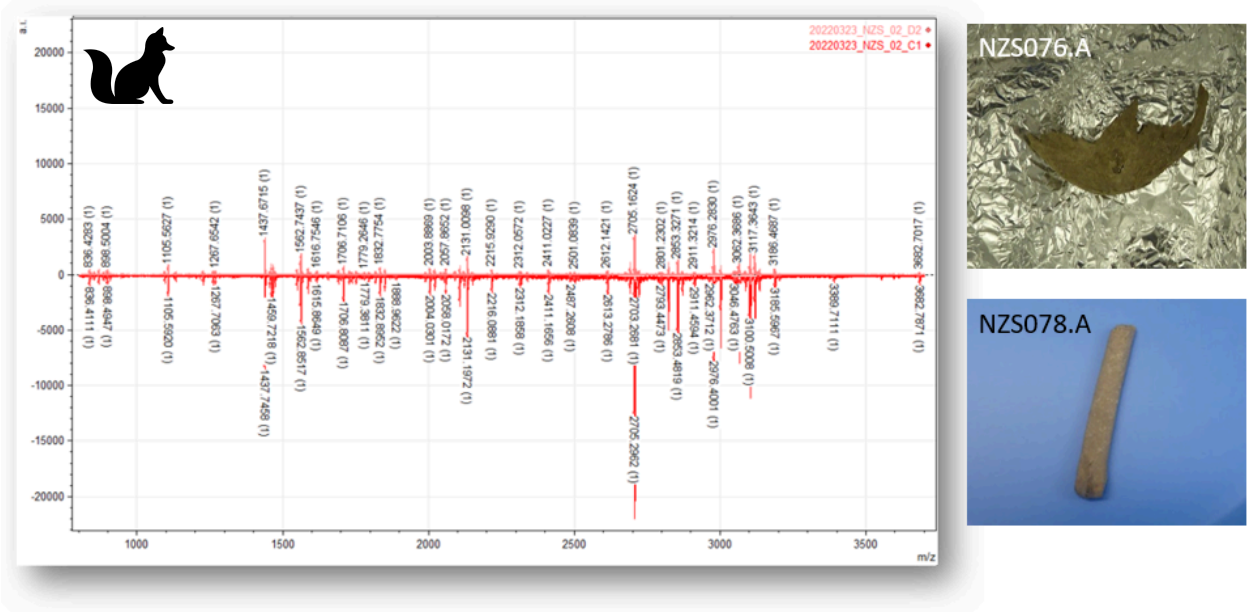
21.4.2. Canids

I identified 6 samples from Nizhnyaya Sooru as canids that could not be further distinguished beyond *Canis* sp. / *Vulpes* sp., but could not be red fox (*Vulpes vulpes*) based on the measured tryptic masses of the α2 484 peptide marker (Tbl.105; see Appendix 03). There are currently no published peptide markers for corsac fox (*Vulpes korsac*) to compare these spectra with. Samples NZS076.A and NZS078.A produced MALDI spectra with isotopic peak distributions at both *m/z* 1437.7 and *m/z* 1457.7 (Fig.31), which are supposed to be individually diagnostic of different species of canids (Buckley et al. 2017). The MALDI spectra of these two samples raise questions as to how reliable the markers published for canids actually are. I also identified a single canid specimen from Tashbulak (TBK337.A), though this sample only retained six collagen peptide markers and could not be identified beyond *Canis* sp. (Tbl.105; see Appendix 03).

Tbl.105 Table of tryptic masses identified in canid samples from Nizhnyaya Sooru & Tashbulak.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS060.A	1105.6	x	1226.7	1453.8	1566.8	x	2131.2	2820.5	2853.5	2869.5	x	2999.6
NZS069.A	1105.6	1210.6?	1226.7	1453.8	1566.8	x	2131.1	2820.5	2853.5	2869.5	x	2999.6
NZS071.A	1105.6	1210.7	1226.7	1453.8	1566.8	x	2131.2	2820.4	2853.5	2869.5	x	2999.4?
NZS076.A	1105.6	x	1226.7	1437.8, 1453.7	1566.8	x	2131.1	2820.4	2853.5	2869.5	x	x
NZS078.A	1105.6	x	1226.7	1437.8, 1453.8	1566.8	x	2131.2	2820.5	2853.5	2869.5	x	2999.8
NZS084.A	1105.6	x	1226.7	1453.8	x	x	2131.2	2820.4	2853.5	2869.5	2853.5	2999.6
TBK337.A	1106.1	x	x	1454.4	x	x	2131.9	2821.4	2854.4	x	x	3000.6

Fig.31 Mirrored MALDI spectra of two canid samples (NZS076.A & NZS078.A) from Nizhnyaya Sooru.



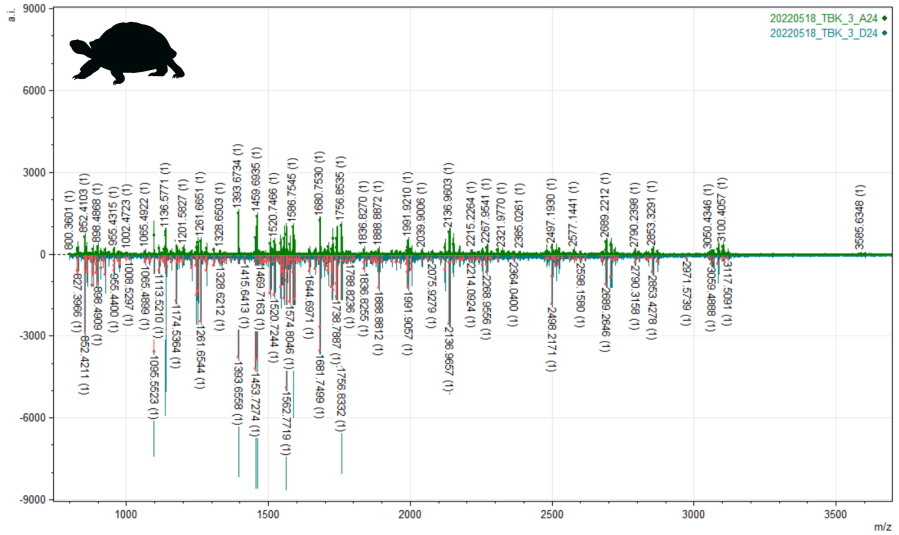
21.4.3. Reptiles

I analyzed a single sample that was morphologically identified as a reptile (TBK118.A; see Appendix 03), specifically “Testudo”. That this sample originated from a tortoise is not in question. The specimen is a fragment of a tortoise plastron (Fig.32), almost certainly from the Central Asian tortoise (*Testudo horsfieldii*), though it is not possible to confirm as much with ZooMS. Although there is a notable lack of published collagen peptide biomarkers for Central Asian reptiles, there are a number of published markers for different species of turtles (de Kock et al. 2023; Harvey et al. 2019). By comparing these markers with the tryptic masses of TBK118.A (Fig.32) I was able to verify a strong similarity between turtle markers and tortoise markers (Tbl.106), with differences at markers α2 978, α2 793, α2 733, α2 658, α2 757, and α2 10. It is possible that this tortoise shares the α1 713 marker with green turtle (*Chelonia mydas*) and the α1 713 marker with leatherback turtle (*Dermochelys coriacea*) (Tbl.107), though in both cases the isotopic peaks on the MALDI spectra of TBK118.A were very small. There is a stronger case for TBK118.A sharing tryptic masses (*m/z* 2853.3, *m/z* 2869.4) with the α1 586 / α1 586+16 markers of leatherback turtles (Tbl.107). LC-MS/MS analysis would be necessary to verify any markers for this tortoise, which has only been identified as *Testudo horsfieldii* by its archaeological context.

Tbl.106 Table of tryptic masses identified in a testudine sample from Tashbulak.

Sample No.	α1 508	α1 309	α2 484	α1 688	α1 889	α1 289	α1 893	α2 393	α1 713	α1 934	α2 454	α1 586	α1 586 (+16)
TBK118.A	1136.	1393.7	1453.7	1459.7	1491.7?	1573.7	1934.9	2105?	2598.1?	2705.2	2790.2	2853.3	2869.4

Fig.32 Mirrored MALDI spectra of a testudine sample (TBK118.A) from Tashbulak.



Tbl.107 Table of published turtle markers (de Kock et al. 2023; Harvey et al. 2019) and TBK118.A markers.

Markers	*C. caretta*	*C. mydas*	*D. coriacea*	*E. imbricata*	*L. kempii*	*L. olivacea*	*N. depressus*	TBK118.A
α2 393	881.9	920	x	x	x	x	x	?
α1 508	1136.5	1136.5	1136.5	1136.5	1152.6	1152.6	1136.5	1136.6
α2 978	1220.7	1220.7	1220.7	1220.7	1220.7	1220.7	1220.7	x
α2 978 (+16)	1236.7	1236.7	1236.7	1236.7	1236.7	1236.7	1236.7	x
α2 574	1355.5	1327.4	x	x	x	x	x	?
α1 309	1393.7	1393.7	1393.7	1393.7	1393.7	1393.7	1393.7	1393.7
α2 484	1453.7	1453.7	1453.7	1443.7	1453.7	1453.7	1453.7	1453.7
α1 688	1459.7	1459.7	1459.7	1459.7	1459.7	1459.7	1459.7	1459.7
α1 889	1490.7	1516.7	1490.7	1490.7	1490.7	1490.7	1490.7	1491.7?
α1 289	1572.7	1572.7	1572.7	1572.7	1572.7	1572.7	1572.7	1573.7
α1 324	1717.8	1731.8	x	x	x	x	x	?
α1 825	1742.9	1768.9	x	x	x	x	x	?
α1 893	1934.0	1960.0	x	x	x	x	x	1934.9
α2 793	2097.0	2097.0	2125	2097.0	2097.0	2097.0	2107.0	x
α2 393	2066.2	2104.3	x	x	x	x	x	2105?
α2 733	2341.1	2353.1	2311.1	2341.1	2341.1	2341.1	2341.1	x
α2 658	2455.3	2455.3	2510.3	2485.3	2455.3	2455.3	2455.3	x
α1 713	2612.8	2598.8	x	x	x	x	x	2598.1?
α1 934	2705.4	2705.4	2705.4	2705.4	2705.4	2705.4	2705.4	2705.2
α2 454	2790.3	2790.3	2790.3	2790.3	2790.3	2790.3	2790.3	2790.2
α1 586	2869.3	2843.3	2853.3	2843.3	2843.3	2843.3	2869.3	2853.3
α1 586 (+16)	2885.3	2859.3	2869.3	2859.3	2859.3	2859.3	2885.3	2869.4
α2 757	2929.5	2929.5	2929.5	2929.5	2929.5	2929.5	2929.5	x
α2 757 (+16)	2945.5	2945.5	2945.5	2945.5	2945.5	2945.5	2945.5	x
α2 10	3007.4	3007.4	3007.4	3007.4	3007.4	3007.4	3007.4	x

21.5. Proteomic Identification of Morphologically Indeterminate Specimens

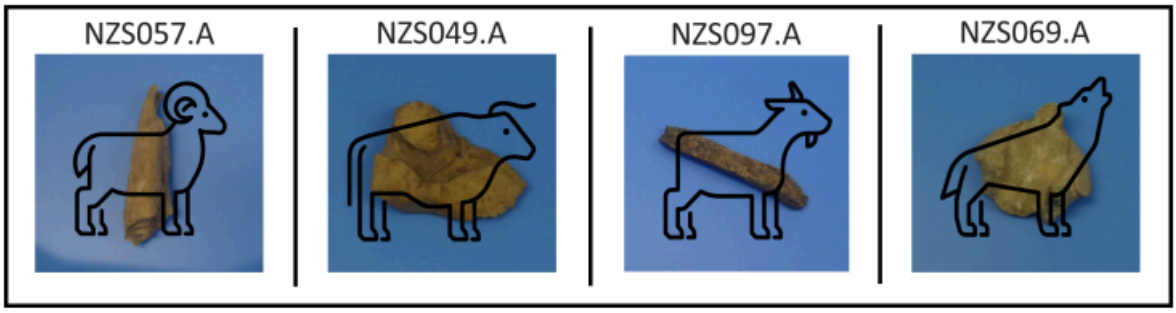
21.5.1. Nizhnyaya Sooru

I was able to use ZooMS to taxonomically identify all 12 samples selected from Nizhnyaya Sooru that could not be identified to a taxonomic group by morphological analysis (Tbls.108–109; Fig.33; see Appendix 03).

Tbl.108 Table of ZooMS-based identifications of indeterminate samples from Nizhnyaya Sooru.

Zooarch ID	ZooMS Identification	Sample No.
Indeterminate	*Bos* sp.	NZS052.A, NZS098.A, NZS219.A
Indeterminate	*Canis* sp. / *Vulpes* sp.	NZS069.A
Indeterminate	*Ovis* sp.	NZS055.A, NZS093.A, NZS204.A, NZS218.A, NZS229.A
Indeterminate	*Ovis* sp. / *Capra* sp.	NZS233.A, NZS236.A

Fig.33 Pictures of four morphologically indeterminate samples from Nizhnyaya Sooru that have been taxonomically identified using ZooMS.



Tbl.109 Table of tryptic masses of NZS samples which could not be assigned morphological identifications.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS049.A	1105.6	1192.7	1208.7	1427.8	1580.9	1648.9	2131.1	2791.9	2852.9	2868.9	3017.7	3032.8
NZS052.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.2	2853.3	2869.3	3017.2	x
NZS055.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	3033.6
NZS057.A	1105.6	x	x	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.3	3033.5
NZS069.A	1105.6	x	1226.7	1453.8	1566.8	x	2131.1	2820.5	2853.3	2869.5	x	2999.6
NZS093.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	3033.6
NZS097.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	3093.6
NZS098.A	1105.6	1182.6	1208.6	1427.7	1580.7	1648.8	2131.1	2792.2	2853.3	x	3017.2	3033.5
NZS127.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.3	2883.4	2899.4	3017.4	3033.5
NZS218.A	1105.6	1182.6	1192.7	1208.7	1580.8	1648.9	2131.2	2792.5	2853.5	2869.6	3017.5	3033.7
NZS219.A	1105.6	1192.7	1208.7	1427.8	1580.8	1648.9	2131.2	2792.5	2853.6	2869.6	3017.6	x
NZS229.A	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.4	3017.4	3033.5

21.5.2. ZK513-1

I was able to use ZooMS to taxonomically identify 64 out of 101 samples selected from ZK513-1 that could not be identified to a taxonomic group by morphological analysis (Tbl.110; see Appendix 03).

Tbl.110 Table of ZooMS-based identifications of indeterminate samples from Trench ZK513-1.

Zooarch ID	ZooMS-Based Identification	No. Samples
Indeterminate	*Bos* sp.	10
Indeterminate	*Cervus* sp. / *Gazella* sp. / *Saiga* sp.	2
Indeterminate	*Ovis* sp.	43
Indeterminate	*Capra* sp.	4
Indeterminate	*Ovis* sp. / *Capra* sp.	5
Indeterminate	Indeterminate	46

21.5.3. Tashbulak

I was able to use ZooMS to taxonomically identify 18 out of 20 samples selected from the Tashbulak faunal assemblage that could not be attributed to any taxonomic group by robust zooarchaeological analysis (Tbl.111; see Appendix 03). I identified the majority of the morphologically non-diagnostic samples as *Bos* sp., though I also identified caprids and equids (Tbl.112). I was also able to use ZooMS to successfully attribute a taxonomic group to samples from Tashbulak that had only been attributed to tentative morphological identifications and broad size-based identifications. Additionally, my ZooMS analysis clarified many of the ambiguous identifications of caprine / cervid / gazelle and revealed the misidentification of a number of samples.

Tbl.111 Table numbering the ZooMS-based identifications of indeterminate samples from Tashbulak.

Zooarch ID	ZooMS-Based Identification	No. Samples
Indeterminate	*Bos* sp.	13
Indeterminate	*Equus* sp.	2
Indeterminate	*Capra* sp.	3

Tbl.112 Table of tryptic masses of morphologically indeterminate samples from Tashbulak.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
TBK005.A	1105.6	1182.6	1198.6	1427.8	1550.8	1649.8	2145.2	2820.4	2883.5	x	x	2999.6
TBK011.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.4	2853.5	2869.4	3017.4	3033.5
TBK028.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.4	3033.5
TBK057.A	1105.6	1182.6	1198.6	1427.8	1550.9	1649.9	2145.1	2819.9	2882.8	x	x	2999
TBK063.A	1105.6	1192.6	1208.7	1427.7	1580.7	1648.8	2131.1	2792.3	2853.4	2869.4	3017.3	3033.4
TBK073.A	1105.6	1192.7	1208.7	1427.8	1580.8	1648.9	2131.2	2792.5	2853.5	2869.5	3017.5	3033.6
TBK097.A	1105.6	x	x	1427.7	1580.7	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	3093.5
TBK098.A	x	x	x	x	x	x	x	x	x	x	x	x
TBK099.A	1105.6	1180.6	1196.6	1427.7	1580.7	1648.8	2131	2792.2	2883.3	2899.3	3017.3	3093.4
TBK112.A	x	x	x	x	x	x	x	x	x	x	x	x
TBK111.A	1105.6	x	1196.6	1427.7	1580.7	1648.8	2131	2792.2	2883.3	2899.3	3017.3	3093.4
TBK139.A	1105.6	1192.7	1208.7	1427.8	1580.8	1648.9	2131.2	2792.3	2853.5	2869.5	3017.5	3033.6
TBK141.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.4	3033.5
TBK143.A	1105.6	1192.6	1208.6	1427.7	1580.7	1648.8	2131	2792.2	2853.3	2869.3	3017.3	3033.4
TBK146.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.3	3033.5
TBK201.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.4	2853.5	2869.5	3017.5	3033.6
TBK203.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.3	3033.4
TBK222.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.4	3033.5
TBK232.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.4	x
TBK327.A	1106	x	x	1428.3	1581.4	1649.4	2131.9	2793.3	2854.4	2870.4	3018.4	x

21.6. Proteomic Identification of Tentative Morphological Identifications

21.6.1. Nizhnyaya Sooru

I was able to use ZooMS to secure identifications for 97% of the samples (n=31) that had only been attributed tentative morphological identifications, due to heavy fragmentation and taphonomic damage (Tbl.113; see Appendix 03). In the course of my analysis, I discovered that the ZooMS-based identifications of 4 of these samples were not consistent with the tentative morphological identifications (Fig.34; Tbls.113–115). I determined that sample NZS068.A, recorded as “Dog?”, was in fact *Ovis* sp. based upon the presence of tryptic masses 1196.7, 1427.8, 1580.8, 1648.9, 2883.6, 3017.5, and 3033.7 (Tbl.115.A). I also determined sample NZS090.A, recorded as “Aves?”, and sample NZS092.A, recorded as “Percidae?”, to both be *Ovis* sp. based on all tryptic masses detected by MALDI (Tbl.115.A). Finally, I determined that sample NZS225.A, recorded as “Capreolus?”, was actually *Ovis* sp. / *Capra* sp. based upon the presence of tryptic mass 1580.8 at the α2 502 marker. Sample NZS058.A did not retain enough markers for identification (Tbl.114).

Tbl.113 Table of ZooMS-based identifications of tentatively identified samples from Nizhnyaya Sooru.

Zooarch ID	ZooMS-Based ID	Sample No.	No. Samples
Bos?	*Bos* sp.	NZS062.A, NZS143.A	2
Canis?	*Canis* sp. / *Vulpes* sp.	NZS084.A	1
Capra?	*Ovis* sp.	NZS163.A, NZS168.A, NZS169.A, NZS199.A, NZS200.A	5
	Ovis sp. / *Capra* sp.	NZS198.A	1
Capra / Ibex?	*Ovis* sp. / *Capra* sp.	NZS212.A	1
Capreolus?	*Ovis* sp. / *Capra* sp.	NZS225.A	1
Cervus?	*Bos* sp.	NZS051.A	1
Dog?	*Ovis* sp.	NZS068.A	1
Lepus?	*Lepus* sp.	NZS080.A	1
Ovis / Capra?	*Ovis* sp.	NZS102.A	1
Ovis?	*Ovis* sp.	NZS159.A, NZS164.A, NZS165.A, NZS201.A, NZS205.A, NZS209.A, NZS217.A, NZS224.A	8
	Ovis sp. / *Capra* sp.	NZS139.A, NZS142.A, NZS160.A, NZS162.A, NZS187.A, NZS203.A, NZS208.A	7
Percidae?	*Ovis* sp.	NZS092.A	1
Vulpes?	*Canis* sp. / *Vulpes* sp.	NZS076.A	1

**Sample No. NZS058.A was morphologically identified as “Ovis / Capra?”, but did not retain enough collagen preservation for a ZooMS-based identification.*

Tbl.114 Table of tryptic masses of sample NZS058.A, morphologically identified as “Ovis / Capra?”.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS058.A	1105.7	x	x	x	x	x	x	x	x	x	x	x

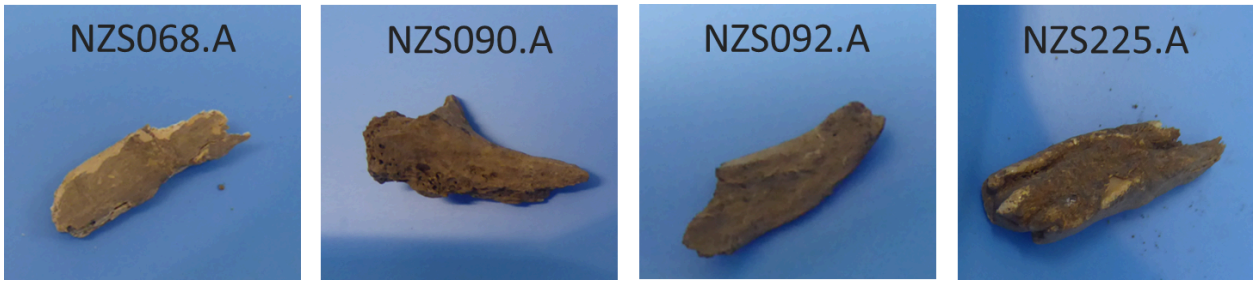


Fig.34 Photos of four NZS samples with conflicting ZooMS-based and morphological identifications, including samples misattributed as "Aves?" (NZS090.A) and "Percidae?" (NZS092.A).

Tbl.115 Table of tryptic masses of NZS samples with conflicting ZooMS-based & tentative morphological IDs.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS068.A	1105.6	x	1196.7	1427.8	1580.8	1648.9	2131.2	x	2883.6	2899.6	3017.5	3033.7
NZS090.A	1105.6	x	1196.7	1427.8	1580.8	1648.9	2131.2	x	2883.6	2899.6	3017.5	3033.7
NZS092.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.2	x	2883.5	2899.5	3017.5	3033.6
NZS225.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	x

21.6.2. ZK513-1

All samples selected from ZK513-1 were limited to size-based identifications, or were otherwise morphologically taxonomically indeterminate (see Appendix 03).

21.6.3. Tashbulak

I was able to use ZooMS to secure identifications for 96% of the samples (n=24) that could only be attributed tentative morphological identifications (n=25) (Tbl.116; see Appendix 03). I determined that 11 of these samples were correctly identified, while 13 were tentatively misidentified (Tbl.116). Sample TBK213.A was tentatively identified as *Bos* sp., while my ZooMS analysis determined that the sample is actually *Capra* sp. Based on the presence of tryptic masses 1180.6, 2883.3, 2899.3 and 3093.4 (Tbl.117). Sample TBK303.A had been tentatively identified as *Equus* sp., but I determined that this sample was *Bos* sp. due to the presence of tryptic masses 1193.1, 1209.1, 1581.2, 1649.3, 2131.7, 2793, 2854.1, 2870.1, 3018.1, and 3034.2 (Tbl.117)– though *m/z* 3018.1 should be interpreted with caution (see Chapter 06).

I further identified a number of tentative morphological misidentifications based upon the peptide mass values measured by MALDI, including the misattribution of *Capra* sp. instead of *Ovis* sp. to sample TBK051.A, of *Ovis* sp. / *Capra* sp. Instead of *Bos* sp. to sample TBK147.A, of *Cervus* sp. instead of *Bos* sp. to sample TBK332.A, of *Gazella* sp. to samples TBK123.A, TBK303.A, and TBK308.A instead of *Ovis* sp. or *Capra* sp., or *Gazella* sp. / *Cervus* sp. instead of *Capra* sp. to sample TBK136.A, and finally of *Sus* sp. instead of *Ovis* sp. to sample TBK290.A (Tbl.117).

Sample No.TBK189.A was morphologically identified as “Ovis / Capra?”, but did not retain enough collagen preservation for a ZooMS-based identification.

Tbl.116 Table of ZooMS-based identifications of tentatively identified samples from Tashbulak.

Morphological Identification	ZooMS-Based Identification	Sample No.	No. Samples
Bos?	*Bos* sp.	TBK086.A, TBK149.A, TBK324.A, TBK271.A, TBK296.A	5
Bos?	*Capra* sp.	TBK213.A	1
Equus?	*Bos* sp.	TBK303.A	1
Capra?	*Capra sp.*	TBK163.A, TBK279.A, TBK014.A, TBK032.A, TBK311.A	5
	Ovis sp.	TBK051.A	1
Ovis / Capra?	*Bos* sp.	TBK147.A	1
	Capra sp.	TBK059.A	1
Cervus?	*Bos* sp.	TBK332.A	1
Gazelle?	*Capra* sp.	TBK303.A, TBK308.A	2
	Ovis sp.	TBK123.A	1
Gazella / Slender Ovis?	*Capra* sp.	TBK091.A	1
	Ovis sp.	TBK124.A	1
Gazella / Deer?	*Capra* sp.	TBK136.A	1
Sus?	*Ovis* sp.	TBK290.A	1

**Sample No.TBK189.A was morphologically identified as “Ovis / Capra?”, but did not retain enough collagen preservation for a ZooMS-based identification.*

Tbl.117 Table of tryptic masses of TBK samples with conflicting ZooMS-based & tentative morphological IDs.

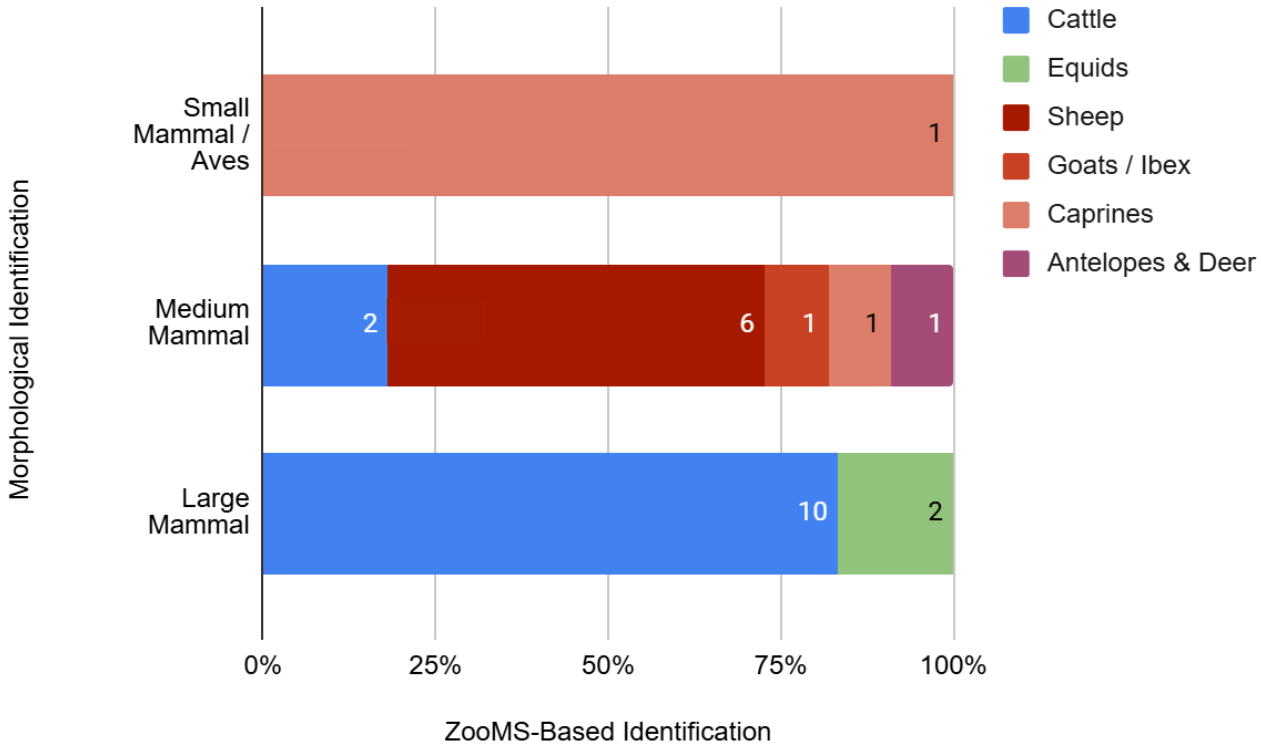
Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
TBK051.A	1105.6	x	1196.6	1427.7	1580.7	1648.8	2131	2792.2	2883.3	289935	3017.3	3033.5
TBK091.A	1105.6	1180.6	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.5	3017.5	3093.5
TBK190.A	1105.5	x	1196.6	1427.7	1580.7	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	3033.5
TBK123.A	1105.6	1180.7	1196.6	1427.8	1580.8	1648.9	2131.1	2792.3	2883.4	2899.4	3017.4	3093.5
TBK136.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	3093.6
TBK147.A	1105.5	1192.6	1208.6	1427.7	1580.7	1648.8	2131.1	2792.3	2853.4	2869.4	3017.3	x
TBK189.A	x	x	x	x	x	x	x	x	x	x	x	x
TBK213.A	1105.5	1180.6	1196.6	1427.7	1580.7	1648.8	2131	2792.2	2883.3	2899.3	3017.3	3093.4
TBK260.A	1105.7	x	1196.8	1427.9	1580.9	1649	2131.3	2792.5	2883.6	2899.6	3017.6	3093.7
TBK290.A	1105.9	x	1197	1428.1	1581.2	1649.2	2131.6	2792.9	2884	2900	3018	3034.1
TBK303.A	1105.9	1193.1	1209.1	1428.2	1581.2	1649.3	2131.7	2793	2854.1	2870.1	3018.1	3034.2
TBK308.A	1105.8	1180.9	1196.9	1428	1581.1	1649.2	2131.5	2792.8	2883.8	2899.8	3017.8	3094
TBK332.A	1105.9	1193	1209	1428.1	1581.2	1649.2	2131.5	2792.8	2853.9	2869.9	3017.9	3034

21.7. Proteomic Identification of Size-Based Morphological Identifications

21.7.1. Nizhnyaya Sooru

I was able to use ZooMS to attribute a taxonomic group to all 25 of the samples selected from Nizhnyaya Sooru that had only been assigned a body size group (Tbl.118; Fig.35; see Appendix 03). This included a caprine sample (NZS223.A) that had been misidentified as “Small Mammal / Aves” (Fig.34). I determined this sample to be *Ovis* sp. / *Capra* sp. based upon all tryptic masses detected by the MALDI (Tbl.119). Amongst “Medium Mammals”, I determined that sample NZS234.A was *Equus* sp., samples NZS082.A and NZS195.A were both *Bos* sp., samples NZS096.A and NZS228.A were both *Cervus* sp. / *Gazelle* sp. / *Saiga* sp., sample NZA097.A was *Capra* sp. (Fig.36), and that samples NZS094.A, NZS129.A, NZS185.A, NZS194.A, NZS196.A, and NZS197.A were all *Ovis* sp. (Tbl.118). I could not discern the taxonomic identity of samples NZS095.A or NZS223.A beyond *Ovis* sp. / *Capra* sp., due to the loss of the diagnostic α2 757 marker (Tbl.119). Amongst the samples morphologically identified as “Large Mammal”, I determined that samples NZS104.A and NZS107.A were *Equus* sp., that sample NZS108.A and NZS221.A were both *Ovis* sp., and that the 10 remaining samples were all *Bos* sp. (Tbl.118).

Fig.35 Bar graph of ZooMS-based IDs of samples with size-based classifications from Nizhnyaya Sooru.



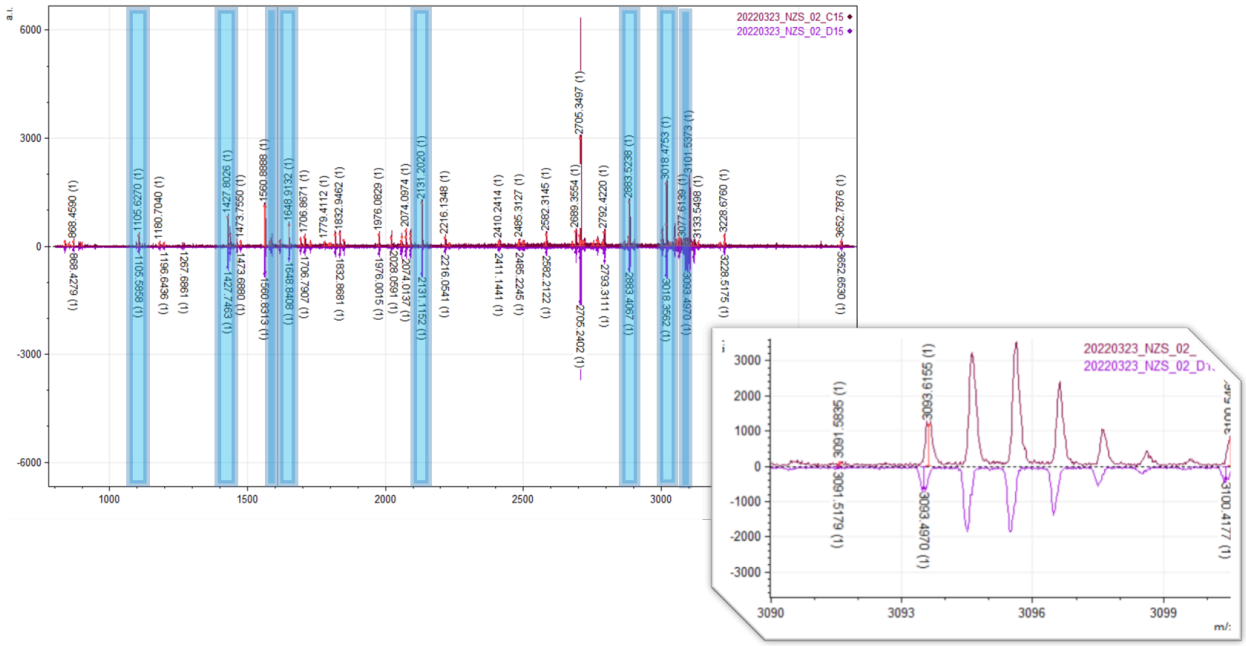
Tbl.118 Table of ZooMS-based IDs of samples with size-based classifications from Nizhnyaya Sooru.

Morphological Identification	ZooMS-Based Identification	Sample No.	No. Samples
Small Mammal / Aves	*Ovis* sp. / *Capra* sp.	NZS223.A	1
Medium Mammal	*Bos* sp.	NZS082.A, NZS195.A	2
	Capra sp.	NZS097.A	1
	Cervus sp. / *Gazella* sp. / *Saiga* sp.	NZS228.A	1
	Equus sp.	NZS234.A	1
	Ovis sp.	NZS094.A, NZS129.A, NZS185.A, NZS194.A, NZS196.A, NZS197.A	6
	Ovis sp. / *Capra* sp.	NZS095.A	1
Large Mammal	*Bos* sp.	NZS106.A, NZS110.A, NZS118.A, NZS124.A, NZS171.A, NZS176.A, NZS180.A, NZS190.A, NZS207.A, NZS222.A	10
	Equus sp.	NZS104.A, NZS107.A	2

Tbl.119 Table of tryptic masses of samples NZS095.A & NZS223.A.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS095.A	1105.6	1180.7	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	x	3017.5	x
NZS223.A	1105.6	1180.7	1196.7	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	x

Fig.36 Mirrored MALDI spectra of NZS097.A with taxonomically diagnostic marker α2 757 (+16) (*m/z* 3093.6).



Tbl.120 Table of tryptic masses of Nizhnyaya Sooru samples morphologically assigned to size-based groups.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Small Mammal												
NZS223.A	1105.6	1180.7	1196.6	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	x
Medium Mammal												
NZS082.A	1105.6	1182.6	1192.7	1208.7	1580.8	1648.8	2131.1	x	2853.4	2869.4	3017.4	x
NZS094.A	1105.6	1180.6	1196.7	1427.7	x	1648.9	2131.1	2792.3	2883.4	x	3017.4	3033.5
NZS096.A	1105.6	x	1196.6	1427.7	1550.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.3	3033.5
NZS129.A	1105.5	x	x	1427.7	1580.7	1648.8	2131.1	2792.3	2883.3	2899.4	3017.3	3033.4
NZS185.A	1105.7	1180.8	1196.8	1427.9	1580.9	1649	2131.2	2792.4	2883.5	2899.5	3017.5	3033.6
NZS194.A	1105.6	x	1196.7	1427.8	1580.8	1648.9	2131.2	2792.5	2883.6	2899.6	3017.5	3033.6
NZS195.A	1105.6	1182.7	1208.7	1427.8	1580.8	1648.9	2131.2	2793.5	2853.6	2869.6	3017.6	3033.7
NZS196.A	1105.6	x	1196.7	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	3033.6
NZS197.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	x	2792.4	2883.5	x	3017.5	3033.6
NZS234.A	1105.6	1182.6	1198.7	1427.8	1550.8	1648.8	2145.1	2820.5	2883.5	2899.5	x	x
Large Mammal												
NZS104.A	1105.6	1182.6	1198.6	1427.8	1550.8	1649.8	2145.1	2820.4	2883.4	x	x	2999.6
NZS106.A	1105.6	1182.7	1208.7	1427.8	1580.8	1648.9	2131.2	2792.4	2853.5	2869.5	3017.5	3033.6
NZS107.A	1105.6	1182.7	x	1427.8	1550.8	1649.8	2145.2	2820.4	2883.5	2899.5	2983.6	2999.6
NZS108.A	1105.6	x	1196.7	1427.8	1580.8	1648.9	2131.2	2792.4	2883.6	2899.6	3017.5	3033.7
NZS110.A	1105.6	1182.6	1208.7	1427.8	1580.8	1648.8	2131.1	2792.4	2853.4	2869.4	3017.4	3033.6
NZS118.A	1105.7	1182.7	1208.7	1427.7	1580.8	1648.7	2131.2	2792.4	2853.5	2869.6	3017.5	3033.7
NZS124.A	1105.6	1182.6	1208.7	1427.8	1580.8	1648.9	2131.2	2792.4	2853.5	x	3017.5	3033.6
NZS171.A	1105.6	1182.6	1208.7	1427.8	1580.8	1648.9	2131.1	2792.4	2853.4	2869.4	3017.4	3033.5
NZS176.A	1105.6	x	1192.7	1208.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.4	3033.5
NZS180.A	1105.5	1182.6	1208.6	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.3	3033.4
NZS190.A	1105.6	1192.7	1208.7	1427.8	1580.8	1648.9	2131.2	2792.5	2853.6	2869.6	3017.5	3033.7
NZS207.A	1105.5	1182.6	1208.7	1427.8	1580.8	1648.9	2131.2	2792.4	2853.5	x	3017.4	3033.5
NZS221.A	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.5	3017.4	3033.5

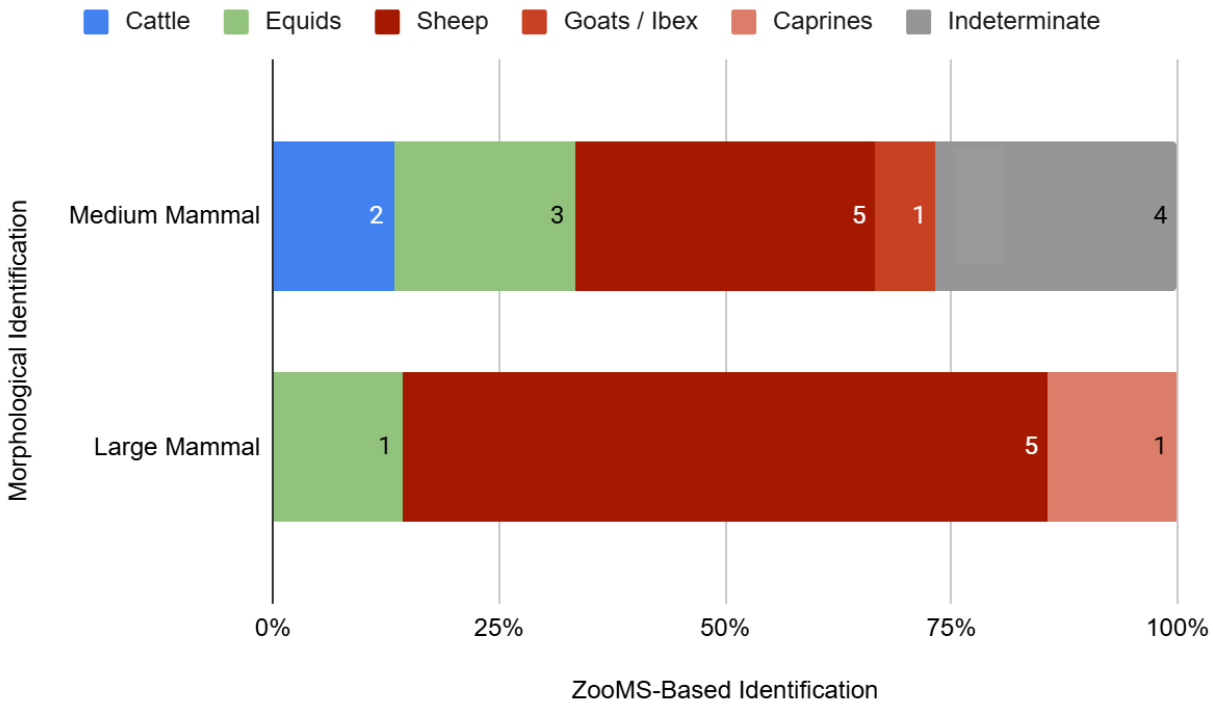
21.7.2. ZK513-1

I was able to use ZooMS to attribute a taxonomic group to 82% (n=18) of the samples selected from Trench ZK513-1 that had only been assigned a body size class (n=22) (Fig.37; Tbl.121; see Appendix 03). Of the 18 samples which were morphologically identified as medium and large mammals and subsequently collagen fingerprinted, there are 11 taxonomic disagreements (Fig.37; Tbls.121–122). These disagreements include specimens initially classified as large mammals being resolved to ZooMS-based caprine identifications, as well as specimens initially attributed to medium mammals being identified with ZooMS as *Equus* sp. or *Bos* sp. (Fig.37; Tbl.121).

Tbl.121 Table of ZooMS-based IDs of samples with size-based classifications from ZK513-1.

Morphological Identification	No. Samples (Zooarch ID)	ZooMS-Based Identification	No. Samples (ZooMS ID)
Medium Mammal	11	*Bos* sp.	2
		Capra sp.	1
		Equus sp.	3
		Ovis sp.	5
Large Mammal	7	*Equus* sp.	1
		Ovis sp.	5
		Ovis sp. / *Capra* sp.	1

Fig.37 Bar graph of ZooMS-based IDs of samples with size-based classifications from ZK513-1.



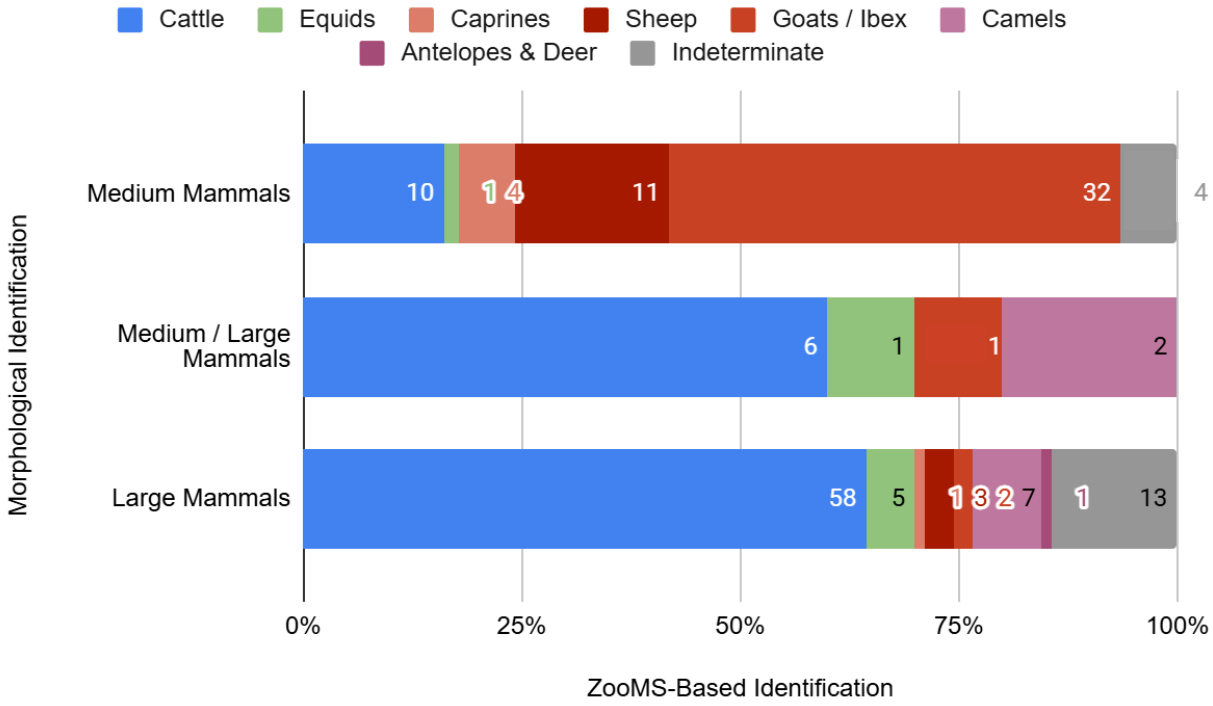
Tbl.122 Table of tryptic masses of ZK513-1 samples morphologically assigned to size-based groups.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Medium Mammal												
ZKG001	1105.5	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.3	3033.4
ZKG002	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.4	3033.5
ZKG003	1105.6	1182.6	1198.6	1427.7	1550.7	1649.8	2145.1	2820.3	2883.4	2899.3	2983.5	2999.5
ZKG004	1105.6	1180.6	1196.6	1427.7	1580.7	1648.8	2131	2792.2	2883.3	2899.3	3017.3	3093.4
ZKG005	1105.6	1192.7	1208.7	1427.8	1580.8	1648.9	2131.1	2792.4	2853.4	2869.4	3017.4	3033.5
ZKG031	1105.6	1182.6	1198.6	1427.7	1550.8	1649.8	2145.1	2820.4	2883.4	2899.4	2983.5	2999.5
ZKG032	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	3033.6
ZKG033	1105.6	1182.7	1198.7	1427.8	1550.8	1649.8	2145.2	2820.4	2883.4	2899.4	x	2999.5
ZKG034	1105.6	1180.6	1196.7	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	3033.5
ZKG055	x	x	x	x	x	x	x	x	x	x	x	x
ZKG056	x	x	x	x	x	x	x	x	x	x	x	x
ZKG057	x	x	x	x	x	x	x	x	x	x	x	x
ZKG058	1105.6	1192.7	1208.7	1427.8	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.4	3033.5
ZKG059	x	x	x	x	x	x	x	x	x	x	x	x
ZKG060	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.7	3033.6
Large Mammal												
ZKG137	1105.6	1180.6	1196.7	1427.8	1580.8	1648.9	x	2792.4	2883.5	2899.5	3018.4	x
ZKG138	1105.7	1180.7	1196.7	1427.8	1580.9	1648.9	2131.3	2792.5	2883.6	2899.7	3017.6	3033.6
ZKG139	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	3033.6
ZKG140	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.3	2792.4	2883.5	2899.5	3017.5	3033.6
ZKG141	1105.7	1182.7	x	1427.9	1550.9	1649.9	2145.3	2820.6	2883.6	2899.6	x	2999.7
ZKG142	1105.8	1180.8	1196.8	1427.9	1581	1649.1	2131.4	2792.3	2883.4	2899.4	3017.4	3033.5?
ZKG143	1105.7	1180.8	1196.8	1427.9	1580.9	1649.1	2131.3	2792.6	2883.7	2899.7	3017.7	3033.8

21.7.3. Tashbulak

I was able to use ZooMS to attribute a taxonomic group to all but 17 of the samples selected from Tashbulak that had only been assigned a body size group by zooarchaeological analysis (n=162); i.e., I was able to refine the identifications of 90% of these samples (Fig.38; Tbl.123; see Appendix 03). I determined that the majority of “Large Mammals” as well as “Medium / Large Mammals” were *Bos* sp., while the majority of “Medium Mammals” were *Capra* sp. (Fig.38; Tbl.123). I identified *Equus* sp., *Bos* sp., and *Capra* sp. samples across all size-based groups (Fig.38; Tbl.123). Interestingly, the majority of the samples I was not able to identify to any taxonomic group with ZooMS had been reported as “Large Mammals” (Fig.38; Tbl.123).

Fig.38 Bar graph of ZooMS-based IDs of samples with size-based classifications from Tashbulak.



Tbl.123 Table of ZooMS-based IDs of Tashbulak samples per body-size group identification.

ZooMS-Based ID	Medium Mammals	Medium / Large Mammals	Large Mammals
Bos sp.	10	6	58
Equus sp.	1	1	5
Ovis sp. / Capra sp.	4	0	1
Ovis sp.	11	0	3
Capra sp.	32	1	2
Camelus bactrianus	0	2	7
Cervus sp. / *Gazella* sp.	0	0	1
Indeterminate	4	0	13

21.8. Proteomic Identification of Ambiguous Morphological Identifications

21.8.1. Nizhnyaya Sooru

I was able to use ZooMS to clarify the taxonomic identity of 83% of samples (n=43) from Nizhnyaya Sooru that were morphologically determined to be “Ovis / Capra” (Tbl.124; see Appendix 03). Two of these were not caprine in origin at all, but instead cattle (NZS099.A) and wild ungulate (NZS231.A) (Tbl.124). Six samples could not be refined beyond (but were confirmed as being) broadly caprine (i.e. *Ovis* sp. / *Capra* sp.), and three did not retain enough collagen for ZooMS-based identification (Tbl.124). Of all of the samples selected from Nizhnyaya Sooru (irrespective of their morphological identifications), I could not identify 24 in total beyond *Ovis* sp. / *Capra* sp., due to the loss of the α2 757 marker (Tbl.125).

Tbl.124 Table of ZooMS-based identifications of ambiguously identified samples from Nizhnyaya Sooru.

Taxon	*Ovis* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	*Cervus* sp. / *Gazella* sp. / *Saiga* sp.	Indeterminable
No. Samples	41	6	1	1	3

Tbl.125 Table of tryptic masses of caprine samples from Nizhnyaya Sooru without the α2 757 marker.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS095.A	1105.6	1180.7	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	x	3017.5	x
NZS122.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	x
NZS133.A	1106.3	1181.4	1197.4	1428.6	1581.7	1649.8	2132.3	2793.8	2884.9	2900.3	3017.6	x
NZS139.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2793.4	2883.5	x	3017.4	x
NZS141.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	x	2883.5	2899.5	3017.4	x
NZS142.A	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.3	2882.4	2899.4	3017.5	x
NZS153.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.5	2883.6	2899.6	3017.6	x
NZS158.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS160.A	1106.2	1181.3	1197.3	1428.5	1581.6	1649.7	2132.1	2791.2	2882	2900.8	3018.8	x
NZS162.A	1105.6	1180.6	1196.6	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.4	x
NZS183.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.1	x	2883.6	2899.6	3017.6	x
NZS187.A	1105.6	x	1196.6	1427.8	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	x
NZS188.A	1105.6	1180.6	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS192.A	1105.6	1180.7	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS198.A	1105.6	1180.6	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS202.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.2	2792.5	2883.6	2899.6	3017.6	x
NZS203.A	1105.6	1180.7	1196.7	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS208.A	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2898.4	3017.4	x
NZS212.A	1105.6	x	1196.7	1427.8	1580.8	1648.9	2131.1	x	2883.5	2899.5	3017.5	x
NZS214.A	1105.6	1180.7	1196.7	1427.8	1580.9	1648.9	2131.2	2792.5	2883.6	2899.6	3017.6	x
NZS223.A	1105.6	1180.7	1196.6	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	x
NZS225.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.1	2792.4	2883.5	2899.5	3017.5	x
NZS231.A	1105.6	x	1196.7	1427.8	1550.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.4	x
NZS233.A	1105.6	1180.7	1196.7	1427.8	1580.8	1648.9	2131.2	2792.5	2883.6	2899.5	3017.5	x

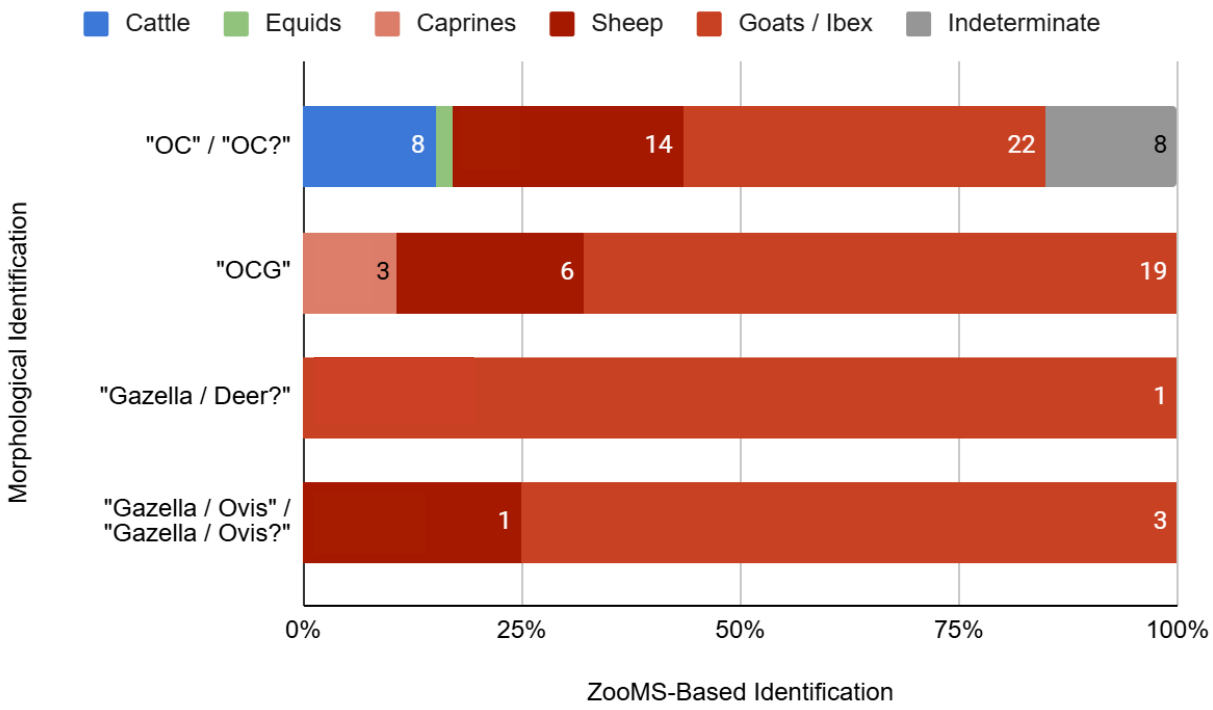
21.8.2. ZK513-1

All samples selected from ZK513-1 were limited to size-based identifications, or were otherwise morphologically taxonomically indeterminate (see Appendix 03).

21.8.3. Tashbulak

Eighty-six of the samples that I selected from Tashbulak had been morphologically identified as “OC”, “OC?”, “OCG”, “Gazella / Deer”, “Gazella / Ovis”, or “Gazella / Ovis?”, as the fragmented remains of these ungulates can be very difficult to distinguish by morphology alone. I was able to use ZooMS to clarify the taxonomic identity of 91% (n=78) of these samples (Fig.39; Tbl.126; see Appendix 03). Eight of the samples morphologically identified as “OC” were actually *Bos* sp. (Tbl.127), and another (TBK128.A) was *Equus* sp. (Fig.39; Tbl.128). I identified the majority of the “OC”, “OC?”, “OCG”, “Gazella / Deer”, “Gazella / Ovis”, and “Gazella / Ovis?” samples as *Capra* sp., while also identifying a substantial number of *Ovis* sp. (Fig.38; Tbl.126). I did not identify any of these samples as *Cervus* sp., *Capreolus* sp., or *Gazella* sp. (Fig.39; Tbl.126). I could not identify three samples (TBK043.A, TBK093.A, TBK166.A) beyond *Ovis* sp. / *Capra* sp., due to the loss of the α2 757 (+16) collagen peptide biomarker (Tbl.129).

Fig.39 Bar graph of ZooMS-based identifications of ambiguously identified fauna from Tashbulak.



Tbl.126 Table of ZooMS-based identifications of ambiguously identified samples from Tashbulak.

Taxon	"OC" / "OC?"	"OCG"	"Gazella / Deer"	"Gazella / Ovis" / "Gazella / Ovis?"
Bos sp.	8	0	0	0
Equus sp.	1	0	0	0
Ovis sp. / *Capra* sp.	0	3	0	0
Ovis sp.	14	6	0	1
Capra sp.	22	19	1	3
Indeterminate	8	0	0	0

Tbl.127 Table of tryptic masses of bovine samples from Tashbulak morphologically identified as "OC"/"OC?".

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
TBK056.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.4	2853.5	2869.5	3017.4	3033.6
TBK147.A	1105.5	1192.6	1208.6	1427.7	1580.7	1648.8	2131.1	2792.3	2853.4	2869.4	3017.3	x
TBK157.A	1105.6	1192.7	1208.7	1427.7	1580.7	1648.8	2131	2792.3	2853.4	2869.4	3017.4	3033.4
TBK175.A	1105.5	1192.7	1208.6	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.4	3033.5
TBK196.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.3	2853.4	2869.4	3017.3	3033.4
TBK212.A	1105.8	1192.9	1208.9	1428	1581.1	1649.1	2131.5	2792.9	2854	2870	3018	3034.1
TBK221.A	1105.7	1192.8	1208.8	1427.8	1580.9	1648.9	2131.2	2792.4	2853.5	2869.5	3017.5	3033.6
TBK293.A	1106	1193.2	1209.1	1428.2	1581.3	1649.4	2131.8	2793.1	2854.2	2870.2	3018.3	3034.4

Tbl.128 Table of tryptic masses of an equid sample from Tashbulak morphologically identified as "OC".

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
TBK128.A	1105.6	1182.6	1198.7´6	1427.8	1550.8	1649.8	2145.1	2819.2	2883.4	2899.4	x	2999.5

Tbl.129 Table of tryptic masses of caprine samples from Tashbulak which did not retain the α2 757 marker.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
TBK043.A	1105.6	1180.6	1196.7	1427.8	1580.8	1648.8	2131.1	2792.2	2883.4	2899.4	3017.4	x
TBK093.A	1105.6	1180.7	1196.7	1427.9	1581	1649	x	2792	2883	2899	3017.8	x
TBK166.A	1105.6	1180.7	1196.7	1428.4	1580.8	1648.9	2131.2	2792.4	2883.5	2899.5	3017.5	x

21.9. Proteomic Correction of Morphological Misidentifications

21.9.1. Nizhnyaya Sooru

I was able to use ZooMS to correct 6 morphological misidentifications of taphonomically damaged samples from NZS (Tbl.130; see Appendix 03). The majority of these consisted of cattle remains morphologically misidentified as caprines or cervids, though one equid sample (NZS226.A) was misidentified as “Bos” and a sheep sample (NZS059.A) was misidentified as “Canis”. I determined that sample NZS070.A was *Bos* sp. (not *Cervus elaphus*) based on the presence of tryptic masses 1208.7 and 1580.8 (Tbls.130–131). Sample NZS213.A, also recorded as “Cervus”, was in fact *Bos* sp., based upon the presence of tryptic masses 1208.7 and 1580.8 (Tbls.130–131). NZS222.A, although recorded as “Ovis”, was also misidentified and my ZooMS analysis established that this sample was actually *Bos* sp. based upon the presence of tryptic masses 1192.7, 1208.7, 2853.3, and 2869.3 (Tbls.130–131).

I also determined that sample NZS099.A was not “Ovis / Capra” as recorded, but *Bos* sp., based upon the presence of tryptic masses 1192.6, 1208.7, 2853.5, and 2869.4 (Tbl.131). Conversely, I determined that sample NZS226.A was not “Bos” as recorded, but *Equus* sp. based upon the presence of tryptic masses 1550.8, 2145.2, 2883.5, 2899.5, and 2999.6 (Tbl.131). Lastly, I determined that sample NZS059.A was *Ovis* sp. (not “Canis”) based on the presence of tryptic masses 1105.6, 1180.6, 1196.6, 1427.7, 1580.8, 1648.8, 2131.1, 2792.3, 2883.4, 2899.4, 3017.4, and 3033.5 (Tbl.131).

Tbl.130 Table of conflicting zooarchaeological and ZooMS-based identifications of Nizhnaya Sooru samples.

Sample No.	Morphological Identification	ZooMS-Based Identification
NZS059.A	Canis	*Ovis* sp.
NZS070.A	*Cervus elaphus*	*Bos* sp.
NZS099.A	OC	*Bos* sp.
NZS213.A	Cervus	*Bos* sp.
NZS222.A	Ovis	*Bos* sp.
NZS226.A	Bos	*Equus* sp.

** “OC” is shorthand for Ovis sp. / Capra sp.*

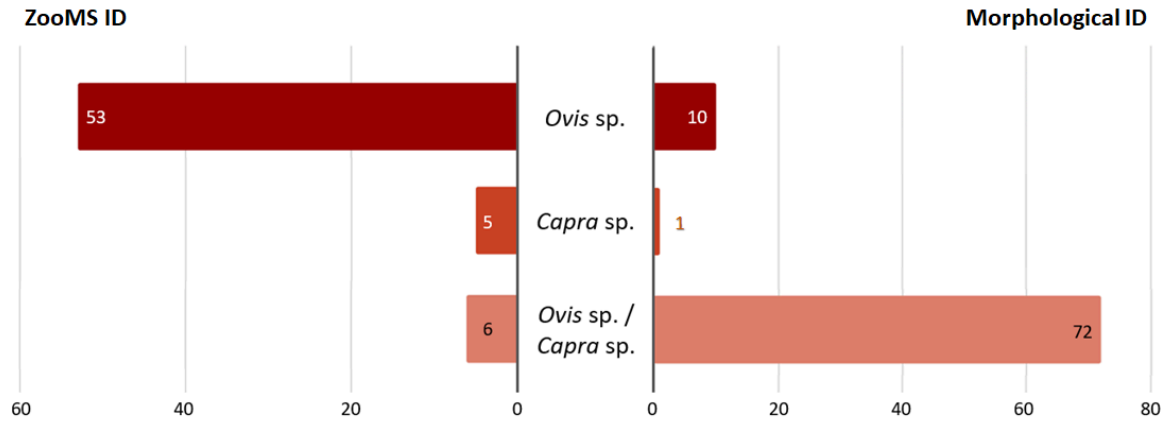
Tbl.131 Table of tryptic masses of NZS samples with conflicting ZooMS-based and morphological IDs.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
NZS059.A	1105.6	1180.6	1196.6	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2899.4	3017.4	3033.5
NZS070.A	1105.6	1192.7	1208.7	1427.8	1580.8	1648.9	2131.2	2792.5	2853.5	2869.5	3017.5	3033.6
NZS099.A	1105.6	1182.6	1192.7	1427.7	1580.8	1648.8	2131.1	2792.4	2853.5	2869.4	3017.4	3033.6
NZS213.A	1105.6	1192.7	1208.7	1427.8	1580.8	1648.9	2131.1	2792.3	2853.3	2869.3	3017.4	x
NZS222.A	1105.6	1192.7	1208.7	1427.7	1580.7	1648.8	2131.1	2792.2	2853.3	2869.3	3017.3	x
NZS226.A	1105.6	1182.7	x	1427.8	1580.8	x	2145.2	2820.5	2853.5	2899.5	x	2999.6

21.9.2. ZK513-1

Using ZooMS, I identified 53 *Ovis* sp., 5 *Capra* sp., and 6 ambiguous caprine specimens from ZK513-1 (Fig.40; see Appendix 03). My identifications are in contrast to morphological identifications published in the ZK513-1 faunal report (Houle et al. 2022), which identified 10 *Ovis* sp., 1 *Capra* sp., and 72 ambiguous caprine specimens (Tbls.39, 43). Importantly, none of the ZKG513 samples which I mass fingerprinted included specimens *morphologically* identified as *Ovis* sp. / *Capra* sp. My ZooMS analysis thus did not help to clarify ambiguous caprine morphological identifications, though future ZooMS analysis of the ZK513-1 faunal assemblage could do so. Both my ZooMS analysis and the faunal report suggest a high ratio of *Ovis* sp. to *Capra* sp. to be characteristic of ZK513-1.

Fig.40 Bar graph of morphological and ZooMS-based identifications of ZK513-1 caprines.



**Not all samples morphologically identified as caprines were subsequently selected for ZooMS analysis, though many morphologically unidentifiable fragments were, leading to an uneven contrast in sample numbers.*

21.9.3. Tashbulak

I identified 21 samples which had been taxonomically misidentified by zooarchaeological analysis (Tbl.132; see Appendix 03). I determined that sample TBK080.A, recorded as “Capreolus”, was *Bos* sp. based on the presence of tryptic masses 1192.6, 1208.6, 1580.8, 2853.4, 2869.4, 3017.4, 3033.4 (Tbl.132). Similarly, I determined that sample TBK151.A was also *Bos* sp. based on the presence of tryptic masses 1192.6, 1208.6, 1427.6, 1580.7, 1648.7, 2853.3, 2869.3, 3017.2, and 3033.4, although this sample had been recorded as “Camelus” (Tbls.132–133). Sample TBK224.A had also been morphologically identified as “Camelus”, and my ZooMS analysis revealed that this sample was actually *Capra* sp. based on the presence of tryptic masses 1180.6, 1196.6, 1427.7, 1580.8, 1648.8, 2792.4, 3017.4, and 3093.4 (Tbls.132–133). Conversely, I determined that sample TBK287.A was actually *Camelus* sp. due to the presence of tryptic masses 1221.9, 1235.9, 1444, 1551.1, 1635.2, 2820.8, and 2992– though it had been recorded as “Ovis” (Tbls.132–133). I have already provided the remaining misidentifications of wild ungulates, caprines, equids, and large bovids (see section “21.6.2.”).

Tbl.132 Table of conflicting zooarchaeological and ZooMS-based identifications of Tashbulak samples.

Sample No.	Morphological Identification	ZooMS-Based Identification
TBK151.A	Camelus	*Bos* sp.
TBK224.A	Camelus	*Capra* sp.
TBK050.A	Capra	*Ovis* sp.
TBK340.A	Capra	*Ovis* sp.
TBK080.A	Capreolus	*Bos* sp.
TBK219.A	Gazella	*Capra* sp.
TBK056.A	OC	*Bos* sp.
TBK128.A	OC	*Equus* sp.
TBK157.A	OC	*Bos* sp.
TBK175.A	OC	*Bos* sp.
TBK195.A	OC	*Bos* sp.
TBK212.A	OC	*Bos* sp.
TBK221.A	OC	*Bos* sp.
TBK293.A	OC	*Bos* sp.
TBK150.A	Ovis	*Capra* sp.
TBK153.A	Ovis	*Capra* sp.
TBK159.A	Ovis	*Capra* sp.
TBK281.A	Ovis	*Capra* sp.
TBK282.A	Ovis	*Capra* sp.
TBK287.A	Ovis	*Camelus* sp.
TBK298.A	Ovis	*Capra* sp.

Tbl.133 Table of tryptic masses of morphologically misidentified samples from Tashbulak.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
TBK050.A	1105.6	x	1196.6	1427.7	1580.8	1648.8	2131.1	2792.4	2883.5	2899.5	3017.4	3033.6
TBK056.A	1105.6	1192.7	1208.7	1427.7	1580.8	1648.8	2131.1	2792.4	2853.5	2869.5	3017.4	3033.6
TBK080.A	1105.6	1192.7	1208.7	1427.8	1580.8	1649.5	2131.2	2792.2	2881.5	2869.6	3017.6	3033.7
TBK128.A	1105.6	1182.6	1198.6	1427.7	1550.8	1648.9	2145.1	2819.3	2853.6	2899.4	x	2999.5
TBK150.A	1105.6	1180.1	1196.6	1427.7	1580.7	1649.8	2131.1	2792.2	2883.4	2899.3	3017.3	3093.4
TBK151.A	1105.6	1180.6	1208.6	1427.6	1580.7	1648.8	2131	2792.2	2883.3	2869.3	3017.2	3033.4
TBK153.A	1105.6	1192.6	1196.7	1427.8	1580.8	1648.7	2131.2	2792.5	2853.3	2899.6	3017.6	3093.7
TBK157.A	1105.6	1180.7	1208.7	1427.7	1580.7	1648.9	2131	2792.3	2883.6	2899.4	3017.4	3033.4
TBK159.A	1105.6	1192.7	1196.6	1427.7	1580.7	1648.8	2131.1	2792.3	2853.4	2899.4	3017.3	3093.4
TBK175.A	1105.5	1180.6	1208.6	1427.7	1580.8	1648.8	2131.1	2792.3	2883.4	2869.4	3017.4	3033.5
TBK195.A	1105.5	1192.7	1208.6	1427.7	1580.7	1648.8	2131	2792.2	2853.4	2869.3	3017.2	3033.4
TBK212.A	1105.8	x	1208.9	1428	1581.1	1648.7	2131.5	2792.9	2853.3	2870	3018	3034.1
TBK219.A	1105.6	1192.9	1196.6	1427.7	1580.7	1649.1	2131	2792.2	2854	2899.3	3017.3	3093.4
TBK221.A	1105.7	1180.6	1208.8	1427.8	1580.9	1648.8	2131.2	2792.4	2883.3	2869.5	3017.5	3033.6
TBK224.A	1105.6	1192.8	1196.7	1427.7	1580.8	1648.9	2131.1	2792.4	2853.5	2899.4	3017.4	3093.6
TBK281.A	1105.9	1180.6	1197	1428.1	1581.2	1648.8	2131.6	2792.9	2883.5	2900.1	3018	3094.2
TBK282.A	1105.9	1181	1197	1428.2	1581.2	1649.3	2131.7	2793	2884	2900.1	3018.1	3094.3
TBK287.A	1105.8	1181	1235.9	1444	1551.1	1649.3	2131.5	2820.8	2884.1	2899.8	x	2992
TBK293.A	1106	1221.9	1209.1	1428.2	1581.3	1635.2	2131.8	2793.1	2883.9	2870.2	3018.3	3034.4
TBK298.A	1105.9	1193.2	1197.9	1428.1	1581.1	1649.4	2131.5	2792.8	2854.2	x	3017.9	3094.1
TBK340.A	1106.1	1180.9	1197.2	1428.4	1581.4	1649.2	2131.9	2793.3	2883.9	2900.5	3018.5	3034.6

21.10. Stratigraphic Distribution of Proteomic Identifications

21.10.1. Nizhnyaya Sooru

The stratigraphic distribution of the ZooMS-based identifications of the selected NZS fauna indicates a consistent presence of sheep (*Ovis* sp.) and caprines throughout all layers, with equids appearing only later in Layers 02–03 (Figs.41–43, Tbl.134; see Appendix 03). These stratigraphic assemblage compositions are reflective of the samples that were selected for this study, as well as the uneven rate of sampling across each cultural layer. Thus, the stratigraphic distributions of ZooMS-based identifications are heavily biased and do not reflect the stratigraphic distributions of the entire NZS assemblage. At the same time, the seeming absence of horse remains until after the Middle Bronze Age (Figs.41–43) weakens arguments for Afanasievo horse domestication (see Chapters 01, 09, 15). The predominance of sheep over goats is very clear until the Middle Bronze – Iron Ages, which are characterized here by far fewer samples. I will examine my ZooMS results for each archaeological period in turn in my "Discussion" chapter (see Chapter 22).

Tbl.134 Table of stratigraphic distributions of ZooMS identifications of samples from Nizhnyaya Sooru.

Layer / Taxon	*Bos* sp.	*Equus* sp.	*Ovis* sp. / *Capra* sp.	*Ovis* sp.	*Capra* sp.	*Cervus* sp. / *Gazella* sp. / *Saiga* sp.	*Canis* sp. / *Vulpes* sp.	*Aves* sp.	*Lepus* sp.	Failed
Layer 02	0	2	1	1	1	1	0	0	0	0
Layer 03	0	2	0	1	0	0	0	0	0	0
Layer 04	4	0	1	11	0	1	0	0	0	0
Layer C	7	0	4	18	0	0	2	1	0	1
Layers 5A/5B	15	0	16	70	0	1	4	0	1	6

Fig.41 Stacked bar graph of ZooMS-based IDs of samples from Nizhnyaya Sooru strata.

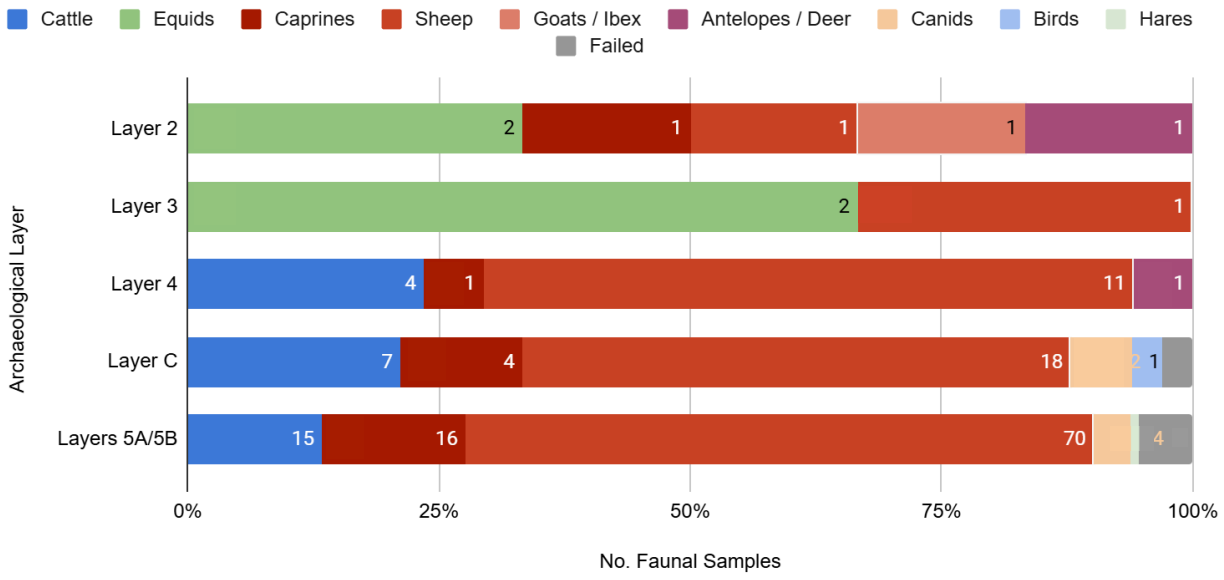


Fig.42 Bar graph of ZooMS-based IDs of samples from Nizhnyaya Sooru strata.

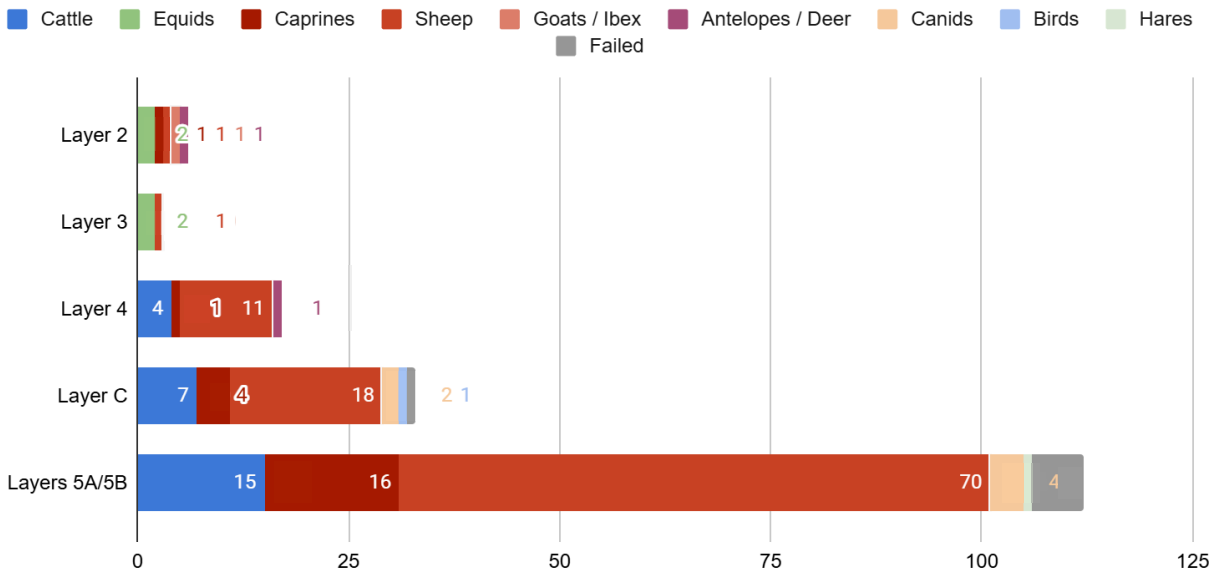
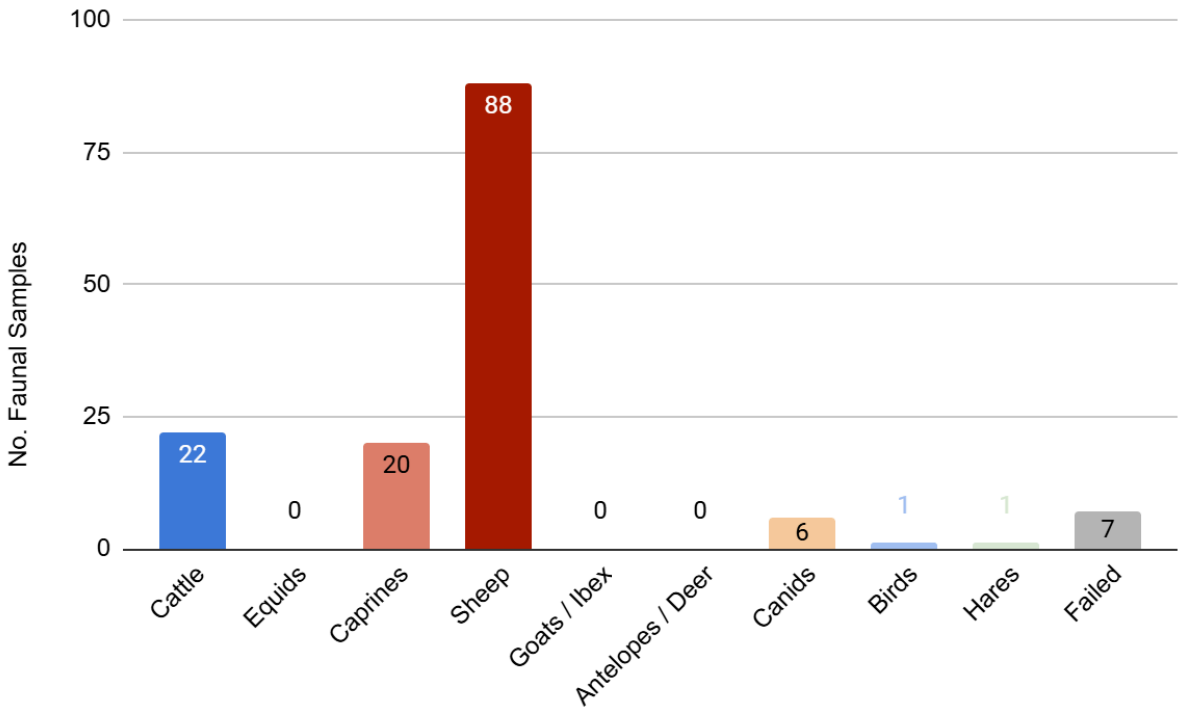


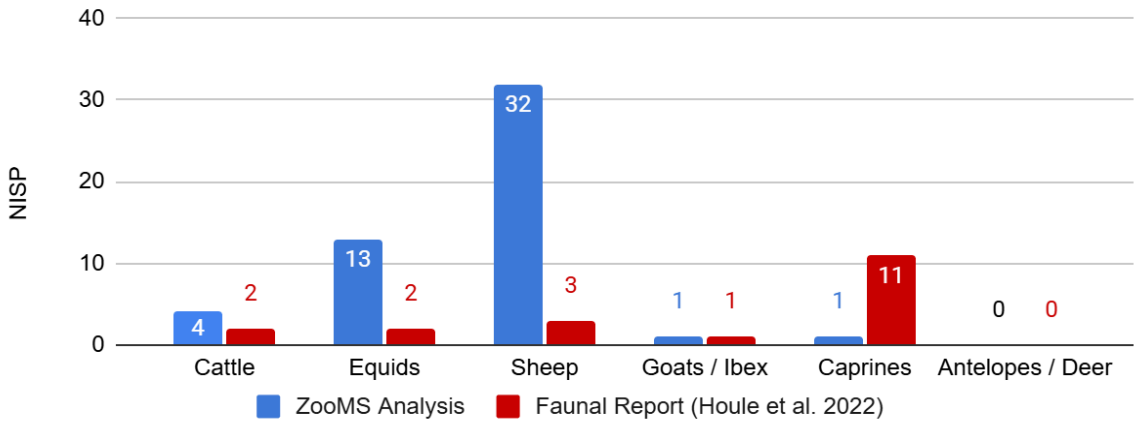
Fig.43 Bar graph of ZooMS-based IDs of samples from the Afanasievo layers of Nizhnyaya Sooru.



21.10.2. ZK513-1

The stratigraphic distribution of my targeted ZooMS-based identifications of fragmented faunal remains selected from the ZK513-1 Trench assemblage can be said to be dominated by *Ovis* sp. in nearly all layers (Tbl.135; Figs.44–46; see Appendix 03). At the same time, the delineation of an already small sample number (143) into 12 groups greatly decreases the resolution of data and complicates any attempts to reconstruct animal economies through time at ZK513-1. Combining the ZooMS data with the zooarchaeological data, as they stand now, does not provide additional insight as the overwhelming majority of the animal bones remain unidentified (see Tbl.135; Figs.44–46). Additional analyses of these remains, ideally using ZooMS, will be necessary for any robust interpretation of animal management strategies and herd compositions through time at ZK513-1. My analysis did greatly help to clarify the ZKG513-1 faunal report, which previously only identified samples selected from Layer 1 as “Medium Mammal” and seven samples from Level 12 as “Large Mammal”. By using ZooMS, I was able to identify caprines, cattle, and equids in Layer 01 as well as equids and caprines in Layer 12 (Tbl.135; Figs.44–46). Furthermore, I was able to enrich the zooarchaeological data from the Eneolithic and Early Bronze Age periods (Fig.44).

Fig.44 Bar graph of morphological and ZooMS-based ID’s from the Eneolithic & EBA layers of ZK513-1.



Tbl.135 Table of stratigraphic ZooMS-based taxonomic distributions of ZK513-1 fauna.

Layer	Radiocarbon	Period (Houle et al. 2022)	*Ovis* sp.	*Capra* sp.	*Ovis* sp. / *Capra* sp.	*Bos* sp.	*Cervus* sp. / *Gazella* sp.	*Equus* sp.	Failed
Layer 01	(none)	Historical	2	1	0	1	0	1	0
Layer 02	(none)	Historical	3	1	0	1	0	0	0
Layer 03	800-990 CE	Early Medieval	1	1	0	1	0	0	0
Layer 04	260-410 CE	Early Medieval	1	0	1	0	0	1	7
Layer 05	80-240 CE	Early Medieval	0	1	1	0	0	0	3
Layer 06	20-140 CE	Iron Age	6	0	0	2	2	3	1
Layer 07	4 BCE-120 CE	Iron Age	3	0	1	2	0	1	3
Layer 08	2020-1780 BCE	Early Bronze Age	1	1	0	3	0	1	9
Layer 09	1890-1690 BCE	Middle Bronze Age	3	1	0	0	0	0	6
Layer 10	1410-1230 BCE	Late Bronze Age	3	0	1	0	0	4	7
Layer 11	2010-1770 BCE	Early Bronze Age	9	0	0	1	0	8	2
Layer 12	2030-1880 BCE	Early Bronze Age	22	0	1	0	0	4	0

Fig.45 Bar graph of absolute ZooMS-based identifications of ZK513-1 fauna per strata, with total number of animal bone fragments in parentheses (Houle et al. 2022).

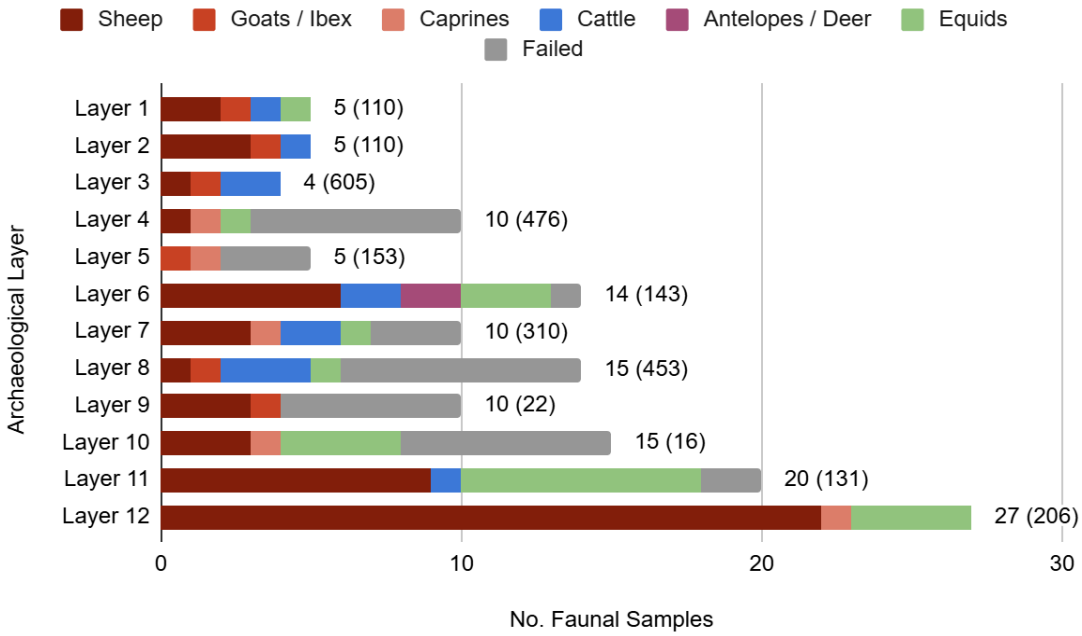
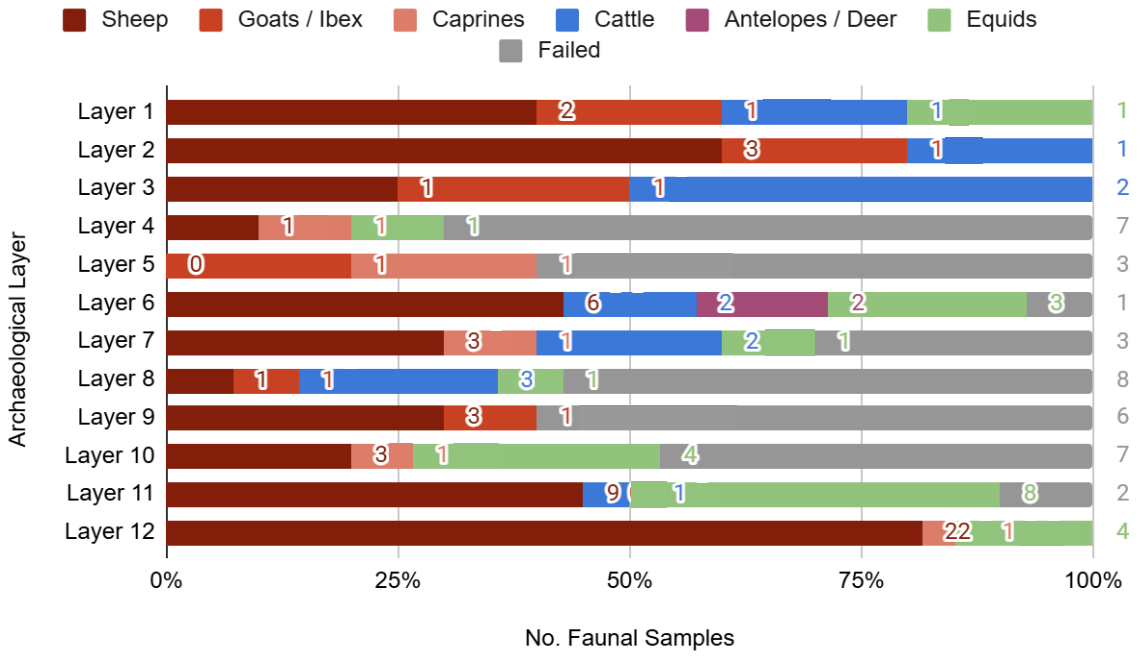


Fig.46 Bar graph of relative ZooMS-based identifications of ZK513-1 fauna per strata.



21.11.3. Tashbulak

Tashbulak is not a stratified site, and thus there is no stratigraphic faunal data to report.

21.12. Proteomic Contribution to Published Regional NISP Data

21.12.1. Bronze Age Southern Siberia

My ZooMS results have contributed substantially to the total body of NISP data available for cattle, equids, and caprines from the Bronze Age settlement sites of Southern Siberia, most dramatically in the context of the Eneolithic and Early Bronze Age (Figs.47–50). Notably, there was not a strong Late Bronze Age component to Nizhnyaya Sooru (see Chapters 12, 15, 20). The contribution of my ZooMS results is most clearly seen in the addition of caprines NISP data, and especially sheep (*Ovis* sp.). For published sources of NISP data, see Chapters 12, 15.

Fig.47 Bar graph of NISP data for cattle (*Bos* sp.) remains recovered from Bronze Age Southern Siberia.

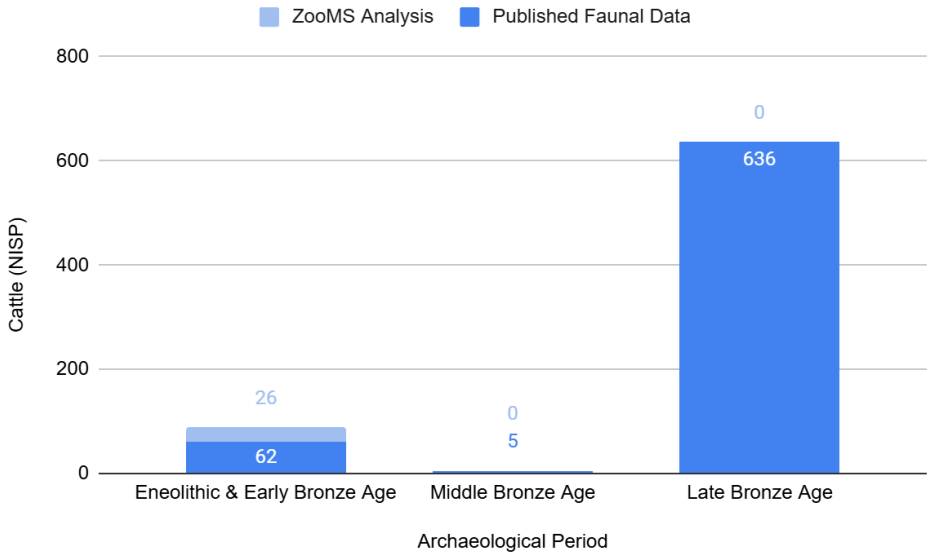


Fig.48 Bar graph of NISP data for equids (*Equus* sp.) remains recovered from Bronze Age Southern Siberia.

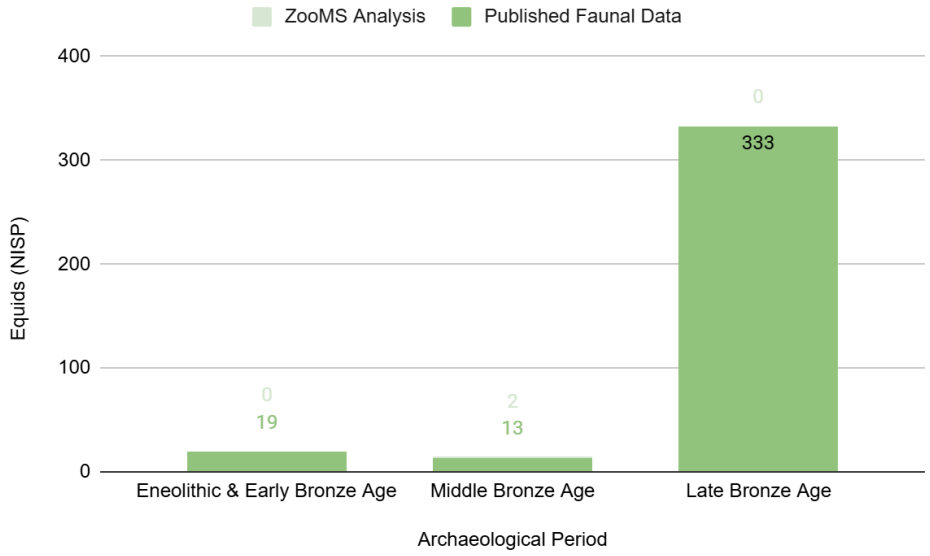


Fig.49 Bar graph of NISP data for *Ovis* sp. & *Capra* sp. remains recovered from Bronze Age Southern Siberia.

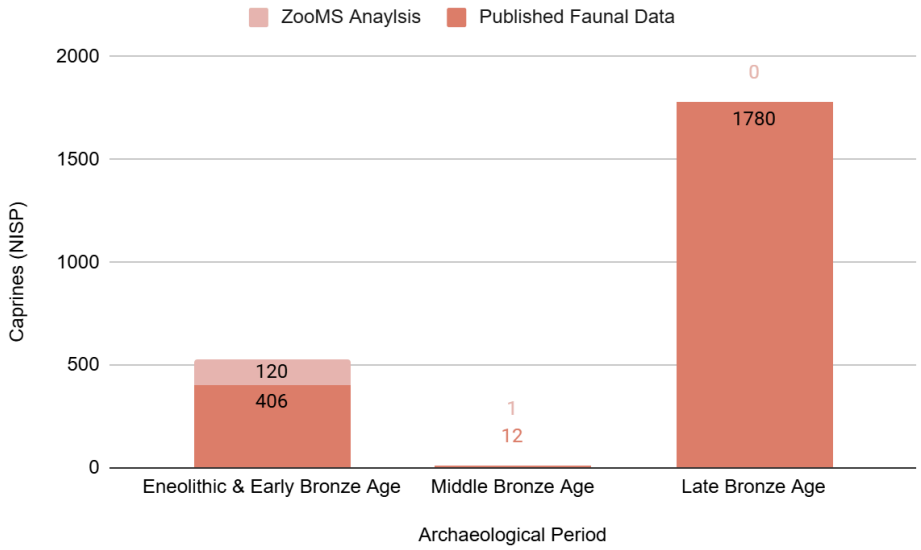
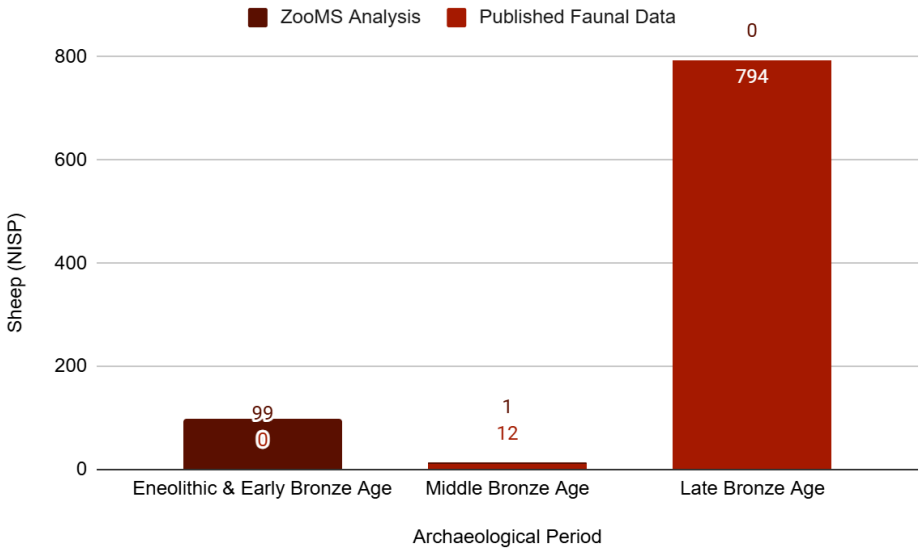


Fig.50 Bar graph of NISP data for sheep (*Ovis* sp.) remains recovered from Bronze Age Southern Siberia.



21.12.2. Bronze Age Outer Mongolia

The ZooMS-based identifications of cattle, equids, and caprines from my analysis have substantially contributed to the overall body of NISP data available from the Bronze Age settlement sites of Outer Mongolia, especially of sheep, and especially in the for the Eneolithic & Early Bronze Age period (which my study was largely focused upon) (Figs.51–54). For published sources of NISP data, see Chapters 12 and 15.

Fig.51 Bar graph of NISP data for cattle (*Bos* sp.) remains recovered from Bronze Age Outer Mongolia.

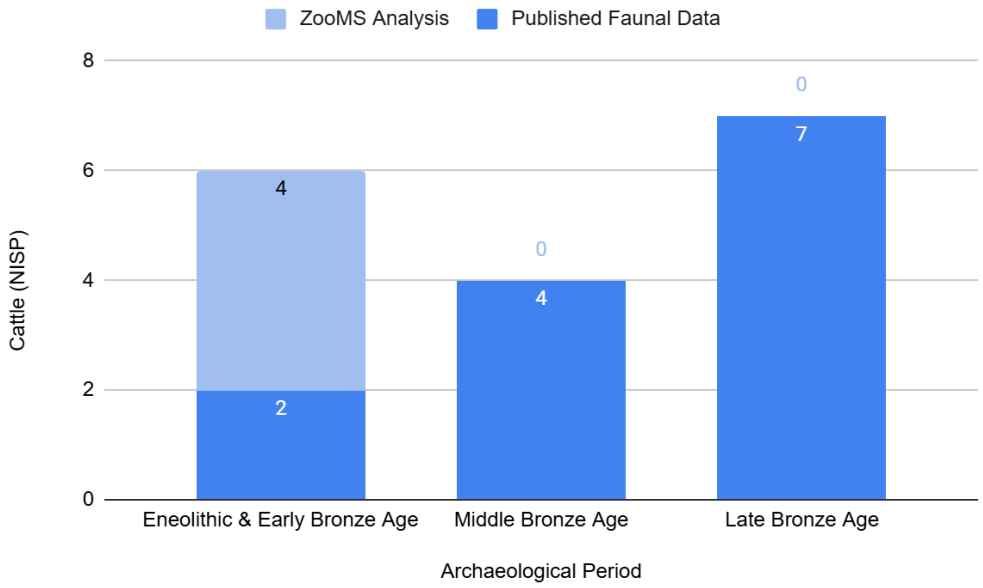


Fig.52 Bar graph of NISP data for equids (*Equus* sp.) remains recovered from Bronze Age Outer Mongolia.

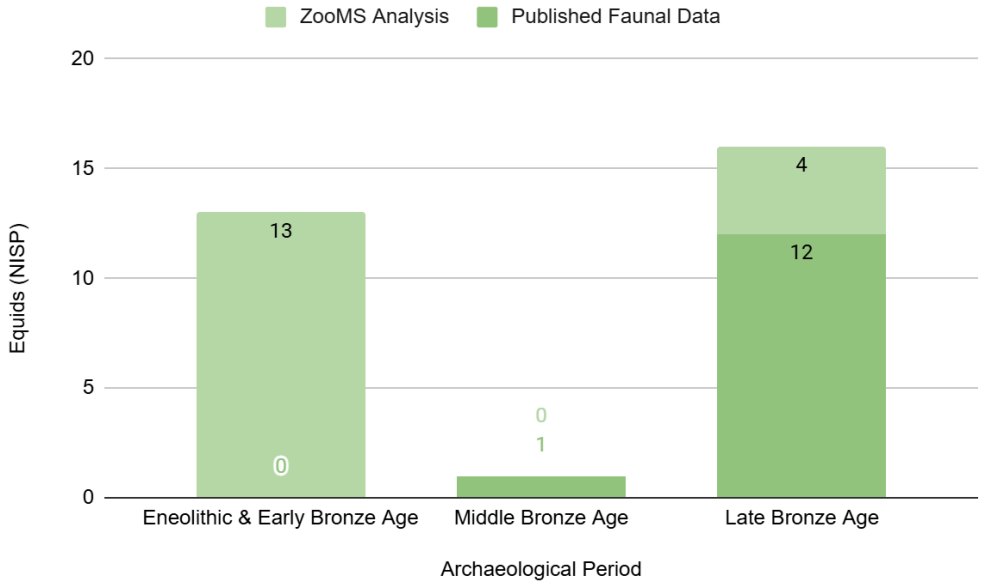


Fig.53 Bar graph of NISP data for *Ovis* sp. & *Capra* sp. remains recovered from Bronze Age Outer Mongolia.

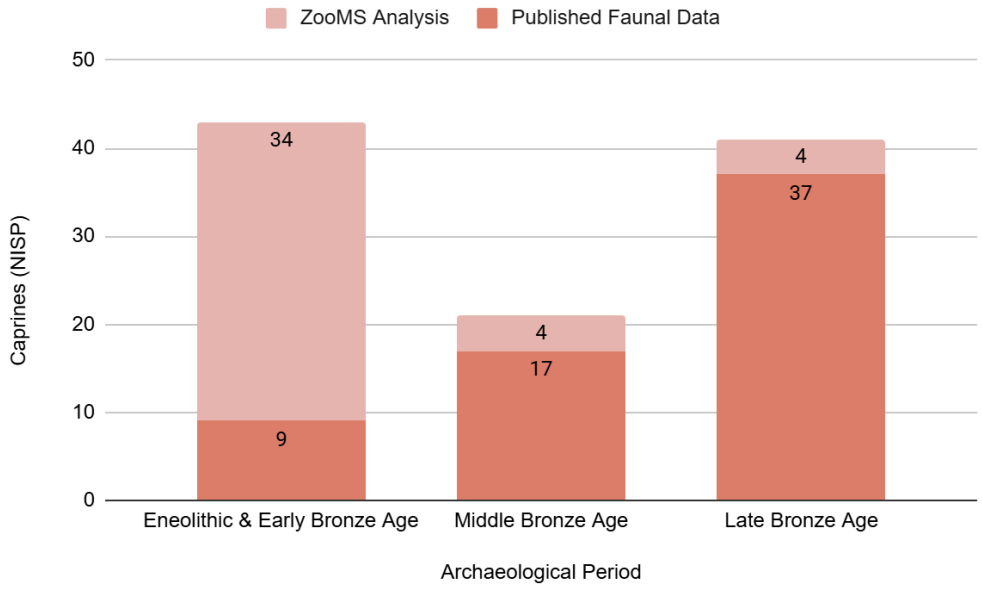
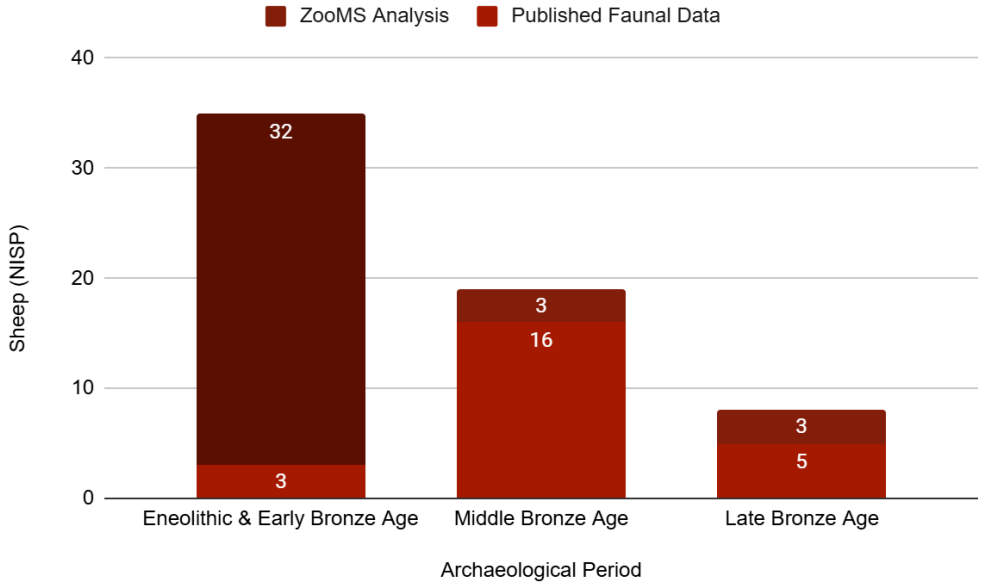


Fig.54 Bar graph of NISP data for sheep (*Ovis* sp.) remains recovered from Bronze Age Outer Mongolia.



21.12.3. Medieval Uzbekistan

The results of my ZooMS analysis represent a solid contribution to the NISP data currently available for cattle, equids, caprines, and especially camels from Medieval contexts in Uzbekistan (Figs.55–58). My ZooMS-based camel identifications significantly contribute to the overall camel NISP from archaeological sites in Uzbekistan in general (Fig.57). For published sources of NISP data, see Chapters 18, 19.

Fig.55 Bar graph of NISP data for cattle (*Bos* sp.) remains recovered from ancient Uzbekistan.

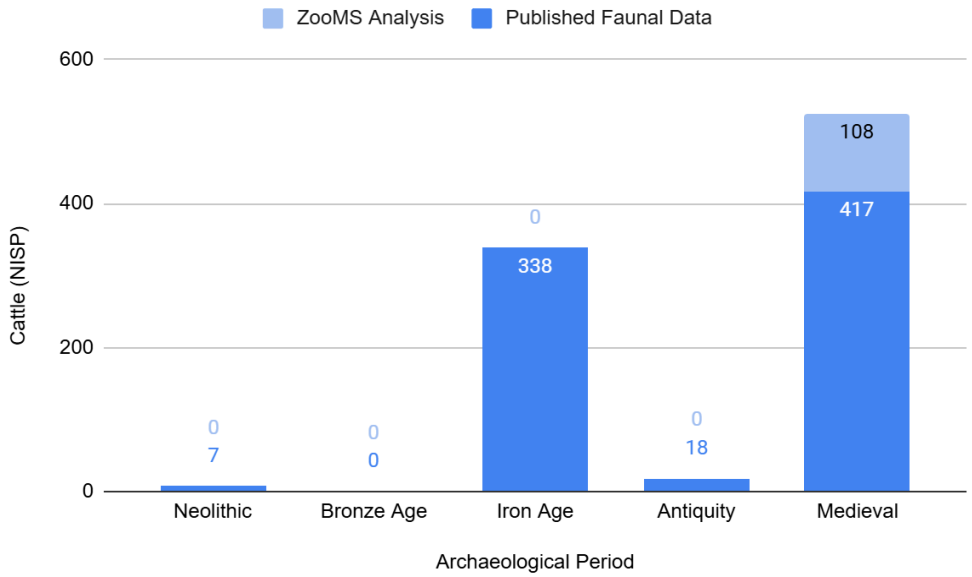


Fig.56 Bar graph of NISP data for equids (*Equus* sp.) remains recovered from ancient Uzbekistan.

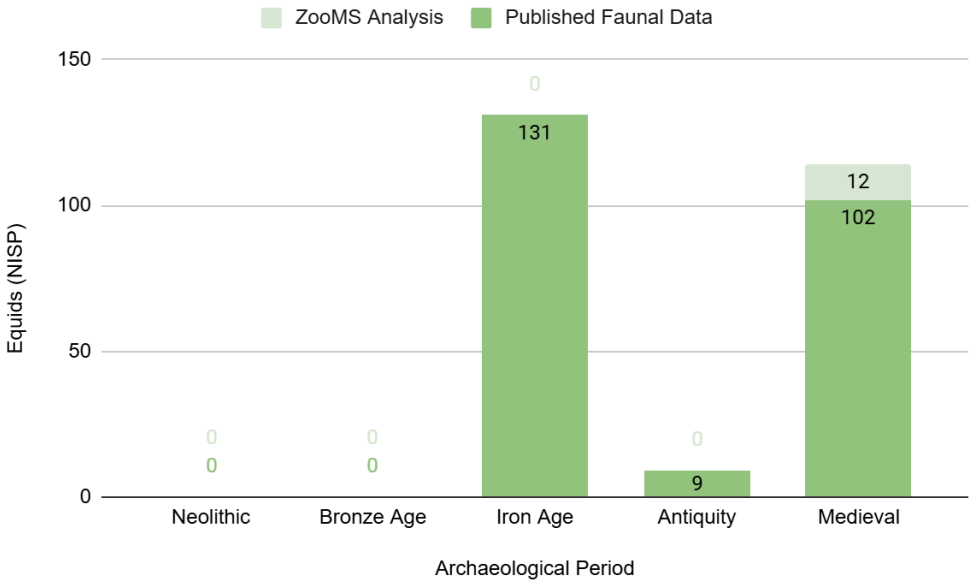
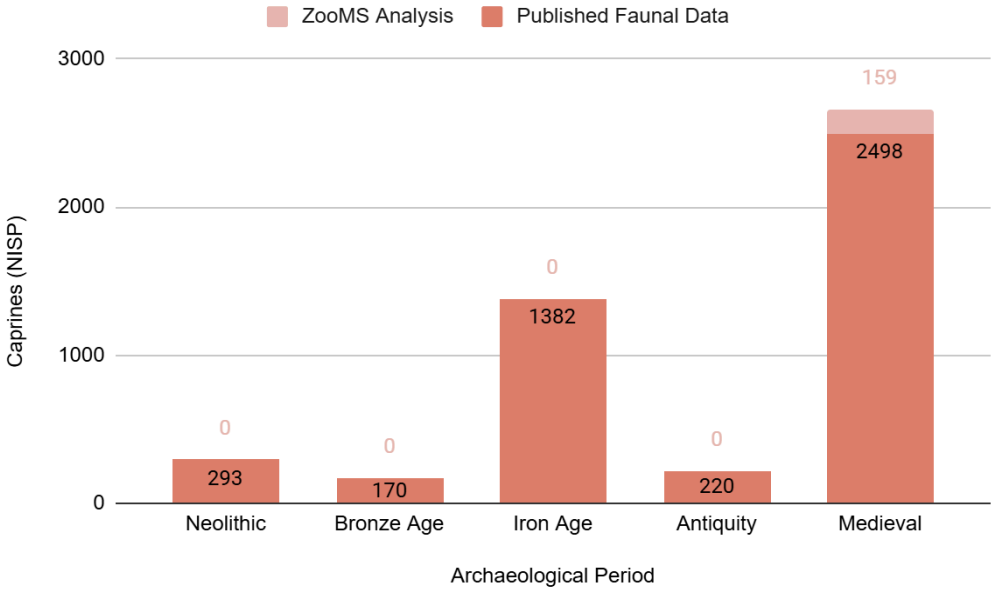


Fig.57 Bar graph of NISP data for camel (*Camelus* sp.) remains recovered from ancient Uzbekistan.

Fig.58 Bar graph of NISP data for *Ovis* sp. & *Capra* sp. remains recovered from ancient Uzbekistan.



22.12. MALDI Collagen Screening of Comparative Specimens

22.12.1. *Gazella subgutturosa*

The tryptic masses measured at all collagen peptide marker sites were consistent in all samples, and were clearly diagnostic of a species of antelope (Tbl.136; Fig.59; see Appendix 03). I was able to predict the probable tryptic masses for all collagen peptide marker sites as measured by MALDI (Tbl.137).

Tbl.136 Table of tryptic masses measured in reference collection specimens of *Gazella subgutturosa*.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
EH04_1	1105.2	1180.3	1196.3	1427.3	1550.3	1648.4	2130.5	2791.5	2882.6	2898.6?	3016.5	3032.6
EH04_2	1105.6	1180.7	1196.7	1427.8	1550.8	1648.9	2131.2	2793.5?	2883.5	2899.5	3017.5	3034.6?
EH04_3	1105.7	1180.8	1196.8	1427.9	1550.9	1649	2131.3	2792.6	2883.7	2899.7	3017.7	3034.9?
EH05_1	1105.3	x	1196.4	1427.4	1550.4	1648.5	2130.6	2791.7	2882.7	2899.7	3016.7	3032.8
EH05_2	1105.7	1182.8	1196.7	1427.8	1550.9	1648.9	2131.2	2792.5	2883.5	2900.5	3017.6	3033.7
EH05_3	1105.6	1180.7?	1196.7	1427.8	1550.8	1648.9	2131.2	2793.4?	2883.5	2900.4?	3017.5	3034.6
EH06_1	1105.6	1182.7	1196.7	1427.8	1550.8	1648.8	2131.1	2793.1	2883.3	2899.3?	3017.2	3033.3
EH06_2	1105.4	1180.5	1196.5	1427.5	1550.5	1648.6	2130.8	2792	2883.1	2899.1	3017.1	3033.2
EH06_3	1105.7	1180.8?	1196.8	1427.9	1550.9	1649	2131.3	2792.6?	2883.7	2899.7	3017.7	3033.8
EH07_1	1105.6	1180.6	1196.7	1427.7	1550.7	1648.8	2131	x	2883.2	x	3017.1	3033.1?
EH07_2	1105.3	1180.4	1196.4	1427.5	1550.5	1648.5	2130.7	x	2883	x	3016.9	3034
EH07_3	1105.7	1180.7	1196.7	1427.8	1550.9	1648.9	2131.2	x	2883.6	x	3017.6	3034.7
EH08_1	1105.5	1180.6?	1196.6	1427.7	1550.7	1648.7	2130.9	x	2883.1	x	3017	3034.2
EH08_2	1106.1	x	1197.2	1428.3	1551.4	1649.5	2131.7	x	2883.1	x	3018	x
EH08_3	1105.6	1180.8?	1196.8	1427.9	1550.9	1649	2131.2	x	2883.7	x	3017.7	x

Tbl.137 Table of suggested tryptic masses of collagen peptide markers in *Gazella subgutturosa*.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Gazella subgutturosa	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4

22.12.2. *Cervus nippon*

The tryptic masses measured at all collagen peptide marker sites were consistent in the two samples (EH01 & EH02) that did produce MALDI spectra with diagnostic peaks (Tbl.130; see Appendix 03). Both of these MALDI spectra were indicative of a deer species (Tbl.139; Fig.60). Although coverage of the sika deer samples was much lower than in the goitered gazelle samples, I was still able to predict the probable tryptic masses for 11 collagen peptide marker sites (Tbl.138).

Tbl.138 Table of suggested tryptic masses of collagen peptide markers in *Cervus nippon*.

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Cervus nippon	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4

Tbl.139 Table of tryptic masses measured in reference collection specimens of *Cervus nippon*.

Sample No.	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
EH01_1	x	x	x	x	x	x	x	x	x	x	x	x
EH01_2	1105	1180.1?	x	1427.1	x	1648.1	2130.3	2792.3	2882.3	x	3017.3	3033.4
EH01_3	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.5	2900.5?	3018.5	3033.7
EH02_1	x	x	x	x	x	x	x	x	x	x	x	x
EH02_2	1105.4	1180.4	x	1427.5	1550.5	1648.6	2130.8	2792	2883	x	x	x
EH02_3	1105.4	1180.5	x	1427.6	1550.6	1648.6	2131?	2793.1?	2883.2	x	x	x
EH03_1	x	x	x	x	x	x	x	x	x	x	x	x
EH03_2	x	x	x	x	x	x	x	x	x	x	x	x
EH03_3	x	x	x	x	x	x	x	x	x	x	x	x

Fig.59 Example MALDI spectra of sample EH06 (*Gazella subgutturosa*) with highlighted markers.

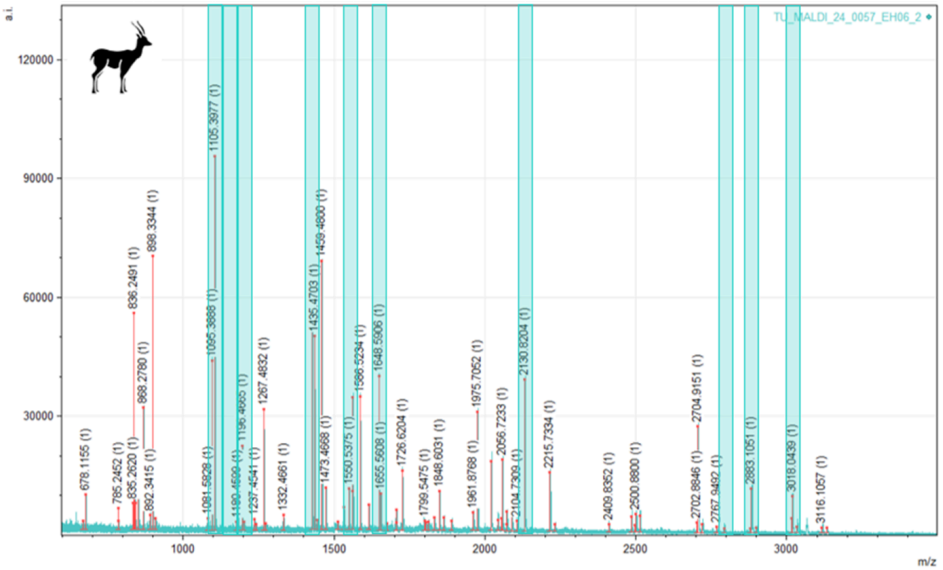
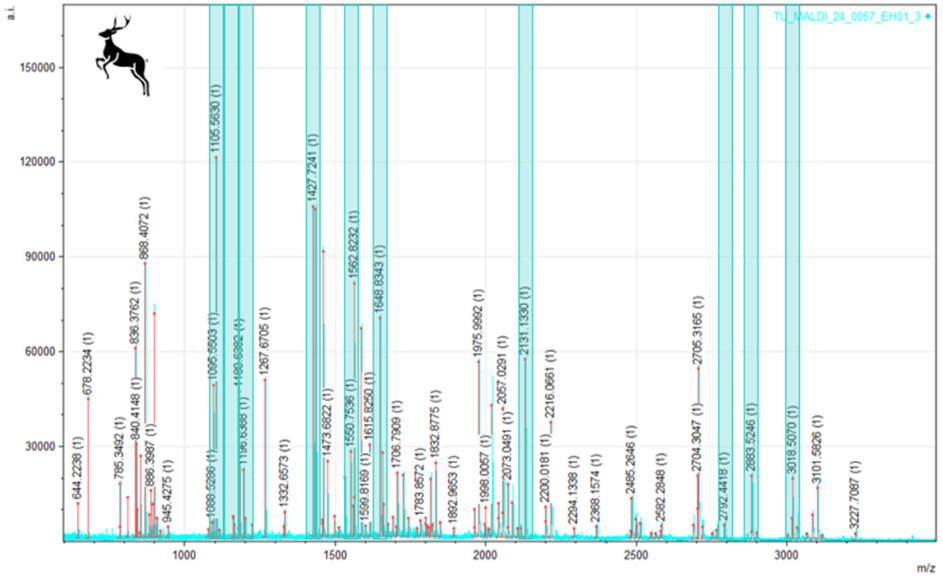


Fig.60 Example MALDI spectra of sample EH01 (*Cervus nippon*) with highlighted markers.



Chapter 22. Discussion

22.1. Nizhnyaya Sooru

22.1.1. Animal Economies

Iron Age Animal Economies (Layer 02)

I selected only 6 samples from the Iron Age occupation Layer (Layer 02) of Nizhnyaya Sooru, as my study is much more concerned with the reconstruction of Afanasievo subsistence lifeways and the emergence of pastoralism in Inner Asia. Five of these samples were selected because they could only be attributed to size-based categories, and the other (NZS227.A) to verify the accuracy of the morphological attribution of "*Ovis* sp.". I was able to use ZooMS to refine the "Medium Mammal" identifications to a mix of caprines and wild ungulates, and the "Large Mammal" identifications to were equids. The presence of horses, caprines, and wild ungulates in Layer 02 suggests a mixed reliance of hunting and herding, though it is unclear if the equids and caprines were wild or domesticated (or both). The Iron Age context strongly suggests that herding would have contributed to subsistence at Nizhnyaya Sooru during this later period of occupation, and the presence of domesticated horses would not be unexpected. Interestingly, the only *Capra* sp. sample I identified from Nizhnyaya Sooru (NZS097.A) was recovered from this layer, possibly suggesting a later reliance on domesticated goat or Siberian ibex.

Middle – Late Bronze Age Animal Economies (Layer 03)

I selected even fewer samples from the Nizhnyaya Sooru Middle–Bronze Age occupation layer (Layer 03) than the Iron Age layer (Layer 02). I identified 2 out of the 3 samples I selected as equids (NZS226.A & NZS234.A), and the third as a sheep (NZS235.A). The presence of equids in both the Middle–Late Bronze Age and Iron Age layers, especially nested within such small sample sizes, suggests a continued reliance on horses at NZS from the Middle Bronze Age onward. All three samples could be wild or domesticated in origin. More interesting in this layer perhaps is the application and utility of ZooMS to clarify morphological identifications. Sample NZS226.A has been misidentified as *Bos* sp. instead of *Equus* sp., and sample NZS234.A (also an equid) could only be morphologically attributed to a "Medium Mammal".

Early Bronze Age Animal Economies (Layer 04)

I did not identify equids in any of the samples (n=17) from the Early Bronze Age layer (Layer 04), which supports a later date for horse domestication in the Central Altai region. This is especially true considering the sample size increase from Layers 02-03, both of which contained multiple equids (Tbl.140). There are many biases, ranging from sampling to discovery to taphonomic, which could be influencing this result. However, the fact remains that I did not identify any equids and as of yet no horse remains recovered from Early Bronze Age Southern Siberian contexts have been verified as domesticated (see Chapter 15). The presence of a

single wild ungulate (NZS195.A) suggests that hunting was still an economic activity during Early Bronze Age occupation at Nizhnyaya Sooru, though likely a secondary one, as the remaining samples were identified as cattle or caprine. Caprines dominated, and I identified 92% of the caprine samples as sheep specifically. I was unable to identify the remaining caprine sample (NZS233.A) as either sheep or goat. Livestock rearing, most especially of sheep, appears to have been the dominant subsistence strategy at Nizhnyaya Sooru during this period.

Eneolithic Animal Economies (Layers C, 5A/5B)

The samples I selected and fingerprinted from the Eneolithic occupation layers of Nizhnyaya Sooru (Layer C, Layer 5A/5B) were overwhelmingly dominated by caprines, especially sheep (n=88), which comprised 82% of the caprines and 61% of the total Eneolithic faunal assemblage (Tbl.141). I was unfortunately unable to identify the remaining caprines (n=20) to either *Ovis* sp. or *Capra* sp., and so it remains unclear if Afanasievo peoples at Nizhnyaya Sooru were exclusively herding sheep or if they were also herding a smaller population of goats. The latter would be consistent with what is currently known of herd compositions from Neolithic Central Asia (see Chapter 19, also Taylor et al. 2021a) as well as much of historical Inner Asia (see Chapter 08), though it is likely that only the sheep would have been dairyed (see Scott et al. 2022). A substantial but secondary representation of cattle (15% of the combined Eneolithic assemblage) and a seeming absence of horses would suggest limited mobility, more conducive to transhumant pastoralism than highly mobile pastoralism (see Chapter 09).

All canid samples that I identified from Nizhnyaya Sooru were also recovered from the Eneolithic layers; these could be either dogs, which could be expected in an assemblage characterized by livestock, or foxes / wolves. The presence of foxes and wolves could occur independently of human hunting activities. This is possibly the case for the Eneolithic layers of Nizhnyaya Sooru, especially considering that the only bird and hare samples I identified were also found in the Eneolithic layers. I did not identify any deer or antelope from these layers, perhaps suggesting that hunting was not altogether common. Higher resolution analyses would be necessary to confirm whether these canid remains are more likely related to the use of dogs to herd sheep and cattle, or the result of either the human hunting of wild canids or an intrusion of wild canids into Nizhnyaya Sooru.

In the context of Afanasievo animal economies, sheep appear to have been domesticated while horses did not, cattle were reared, and the hunting of small game may have been preferred to antelope and deer hunting. This could already be said to sharply contrast with the later prehistory of Nizhnyaya Sooru, where both equids and antilopines / cervids are represented. The results of the ongoing analysis of the Nizhnyaya Soorufauna should greatly clarify many of the questions that I have raised here, though subsequent genomic analysis would also help to clarify Afanasievo reliance on hunting versus herding. ZooMS, like any other archaeological method, is best employed in tangent with other robust methods and lines of evidence. At the same time, the results of my ZooMS analysis have already provided valuable new insights into Eneolithic subsistence at Nizhnyaya Sooru.

22.1.2. Taxon-Specific Management

Cattle

Cattle were clearly an important part of Eneolithic and Early Bronze Age animal husbandry at Nizhnyaya Sooru (Tbl.140), which is in keeping with the little that we know of Afansievo pastoralism (see Chapters 01, 09–15). ZooMS cannot be used to distinguish between yak and taurine cattle, and yak have been reported from Afanasievo occupation layer of Uznezya-I, though this assemblage was commingled with materials from later periods (Kostinev 2005). The early distribution of yak across Inner Asia remains poorly understood (see Tumurbaatar & Makarewicz 2022), though yak are not generally associated with Afanasievo animal economies. Taurine cattle, or the wild aurochsen forebears, are more likely candidates for the Eneolithic and Early Bronze Age bovines recovered from Nizhyaya Sooru. The absence of cattle after the Early Bronze Age is much more likely reflective of sampling biases than any disruption in cattle rearing, though there is currently no faunal report to compare my results with.

Tbl.140 Table of zooarchaeological and ZooMS-based identifications of cattle from Nizhnyaya Sooru.

Period	Eneolithic		Early Bronze Age	Middle – Late Bronze Age	Early Iron Age	*Historical / Modern
Layer	Layer 5A / 5B	Layer C	Layer 04	Layer 03	Layer 02	Layer 01
ZooMS ID	15	**7**	4	0	**0**	**0**

**No samples were selected from Layer 01.*

Equids

I did not identify any equids in the earliest occupation layers of Nizhnyaya Sooru (Tbl.141), and have thus found no supporting evidence for Afansievo or pre-Late Bronze Age horse domestication in Southern Siberia. My identification of equids in the later Bronze Ages and Early Iron Age is not at all surprising, as it is known that horse culture exploded across Eurasia during this period, most especially in Inner Asia (Taylor 2024; see also Chapter 15). That being said, the fact that I did not identify any equid in earlier layers does not necessarily mean that domesticated horses were not present (though this is unlikely), nor that equids such as Przewalskii's horse (*Equus przewalskii*) were not being hunted (this is far more likely).

Tbl.141 Table of zooarchaeological and ZooMS-based identifications of equids from Nizhnyaya Sooru.

Period	Eneolithic		Early Bronze Age	Middle – Late Bronze Age	Early Iron Age	*Historical / Modern
Layer	Layer 5A / 5B	Layer C	Layer 04	Layer 03	Layer 02	Layer 01
ZooMS ID	0	**0**	0	2	2	**0**

**No samples were selected from Layer 01.*

Caprines

Caprines were the most abundant of all the taxa identified at Nizhnyaya Sooru (~ca. 80%), though selection bias undoubtedly plays into their high representation. I determined that over 65% of the caprines I identified were *Ovis* sp., which is not a relic of sample selection. The dominance of *Ovis* sp., especially in the Eneolithic & Early Bronze Age layers (which I selected for) is in accord with recent finding of the importance of sheep husbandry and dairying across the ancient Eurasian Steppe (Scott et al. 2022; Wilkin et al. 2020) (Tbl.142). It is very likely that Afansievo peoples were milking sheep at Nizhnyaya Sooru, though a shotgun proteomic analysis of human dental calculus or pottery sherd residues recovered from the Eneolithic layers of the site would provide stronger insight (see Chapter 04), if any such materials have been recovered.

Tbl.142 Table of zooarchaeological and ZooMS-based identifications of caprines from Nizhnyaya Sooru.

Period	Eneolithic		Early Bronze Age	Middle – Late Bronze Age	Early Iron Age	*Historical / Modern
Layer	Layer 5A / 5B	Layer C	Layer 04	Layer 03	Layer 02	Layer 01
ZooMS ID	101	32	12	1	3	0

**No samples were selected from Layer 01.*

Antilopines & Cervids

Very few antelopes / deer were recovered from Nizhnyaya Sooru, and so it can only be suggested that their hunting formed a small part of the prehistoric economic activities, at least during the Early Bronze and Iron Age (see Tbl.143).

Tbl.143 Table of zooarchaeological and ZooMS-based identifications of antilopines & cervids from NZS.

Period	Eneolithic		Early Bronze Age	Middle – Late Bronze Age	Early Iron Age	*Historical / Modern
Layer	Layer 5A / 5B	Layer C	Layer 04	Layer 03	Layer 02	Layer 01
ZooMS ID	0	0	1	0	1	0

**No samples were selected from Layer 01.*

22.2. ZK513

22.2.1. Animal Economies

Iron Age Animal Economies (Layers 06-07)

I was able to use ZooMS to identify 20 animal bone fragments from the Iron Age layers of ZK513-1, including the only antilopines / cervids from my analysis (n=2). The other taxa I identified were *Ovis* sp., *Capra* sp., *Ovis* sp. / *Capra* sp., *Bos* sp., and *Equus* sp., which is mostly in line with the original report (Houle et al. 2022). The original faunal report did not identify antilopines / cervids or goats / ibex. Thus, there is an element of hunting during the Iron

Age occupation at ZK513 that had previously been undetected. The largest number of bone fragments accounted for in both the original report (Houle et al. 2022) and my own study are caprines, suggesting that sheep and goat pastoralism were the main economic activity of this period. It is unclear which of the specimens I identified were wild and which were domesticated, though domesticated horses should be expected at an Iron Age site in Outer Mongolia (see Chapters 11-15).

Middle–Late Bronze Age Animal Economies (Layers 09-10)

I identified 12 animal bone fragments from the Middle and Bronze Age layers using ZooMS, most of which were *Ovis* sp., *Capra* sp., and *Ovis* sp. / *Capra* sp., amongst a handful of equid specimens (n=4). The original faunal report listed, in total, only a single *Ovis* sp. / *Capra* sp. fragment and a single *Bos* sp. fragment (Houle e al. 2022). While I did not identify cattle in the course of my ZooMS analysis, there remain 26 fragments from this layer which have not been identified morphologically or proteomically, and there is no reason to suspect that cattle remains would not number among them. There is currently no zooarchaeological evidence of hunting at ZK513 prior to the Iron Age, though hunting very well may have taken place. It is clear that caprine pastoralism was likely the main economic activity during the Middle and Late Bronze Ages, and it seems unlikely that the caprines from this layer would all be wild. From the evidence we currently have, it does not appear that domesticated horses were present during this period.

Eneolithic–Early Bronze Age Animal Economies (Layers 08, 11-12)

Using ZooMS, I identified 32 *Ovis* sp., 1 *Capra* sp., and 1 *Ovis* sp. / *Capra* sp. fragments from the earliest layers of ZK513; when combined with the 14 caprines identified in the faunal report (Houle et al. 2022), a familiar picture of caprine pastoralism as a primary economic activity emerges. I also identified 4 cattle bones and 13 equid bone fragments which supplement the 2 cattle bones and 2 equid bones previously identified (Houle et al. 2022). The equid bones which have been submitted for aDNA analysis have been identified as the wild Pleistocene *Equus ovodovi*, and there is no indication that domesticated horses were present during the Eneolithic & Early Bronze Age periods. The seeming absence of equids during the Middle and Late Bronze Ages suggests instead that wild equids were hunted during the earliest phases of occupation at ZK513-1, and that domesticated horses were not exploited until the Iron Age (or shortly before).

22.2.2. Taxon-Specific Management

Cattle

Cattle (*Bos* sp.) are nearly omnipresent throughout all phases of human occupation at ZK513, and my ZooMS analysis has confirmed their presence as far back as 2010-1770 BCE (Tbl.143). The presence of cattle so early suggests that pastoralism, or at least cattle rearing, has been a component of human subsistence at ZK513 since its earliest phases of occupation (excluding

Layer 12, the earliest layer). The cattle remains that I was able to identify from Layer 11 (2010-1770 BCE) and Layer 08 (2020-1780 BCE) at ZK513-1, are to date the oldest archaeological cattle remains to have been *securely* identified from Outer Mongolia (see Houle et al. 2022, also Chapter 12). Houle et al. (2022) report 206 unidentifiable fragments from Layer 12, only 27 of which were selected for my study (Fig.22), and it is very possible that a follow-up ZooMS study of these remaining fragments would identify the remains of *Bos* sp. among them. The same can be said for Layer 10 and Layer 05, the only other layers that cattle remains have not been identified by zooarchaeological analysis or ZooMS (Tbl.144).

Tbl.144 Table of zooarchaeological and ZooMS-based identifications of cattle from ZK513-1.

Period	Eneolithic & Early Bronze Age			Middle Bronze Age	Late Bronze Age	Iron Age		Early Medieval			Historical	
Layer	Layer 12	Layer 11	Layer 08	Layer 09	Layer 10	Layer 07	Layer 06	Layer 05	Layer 04	Layer 03	Layer 02	Layer 01
Zooarch ID	/	/	**1**	**1**	/	/	**3**	/	**1**	**2**	**1**	**2**
ZooMS ID	/	**1**	**3**	/	/	**2**	**2**	/	/	**2**	**1**	**1**

The very early and consistent presence of cattle that both my ZooMS results and the initial faunal analysis (Houle et al. 2022) have been able to identify strongly support the theory that Eneolithic / Early Bronze Age Afanasievo peoples introduced domesticated cattle into Outer Mongolia (see Houle et al. 2022, also Chapters 01, 06, 09–10, 15). The aDNA analysis of the earliest cattle samples from ZK513 would provide a higher resolution taxonomic identification and facilitate lineage reconstruction of any samples securely identified as domesticated cattle (see Chapter 04). Should future studies securely identify the presence of domesticated cattle in the Early Bronze Age layers (Layers 12, 11, & 08), the role of both Afanasievo migrations into the Eastern Eurasian Steppe as well as the role of and mountains and foothills would be further emphasized in the story of domesticated animal dispersal from West Asia into Inner Asia.

Equids

I identified equids in the Bronze Age, Iron Age, Medieval, and historical layers of the ZK513-1 Trench– including in the earliest Eneolithic and Bronze Age Layers (Tbl.145). These layers correspond with the current data for the introduction of domesticated horses (DOM2) into Outer Mongolia (Houle et al 2022; Librado et al 2021; see also Chapter 01, 06, 09, 11, 15). The four equid samples that I identified in the earliest layer (Layer 12; ca. 2030-1880 BCE) had the potential to be the earliest discovered domesticate horses in Outer Mongolian archaeological contexts (see Chapter 11). These four samples were subsequently submitted for AMS radiocarbon dating and genomic analysis and determined not to be *Equus caballus* but *Equus ovodovi*, an extinct Late Pleistocene / Early Holocene equid (Pan et al. 2024; see Appendix 03).

Wild horses were known to have been hunted in Outer Mongolia during the Bronze Age (Taylor et al. 2024), and the recovery of wild equids here is not surprising. At the same time, the identification of *Equus ovodovi* in an Eneolithic context has established that this equid was known to and preyed upon by early Mongolian peoples. Previous morphological identifications of domesticated horses in Bronze Age archaeological sites are thus even more questionable

than previously suggested (see Chapter 15). I believe that collagen peptide mass fingerprinting with chymotrypsin (as opposed to trypsin) would be an effective way to screen for domesticated horses in future ZooMS analyses, especially in Central Eurasian contexts, as *Equus ovodovi* is closer related to stenoids than caballoids (see Paladugu et al. 2023).

Tbl.145 Table of zooarchaeological and ZooMS-based identifications of equids from ZK513-1.

Period	Eneolithic & Early Bronze Age			Middle Bronze Age	Late Bronze Age	Iron Age		Early Medieval			Historical	
Layer	Layer 12	Layer 11	Layer 08	Layer 09	Layer 10	Layer 07	Layer 06	Layer 05	Layer 04	Layer 03	Layer 02	Layer 01
Zooarch ID	**1**	**1**	/	/	/	**1**	**1**	**2**	/	**2**	**1**	**1**
ZooMS ID	**4**	**8**	**1**	/	**4**	**1**	**3**	/	**1**	/	/	**1**

Caprines

My ZooMS results have established the presence and possibly dominance of *Ovis* sp. in nearly all levels of ZK513, including in layers where caprines had been previously undetected (Tbl.146). I was able to identify sheep (Ovis sp.) in Layers 02, 04, and 07-11 and goats (*Capra* sp.) in Layers 02, 03, 05, 08, and 09, where they had not been identified in the initial reports (i.e. Houle et al. 2022). My results demonstrate the utility of using ZooMS to refine the size-based taxonomic identifications of fauna from the Bronze Age assemblages of Central Eurasia, as well as to securely attribute taxa to morphologically unidentifiable fragments from these contexts. As far as I am aware, the sheep (n= 22) and ambiguous caprine (n=1) that I identified from Layer 12 (2030-1880 BCE) of ZKG513-1 are the oldest *securely* identified archaeological sheep and caprine remains recovered from Outer Mongolia (see Houle et al. 2022 and Chapter 11). It is unclear whether these belonged to livestock or wildstock (or both).

Tbl.146 Table of zooarchaeological and ZooMS-based identifications of caprines from ZK513-1.

Period	Eneolithic & Early Bronze Age			Middle Bronze Age	Late Bronze Age	Iron Age		Early Medieval			Historical	
***Ovis* sp.**												
Layer	Layer 12	Layer 11	Layer 08	Layer 09	Layer 10	Layer 07	Layer 06	Layer 05	Layer 04	Layer 03	Layer 02	Layer 01
Zooarch ID	**3**	/	/	/	/	/	**5**	/	/	**1**	/	**1**
ZooMS ID	**22**	**9**	**1**	**3**	**3**	**3**	**6**	/	**1**	**1**	**3**	**2**
***Capra* sp.**												
Zooarch ID	**1**	/	/	/	/	/	/	/	/	/	/	**1**
ZooMS ID	/	/	**1**	**1**	/	/	/	**1**	/	**1**	**1**	**1**
Caprines (*Ovis* sp., *Capra* sp., *Ovis* sp. / *Capra* sp.)												
Zooarch ID	**8**	**1**	**4**	**1**	/	**25**	**7**	**1**	**9**	**6**	**5**	**14**
ZooMS ID	**23**	**9**	**2**	**4**	**4**	**4**	**6**	**2**	**2**	**2**	**4**	**3**

A recent mtDNA study has established the presence of domesticated sheep at Nizhnyaya Sooru (see Chapters 12–14) during the Bronze Age in the Central Altai region (Hermes et al. 2020). The presence of domesticated sheep during the Early Bronze Age period of occupation at ZK513 would support the theory that Afansievo peoples initially introduced livestock into Outer Mongolia (see Chapter 09, 15); this is especially true considering the presence of cattle in these early occupation layers. At the same time, wild caprines in these layers would not be unexpected, especially considering the presence of wild equids in the earliest Bronze Age layer of ZK513-1 (Pan et al. 2024, in press.). Caprine samples from Layer 12 have been selected for subsequent aDNA analysis. The application of aDNA analysis to the caprines samples from ZK513-1 would provide invaluable insight into the timing and spread of sheep domestication into Outer Mongolia.

Antilopines & Cervids

Cervids and gazelle were identified with both zooarchaeology and ZooMS, but only in the Late Iron Age and Early Medieval strata (Tbl.147). It is very possible that there are more cervids and gazelle represented in the lower layers of ZK513-1, just as it is possible that hunted game were processed and disposed of in a different area of the ZK513 site. Taken at face value, the very limited evidence that we do have could suggest that hunting was more prevalent during the later periods of human occupation at ZK513-1. As ZooMS cannot be used to discriminate between argali and domesticated sheep, Siberian ibex and domesticated goat, or wild versus domesticated horses, it is difficult to argue for hunting or herding prevalence at ZK513 based off of the other ZooMS-based taxonomic identification associated with the later layers.

Both ZooMS-based and zooarchaeological identifications of cattle are associated with nearly every cultural layer of ZK513 (Tbl.144), suggesting that hunting was never the sole economic activity at ZK513. It need not be the case that cattle were being butchered for meat, however, as butchery marks have so far only been recorded on caprine remains (Houle et al. 2022). A much larger number of samples from the faunal assemblage will need to be submitted for ZooMS before any stronger conclusions can be drawn about the exploitation of cervids and gazelle at ZK513-1. There are currently no stratified archaeological settlement sites in Western Mongolia with a faunal assemblage for comparison or inference (see Chapters 11–15).

Tbl.147 Table of zooarchaeological and ZooMS-based identifications of antilopines & cervids from ZK513-1.

Period	Eneolithic & Early Bronze Age			Middle Bronze Age	Late Bronze Age	Iron Age		Early Medieval			Historical	
Layer	Layer 12	Layer 11	Layer 08	Layer 09	Layer 10	Layer 07	Layer 06	Layer 05	Layer 04	Layer 03	Layer 02	Layer 01
Zooarch ID	/	/	/	/	/	/	/	/	/	**1**	/	/
ZooMS ID	/	/	/	/	/	/	**2**	/	/	/	/	/

22.3. Tashbulak

22.3.1. Animal Economies

The combined archaeobotanical (see Chapter 18) and faunal evidence from Tashbulak suggests that agropastoralism was the predominant subsistence strategy at Tashbulak. A wide variety of fruits, legumes, and grains appear to have been cultivated alongside the rearing of goat, sheep, cattle, and horses (or onagers, etc.) (see Chapter 18). These findings support the theory that Medieval pastoralists in Transoxiana adapted their subsistence practices around the onset of the Medieval Climate Anomaly (see Chapter 19), though it may also be the case that agropastoralism was being practiced in the highlands prior to this aridification event. The presence of agriculture, metallurgy, and cattle rearing suggests that the pastoralists of Tashbulak were not especially mobile, even though equids and camel remains (Fig.61) were recovered in limited numbers.

Fig.61 Photograph of a camel maxilla recovered from Tashbulak (photographed by Eden Hill).

22.3.2. Taxon-Specific Management

<u>Cattle</u>

I identified the majority (~32%) of the fragments from Tashbulak as *Bos* sp.; without a faunal report to compare my results to, I cannot say if this is in line with the zooarchaeological analysis or if it is higher, as tends to be the case with ZooMS-based bovine identifications (see Chapter 05). A large number of cattle does not suggest that the inhabitants of Tashbulak were highly mobile, even if the site can be interpreted as a mix of sedentary metallurgists and semi-nomadic herders. In lieu of mortality data, it is unclear if these cattle were slaughtered for meat or were also milked. A large number of cattle is also in keeping with what has so far been observed in

the faunal assemblages of Medieval Uzbekistan, subject to taphonomic and sampling bias though these observations may be (see Chapter 02).

Equids

A low representation of equids (~3%) further suggests that the pastoralist component of Tashbulak was not especially mobile. It is unlikely that the zooarchaeological report will differ greatly in this respect. Horses were probably managed at Tashbulak for transportation as well as for herding livestock. Equids are not uncommonly recovered from Medieval archaeological sites in Uzbekistan (see Chapter 19), though the highland elevation of Tashbulak provides a more unique context.

Camelids

My ZooMS-based identification of 10 camel bone fragments at Tashbulak is intriguing. Camels are better suited to arid lowland environments, such as deserts, than highlands and mountains (see Chapter 07). It may be the case that the Medieval pastoralists of Tashbulak began rearing small numbers of camels due to their general resilience and ability to browse on shrubs and other non-grasses (see Chapter 07). The inclusion of camels into highland herds may have been a strategic adaptation in the face of climate change and increasing aridification, especially considering the consistent underrepresentation of camels in both the prehistoric and historical faunal assemblages of Transoxiana, Bactria, and Khorezm (Fig.61; see Chapter 21) and Central Asia more broadly (see Chapter 08).

The presence of camels at a settlement site that specialized in metal crafting might also suggest consistent long-distance trade, especially under Qarakhanid rule, as the Qarakhands were instrumental in the intensification of Trans-Eurasian trade (see Chapter 18). As far as I am aware, my results are the first to use ZooMS to establish the presence of camels at a Medieval Transoxian archaeological site– highland or lowland (see Chapter 19). Our understanding of Transoxian camel exploitation especially would be enhanced by the continued application of ZooMS to fragmented faunal assemblages. My own ZooMS data has already contributed significantly to the overall NISP data variable for camels from archaeological sites in Uzbekistan, representing more than half of the data published for the medieval period (see Chapters 18–19).

Caprines

The overwhelming majority of the caprine samples I taxonomically identified with ZooMS were *Capra* sp. as opposed to *Ovis* sp. – including specimens that had been morphologically and non-tentatively identified as “Ovis”. This suggests that the dominance of *Capra* sp. is not just the result of morphologically ambiguous caprine bone fragments being more likely to be goat, but also that there were more goats than sheep present at Tashbulak. It is highly unlikely that these were predominantly wild goats, due to the Medieval context (see Chapter 19) and the presence of cattle (see Chapter 08). The preference for goat rearing instead of sheep rearing that can be inferred at Tashbulak is drastically opposed to the Bronze Age pastoralist strategies of Inner

Asian settlement sites such as Nizhnyaya Sooru and ZK513, which were sheep-focused. My ZooMS results are the first to establish a high goat to sheep ratio in a Medieval Transoxian context (see Chapter 19).

Goats are more resilient than sheep and are better adapted to both arid and highland environments (see Chapter 07). It is unsurprising that the Medieval pastoralists of Central Asia, who were undoubtedly more diversified and would have had more options than their prehistoric predecessors, would prefer to rear goats in the highland regions– especially following the onset of the Medieval Climate Anomaly (see Chapters 18–19). The preference for goat rearing at Tashbulak, combined with the low recovery of wooling artifacts (see Chapters 17–18), further suggests that wool production was not a primary economic activity. Although Tahsbulak is located in textile-rich Ustrushna, the site appears to have been a mining settlement with an agropastoralist subsistence component (see Chapters 18–19). It does not seem likely that large quantities of raw wool and yarn were produced at Tashbulak, or that artisans were manufacturing woolen textiles at Tashbulak on a large scale.

In all likelihood, there were enough wool-producing animals and wooling implements to maintain the day-to-day textile needs of Tashbulak, but not enough for commercial purposes. This suggests that the woolen textile industry of Medieval Transoxiana was unlikely to have been based in the highlands, or at least not in highland settlements which were centered around mining and metallurgy. If goats were more often managed in the highlands, then perhaps sheep (which produce larger quantities of wool, and have long been favored in Eurasia for dairying; Scott et al. 2022) were more prevalent in the lowlands of Ustrushna and Transoxiana more generally. There are currently not enough archaeological data to make any strong assertions, though it may be the case that the wool and woolen textiles of Ustrushna that were used for commercial purposes were produced at lower elevations.

Antilopines & Cervids

I only identified a single deer / antelope specimen (TBK126.A), suggesting that wild game hunting was not a primary economic activity at Tashbulak. My results also suggest that neither boar hunting or pig rearing were commonly (if at all) practiced at Tashbulak, supporting the observance of an Islamic diet. That being said, the extent of Islamification in the highlands of Transoxiana under Qarakhanid rule cannot be addressed by zooarchaeology and ZooMS alone. The recovery of grape seeds on the other hand might suggest grape cultivation and viniculture, and thus the consumption of alcohol (see Chapter 17). At the same time, the presence of grape seeds does not make a strong case for wine production or consumption; the inhabitants could have just as easily been eating grapes and drinking grape juice.

Perhaps the single most important line of evidence for Islamic observance at Tashbulak is the traditional Muslim cemetery (see Chapter 18). Islamic burials do not necessarily mean that the majority of Islamic tenets and practices were being adhered to, but they do indicate the presence of an Islamic identity as well as (at the very least) the desire to at least *appear* to follow Islamic lifeways. The realities of religious observance do not always concur with the

expectations of religious observance, and Islamic burials do not necessarily guarantee that Islamic dietary taboos were strictly adhered to at Tashbulak. From the limited evidence available, it appears that Islamification was present even in the highland pastoralist regions of Transoxiana by the time of the Qarakhanids, at least in mixed contexts where urbanism and metallurgy were being practiced alongside livestock rearing.

Chickens

More and more evidence of chicken management at Tashbulak is being uncovered. My ZooMS results support the eggshell PMF results establishing the presence of domesticated chickens at Tashbulak (Peters et al. 2024). This further suggests that the inhabitants of Tashbulak engaged in agropastoralism as opposed to mobile pastoralism, and are unlikely to have been “nomads”. Chicken management was not limited to highly elevated sites and was widespread through Uzbekistan (Peters et al. 2024), suggesting that neither the prehistoric nor Medieval peoples of Uzbekistan were generally nomadic peoples (see also Chapter 09).

22.4. Collagen Peptide Marker Screening

The results of my collagen peptide marker screening study of goitered gazelle (*Gazella subgutturosa*) and sika deer (*Cervus nippon*) collagen suggest that the tryptic masses of twelve common collagen peptide markers are likely identical in both species. Tandem mass spectrometry (see Chapter 04) would be necessary to estimate the actual amino acid sequences of the collagen peptide markers and verify my suggestions, or identify any additional markers. My MS data results do not suggest that MALDI could be used to discern goitered gazelle or sika deer from gazelles such as mountain gazelle (*Gazella gazella*), Thomson's Gazelle (*Eudorcas thomsonii*), or Grant's Gazelle (*Nanger granti*), from African steenbok (*Raphicerus campestris*), from Eurasian antelopes such as saiga antelope (*Saiga tatarica*) or impala (*Aepyceros melampus*), or from cervids such as elk / moose (*Alces alces*), red deer (*Cervus elaphus*), Irish elk (*Megaloceros giganteus*), chital deer (*Axis axis*), fallow deer (*Dama dama*), or elaphure (*Elaphurus davidianus*) (Tbl.148).

My results do suggest that MALDI could be used to discern goitered gazelle (*Gazella subgutturosa*) and sika deer (*Cervus nippon*) from African antelopes such as roan antelope (*Hippotragus equinus*), sable antelope (*Hippotragus niger*), hartebeest (*Alcelaphus buselaphus*), springbok (*Antidorcas marsupialis*), hirola (*Damaliscus hunteri*), tsessebe (*Damaliscus lunatus*), waterbuck (*Kobus ellipsiprymnus*), kob (*Kobus kob*), Kirk's dik-dik (*Madoqua kirkii*), oribi (*Ourebia ourebi*), and grey rhebok (*Pelea capreolus*), from Tibetan antelope (*Pantholops hodgsonii*), from roe deer (*Capreolus capreolus*), and from the North American mule deer (*Odocoileus hemionus*) and white-tailed deer (*Odocoileus virginianus*) (Tbl.149).

The results of my study are preliminary. Without published collagen peptide markers for other Inner Asian taxa such as Prezewalskii's gazelle (*Procapra prezewalskii*), Mongolian gazelle (*Procapra gutturosa*), Siberian roe deer (*Capreolus pygarus*), Siberian musk deer (*Moschus*

moschiferus), Altai wapiti (*Cervus canadensis*), and Bactrian wapiti (*Cervus elaphus bactrianus*), it is unclear whether or not ZooMS can be used to discriminate between them. The majority of the the antelopes that are likely discernable from goitered gazelle (*Gazella subgutturosa*) and sika deer (*Cervus nippon*) using MALDI are African, though Tibetan antelope (*Pantholops hodgsonii*) present as many as three collagen peptide marker differences. It is possible that additional peptide markers could be identified that could distinguish between goitered gazelle and sika deer and other antilopines and cervids. LC-MS/MS-based marker development would be worth pursuing for both taxa, as well as other Inner Asian antilopines and cervids.

Tbl.148 Table of species with collagen peptide markers that likely differ from *C. nippon* & *G. subgutturosa.*

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Alcelaphus buselaphus	1105.6	1180.6	1196.6	1427.7	**1590**	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Antidorcas marsupialis	1105.6	1180.6	1196.6	1427.7	**1532.8**	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Capreolus capreolus	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	**3043.4**	**3059.4**
Hippotragus equinus	1105.6	1180.6	1196.6	1427.7	**1580.8**	1648.8	2131.1	2792.4	2883.4	2899.4	3043.4	**3059.4**
Hippotragus niger	1105.6	1180.6	1196.6	1427.7	**1580.8**	1648.8	2131.1	2792.4	2883.4	2899.4	3043.4	**3059.4**
Kobus ellipsiprymnus	1105.6	**1150.6**	**1166.6**	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Kobus kob	1105.6	**1150.6**	**1166.6**	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Madoqua kirkii	1105.6	**1166.6**	**1182.6**	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3043.4	**3059.4**
Odocoileus hemionus	1105.6	1180.6	1196.6	1427.7	**1593.8**	1648.8	2131.1	2792.4	2883.4	2899.4	**3043.4**	**3059.4**
Odocoileus virginianus	1105.6	1180.6	1196.6	1427.7	**1580.8**	1648.8	2131.1	2792.4	2883.4	2899.4	**3043.4**	**3059.4**
Ourebia ourebi	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3043.4	**3059.4**
Pantholops hodgsonii	1105.6	1180.6	1196.6	1427.7	**1580.8**	1648.8	2131.1	2792.4	**2857.4**	**2873.4**	3017.4	3033.4
Pelea capreolus	1105.6	**1150.6**	**1166.6**	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4

Tbl.149 Table of species with collagen peptide markers that likely agree with *C. nippon* and *G. subgutturosa.*

Species	α1 508	α2 978	α2 978 (+16)	α2 484	α2 502	α2 292	α2 793	α2 454	α1 586	α1 586 (+16)	α2 757	α2 757 (+16)
Aepyceros melampus	1105.6	1180.6	1196.6	1427.7	x	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Alces alces	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Axis axis	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Cervus elaphus	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Dama dama	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Elaphurus davidianus	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Eudorcas thomsonii	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Gazella gazella	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	x	x	x	3017.4	3033.4
Elaphurus davidianus	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Nanger granti	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Raphicerus campestris	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4
Saiga tatarica	1105.6	1180.6	1196.6	1427.7	1550.8	1648.8	2131.1	2792.4	2883.4	2899.4	3017.4	3033.4

23. Conclusion

23.1. Archaeological Sites

Here I used ZooMS to enrich the faunal data available from three Inner Asian archaeological sites in order to better understand the animal economies and human-animal relationships which characterized them. The research questions I investigated included when the earliest evidence of domesticated animal husbandry arises in relation to which archaeological cultures, which herd compositions were the most prevalent in different spatial and temporal contexts, which modes of pastoralism can be inferred from these contexts, and what evidence exists for economies specializing in secondary animal products. My application of ZooMS was not to taxonomically identify as many animal bone fragments as possible but to target key specimens of interest, such as morphologically indeterminate or ambiguous specimens and possible early domesticates. I will overview how my ZooMS analyses contributed to our understanding of each of the archaeological sites below.

23.1.1. Nizhnyaya Sooru

I was able to use ZooMS to securely identify morphologically unidentifiable and taxonomically ambiguous animal bones and teeth recovered from the stratified settlement site of Nizhnyaya Sooru in the Central Altai of Southern Siberia. My targeted ZooMS analysis helped to refine the taxonomic profile of Nizhnyaya Sooru throughout the Eneolithic, Bronze Age, and Iron Age layers of human occupation and have provided new insights into prehistoric lifeways and human-animal relationships in the Altai. These insights include a preference for sheep husbandry that persists into the Iron Age, where goats seem to appear for the first time. The prevalence of caprine exploitation throughout all periods of occupation at Nizhnyaya Sooru is clear even considering the sampling bias that is the result of my selection for morphologically ambiguous caprine specimens. These results align well with recent studies indicating that Eneolithic & Early Bronze Age peoples of the Western Steppe, from where the Afanasievo initially migrated into Inner Asia, relied primarily on sheep husbandry (see Chapters 01, 09).

My results also support Afanasievo models of domesticated caprine and cattle introduction into Inner Asia (see Chapters 01, 06, 09, 15). Additional insights from my ZooMS analysis include that there remains an absence of equids until the Middle Bronze Age, as well as a minimal reliance on the hunting of deer and antelope throughout all periods. Here my results do not support early models of horse domestication, especially not in Afanasievo contexts (see Chapters 01, 06, 09, 15), but instead support a later Bronze Age date (though it remains unclear if any of the equids I identified were domesticated). Finally, I identified several sheep (*Ovis* sp.), goat (*Capra* sp.), and equid (*Equus* sp.) samples for subsequent radiocarbon and aDNA analysis, paving the way for multiproxy biomolecular and biogeochemical studies into the initial emergence of animal domestication and pastoralism in Inner Asia. These analyses are currently ongoing, and any livestock identified will help to refine our understanding of animal domestication and dispersal events in Inner Asia.

23.1.2. ZK513

My ZooMS study of ZK513 fauna from Trench ZK513-1 was designed to screen for candidate specimens suitable for aDNA-based identification of domesticated animals, and this work is currently ongoing. The genomic analysis which has been conducted has identified, for the first time, *Equus ovodovi* in an Outer Mongolian Bronze Age context (Pan et al. 2024). The discovery of these specimens emphasizes the complexity of identifying equid remains in prehistoric assemblages and the level of caution that must be observed in the reporting of both morphological and ZooMS-based identifications. A more thorough and systematic ZooMS analysis of the remaining ZK513-1 faunal assemblage would undoubtedly provide critical insight into the animal economies of Eneolithic and Early Bronze Age Mongolia, a period for which there is a true dearth of information (see Chapters 11–15).

From this selection of fragmented faunal remains (n=142), I was able to further use ZooMS to provide valuable insight into the animal economies of prehistoric Outer Mongolia. My identification of sheep (*Ovis* sp.), goat (*Capra* sp.), and cattle (*Bos* sp.) in the earliest layers of ZK513-1 support the hypothesis that Afanasievo peoples introduced certain domesticated animals into Outer Mongolia (see Chapters 01, 06, 09, 15). That the Eneolithic equids I identified were determined to be *Equus ovodovi* instead of *Equus caballus* (Pan et al. 2024; Appendix 03) further refutes the idea that Afanasievo peoples also introduced domesticated horses into Outer Mongolia (see Chapters 01, 06, 09, 15). My identification of potential livestock in the earliest occupation layers at ZK513 suggests that pastoralism was an early subsistence strategy and a consistent economic activity even into the historical period, though higher resolution identifications (e.g. aDNA analysis) would be necessary to confirm that these specimens were in fact livestock as opposed to wildstock.

My ZooMS-based identification of *Cervus* sp. and *Gazelle* sp. in the Iron Age and Medieval layers also suggests that hunting may have become more prevalent in the later occupation phases of ZK513, though the sample sizes are much too small to draw any firm conclusions. The stratigraphic distribution of all ZooMS-based identifications can be said to be dominated by sheep in nearly all layers. At the same time, the delineation of an already small sample number (n=143) into 12 groups greatly decreases the resolution of data and complicates any attempts to reconstruct animal economies through time at ZK513. Combining the ZooMS data with the zooarchaeological data (Houle et al. 2022), as they stand now, also does not provide additional insight as the overwhelming majority of the animal bones remain unidentified. Additional analyses of these remains, ideally ZooMS, will be necessary for any robust interpretation of animal management strategies and herd compositions through time at ZK513-1.

23.1.3. Tashbulak

My Tashbulak ZooMS study was tactical as opposed to all-encompassing. While I was able to refine, clarify, and correct several taxonomic identifications provided by zooarchaeology, my results do not fully reflect the taxonomic distribution of all of the animal bones recovered from Tashbulak– just as the animal bones recovered do not fully reflect the animals reared and

slaughtered at Tashbulak (see Chapters 02, 18–19). The pattern that emerged from the faunal samples I selected from Tashbulak is biased towards caprines (see Chapter 20), as I specifically selected caprine samples that ZooMS could ideally provide higher resolution taxonomic identifications for (see Chapter 05). The higher representation of cattle could also be the result of preservation bias (see Chapter 02), and is a phenomenon commonly observed in ZooMS-based assemblage analysis (see Chapter 05). While my results do not accurately reflect the herd compositions of Tashbulak, there are a number of circumstances and behaviors that can be inferred from my results.

It is evident that goats (*Capra* sp.) were reared in much higher numbers than sheep (*Ovis* sp.), a divergence from the strategies observed in the Bronze Age assemblages of Southern Siberia and Mongolia. The preference for goat rearing is unsurprising, considering the arid highland context of Tashbulak. More unexpected is my confirmation of the presence of camels, which are not typically associated with or herded in mountainous zones. My results, which I understand to be the first ZooMS-based identifications of camels, sheep, and goats in Medieval Transoxian contexts, support the hypothesis that climate change drove agropastoralist adaptations in highland settlements. Finally, my results do not suggest that the people of Tashbulak ignored Muslim dietary taboos. Combined with the burial archaeology, it is likely that the inhabitants of Tashbulak observed both the funerary and dietary customs of Islam under Qarakhanid rule.

23.2. Bronze Age Animal Economies

One of the most prevalent discussions in Inner Asian archaeology is the role of the Afanasievo archaeological culture in introducing livestock into areas of Inner Asia such as Southern Siberia and Outer Mongolia. Whether or not domesticated horses were being managed by Afanasievo peoples has also been debated. Scholars are not always in agreement about what Afansievo even means, though there is a consistent association with the Eneolithic and Early Bronze Age. The animal economies of Inner Asia that date back to these archaeological periods are difficult to reconstruct due to the limited number of faunal remains that have so far been recovered from archaeological contexts. There are also a number of issues which complicate attributing taxonomy to these remains, including taphonomic loss, morphological plasticity, biometric overlap between related species, the discrimination of wild from domesticated fauna, access to specialist training, access to reference collections, and the availability of published genomes and peptide markers.

The aforementioned issues present significant challenges for zooarchaeologists using morphometric methods as well biogeochemical and biomolecular approaches. Although emphasis has been increasingly placed on the value of methods such as stable isotope analysis, radiocarbon dating, aDNA analysis, and paleoproteomics, these methods have their own limits and caveats and cannot replace zooarchaeology. The multiproxy analysis of faunal remains recovered from sites that have been mindfully excavated has resulted in new revelations into prehistoric lifeways and animal domestication histories that sometimes conflict with older interpretations of archaeological data. Consequently, there has been some

disagreement and inconsistent reporting throughout decades of scholarship about the presence of domesticated animals in the prehistoric faunal assemblages of Inner Asia. Examples include conflicting reports about the same equid remains from Afanasievo contexts as well as the same suid and bovine remains from Neolithic Mongolian sites.

Certain faunal data recovered from Afanasievo contexts have been further compromised by assemblage commingling and stratigraphic disarray. That is not to say that these data are not valuable, so much as there are limits to what can be inferred from them. There is a need for transparency when incorporating these data into analyses such as herd composition reconstructions and arguments for different subsistence strategies and economic activities. That being said, these data are precious, and we are fortunate to have them. There are more faunal data available from Afanasievo settlement sites than from the settlement sites of any other Bronze Age archaeological culture of Southern Siberia or Outer Mongolia, and there is currently little that can be said about the human-animal relationships which characterize these regions and periods of Inner Asia. The discovery of new settlements such as ZK513 and Biluut III, the renewed excavations of settlements such as Nizhnyaya Sooru, and new faunal analyses of large assemblages that incorporate targeted biogeochemical and biomolecular approaches has begun to clarify these relationships.

Here I have used ZooMS to taxonomically identify a selection of fragmented animal bones from Nizhnyaya Sooru and ZK513. There is some evidence of wild game hunting at both sites during their Eneolithic & Early Bronze Age periods of occupation, though neither deer nor antelope remains were recovered from either. There is no evidence of horse domestication at either site, while wild equid remains were recovered from ZK513-1. The faunal data instead suggest that caprine husbandry, supplemented by cattle husbandry on a much smaller scale, predominated at both sites during the earliest periods of human occupation. These data support models of domesticated animal dispersal that are driven by human migrations from the Western Eurasian Steppe into the Eastern Eurasian Steppe and the Inner Asian Mountain Corridor. Importantly, ZooMS cannot discriminate wild caprines or cattle from their domesticated counterparts, and so it can not be determined from my results alone how many of these remains were the result of herding domesticated sheep and cattle versus hunting argali and aurochsen. The most up to date analysis of fauna from Nizhnyaya Sooru has yet to be published, further complicating the interpretation of my ZooMS data. My data has helped to refine the faunal report for ZK513 (Houle et al. 2022), emphasizing the role that sheep husbandry played at the site during the Eneolithic & Early Bronze Age.

23.3. Prehistoric Horse Domestication

“...the limited nature of the region’s early archaeofaunal record, absence of quality reference collections for morphological identifications, and the lack of reliable morphological criteria for distinguishing wild lineages from domestic, have prevented a conclusive assessment of the timing of early domestic horse use....” (Taylor et al. 2024)

Modern horses (i.e. DOM2 lineage horses) were domesticated from wild horses (*Equus ferus*) in the Western Eurasian Steppe ca. 4000 years ago (Librado et al. 2021; see also Chapters 06). The timing and the mechanisms of their dispersal into the Eastern Eurasian Steppe remain unclear, though the presence of wild equids and the seeming absence of domesticated horses from the oldest occupation layers of the ZK513 site refutes an earlier timeline for horse domestication in Western Mongolia (Pan et al. 2024). It has been speculated that domesticated horses were introduced into the Mongolian Plateau via Tuva (see Chapter 10) ca. 1500 BCE (Honeychurch 2015; Houle 2016; see also Chapters 09, 15). The Altai Mountains have also been suggested as a route of dispersal, though the near absence of horse remains recovered from Bronze Age contexts in Western Mongolia has rendered this scenario far less likely (Houle 2016). It is also unlikely that Afanasievo archaeological culture, which has never been securely associated with domesticated horse remains (see Chapters 09, 15), introduced domestic horses from the Western Eurasian Steppe into the Mongolian Plateau through the Altai Mountains during the Eneolithic and Early Bronze Age.

Although the pathway of horse husbandry into Outer Mongolia has not yet been identified it is clear that domesticated horses were present by at least the Late Bronze Age (Honeychurch 2015; Houle 2016; Lepetz et al. 2019; Taylor 2017, 2024; Taylor et al. 2016; 2020a,b, 2024). The advent of horse domestication and eventually horseback riding would have, in all likelihood, coincided with pastoralist intensification resulting from increased mobility and social complexity (Taylor 2017; Taylor et al. 2016, 2020b; Ventresca Miller et al. 2022). These changes are most evident in the archaeological record of the Late Bronze Age, though whether that is an accurate reflection of historical process or a result of taphonomic and discovery biases remains unclear. There is solid evidence for horse husbandry practices by the Late Bronze Age, marking a clear turning point for economic and social transformation in Outer Mongolia, though the driving mechanisms behind this phenomenon are not known (see Taylor et al. 2017). My own results refute the idea that horses were being domesticated in Outer Mongolia or Southern Siberia before the Late Bronze Age, though future excavations and faunal analyses may prove otherwise.

23.4. Medieval Animal Economies

The questions attached to Qarakhanid era Transoxiana (the region within Uzbekistan that Tashbulak is situated within) are very different from the questions surrounding the earliest animal husbandry practices in the Altai and Khangai Mountain regions. Livestock rearing and the riding of both horses and camels were well-established in Transoxiana by the Medieval period, though the ratios of sheep to goats that characterized herds through different periods is essentially unknown. The logistics of secondary animal products are also unclear, such as which animals were most often utilized for wool production, who raised these animals and where, who utilized the raw wool to manufacture woolen textiles, and on which scales and in which locations were these textiles produced. The rise of Islamic regimes in Medieval Transoxiana led to widespread religious conversion, though how this shift in religious identity played out in subsistence practices across different Transoxian contexts is not well understood.

Archaeological practice in Uzbekistan has its roots in Soviet era archaeology and maintains many of the same priorities and perspectives. Although recent initiatives, especially involving collaborations with Chinese scientists, are leading to an increase in zooarchaeological training, the collection and analysis of faunal data has been historically ignored. There are limited zooarchaeological data to interpret, though the data that are available do not indicate a dramatic shift in animal economies that coincide with Islamification in Uzbekistan (see Chapter 17). The available data also rarely discriminate between sheep and goat remains, complicating assemblage interpretations and obscuring what could be inferred about animal management strategies in different contexts. Related questions include whether secondary product manufacture, such as of woolen textiles, was more prevalent in urban or agricultural contexts.

Here I used ZooMS to refine the taxonomic identifications of certain faunal specimens recovered from Tashbulak in an effort to address these gaps in our understanding about Medieval Transoxian animal economies. My ZooMS results, combined with other lines of archaeological evidence such as archaeobotanical analysis and the peptide mass fingerprinting of bird eggshells (see Chapters 02, 04–05), indicate that Tashbulak maintained an agropastoralist economy (see Chapters 09, 19). The animal husbandry component was primarily centered upon goat rearing, though sheep, cattle, horses, camels, and chickens were also managed. There is no faunal evidence to suggest that the majority of the peoples of Uzbekistan were more engaged in mobile pastoralism than agropastoralism (see Chapters 09, 19), though the faunal assemblage recovered from Tashbulak may reflect changes in animal management strategies that were driven by climate change (see Chapters 18–19). The publication of currently ongoing zooarchaeological analysis from Medieval sites at lower elevations should help to clarify how the animal economy of Tashbulak fit into the larger picture of Medieval animal economies in Transoxiana.

23.5. Medieval Wooling Economies

My results also suggest that neither wool nor woolen textiles were being manufactured on a commercial scale at Tashbulak, though the presence of camels and equids may emphasize the importance of long distance trade at Tashbulak. It may be the case that the wool and textile industries of Ustrushna were concentrated in the lowlands, or were kept separate from mining and metallurgist industries. The current state of the archaeological data does not seem to support or refute wooling economies in Medieval Transoxiana outside of Tashbulak, either in urban or agricultural contexts (see Chapters 17–19). More research and data, and the publication of said research and data, will be necessary to further explore the logistics of Medieval wooling economies in Transoxiana.

23.6. Medieval Camel Exploitation

Camel remains are rarely recovered from the archaeological sites of Inner Asia, even in Silk Road period contexts (see Chapters 18–19). My ZooMS-based identification of 10 camel specimens from Tashbulak establishes that they were being managed in highland urban contexts during the Qarakhanid period, likely in connection to trade. Whether or not they were being exploited for more than transportation is unclear; future shotgun proteomic analysis of dental calculus from individuals buried at Tashbulak might clarify whether or not they were being milked as well (Chapter 04). The presence of camels at Tashbulak might also indicate an evolving agropastoralist strategy that was adapting in response to aridification and the Medieval Climate Anomaly. Camel management in lowland, agricultural, and urban contexts more broadly during the Medieval period of Transoxiana remains unclear, in lieu of more archaeological data.

23.7. Inner Asian Caprine Husbandry

Researchers have speculated that domesticated sheep (*Ovis aries*), goats (*Capra hircus*), and taurine cattle (*Bos taurus*) disseminated into Inner Asia as part of a complex process of human migration, trade, and cultural exchange ca. 8,000 years ago (see Chapter 06). Genetic and genomic studies have established that sheep and goats were domesticated ca. 8,000-11,000 years ago in the Fertile Crescent and disseminated eastward into Central Asia and eventually the Mongolian Plateau (see Chapter 06). It is very evident from the available archaeological data that caprines have been managed in Inner Asia at least since the Eneolithic & Early Bronze Age (see Chapters 09, 15); less clear is the relationship between sheep husbandry and goat husbandry in different contexts. The ratios of sheep to goat managed in these ancient herds are poorly understood and critically underutilized in Inner Asian mortality profile reconstructions (see Chapters 02, 15, 19).

The method I have used for my doctoral work, ZooMS, is especially useful for clarifying the sheep / goat ratios which characterize archaeofaunal assemblages (see Chapters 05–06). I was able to establish that sheep (*Ovis* sp.) were more commonly represented than goats (*Capra* sp.) throughout all periods at Nizhnyaya Sooru but the Iron Age (where they occur in equal representation). Sheep remains are also represented in higher numbers than goats throughout all periods of occupation at ZK513. These sites are temporally, spatially, and culturally adjacent, and their shared preference for sheep husbandry is completely in accord with recent archaeological data. In contrast, my ZooMS results establish a clear prevalence of goats over sheep at Tashbulak, which as a Medieval site in Uzbekistan is not as adjacent with Nizhnyaya Sooru and ZK513.

The preference observed at Tashbulak is likely related to the higher and drier environment that is more conducive to managing goats, though there may very well be other factors driving this inverse pattern of caprine exploitation, perhaps related to differing strategies in secondary product specialization. Age-at-death data would be necessary to reconstruct mortality profiles as Tashbulak, ZK513, or Nizhnyaya Sooru, and that data is currently not available. While culling

patterns are currently unavailable for interpretation, tentative inferences can still be drawn based upon the ecological requirements and behavioral differences between sheep and goat (see Chapter 07) as well as contextual trends.

It is apparent that the far western reaches of Inner Asia which border the Western Eurasian Steppe, such as Southern Siberia and Outer Mongolia, engaged primarily in sheep husbandry during the Eneolithic & Early Bronze Age; this is most likely the result of contact with Afansievo peoples migrating into the Inner Asian Mountain Corridor. The higher representation of goat as opposed to sheep at Tashbulak may not apply to Medieval Transoxiana in general, so much as highland settlements populated by agropastoralists. It is possible that lowland settlements during the same time period preferred to rear higher numbers of sheep, especially in an area noted for woolen textile production. It is also possible that broad areas of Transoxiana adapted goat husbandry as a response to aridification, following the Medieval Climate Anomaly (see Chapters 18–19). The publication of zooarchaeological analyses which are currently underway will ideally help to clarify the history and modes of caprine pastoralism in ancient Transoxiana.

23.8. Faunal Data Enrichment

For all three sites, I was largely successful in my goal to verify morphological identifications, identify and correct any misidentifications, and to refine the morphological taxonomic attributions of fragments that were limited to tentative attributions, ambiguous attributions, size-based mammal classes, or were otherwise indeterminate. I identified 6 samples from Nizhnyaya Sooru and 21 samples from Tashbulak that had been morphologically misidentified, and was able to assign a genus-level identification to all of them. In regards to morphologically indeterminate samples,I was able to identify 100% (n=12) of samples selected from Nizhnyaya Sooru, 64% (n=64) of the samples selected from ZK513-1, and 90% (n=18) of samples selected from the Tashbulak.

I was also able to use ZooMS to secure identifications for 97% (n=31) of the tentatively identified samples from Nizhnyaya Sooru and 96% (n=24) of the tentatively identified samples from Tashnulak; all samples selected from ZK513-1 were limited to size-based identifications, or were otherwise morphologically taxonomically indeterminate. Of samples that could only be morphologically attributed to a size based group, I was able to identify 100% (n= 25) of the samples selected from Nizhnyaya Sooru, 82% (n=18) of the samples selected from ZK513-1, and 90% (n=162) of the samples selected from Tashbulak.

I was further able to use ZooMS to clarify the taxonomic identity of 83% of samples (n=43) from Nizhnyaya Sooru that could only be ambiguously identified based upon morphology. Finally, 86 of the samples that I selected from Tashbulak had only been ambiguously morphologically identified, and I was able to use ZooMS to identify 91% (n=78) of these samples. As already noted, all samples selected from ZK513-1 were limited to size-based identifications or were otherwise morphologically taxonomically indeterminate.

Equids

I was able to identify *Equus* sp. samples in the Eneolithic & Early Bronze Age layers of Trench ZK513-1 in the course of my analysis. These samples were subsequently submitted for aDNA analysis, as intended, and determined to be *Equus ovodovi* (Pan et al. 2024). I did not identify any equids in the Eneolithic & Early Bronze Age layers of Nizhnyaya Sooru, though the results from Pan et al. (2024) suggest that caution is due when attributing species-level identifications to any equid remains recovered from Eneolithic & Early Bronze Age Southern Siberia.

Camels

I was able to securely identify 10 animal bones from Tashbulak as *Camelus* sp. (*Camelus bactrianus* when taken in context). My results represent, to my knowledge, the only proteomic identification of camel remains from Transoxiana and currently double the combined published NISP of camel remains recovered from Medieval contexts in Uzbekistan (see Chapter 19).

Caprines

I was able to identify caprines from the Eneolithic & Early Bronze Age layers of both Nizhnyaya Sooru and ZK513. These samples have since been submitted from radiocarbon and mtDNA analysis, which are to my knowledge currently underway. Ideally the results of these additional biogeochemical and biomolecular analyses will help to reconstruct the maternal lineages and thus domestication histories of domesticated sheep and goats in Inner Asia.

Antelopines & Cervids

I was able to identify, at a low resolution, antelopes / deer from all three archaeological sites. I identified a single ambiguously antilopine or cervid specimen from an Early Bronze Age occupation layer of Nizhnyaya Sooru, and another from an Early Iron Age layer. This suggests that while hunting was taking place during the Bronze and Iron Age, it was not a predominant activity- though, comparison with the full zooarchaeological report would be necessary to verify this.

I also identified two ambiguously antilopine or cervid specimens from an Iron Age occupation layer at ZK513-1, suggesting a similar story for the culturally adjacent site of ZK513. Finally, I identified a single ambiguously antilopine or cervid specimen from Tashbulak, also suggesting that hunting was not a primary economic activity; all of the archaeological data recovered from Tashbulak instead suggests an agropastoralist economy.

23.9. Collagen Peptide Marker Screening (MALDI-TOF)

The collagen peptides of goitered gazelle (*Gazella subgutturosa*) and sika deer (*Cervus nippon*) are not distinguishable using MALDI, at least not based upon the twelve markers most

commonly measured and compared for mammalian taxa (see Chapters 05, 21). With the current library of published collagen peptide markers, ZooMS also cannot be used to distinguish these species from mountain gazelle (*Gazella gazella*), Thomson's Gazelle (*Eudorcas thomsonii*), Grant's Gazelle (*Nanger granti*), African steenbok (*Raphicerus campestris*), saiga antelope (*Saiga tatarica*), impala (*Aepyceros melampus*), elk / moose (*Alces alces*), red deer (*Cervus elaphus*), Irish elk (*Megaloceros giganteus*), chital deer (*Axis axis*), fallow deer (*Dama dama*), or elaphure (*Elaphurus davidianus*) (see Chapter 21). It is possible that these species may be distinguished based upon additional markers, though LC-MS/MS analysis would be necessary for verification.

MALDI can be used to discriminate goitered gazelle / sika deer from roan antelope (*Hippotragus equinus*), sable antelope (*Hippotragus niger*), hartebeest (*Alcelaphus buselaphus),* springbok (*Antidorcas marsupialis*), hirola (*Damaliscus hunteri*), tsessebe (*Damaliscus lunatus*), waterbuck (*Kobus ellipsiprymnus*), kob (*Kobus kob*), Kirk's dik-dik (*Madoqua kirkii*), oribi *(Ourebia ourebi),* grey rhebok (*Pelea capreolus*), Tibetan antelope (*Pantholops hodgsonii*), roe deer (*Capreolus capreolus*), North American mule deer (*Odocoileus hemionus*), and white-tailed deer (*Odocoileus virginianus*) (see Chapter 21). Ideally future LC-MS/MS studies will be conducted to develop markers for Inner Asian antilopines and deer, namely Prezewalskii's gazelle *(Procapra prezewalskii*), Mongolian gazelle (*Procapra gutturosa*), Siberian roe deer (*Capreolus pygarus*), Siberian musk deer (*Moschus moschiferus*), Altai wapiti (*Cervus canadensis*), and Bactrian wapiti (*Cervus elaphus bactrianus*).

23.10. Future Directions

I have endeavored in this dissertation to synthesize several important resources, ranging from relevant Soviet era theoretical texts and archaeological reports to species-specific ecological requirements and zooarchaeological criteria. There is currently a disconnect between many modern researchers and the older body of archaeological literature that is the fruit of older archaeological practices, and thus the foundation of Inner Asian archaeological data. This disconnect is not limited to significant language barriers, but also to a lack of historical and theoretical awareness. It is important that modern day researchers understand what this older body of archaeological data consists of, why it is shaped the way it is, and that they are transparent in their reporting when pulling from this data for their own research purposes.

There is also currently a disconnect between zooarchaeologists and archaeological scientists. Many zooarchaeologists do not have a firm understanding of biochemistry, proteomics, or wet labwork, and many archaeological scientists do not have a firm understanding of faunal analysis let alone archaeological theory or fieldwork. Here I have endeavored to provide brief and accessible overviews of these topics, so that researchers more firmly rooted in either “camp” can better understand the other. It is for this purpose, to facilitate collaboration and understanding, that I have endeavored to provide both the morphometric and biomolecular criteria that have been published for the key Inner Asian taxa that characterize the animal economies, and thus faunal assemblages, of ancient Inner Asia. Zooarchaeology and ZooMS in

concert truly have the potential to revolutionize our understanding of these human-animal relationships.

The continued use of ZooMS to discern sheep bones from goat bones is critical for refining our limited understanding of sheep to goat ratios of ancient Inner Asian herds. The combination of refined caprine identifications with robust zooarchaeological analysis opens up the possibility of reconstructing the high-quality mortality profiles which have as of yet been chronically absent from Inner Asian zooarchaeological studies (see Chapters 02, 15, 19). Neither ZooMS nor zooarchaeology, combined or individually, are currently able to confidently discriminate between domesticated and wild mammal remains (though zooarchaeology is the more-suited method between the two). However, ZooMS is an ideal screening method for samples that would be ideal candidates for AMS radiocarbon and higher-resolution mtDNA and genomic studies (see Chapters 03–04). The zooarchaeological analysis of faunal remains that have been screened with ZooMS, chronologically verified with AMS radiocarbon dating, and verified as having been domesticated with aDNA analysis, opens the door for much deeper animal husbandry studies.

The continued development of LC-MS/MS verified collagen peptide markers for Inner Asian fauna would greatly enhance this endeavor, as markers are still absent for many key species-most especially for non-mammalian species such as birds and reptiles (see Chapters 05, 20–21). Finally, I would also strongly recommend that any future ZooMS analyses of Eneolithic & Early Bronze Age fauna from Southern Siberia, Outer Mongolia, and adjacent regions involve the use of chymotrypsin on samples determined to be *Equus* sp., to further distinguish stenoids from caballoids and possibly identify (with follow up aDNA analysis) the oldest DOM2 remains available in the Inner Asian archaeological record (see Chapters 01, 06, 09, 15).

My main research goals for my own study were to use ZooMS to clarify patterns of sheep versus goat exploitation in different archaeological contexts, to search for camel remains in Medieval contexts, and to identify potential Eneolithic & Early Bronze Age livestock for subsequent radiocarbon and aDNA analysis. I am proud to say that I was able to achieve all of these in the course of my doctoral work, and thus contribute to our understanding of the ancient animal economies of Inner Asia. I was also able to use ZooMS to clarify faunal reports from Inner Asian archaeological sites by refining tentative, ambiguous, and size-based morphological identifications, as well as identifying misidentified and otherwise indeterminate specimens. Thus, I truly believe that the targeted application of ZooMS to faunal remains of relevant interest to driving research questions, combined with robust zooarchaeological analysis, will transform our understanding of the subsistence strategies and human-animal relationships of ancient Inner Asia. I am excited to see that scholars and scientists seem to be in agreement on this point, and look forward to what the next decade of archaeological collaboration, innovation, and research will reveal.

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Appendix 01–First Author Publication

Manuscript A

Hill, E., & Albarella, U. (2024). An international, open-access dataset of dental wear patterns and associated broad age classes in archaeological cattle mandibles. Scientific Data, 11(1), 713.

https://www.nature.com/articles/s41597-024-03377-y

scientific data

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DATA DESCRIPTOR

An international, open-access dataset of dental wear patterns and associated broad age classes in archaeological cattle mandibles

Eden Hill[1,2] & Umberto Albarella[3]

Zooarchaeologists investigate past interactions between animals, humans, and their environments by analyzing the remains of archaeological fauna. Age-at-death distributions are fundamental to faunal analysis and are often estimated by comparing exposed dentine patterns to standardized tooth wear stages that have been associated with relative age classes. We present Bubona, an international dataset of dental wear patterns and associated broad age classes in archaeological cattle mandibles. Our open-access dataset of 1460 data entries from nine counties is being used to create tooth-type specific reference tables of probable age class attribution for cattle mandibles lacking complete dentition. Bubona is a valuable resource for the innovation of new systems of age estimation for cattle and it is the creators hope that researchers will continue to both help expand the dataset by contributing their own data, as well as utilize the data to refine and innovate age-at-death estimation methods.

Background & Summary

Zooarchaeologists use a variety of methods to reconstruct profiles of animal assemblages from archaeological sites[1]. The age-at-death distributions of archaeological fauna can help to address many archaeological questions, ranging from hunting patterns to husbandry regimes, ritual behavior, cultural preferences etc. Their estimation is a critical aspect of zooarchaeological research[2,3]. The relative age-at-death of archaeological fauna is generally estimated through the examination of bones and teeth, which are commonly recovered and exhibit determinate growth[1–4].

A fundamental zooarchaeological method which utilizes teeth to estimate the relative age-at-death of archaeological animal remains is the analysis of dental eruption and attrition[3]. Dental age in cattle may in turn be associated with broad or narrow chronological age classes (e.g.[5–12]). Bubona was created to synthesize Grant's[6] tooth wear stages with O'Connor's[12] broad age classes (Table 1) in an open-access dataset, in order to facilitate the age class attribution of cattle mandibles lacking complete posterior dentition. An additional age class, *Neonatal*, has been adapted into O'Conner's original criteria[12].

Age-at-death frequency distributions, known as mortality profiles, derived from assemblages of wild animals (such as aurochs) can be utilized to extrapolate hunting tactics, seasonal killing, and seasonal occupation[3,13–15]. The mortality profiles of assemblages containing domesticated animals (such as cattle) may be interpreted to infer herd specialization and livestock management practices[10,16–21]. The value of age-at-death data cannot be understated and the authors are in the process of using Bubona to create and publish reference tables which correlate the development of the fourth premolars and molars with broad age classes (publication forthcoming). We strongly encourage researchers to submit their own data to be incorporated into Bubona, especially welcome data from archaeological contexts outside of the United Kingdom. Any submitted data would be vetted by the authors before inclusion into our dataset. We also whole-heartedly welcome other researchers to use our dataset to develop additional age-at-death estimation methods, or refine existing ones.

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Age Class	Criteria
Neonatal	Fourth deciduous premolar not in wear
Juvenile	Fourth deciduous premolar in wear; first permanent molar not yet in wear
Immature	First permanent molar in wear; second permanent molar not yet in wear
Subadult	Second permanent molar in wear; third permanent molar not yet in wear
Adult	Third permanent molar in wear but not heavily worn; wear stage a - i*
Elderly	Third permanent molar heavily worn; wear stage j or beyond*

Table 1. O'Connor's broad age classes (1988). *Wear stages as defined by[6].

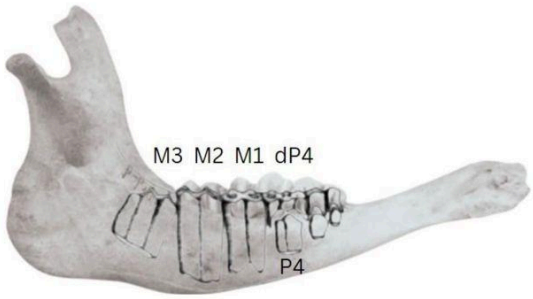

Fig. 1 Dental schema of a cattle mandible adapted from[1].

Methods

Bubona is a collation of 1460 tooth eruption and wear data derived from both prerecorded and independently examined cattle mandibles housed in university collections and recovered from archaeological sites and across the world. The details of our data selection, collection, and compilation are described below.

Data selection. Two criteria were observed in the selection of archaeological cattle and aurochs mandibles; (i) the presence of at least two molars or fourth premolars and (ii) the presence of erupted third molars, or the furthest back erupted molar if the third molar had not yet erupted.

The presence of at least two molars or fourth premolars is a useful criterion because[12] system of age classification is dependent upon the eruption and wear of molars/fourth premolars in association with one another. These teeth are abbreviated as dP4, P4, M1, M3, and M3 (Fig. 1). The examination of mandibles with at least two recordable teeth also reveals incidence of tooth wear stages which do not form parameters for age classes; e.g. it is the recording of tooth wear stages of the remaining molars and fourth premolar of an elderly mandible which reveals which non-M3 tooth stages are frequently exhibited by elderly individuals.

The direct attribution of the cattle mandibles to O'Connor's broad age classes[12] as opposed to Grant's mandibular wear stages[6] is possible only in mandibles which have the furthest back erupted molar present. Accordingly, only mandibles with erupted third molars or the furthest back erupted molar if the third molar had not yet erupted were incorporated into Bubona.

Data collection. Pre-recorded data was included in our personally owned data[22–26], and provided by Veronica Aniceti[27,28], George Kazantzis[29,30], Mauro Rizzetto[31–43], Sofia Tecce (unpublished data from Rectory Farm, Lincolnshire, UK), Angela Trentacoste[44,45], and Lizzie Wright[46–48]. Additional data was pulled from published sources[11,49–57].

Independently recorded cattle mandibles were selected from multiple sites across France, Germany, and the UK (Chaplin Treasury, no known publication; Dangstetten Roman Camp[58]; Gurness[59,60]; Inveresk Gate[61]; Jarlshof[62]; Lazenay[63]; Links of Noltland[64]; Newstead[65]; Perth High Street[66]; Skeleton Green[67]) and analyzed by one of us (EH) in accordance with Grant[6] and O'Connor[12]. Modern cattle mandibles from Germany, Oman, Turkey, and the UAE were also selected from the Tübingen University zooarchaeological collections. In total, cattle mandibles from 9 countries have been incorporated into Bubona (Fig. 2).

Access to the assemblage from the Lazaney site was facilitated by Robin Bendry and the University of Edinburgh, where the materials were being housed at the time of data collection. The assemblage from Skeleton Green was examined at the University of Sheffield (on loan from Hertford Museum). The remaining assemblages were examined at the National Museum Stores in Edinburgh under the supervision of Zena Timmons by permission of Jerry Herman and the National Museum of Scotland. The assemblage from Dangstetten Roman Camp, and all modern mandibles, were examined at the University of Tübingen zooarchaeological collections under the supervision of Angel Blanco-Lapaz by permission of Britt Starkovich.

Fig. 2 Map of countries represented in Bubona.

Data entry. Data recorded from all mandibles selected was entered into an Excel spreadsheet organized by (i) archaeological site or modern context (see 'Data Collection'), (ii) chronological context (iii) tooth wear stages[6] recorded for each mandibular tooth (dP4, P4, M1, M2, M3), and (iv) age classes ([12], with the added class on *Neonatal*) recorded for each mandible. C represents crypt, V represents visible, H represents half-erupted, E represents erupted, and U represents unworn. The age class *Neonate* has been added to O'Connor's age classes and is assigned to mandibles with an unworn dP4 (Table 1).

Reference publications and DOIs of faunal and archaeological reports and datasets were also included for each entry whenever possible.

Taxa inclusion. Bubona is composed of tooth wear stage and age class data recorded for archaeological and modern domesticated cattle (*Bos taurus*) and aurochs (*Bos primigenius*).

Data Records

The dataset is freely available as an .xlsx file on Zenodo[68]. Bubona includes 1460 data entries for cattle and aurochs mandibles recovered from 79 archaeological sites and 5 modern contexts. All entries have been associated with (i) an archaeological site or modern context, (ii) a chronological context (iii) tooth wear stages[6] recorded for each mandibular tooth (dP4, P4, M1, M2, M3), and (iv) age classes[12] recorded for each mandible.

Technical Validation

Bubona is composed of lower posterior (dP4/P4, M1, M2, M3) tooth wear stages and broad age classes recorded in cattle and aurochs mandibles exhibiting the presence of at least two molars or fourth premolars as well as the presence of erupted third molars (or the furthest back erupted molar if the third molar had not yet erupted). All mandibles have been assigned a unique Bubona ID that is clearly associated with their original ID and all tooth wear stages and age classes can be checked either against their original datasets or the original data.

In the case of original data, occlusal and buccal/lingual photographs taken of the mandibles that were selected for inclusion in Bubona and independently recorded in either the University of Sheffield, the University of Edinburgh, or the National Museum Stores in Edinburgh in 2018 or the University of Tübingen in 2023 are available for review on Zenodo[55,68].

Code availability

No custom code has been used in the creation of the Bubona Dataset.

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Author contributions

Eden Hill recorded and photographed all independently scored mandibles, collected data from published sources, compiled all data into one dataset, uploaded the dataset and photographs onto Zenodo, created the Bubona logo, and composed this manuscript. Umberto Albarella provided personal data, collected the personal data of others, reviewed the dataset, and edited this manuscript.

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Competing interests

The authors declare no competing interests.

Additional information

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Appendix 02–Middle Author Publication

Manuscript B

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ORIGINAL ARTICLE

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Genome-wide population affinities and signatures of adaptation in hydruntines, sussemiones and Asian wild asses

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Abstract

The extremely rich palaeontological record of the horse family, also known as equids, has provided many examples of macroevolutionary change over the last ~55 Mya. This family is also one of the most documented at the palaeogenomic level, with hundreds of ancient genomes sequenced. While these data have advanced understanding of the domestication history of horses and donkeys, the palaeogenomic record of other equids remains limited. In this study, we have generated genome-wide data for 25 ancient equid specimens spanning over 44 Ky and spread across Anatolia, the Caucasus, Central Asia and Mongolia. Our dataset includes the genomes from two extinct species, the European wild ass, *Equus hydruntinus*, and the sussemione *Equus ovodovi*. We document, for the first time, the presence of sussemiones in Mongolia and their survival around ~3.9 Kya, a finding that should be considered when discussing the timing of the first arrival of the domestic horse in the region. We also identify strong spatial differentiation within the historical ecological range of Asian wild asses, *Equus*

Jianfei Pan and Xuexue Liu contributed equally to this study.

For affiliations refer to page 11.

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hemionus, and incomplete reproductive isolation in several groups yet considered as different species. Finally, we find common selection signatures at *ANTXR2* gene in European, Asian and African wild asses. This locus, which encodes a receptor for bacterial toxins, shows no selection signal in *E. ovodovi*, but a 5.4-kb deletion within intron 7. Whether such genetic modifications played any role in the sussemione extinction remains unknown.

KEYWORDS
ancient DNA, *ANTXR2*, Asian wild ass, European wild ass, extinction, Sussemione

1 | INTRODUCTION

The equid family emerged from multi-toed dog-sized ancestors ~55 Mya in northern America, and diversified across the world into over a hundred taxa since (MacFadden, 1986). This once flourishing family, which included both grazers and browsers (Owen-Smith, 2013), is, however, only represented by a single genus today, *Equus* (Orlando, 2015). Together with the horse (*Equus caballus*) and the donkey (*Equus asinus*), this genus comprises three African species of zebras (*E. burchelli*, *E. grevyi* and *E. zebra*), as well as two species of Asiatic wild asses (Vilstrup et al., 2013), one (*Equus kiang*) native to Tibetan area, and another (*Equus hemionus*), historically distributed from the Arabian peninsula to the Manchuria (Rosenbom et al., 2015), and now restricted to discontinuous patches in Iran, Turkmenistan, Mongolia and China (Kaczensky et al., 2020) (Figure 1).

The evolutionary history of the *Equus* genus is colourful. It emerged in Northern America ~4–4.5 Mya (Orlando et al., 2013), and dispersed multiple times into the Old World (Jónsson et al., 2014). The ancestors of the so-called stenonine lineage crossed Beringia ~2.6 Mya, and eventually diverged into the zebra and the African ass subgroups ~1.7 Mya, which both reached Africa independently (Jónsson et al., 2014). The ancestors of the horse first crossed Beringia ~1 Mya, extending the geographic span of the so-called caballine lineage into Eurasia (Vershinina et al., 2021). Other caballine dispersals from the New World into the Old World, coincident with global Ice Ages, are documented (e.g. ~120 Kya; Vershinina et al., 2021). However, since the American palaeontological record shows no equid members from after ~12 Kya to the colonization period, the family is generally considered to have become extinct in its original homeland at the end of the Late Pleistocene (or during the first half of the Holocene, according to the persistence of horse-like environmental DNA in sediments dated to ~4–8 Kya; Wang et al., 2021).

The equid family provides many examples of extinctions in the recent past, outside of their American homeland. The quagga zebra (*E. quagga*) from South Africa and the European tarpan (*Equus ferus ferus/sylvaticus*) became, for example, extinct no later than at the late 19th/early 20th century (Olsen, 2006). Palaeoclimatic niche models have also suggested that the European wild ass, *Equus hydruntinus*, survived in patchy isolated regions across their European, Southwest Asian and Caucasian, until they became globally extinct ~2.5 Kya (Crees & Turvey, 2014). Furthermore, ancient DNA work has revealed that the so-called sussemione (*Equus ovodovi*) survived into the Altay region until at least ~32 Kya (Druzhkova et al., 2017; Vilstrup et al., 2013), and in China until ~3.4 Kya (Cai et al., 2022; Catalano et al., 2020), although palaeontological archives previously suggested considerably deeper extinction times into the Middle Pleistocene (Vasiliev, 2013).

In the last decades, ancient DNA has emerged as a powerful tool to study past population dynamics (Orlando & Cooper, 2014). In equids, most of the ancient DNA work has, however, focused on elucidating the domestication history of the horse (reviewed in Orlando et al., 2021), and the donkey (Todd et al., 2022), in which palaeogenomic archives from several hundreds of ancient animals have been characterized (Librado et al., 2021; Librado et al., 2024). While 26 ancient genomes and two almost complete mitochondrial genomes have been sequenced for *E. ovodovi* (Cai et al., 2022; Druzhkova et al., 2017; Vilstrup et al., 2013), the genetic characterization of *E. hydruntinus* has been limited to a handful of partial or pseudo-complete mitochondrial genomes (Bennett et al., 2017; Catalano et al., 2020; Orlando et al., 2006, 2009), and three nuclear genomes (Özkan et al., 2024).Moreover, ancient genome data for their closest phylogenetic relatives, the Asian asses (*E. hemionus*), are still lacking. Therefore, whether these species have evolved in isolation or interbred, and whether their populations were structured in various regional groups, remain unknown.

In this study, we applied ancient DNA shotgun sequencing to characterize the genetic variation in 25 equid archaeological remains at the genome-wide scale. These include the nuclear genome of a >44.1 Ky-old specimen from Emine-Bair-Khosar Cave, Ukraine, morphologically identified as *E. hydruntinus*, as well as four specimens from Mongolia, genetically identified as *E. ovodovi*, and 20 Asian wild asses from western Russia, Georgia, Iran, Kyrgyzstan and Tajikistan (Table S1). Our analyses confirm the close phylogenetic relationship between *E. hydruntinus* and Asian wild asses, but reveal strong spatial differentiation within the historical ecological range of *E. hemionus*, with eastern Iran representing an historical contact zone between a first subgroup spanning Central and East Asia and a second in and around the Caucasian region, Anatolia and Syria. Our work also uncovers the presence of *E. ovodovi* in Mongolia ~3.9 Kya, in stratigraphic layers that were previously considered to be associated with the horse, *E. caballus*, challenging previous

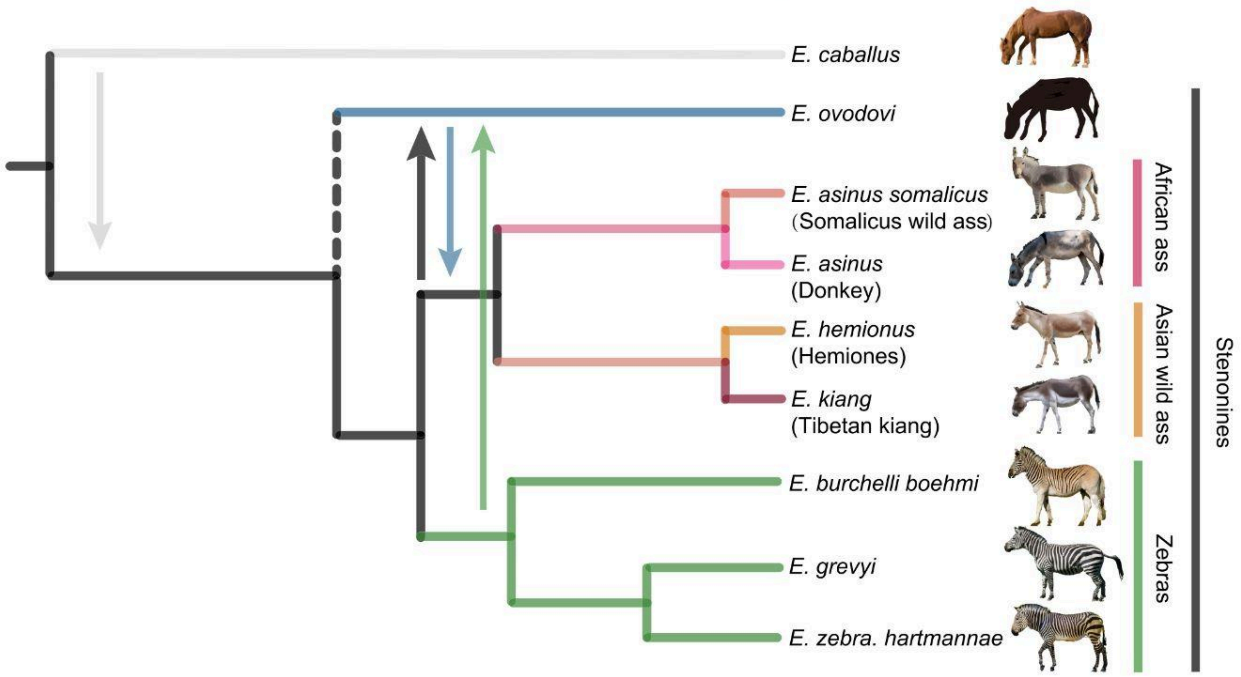

FIGURE 1 Phylogenetic relationships within the *Equus* genus. Phylogenetic relationships are according to Jónsson et al., 2014. The phylogenetic placement of *E. ovodovi* remains ambiguous and difficult to solve, in part due to a history of pervasive gene-flow between various lineages, with different contributions into and from the most recent common ancestors of zebra and assess, respectively (Cai et al., 2022). It is, thus, shown with dashed line.

assumptions about the timing and arrival of the domestic horse in Mongolia. Finally, our work further discloses selection signatures for the *ANTXR2* gene in all stenonine equids investigated except *E. ovodovi*. The role that this cellular receptor for *Bacillus anthracis* may have played in the extinction process of *E. ovodovi* remains to be addressed.

2 | MATERIALS AND METHODS

2.1 | Samples

In this study, a total of 25 equid archaeological remains spread across Anatolia, the Caucasian region, Iran, Central Asia and Mongolia were collected for DNA analysis. These specimens include: four *E. ovodovi* (ZKG, ~3.9 Kya) from Mongolia; one *E. hydruntinus* (Ba2-2343, >44.1 Kya) from the Emine-Bair-Khosar Cave (van Asperen et al., 2012); 20 Asian wild asses from 10 archaeological sites: Godin Tepe (GT, ~3.3–5.2 Kya), Shahr-i Qumis (AM803, ~2.2 Kya) and Yanik Tepe (YTF0148, ~4.8 Kya) from Iran; Kvartshelebi from Georgia (GNM44 and GNM47B, ~4.8 Kya); Oroshaemoei (LR18x57, ~7.6 Kya), Aygurskiy (KAU52, ~5.5 Kya) and Sharakhalsun (BZNKx689, ~4.8Kya) from Russia; Semetey from Kyrgyzstan (SMT1, ~5.4 Kya); Kurteke from Tajikistan (KTK1 and KTK2, ~2.1 and 3.7 Kya, respectively) and Alay from Kyrgyzstan (ALA, ~12.1 Kya) (Figure 2a, Table S1). We also included previously published genome sequences of equid species for comparison, including from three extinct *E. hydruntinus* specimens (Özkan et al., 2024), as detailed in Table S1.

2.2 | Ancient DNA extraction, library construction and sequencing

Ancient DNA analyses were carried out in the clean lab facilities of the Centre for Anthropobiology and Genomics of Toulouse (CAGT), except for specimen Ba2-2343, which was processed in the ancient DNA facilities of the Centre of new Technologies, University of Warsaw (CeNT). At CAGT, DNA extraction was based on 50–630 mg of bone or tooth powder (Table S1). Wet lab procedures at CAGT are fully described in previous work (Librado et al., 2021), and involved the incubation of DNA extracts with the USER™ enzymatic mix to reduce the fraction of nucleotide mis-incorporations in downstream analyses. Wet lab procedures at CeNT are described by Popović et al. (Popović et al., 2021).

2.3 | Read processing, trimming and alignment

Raw paired-end fastq files were demultiplexed, trimmed, and collapsed when showing sufficient sequence overlap using AdapterRemoval v.2.3.0 (Schubert et al., 2016). Reads shorter

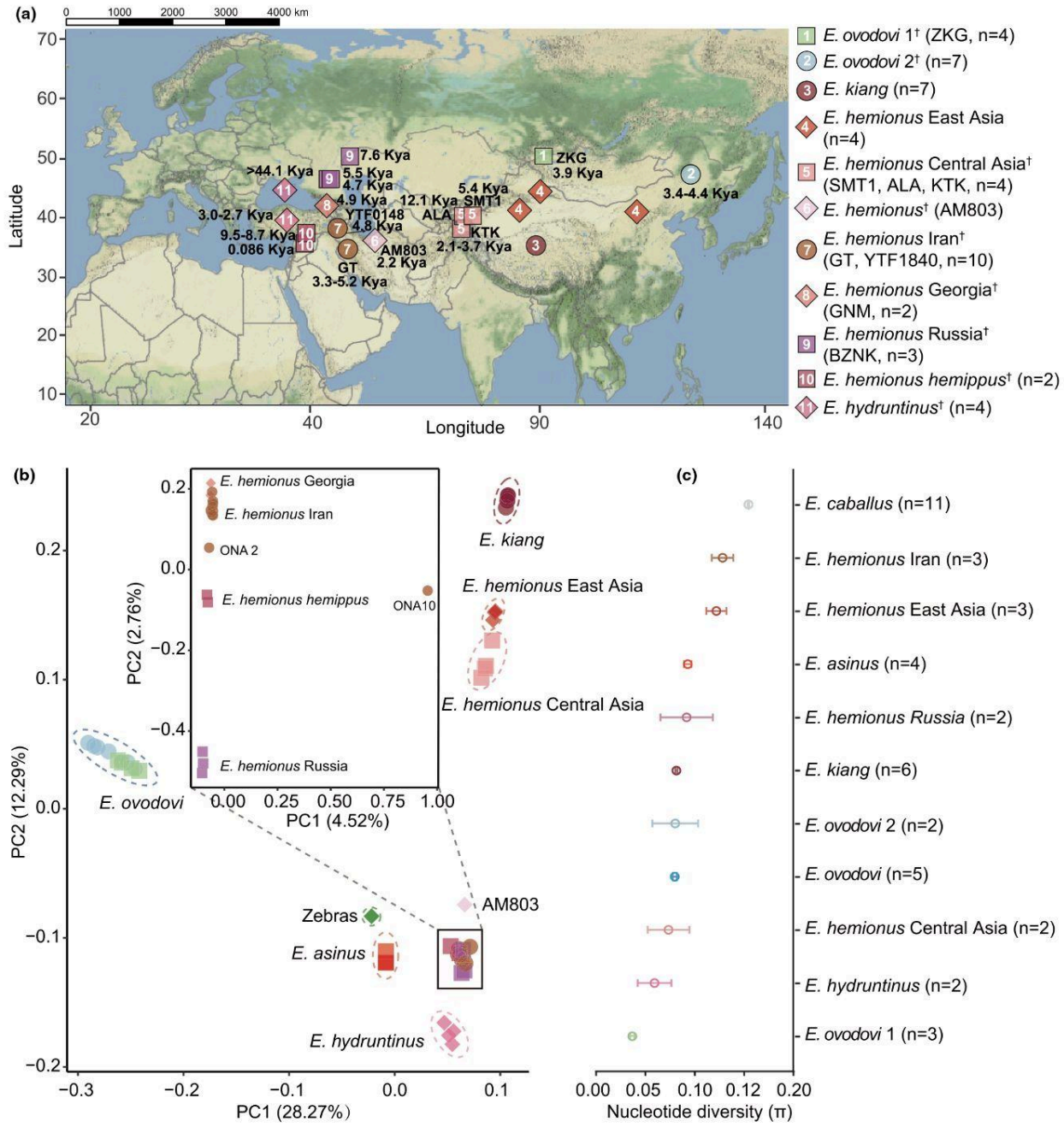

FIGURE 2 Geographical distribution and genetic diversity. (a) Sample map. Archaeological sites, sample names and temporal information are provided (see Table S1 for more details). BP = Before Present; '†' indicates ancient samples. (b) PCA of autosomal variation within stenonine genomes (main plot, $n = 56$) or restricted to *E. hemionus* from Russia, Iran and Georgia, Syrian hemippes, and *E. hydruntinus* (zoomed-in box, $n = 19$). (c) Pairwise nucleotide diversity (π) within each group, based on the distribution of pairwise autosomal differences, limited to samples showing sufficient genome coverage.

than 25 bp were excluded. Sequences were then mapped using Bowtie2 (v2.5.3) against the donkey nuclear reference sequence (GCF_016077325.2), following parameters recommended by (Poullet & Orlando, 2020), and using Paleomix v1.12 (Schubert et al., 2014). Indel realignment was performed using the IndelRealigner from GATK (McKenna et al., 2010), and sequence alignments were filtered to include only those with a minimal mapping quality of 25, while removing PCR duplicates. The average coverage across samples was ~1.10 X (median = 1.03 X; range = 0.11–3.38 X; Table S1). Furthermore, we assessed the

presence of post-mortem DNA damage signatures, including nucleotide mis-incorporation and base compositional patterns, using mapDamage2 v.2.0.8 (Jónsson et al., 2013). Taxonomic and sex identification were carried out using the Zonkey pipeline (Paleomix 1.3.8) on BAM alignments files against the EquCab2 horse nuclear reference (Wade et al., 2009), obtained according to the same procedure (Schubert et al., 2017). The sequence data for the 25 specimens other than those analysed here for the first time were subjected to the same procedure to provide comparative data (Table S1).

2.4 | Mitochondrial sequencing data processing

We used Paleomix v1.12 (Schubert et al., 2014) as described above, to map the sequences against eight distinct mitochondrial reference sequences (*E. asinus* (CM027722.2), *E. burchellii quagga* (NC_044858.1), *E. grevyi* (NC_020432.2), *E. hemionus* (NC_016061.1), *E. hydruntinus* (OP448588.1), *E. kiang* (NC_020433.1), *E. ovodovi* (KY114520.1) and *E. zebra* (NC_018780.1)). To maximize sequence coverage, we selected the alignment maximizing coverage to call the mitochondrial haplotypes using BCFTOOLS v.1.17, ignoring alignments with mapping qualities below 25, individual bases with quality scores lower than 30 and sites showing coverage strictly inferior to 5. A total of 34 additional mitochondrial sequences were obtained from GenBank (see Table S2 for detailed information) for Maximum Likelihood (ML) phylogenetic reconstruction using IQtree v.1.6.12 (Nguyen et al., 2015), assessing node support from 100 bootstrap pseudo-replicates.

2.5 | Genomic variation calling

All samples in our dataset were pseudo-haploidized for their autosomal variation, following the methodology outlined by Librado (Librado et al., 2021), using ANGSD v. 0.933-86-g3fefdc4 (htslib: 1.10.2-106-g9c35744). This procedure returned a total of 2,688,203 nucleotide transversions covered in at least 80% of the total number of samples (average sample missingness = 49.26%).

2.6 | Principal component analysis (PCA)

We constructed PCA analyses using PLINK (v1.90b4.9) (Chang et al., 2015), considering SNPs with a minimum allele frequency (MAF) of 0.05. Analyses were repeated on two data sets. The first included all samples, excepting the 11 *E. caballus* specimens that were included as phylogenetic outgroups (leaving a final set of 1,334,833 transversion SNPs; Figure 2b, main panel). The second analysis was restricted to the samples of *E. hemionus* from Russia, Iran and Georgia, hemippes and *E. hydruntinus* ($N = 19$) to focus on the population structure of the European and Asian wild asses (372,946 transversion SNPs; Figure 2b, zoomed-in panel).

2.7 | Neighbour-joining phylogeny, genetic continuity and population modelling

Phylogenetic relationships were evaluated by reconstructing a BioNJ Neighbour-Joining tree using the set of 1.33 million nucleotide transversions. The matrix of pairwise genetic distances (calculated as 1-ibs, identity-by-state) was generated using PLINK (v1.90b4.9), and served as the input for BioNJ phylogenetic tree reconstruction with FastME v.2.1.4 (Lefort et al., 2015). Node support values were estimated through 100 bootstrap pseudo-replicates, masking for clarity values inferior to 70 (Figure 3b).

2.8 | Ancestry modelling

Genetic ancestry profiles were obtained from ADMIXTURE (v. 1.3.0) (Alexander et al., 2009) ($N = 67$), considering K values from 2 to 10. The optimal number of K ancestry components was determined as $K = 6$ following Cross Validation, with default parameters. A total of 100 bootstrap pseudo-replicates were considered to assess the confidence range of each individual genetic ancestry proportion (Figure 3c and Figures S3,S4).

2.9 | Gene flow and signatures of introgression

We tested the presence of gene flow between the different lineages identified using both phylogenetic reconstruction with migration edges, as implemented by the TreeMix v.1.13 software (Pickrell & Pritchard, 2012), and the Fbranch statistics (f_b), as calculated by Dsuite (Version 0.5 r48) (Malinsky et al., 2021). Both analyses were carried out considering the set of 1,114,884 quality-controlled variants covered in at least 90% of the samples, leaving horse as outgroup ($N = 56$). The optimal number of migration edges for TreeMix ($m = 4$; Figure S6) was determined using the mixed linear model implemented in the optM v.0.1.6 R package (Fitak, 2021). Node support was assessed using modified scripts from BITE (Milanesi et al., 2017), and considering a total of 100 pseudo-replicates (Figures S7,S8). We scanned the genome variation for patterns of introgression, computing f_d statistics (Malinsky et al., 2021) using the Dinvestigate function within Dsuite (Version 0.5 r48), considering sliding windows of 20 SNPs and 5-SNPs increment and the NJ tree topology obtained from FastME v.2.1.4 (Lefort et al., 2015). Genomic regions showing at least three consecutive windows within the top 99.9th f_d percentile provided a list of candidates for introgression. We also assessed the same genomic windows for the Weir and Cockerham F_{ST} fixation index (Leviyang & Hamilton, 2011), considering each population pair in VCFTOOLS (0.1.17) (Danecek et al., 2011). NJ phylogenetic trees were reconstructed within the top 99.9% f_d windows as a further control for gene flow, following previously described methodology (Rocha et al., 2023) (Figure 5a).

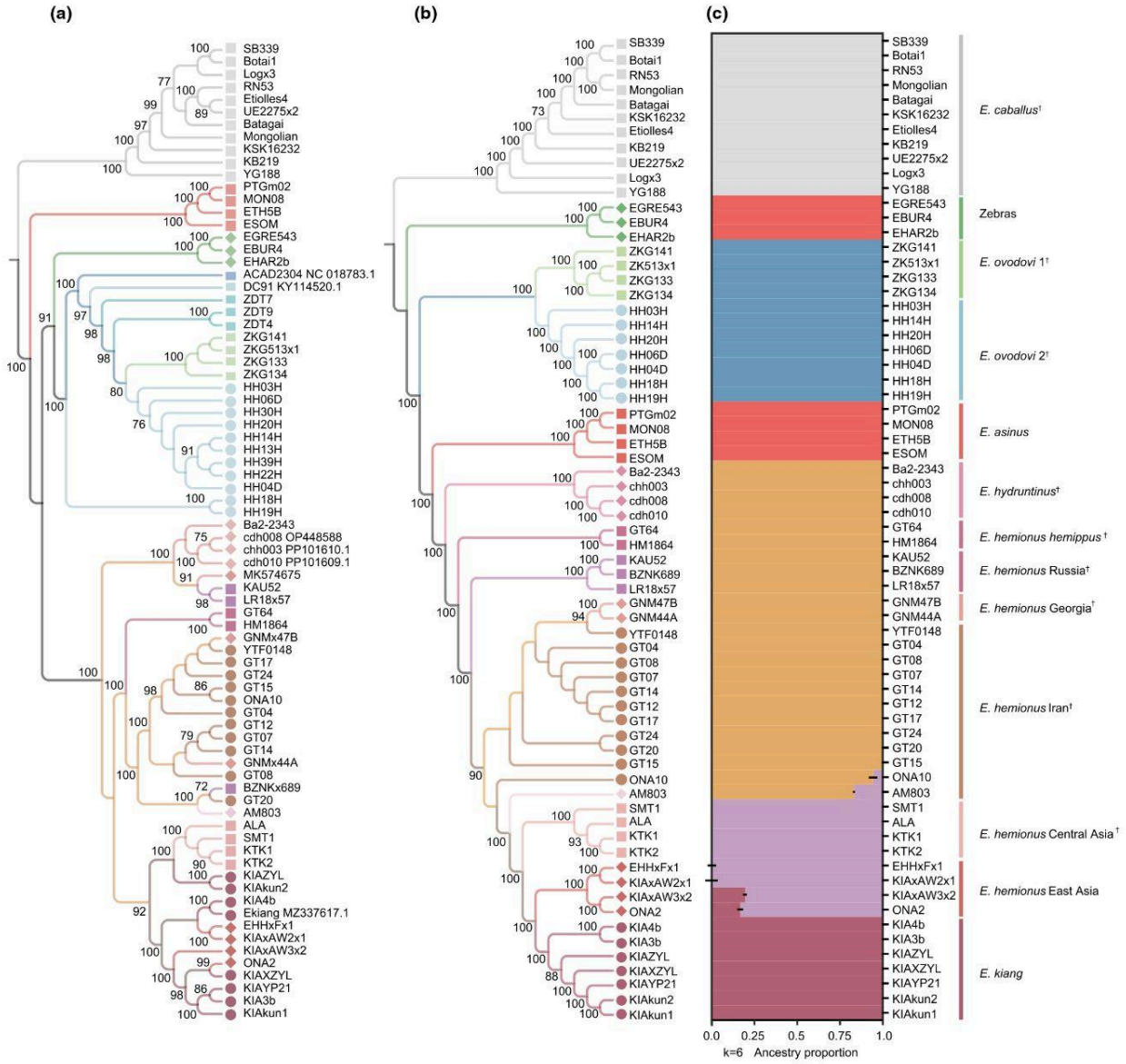

FIGURE 3 Genetic affinities. (a) IQtree Maximum Likelihood phylogenetic tree based on complete mitochondrial DNA sequences. The tree is rooted on horses, and was built using the TVM+F+R3 substitution model. The numbers on each node represent bootstrap supports in percentage (≥70% for clarity). (b) Neighbour-Joining tree constructed using autosomal genome transversions. (c) ADMIXTURE analysis for all samples with the optimal $K=6$ number of ancestry components. The black bars indicate confidence intervals, estimated from bootstrap resampling.

2.10 | Selection signatures

We next used Ohana (Cheng et al., 2022) to look for selection signatures within 50 kb windows (step-size = 5 kb) (Rocha et al., 2023) and across five ancestry components representing the following taxonomic lineages: *E. ovodovi* (Group 1, $n=7$), *E. asinus* (Group 2, $n=4$), *E. kiang* (Group 5, $n=7$), *E. hemionus* from Central and East Asia (Group 4, $n=6$), and the remaining wild asses, including *E. hemionus* from Iran, Russia, Georgia, hemippes and *E. hydruntinus* (Group 3, $n=11$) (Figure 6a,b). For these analyses, positions not covered in at least 90% of the samples were disregarded and MAF was set to 2%. We first obtained the joint distribution of allele frequencies across all ancestral components using Nemeco, and then identified covariance outlier regions using *selescan*, which implements a likelihood model for each individual locus. Functional gene annotation available for protein coding genes within the top 99.5% of each component were obtained from the Ensembl BioMart online genomic database (https://grch37.ensembl.org/info/data/biomart/index.html) and visualized through the OmicShare platform (https://www.omicshare.com/tools) (Figure 6d).

3 | RESULTS

3.1 | Genome sequencing and species identification

We collected one specimen morphologically-identified as *E. hydruntinus* (Figure S1) and associated with a non-finite radiocarbon date (>44,080 Before Present, BP; IntCal20) (Reimer et al., 2020), as well as of archaeological equid remains from across Anatolia, the Russian steppes, Georgia, Iran, Central Asia and Mongolia (Figure 2a; Table S1). These specimens were processed for ancient DNA analysis in the ancient DNA facilities of the Centre for Anthropobiology and Genomics of Toulouse ($N=24$) and those of the Centre of New Technologies University of Warsaw ($N=1$, *E. hydruntinus*) (Supplementary information). DNA preservation levels were compatible with genome characterization through shotgun sequencing at 0.1- to 3.4-fold average depth-of-coverage (median = 1.0-fold), from relatively limited sequencing efforts (37.0–465.5 million read pairs at CAGT and 297.7 single end reads at CeNT; Table S1).

Species identification in Zonkey (Schubert et al., 2017) indicated the clustering of all specimens together within Asian wild asses, except for specimens from Mongolia (ZKG, ~3.9 Kya), not matching the default reference panel of extant *Equus* species. ML phylogenetic reconstruction, including representatives of all ancient and modern *Equus* taxa ever characterized genetically, supported the mitochondrial clustering of ZKG specimens within a monophyletic clade consisting of all other *E. ovodovi* specimens previously sequenced ($n=16$; Figure 3a). The NJ phylogeny reconstructed from autosomal transversion SNPs further confirmed the clustering of ZKG specimens as a sister group to ~3.4–4.4 Ky-old *E. ovodovi* specimens from China (Figure 3b). Moreover, the pairwise genetic distances between ZKG and the other *E. ovodovi* specimens from China were found to be considerably lower than those between any such groups and other Asian wild asses investigated in this study (Figure S2). ADMIXTURE analyses based on the optimal number of genetic components ($K=6$) also indicated that the ZKG specimens exhibited a genetic makeup similar to that of the *E. ovodovi* specimens from China, and maximized a genetic component that was private to this group (Figure 3c and Figure S3,S4). Combined, these analyses indicate that the 4 ZKG specimens belonged to a subpopulation of *E. ovodovi* living ~3.9 Kya in Mongolia, ruling out any possible assignment to the horse species (*E. caballus*).

3.2 | Genetic structure and diversity

We further scrutinized the result of the PCA analysis to assess the genetic affinities amongst different wild asses (sub-) species (Figure 2b). While the first principal component (PC1) mainly separated *E. ovodovi* from the European and Asian wild assess, the second principal component (PC2) provided further resolution into various groups of affinities amongst *E. hydruntinus*, hemippes and *E. hemionus* specimens. In particular, the European wild ass (*E. hydruntinus*) and the Tibetan kiang (*E. kiang*) appeared at the opposite ends of PC2, with various *E. hemionus* occupying intermediate positions (Figure 2b). Those specimens from western Russia (BZNK), Anatolia and Syria (*E. h. hemippus*), and the Caucasus (Godin Tepe, GT; Georgia, GNM) clustered together with two onager specimens (ONA2 and ONA10), relatively close to European wild asses. In contrast, the *E. hemionus* specimens from Central Asia (SMT1, ALA and KTK) placed at the other end of PC2, near Asian wild asses from East Asia and Tibetan kiangs. Such affinities were supported in both NJ and ML phylogenetic reconstructions (Figure 3b and Figure 4c respectively). This indicated a strong phylogeographic structure within Asian wild asses, separating those populations located west of the Caspian Sea from those located in the eastern range of Central Asia (Kyrgyzstan and Tajikistan), China and Tibet. Interestingly, the genomic makeup of the specimen AM803 from Shahr-i-Qumis, Iran shows a mixture of the two genetic components maximized in the two groups of Asian asses west of the Caspian Sea, and in Central Asia and China, both apparent in ADMIXTURE (*E. hemionus* Iran = 83.2 ± 0.6% and *E. hemionus* East Asia = 16.8 ± 0.6%; Figure 3c), TreeMix (Figure 4a), and branch-specific f_b statistics (Figure 4b) analyses. This reveals the region extending from eastern Iran across most of Central Asia represented as a contact zone around ~2.2 Ky BP (i.e. the radiocarbon date of AM803; Table S1).

ADMIXTURE analyses further provided evidence of gene flow between Tibetan kiangs and two *E. hemionus* specimens, including one (KIAxAW3x2) from Xinjiang, North-West China (*E. hemionus* East Asia = 80.4 ± 1.2% and *E. kiang* = 19.6 ± 1.2%; Figure 3c). This confirmed previous phylogenetic findings, reporting mitochondrial haplotype sharing between Tibetan kiangs and so-called Dziggetai hemiones (Bennett et al., 2017). The second such specimen was sampled from a zoo (ONA2) showed a similar genomic composition, consisting of 83.3 ± 1.8% *E. hemionus* East Asia ancestry and 16.7 ± 1.8% of *E. kiang* ancestry. Interestingly, the second zoo specimen (ONA10) also showed evidence of admixture, suggesting a history of pervasive admixture between main population subclusters in captivity (*E. hemionus* Iran = 94.4 ± 2.6% and *E. hemionus* Central Asia = 5.6 ± 2.6%).

ML and NJ phylogenetic reconstructions based on mitochondrial and autosomal DNA variation supported a monophyletic cluster of *E. hydruntinus*, branching off a sister clade of Asian wild asses (Figure 3b). TreeMix ML reconstructions allowing for four migration edges revealed, however, a more complex phylogenetic history, in which the close proximity of *E. hydruntinus* and *E. hemionus* from Russia was strongly supported (Figure 4a). In this analysis, *E. hydruntinus* specimens were modelled to have received a ~ 24% genetic contribution from a lineage basal to all wild asses, which explains their deeper phylogenetic placement in the NJ phylogenetic tree (Figure 3b). *E. hydruntinus* was also modelled to have contributed genetic material (~11%) to Syrian hemippes (*E. h. hemippus*), and branch-specific f_b statistics support significant gene flow between these groups (Figure 4b). Combined, these analyses support a history of contact between *E. hydruntinus* and Asian wild ass populations from Syria and western Russia,

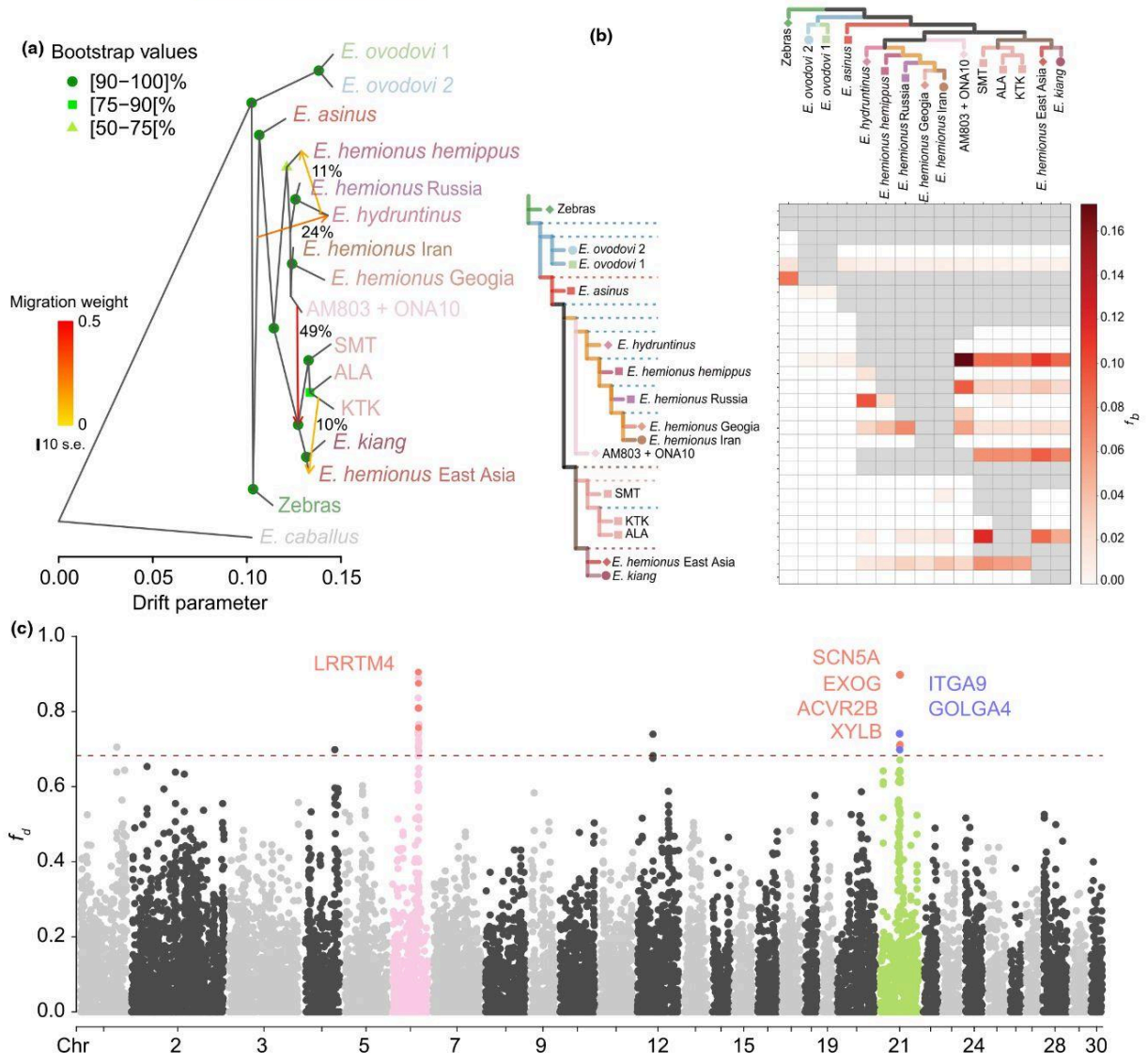

FIGURE 4 Gene flow between various equine groups. (a) TreeMix Maximum Likelihood phylogenetic tree. Coloured arrows represent migration edges, with the colour scaled according to migration weight, indicated in %. The shapes reported on the internal nodes represent increasing bootstrap support. (b) Branch-specific f_b statistics analyses. Significant values of f_b statistics indicate an excessive sharing of derived alleles between the branch of the tree represented above the figure, and the equid species or node presented vertically. The intensity of the red colour reflects statistical support for gene flow, while the grey colour indicates combinations that cannot be tested. (c) Genome scan for gene flow between AM803 and ONA10 and the group of Asian wild asses located East of the Caspian Sea (i.e. Central Asia, East Asia and *E. kiang*), using windows of 20 SNPs (stepsize = 5 SNPs). The red dashed line represents the top 99.9% cutoff. Genes within the top 99.9% f_d and supported by at least three consecutive windows were considered as candidate genes for adaptive introgression.

in line with previous mitochondrial analyses revealing the inclusion of *E. hydruntinus* within a larger, paraphyletic group of Asian wild asses (Bennett et al., 2017). Whether other European wild ass populations located further west of the species' distribution range also showed significant admixture with Asian wild asses remains unknown in the absence of nuclear genome data from *E. hydruntinus* specimens outside of southwest Asia and northwest Russia. However, we noticed that Asian wild asses from Iran and Georgia did not show evidence of gene flow with *E. hydruntinus*. This suggests that the contact zone between *E. hydruntinus* and *E. hemionus* was restricted to the most western range of southwest Asia and the northern range of the Caucasus mountain range, and did not spread further east than eastern Anatolia and the Levant (Figure 2a).

In addition to unveil a strong phylogeographic structure, our analyses also revealed important demographic differences within Asian

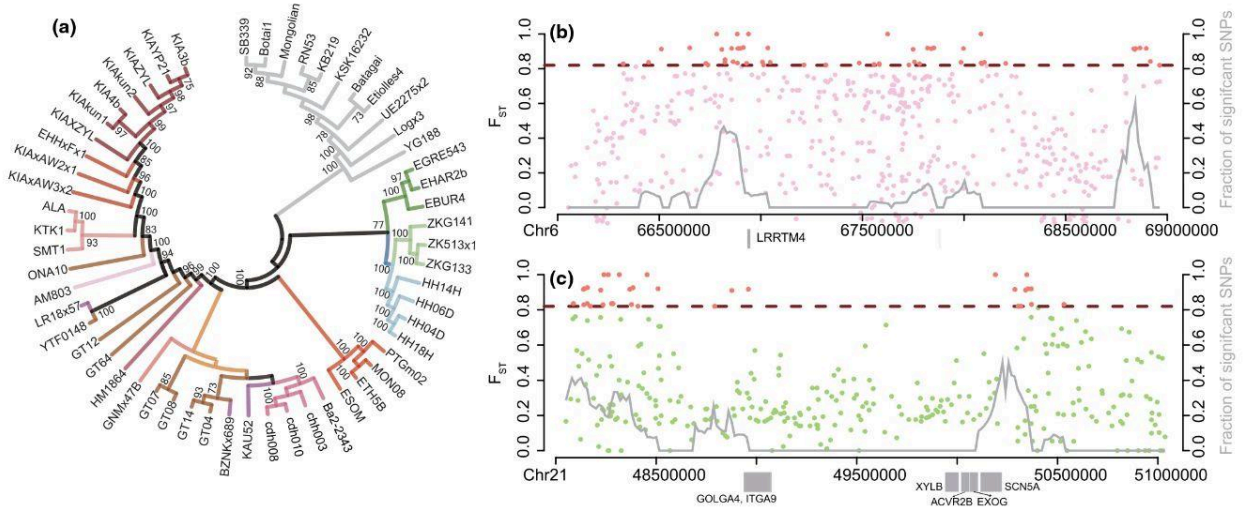

FIGURE 5 Adaptive introgression. (a) Phylogenetic tree for those genomic regions in the genomes of AM803 and ONA10 potentially introgressed from the group of Asian wild asses located East of the Caspian Sea (i.e. Central Asia, East Asia and *E. kiang*). The numbers on each node represent bootstrap supports in percentage (≥70% for clarity). (b, c) F_{ST} fixation indices between Asian wild asses from Eastern Asia plus AM803 and ONA10, and those from west of the Caspian Sea for the candidate introgressive region on chromosomes 6 (b) and 21 (c). Red dots indicate significant SNPs, while pink and green dots refer to chromosomes 6 and 21, respectively (as shown in Figure 4c). The grey line represents the fraction of significant SNPs at the position considered.

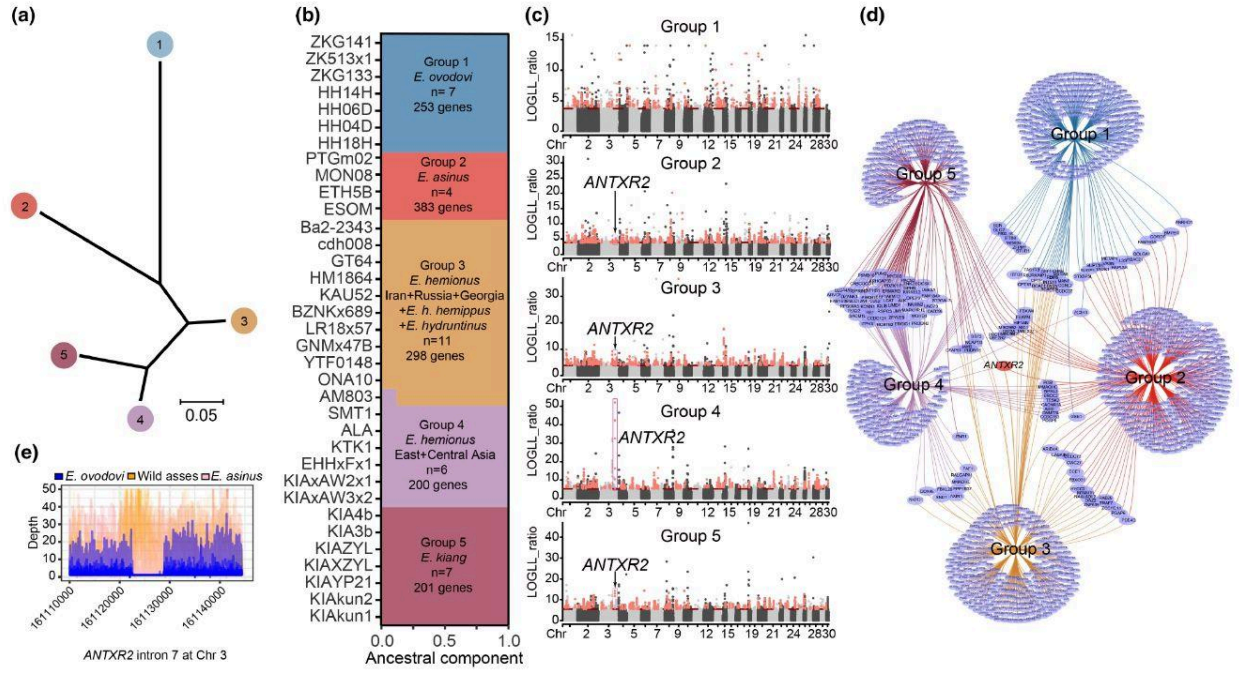

FIGURE 6 Signatures of genetic adaptation in various equine groups. (a) Estimated unrooted tree topologies of ancient ancestry components inferred by Ohana for $K = 5$. (b) Ancestral admixture components and the number of candidate genes for selection in each cluster (cutoff 99.5%). (c) Log-likelihood ratio with the regions comprising at least three consecutive windows within the top 99.5% percentile considered as selection candidates (window size = 50 kb, stepsize = 5 kb). (d) Venn network of annotated protein coding genes located within the candidate regions. (e) Cumulative depth-of-coverage profile within the *ANTXR2* gene.

wild ass populations. The nucleotide diversity of those specimens from Central Asia was more limited than that estimated in northwest Russia, East Asia and Iran (Figure 2c). It was in fact comparable to that measured in *E. hydruntinus* and *E. ovodovi* (Figure 2c), the two extinct species analysed in this study. This indicates populations of limited sizes between 2.0 and 12.1 Ky BP (i.e. the radiocarbon range of

the corresponding specimens; Table S1), in line with the local extinction of this group throughout Central Asia, except in the Badkhyz Reserve from Turkmenistan (Kaczensky et al., 2020).

3.3 | Selection and adaptive introgression

The analyses reported above supported an admixed genomic makeup between the AM803 and ONA10 specimen with Asian wild asses from Eastern Asia (Figure 4a,b and Figure S5). We further scrutinized the AM803 and ONA10 genomes for evidence of adaptive introgression, first identifying those genomic windows of 20 SNPs showing surprisingly-high f_d values in Dsuite (Malinsky et al., 2021), indicative of admixture between AM803 and ONA10 on the one hand, and Asian wild asses from Eastern Asia on the other hand (Figure 5a). Focusing on regions showing at least three such consecutive windows revealed three candidate loci for adaptive introgression on chromosomes 6 and 21 (Figure 4c). We then calculated, within those regions, F_{ST} values between Asian wild asses from Eastern Asia and those from west of the Caspian Sea, but grouping AM803 and ONA10 with the former. Finding high F_{ST} values would depict genomic regions in which the AM803 and ONA10 samples show an Eastern Asian genomic background strongly differentiated from that present west of the Caspian Sea (Figure 5b,c). It would, thus, suggest that the genetic introgression detected may be adaptive.

We found that positions 66,735,924 and 68,324,246 of chromosome 6 depicted a genomic region showing an excess of high F_{ST} values (≥99.9% percentile; Figure 5b). This region only included one protein coding gene, *LRRTM4*, which is a trans-synaptic adhesion protein regulating glutamatergic synapse assembly on the dendrites of central neurons (Table S3) (Sinha et al., 2020). The genomic region between positions 48,910,707 and 50,321,289 of chromosome 21 showed similar f_d and F_{ST} profiles (Figure 5c, Table S3,S4). It encompassed six protein coding genes, with essential roles in the removal of the RNA primer (Karlowicz et al., 2022), Golgi assembly, and spermatogenesis and male fertility (Guo et al., 2020), cell proliferation (Xu et al., 2021), cardiac electrophysiological function (Li et al., 2018), glucose metabolism and lipogenesis (Guo et al., 2022) and insulin sensitivity (Swan et al., 2024) respectively. In light of the relatively limited annotations available in the donkey reference genome, further work is needed before the potentially adaptive introgression signal identified can be confirmed and their functional consequences identified.

To further investigate the adaptive history of European and Asian wild asses as well as *E. ovodovi*, we searched for selection signatures in the equine genome using the ancestry-aware methodology implemented in Ohana (Cheng et al., 2022). More specifically, we supervised the analysis by defining five groups, including *E. ovodovi* (Group 1), donkeys (Group 2) and three groups of Asian wild asses reflecting the population structure uncovered above (*E. hydruntinus* and/or *E. hemionus* from Iran and west of the Caspian Sea, Group 3; *E. hemionus* from Central and East Asia, Group 4; and *E. kiang*, Group 5) (Figure 6a,b). We then calculated the average of the SNP-based LogLikelihood ratio returned by Ohana within 50 kb genomic windows, and considered the top 99.5% ranked values, requiring support from three consecutive windows, as candidates for selection in each ancestry component (Figure 6c,d).

Strikingly, the genetic component characterizing each of the Groups considered returned a set of candidate genomic regions including between 200 and 383 annotated protein coding genes (Figure 6d, Tables S5–S14). The number of shared candidates for selection not only recapitulates the phylogenetic affinities between these groups, but also supports the adaptive nature of the signal identified as Central and East Asian *E. hemionus* (Group 4) share more adaptive signatures with *E. kiang* (Group 5), endemic to East Asia, than with *E. hydruntinus* and/or *E. hemionus* from Iran and west of the Caspian Sea (Group 3). Importantly, one gene, *ANTXR2*, was identified as a selection candidate in all stenonine lineages investigated in this study, except *E. ovodovi* (Figure 6d,e and Table S14). The loss of *ANTXR2* expression in mice is known to enhance resistance to bacterial toxins (Banks et al., 2005), and *ANTXR2* featured amongst selection candidates previously identified while scanning the genomes of Przewalski's horses (Gaunitz et al., 2018), or plains zebras (Dickson, 2021). Combined with our results, the available evidence may indicate that this locus played a central role during equine evolution in response to infectious diseases, especially through its role in the cellular uptake of bacterial toxins.

4 | DISCUSSION

In this study, we have generated genome-wide sequence data for 25 ancient equids, mainly from members of the *E. hemionus* species, but also from two extinct equine species (*E. hydruntinus* and *E. ovodovi*). We produced the first nuclear genome from a specimen morphologically identified as *E. hydruntinus*, which complements the three genome sequences from Özkan et al., 2024 that were assigned to this species based on phylogenetic placement. Clustering of the four specimens within a single monophyletic group confirms this assignment.

The four *E. ovodovi* genomes characterized here also complement those reported Cai et al., 2022, at the archaeological site of Honghe, China, which documents, for the first time, the presence of the species in Mongolia until ~3.9 Kya (Houle et al., 2022) for elements on the stratigraphic context. Interestingly, *E. ovodovi* belongs to a group of equids called Sussemiones, which was once considered extinct since the Middle Pleistocene (Druzhkova et al., 2017). However, palaeogenetic studies have revealed their survival up until the Late Pleistocene in the Altay region (Vilstrup et al., 2013), and at least until ~3.4–4.4 Kya in Inner Mongolia and China (Cai et al., 2022), and now at approximately the same time in Mongolia. Extensive DNA survey of equine remains across East Asia, including after 3.4 Kya, should be carried out to elucidate the exact geographical range and extinction timing of this species. For now, the relatively limited genetic diversity present amongst the specimens sequenced, especially

from Mongolia, may indicate ongoing demographic declines locally (Figure 2c). More globally, the selection scan presented here shows no evidence of positive selection in the region containing *ANTXR2* for this species, in contrast to what is observed for other stenonines. Further work is needed to understand not only the exact role that this gene may have played in equid survival to infectious diseases in equids, but also the functional consequences of the 5.4-Kb deletion specific to *E. ovodovi* (Figure 6e).

Importantly, the four *E. ovodovi* specimens sequenced in this study were thought at the time of their discovery as possibly representing the earliest domestic horses to have spread into Mongolia, as their associated age is coincident with the previously reported expansion of modern domesticated horses outside their original homeland (Librado et al., 2021). The identification reported here rejects this view, and the earliest genetic evidence for the presence of domestic horses in Mongolia available so far remains in the Bronze Age, some ~3.2–3.1 Kya (Fages et al., 2019; Librado et al., 2024), in line with archaeological evidence for hippophagy (Taylor et al., 2018), horse milking (Ventresca Miller et al., 2022) and bridling (Taylor et al., 2017) around ~3.4–3.2 Kya, ~3.2 Kya and ~3.2–3.0 Kya respectively. That we identified other equid taxa than the horse in northwest Russia around ~4.7 and 5.5 Kya is also central to ongoing debates about the timing of horse domestication in the Pontic-Caspian region. The presence of equine beta-lactoglobulin peptides has indeed been reported from dental calculus of two early Bronze age human individuals contemporary to the onset of the Yamnaya cultural horizon (Wilkin et al., 2021). While the primary sequence of such peptides is identical across all species belonging to the *Equus* genus, these data were interpreted as evidence for the consumption of horse milk at the time, due to horses being the only alleged *Equus* species in the region (Wilkin et al., 2021). This interpretation implied that horses were already domesticated around ~4.5–5.3 Kya. More extensive palaeoproteomic surveys of the region, however, failed to replicate these findings, supporting Neolithic and Early Bronze Age dairying practices focused exclusively on sheep in the North Caucasian steppes, with *Equus*-specific peptides appearing no earlier than the early Iron Age (~3 Kya) (Scott et al., 2022). Together with genetic evidence supporting the demographic and geographical expansion of domesticated horses no earlier than ~4.2 Kya (Librado et al., 2021, 2024), our findings caution against previous reports of horse milking and established horse domestication in the region as early as ~4.5–5.3 Kya.

Moreover, our genome analyses revealed that the four *E. hydruntinus* specimens investigated here shared nuclear genetic affinities with Asian wild asses from north-western Russia and with Syrian hemippes. This is consistent with the geographic origins of the *E. hydruntinus* samples (Ukraine and Anatolia), and suggests population groups living at least partly in sympatry and not completely reproductively isolated. The exact genomic makeup of those *E. hydruntinus* groups inhabiting their more western distribution range, which extended as far as western Europe (Strani & Daniel., 2023) until ~2.5 Kya (Crees & Turvey, 2014), remains to be characterized to delineate the geographic extent of such genetic exchanges. More extensive palaeogenomic analyses charting the genetic diversity of hydruntines across space and time are, thus, needed to understand the impact of past glacial climate changes, human hunting, as well as the temporal dynamic and the genomic footprints of extinction, following inspiring studies carried out on woolly mammoths (Rogers & Slatkin, 2017; van der Valk et al., 2022).

Our analyses also support that the Tibetan kiang emerged from *E. hemionus* populations located at the Eastern range of their distribution, and provide additional evidence of gene flow between those two groups beyond mitochondrial haplotype sharing (Bennett et al., 2017). This finding lends support for classifications considering both taxa as *E. hemionus* subspecies, despite both groups carrying different karyotypes (Musilova et al., 2009), a situation reminiscent to what reported for *E. caballus* and *E. przewalski*, which also show different karyotypes (Ahrens & Stranzinger, 2005), but can have viable and fertile hybrid offspring (Der Sarkissian et al., 2015). Rather than reproductive isolation, the strong phylogeographic pattern unveiled amongst *E. hemionus* and *E. kiang* populations is indicative of isolation-by-distance from the Caucasian range to Kyrgyzstan, Tajikistan and East Asia, with eastern Iran representing an important contact zone between two main genetic subgroups. Unravelling the exact boundaries of this contact zone within Central Asia, and their possible shifts in the face of climate change and/or human activities will require further genome sequencing in the region throughout the Late Pleistocene and the Holocene, and until their local extirpation and global decline in the 19th and 20th centuries.

AUTHOR CONTRIBUTIONS

L.O. conceptualized and coordinated the study. P.M. and L.O. provided funding. H.D., A.F.M., B.S., S.S., E.H., A.P., J.-M.A., P.O., P.W., P. K., M.M., D.L., S.R., S.H., T.H., J.-L.H., E.H., R.B., K.S., B.R., S.S., A.A., N.S., A.S.G., G.S., J.L.G., J.B., A.B.B., A.A.K., K.R., C.W., N.V., J.-L.A., E.C. and W.T.T.T. provided samples. E. N. van A. performed the morphological description of *E. hydruntinus* specimen. R.B., J. L.G., S.R., E.H., M.M. and W.T.T.T. described the archaeological contexts. S.S. performed the wet-lab work at CAGT, with input from L.O. M.B. and D. P. performed the wet-lab work and sequencing at CeNT. J.P., X.L. and L.O. performed data analysis. L.O. wrote the manuscript, with input from J.P. and X.L. All authors revised the manuscript and approved the publication. J.P. and X.L. prepared the figures and tables, with input from L.O.

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CONFLICT OF INTEREST STATEMENT

The authors declare that they have no competing interests.

DATA AVAILABILITY STATEMENT

All code related to this analysis is available in open depository of GITHUB: https://github.com/xuefenfei712/aDNA. All collapsed, and paired-end sequence data sequenced in this study are available in compressed fastq format through the European Nucleotide Archive with the deposited code of PRJEB76252.

BENEFIT-SHARING STATEMENT

This research addresses the population genetics of hydruntines, sussemiones and Asian wild asses. We have ensured that all raw data are provided, together with well-documented scripts and instructions for data analyses. All sample providers are included in the Acknowledgements section.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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Appendix 03–Supplementary Data

Nizhnyaya Sooru

All ZooMS spectra and sample data spreadsheets have been uploaded to Zenodo, under embargo pending future publication.

- Spectra: 10.5281/zenodo.14678978
- Data: 10.5281/zenodo.14679054

ZK513-1

All ZooMS spectra and sample data spreadsheets have been uploaded to Zenodo, under embargo pending future publication.

- Spectra: 10.5281/zenodo.14678840
- Data: 10.5281/zenodo.14678815

Tashbulak

All ZooMS spectra and sample data spreadsheets have been uploaded to Zenodo, under embargo pending future publication.

- Spectra: 10.5281/zenodo.14678569
- Data: 10.5281/zenodo.14678632

Collagen Peptide Marker Screening (MALDI)

All ZooMS spectra have been uploaded to Zenodo, under embargo pending future publication. All sample data is available in this dissertation, in my “Materials & Methods” chapter and below.

- Spectra: 10.5281/zenodo.14679087
- Spreadsheet: Chapter 20, Section 20.2 (Tbl.92)

Tbl.92 Table of reference collection species, sample numbers, lab codes, and weights.

Species	Collections Sample No.	Lab Sample No.	Lab Sample Weight
Gazella subgutturosa	CE74	EH01	6.42 mg
Gazella subgutturosa	CE75	EH02	4.88 mg
Gazella subgutturosa	CE76	EH03	5.44 mg
Gazella subgutturosa	AT2	EH04	11.35 mg
Gazella subgutturosa	A32	EH05	5.6 mg
Cervus nippon	AT38	EH06	8.04 mg
Cervus nippon	AT44	EH07	6.08 mg
Cervus nippon	AT194	EH08	7.4 mg