



universität
wien

MASTERARBEIT | MASTER'S THESIS

Titel | Title

Application of paleoproteomics (ZooMS) for understanding past dietary habits of humans and hyenas at the Paleolithic site Tsagaan Agui (Mongolia)

verfasst von | submitted by

Verena Penninger BSc

angestrebter akademischer Grad | in partial fulfilment of the requirements for the degree of

Master of Science (MSc)

Wien | Vienna, 2025

Studienkennzahl lt. Studienblatt |
Degree programme code as it appears on the
student record sheet:

UA 066 827

Studienrichtung lt. Studienblatt | Degree pro-
gramme as it appears on the student record
sheet:

Masterstudium Evolutionäre Anthropologie

Betreut von | Supervisor:

Assoz. Prof. Aikaterini Douka PhD

Note of Thanks:

I would like to thank all people that were directly and indirectly involved in supporting me to finally complete my Master's thesis.

First, I would like to thank my parents, Bettina and Christian, for supporting me my whole life, for making a good education possible and for being constant advisors.

I would also like to thank my brother, David, for believing in me and my skills and for being the best big brother I will always look up to.

The next thanks go to my great love Thomas, without whom I would not feel complete, for being at my side no matter what and for the trust he has in me and my abilities.

Of course, I would like to thank Katerina Douka for her supervision and guidance during the whole project, for the trust she has placed in me and for her supportive nature.

Further thanks to Lidia Martin, who was a constant help, especially with Zooms related things.

Also, I would like to thank Maddalena Gianni for training me in the lab and for being patient and friendly the whole time.

I would furthermore like to thank Arina Khatsenovich for providing the material and for her advice and feedback on the results and the thesis itself.

Finally, I would like to thank Laura van der Sluis for being a kind and supportive contact person in all lab-related concerns.

Not to forget, I would also like to thank the University of Vienna, the Department of Evolutionary Anthropology and the Douka Lab in particular for making the work on the thesis possible in the first place.

Abstract

ZooMS, a paleoproteomic method that relies on the analyses of collagen and keratinous materials from archaeological sites, is particularly useful for rapid taxonomic identifications of fragmented bone assemblages. The samples for this study derived from the Paleolithic cave site Tsagaan Agui in southern Mongolia. The site has yielded a large lithic industry (Middle Paleolithic), numerous bones; some with cut-marks, cracking fractures and secondary treatment from humans; as well as hyena coprolites and digestion-eroded bones. In this work, 566 Pleistocene-age bones were analyzed with ZooMS. Of these, 276 bones retrieved during excavation and 287 bone fragments showed signs that were nibbled or digested by hyenas, partly extracted from coprolites. In total, 95 % of bones showed excellent collagen preservation; the digested samples showed a 98 % success rate in collagen preservation. The identified ZooMS taxa include equids (the largest fraction with 42 %), camels, antelopes, rhinos, beavers, felids, canids, leopards, bear, foxes, goat, mouse, rats, badger, birds and some less well defined bovids/cervids, together indicating a distinct Eurasian fauna complex. Four bone samples were radiocarbon dated, the oldest to 49.4-43.8 ka cal BP and was taxonomically identified as *Pantholops hodgsonii*. Both humans and hyenas targeted camels, equids and medium-sized bovids. Hyenas expanded their diet with cervids, rhinos, rodents, leopards, felids, bears and other carnivores. The faunal record, mostly consisting of migratory ungulates, indicates the abundance of grass/plants as well as water sources, not clearly visible today. This suggests a temperate environment for part of the period the site was occupied. Ultimately, this work identifies in more detail the prehistoric fauna that lived in and around an important Paleolithic human shelter in Central Asia, and died by predators that include both humans and hyenas, offering important new insights.

Key words: ZooMS, paleoproteomics, Paleolithic, radiocarbon dating, Tsagaan Agui, Central Asia, Eurasian fauna, cave hyena

Table of Contents:

1. Introduction	6
1.1. Paleoproteomics	7
1.1.1. Development of the field	7
1.1.2. Ancient Proteins	9
1.1.3. Collagen Fingerprinting	12
1.2. Overview of the Paleolithic period, with focus on Eurasia	16
1.3. The archeological site of Tsagaan Agui	20
2. Material and Methods	23
2.1. Material	23
2.1.1. Non-digested bones	23
2.1.2. Hyena-digested bones	24
2.2. Methods	24
2.2.1. Collagen peptide mass fingerprinting (ZooMS)	24
2.2.2. Radiocarbon Dating	26
3. Results	28
3.1. ZooMS results	28
3.1.1. Non-Digested Samples	30
3.1.2. Digested Samples	32
3.1.3. ZooMS results in context with the archaeological layers	34
3.2. Radiocarbon dates	35
4. Discussion	37
4.1. Success rate of digested samples	37
4.2. Faunal Assemblage at Tsagaan Agui	37
4.3. Chronological Data	50
4.4. Insights into Paleoecology and Diet	51
5. Conclusion	57
6. Bibliography	59
7. List of Illustrations	68

8. Table Directory	70
9. Appendix	71

1. Introduction

Bone is one of the most common types of remains excavated at archaeological and paleontological sites. Bones survive for millennia, preserving not only their inorganic matrix but also some of their biomolecular components. The identification of bones is essential for research disciplines such as paleontology, archaeology and paleoanthropology. However, bones found buried at sites are often fragmented beyond morphological recognition, which is why alternative methods for bone identification have been introduced in the last two decades. These methods rely on the extraction of biomolecules, such as aDNA and proteins, the most abundant of which is collagen. One such method is ZooMS (short for Zooarchaeology by Mass Spectrometry), a paleoproteomic methodology that is based on the principles of peptide mass fingerprinting (Brown et al. 2021). The method was first introduced in 2009 (Buckley et al. 2009) and is now a rapidly growing technique due to its potential for rapid taxonomic identification of large bone assemblages and its minimally destructive and cost-effective character, at the same time (Richter et al. 2022). The application of ZooMS has led to important discoveries in the last decade, such as the discovery of Denisova 11 (“Denny”), the first-generation hybrid offspring of a Neanderthal mother and a Denisovan father (Brown et al. 2016) or the identification of the earliest known domestic sheep in Africa (Coutu et al. 2021).

In this thesis, I use ZooMS to taxonomically identify 566 bone samples from the Paleolithic cave site Tsagaan Agui in Mongolia, excavated by Dr. Arina M. Khatsenovich (Institute of Archaeology and Ethnography SB RAS). Tsagaan Agui lies in the southern Gobi Altai region and has yielded numerous lithic artefacts, a large bone industry as well as fauna and floral remains. There is also evidence for human-animal interactions in the form of cut-marks on some bones. The findings indicate intense human and animal occupation; however, no human remains have been found so far (Khatsenovich et al. 2022).

The 566 bones from Tsagaan Agui analyzed here consisted of two groups of samples; fragmented bones and hyena-digested bones partly extracted from coprolites. The application of ZooMS on these bones aimed primarily at determining their taxonomic identification, as well as the degree of collagen preservation between hyena-digested and undigested bones. Finally, selected samples underwent radiocarbon dating to assess the age of the identified fauna. Ultimately, the data produced here aims at expanding our understanding of human

evolution by identifying prehistoric fauna living and dying close to an important Paleolithic human shelter in Central Asia and elucidate human-animal interactions, diet and the environment they lived in.

1.1. Paleoproteomics

The study of ancient proteins, or else paleoproteomics, allows us to explore fundamental questions about past organisms, biology and ecology through mass spectrometry-based approaches. It is a rapidly growing field with diverse applications that range from taxonomic identifications of fragmented bones, investigation of phylogenetic relationships (also of extinct species), to the analysis of past diet through proteins found in dental calculus and residues in pottery. This is possible, because proteins can persist for millions of years in protected environments. In addition to being part of a biological tissue, proteins can for example also be found in textiles, building materials or paints. Their ubiquity and longevity make them perfectly suited for reconstructing biological and cultural history and can therefore rightly be described as an important “*bioarchive of the past*” (Warinner et al. 2022).

1.1.1. Development of the field

The origin of paleoproteomics lies back in the 20th century even before the discovery of the structure of DNA. In the 1930s scientists were interested in determining the blood groups of mummies through antisera and later in the 1950s the so-called *paleobiochemistry* was developed as a new scientific discipline by Phil Abelson. In the 1950s, Abelson and other members of the Geophysical Laboratory successfully recovered for the first time amino acids from fossils (Abelson 1955). These early discoveries paved the way for what has become the field of paleoproteomics today. Yet, problems concerning contamination, cross-reactivity, diagenetic variability or the difficulty of replicating the experiments impeded the development of the field. In the 1970s and 1980s the interest in ancient proteins arose again, this time through the use of immunological assays. ELISA was developed to gain more relevant immunological information for taxonomic systematics, but the replication of the results remained a constant issue. Over the next two decades immunological approaches in the field of paleoproteomics decreased, also because it remained difficult to understand which proteins were immunologically detected (Schweitzer et al. 2002).

Hence, protein sequencing was the only way forward. The first successful recovery of an ancient protein sequence was achieved using Edman degradation methodologies (Huq et al. 1990) but even this was limited to its application because it required pristine and unmodified proteins to be preserved. The major breakthrough came with the development and broader application of mass spectrometric methods. The innovative application of soft-ionization mass spectrometry as well as isotopic analysis, to ancient proteins by Peggy Ostrom and colleagues (Ostrom et al. 2000) is considered a seminal point in the development of the field.

Peptide Mass Fingerprinting (PMF) was developed in 1993. This method is applied to identify proteins by the masses of the peptides that result during enzymatic digestion (Collins et al. 2010). Decisive for its development was the former innovation of the matrix-assisted laser desorption/ionization (MALDI) soft ionization method in 1987, which enabled the ionization of large non-volatile molecules, like peptides, without being fragmented (Karas & Hillenkamp 1988; Tanaka et al. 1988). It is often combined with a Time of Flight (ToF) mass analyzer, that measures the time it takes for each peptide ion to extend across the flight tube. The MALDI-TOF mass spectrometry system has a large mass range and is ideally used for individual proteins or mixtures with a valid composition (Richter et al. 2022). If type I collagen (COL1) is used for PMF it is referred to as ZooMS, an acronym emphasizing the roots of the method not only in zooarchaeology but also in mass spectrometry (Buckley et al. 2009).

The taxonomic discrimination of sheep and goat bones in 2010 can be seen as the first widespread use of MALDI-TOF MS in the field of archaeology (Buckley et al. 2010). Other analytical techniques in ancient protein identifications beside peptide mass fingerprinting are amino acid analyses, immunoassays and liquid chromatography – tandem mass spectrometry (LC-MS/MS). Usually LC-MS/MS approaches are usually bottom-up identifications, but there are also top-down approaches that can be used to identify a protein while it is in its native state offering the potential to gain information about protein fragmentation and posttranslational modifications (PTMs) and therefore help understanding protein survival and degradation (Hendy 2021).

Paleoproteomics is undoubtedly a revolutionizing way to study the past record, allowing us to broaden our knowledge of evolution, phylogeny, human diet, art and many other aspects; but

certain challenges still remain. These are for example difficulties concerning protein recovery and measurement, insufficient databases or sources of contamination. And although mass spectrometry became the go-to tool in paleoproteomics, immunological approaches like the potential of immunoaffinity chromatography to target or enrich specific proteins before sequencing them offer promising potential for the future. The same applies for other non-MS based technologies like massively parallel sequencing by nanopore, fluorosequencing and image-based Edman, although those approaches are for now not ideally suited for paleoproteomics due to unexpected modification in ancient samples and autofluorescence caused by diagenesis (Warinner et al. 2022).

1.1.2. Ancient Proteins

Proteins are large biomolecules made up from amino acids folded into a complex three-dimensional form. The amino acid sequence is encoded by DNA and then transcribed into RNA and ultimately translated into proteins. Due to the fact that proteins preserve part of the heritable genetic code they are suited for phylogenetic reconstructions and taxonomic identifications (Whitford 2013).

Certain proteins are commonly used in paleoproteomics. The most frequently analyzed one is Type 1 collagen, COL1. It can be derived from bone, dentine, antler, ivory, parchment, leather and other soft tissue (Richter et al. 2022). More information about collagen and its proteomic analysis follows in the next chapter (1.1.3.). Another group of proteins are keratins that allow the identification of wool, horn, hair, feathers and similar substrates. After collagens α -keratins and corneous β -proteins, CBPs – or formerly known as β -keratins – are the most relevant structural protein classes in vertebrates and they can, just like collagens, be taxonomically distinguished with PMF. Keratinous tissues do not remodel nor mineralize, which means they are more predisposed to degradation than mineralized proteins (McKittrick et al. 2012) and are therefore less likely to be found in an archaeological context.

The protein amelogenin (AMEL as associated gene) is commonly analyzed in the last decade and it can be used for sex typing in humans (Mannucci et al. 1994) and some animals. Amelogenin is part of the enamel matrix and due to sequence differences and deviations in the expression level, in monotremes, marsupials, eutherian mammals and nonmammalian species it allows for sex discrimination (Warinner et al. 2022). Besides collagens, keratins and amelogenin, fibroin - as the dominant protein in archeological silk - can also be analyzed to

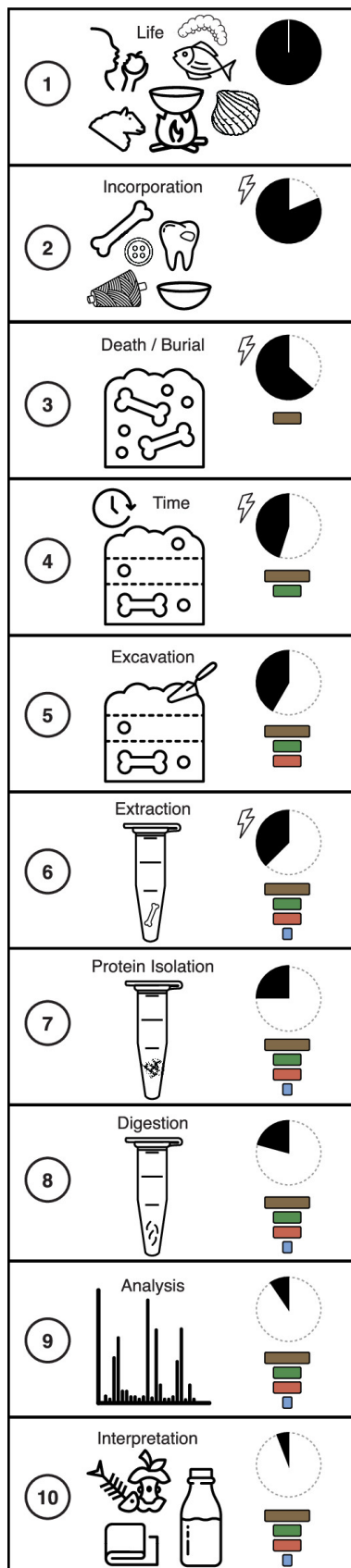


Figure 1: Different stages of protein incorporation and recovery in an archaeological sample ranging from the ancient life to present interpretation (Warinner et al. 2022).

identify silk textiles and their species of origins (Degano et al. 2011). Another example is the milk beta-lactoglobulin, which is probably the most frequently tested ancient food protein (Brownlow et al. 1997). Finally, osteocalcin has been one of the first proteins to be analyzed from archaeological bones (Ulrich et al. 1987; Huq et al. 1990).

Ancient proteins can be found in bone, dentine, enamel, avian eggshells, mollusc shells, mummified remains or plant macroremains. Proteomes, the collection of proteins in a specific tissue, often show high complexity and a wide range of protein expressions. LC-MS/MS is used to profile such proteomes but characterizing them remains challenging. If protein mixtures derive from more than one proteome it is referred to as metaproteomes like the mixtures found in microbiomes, food remains, residues, diseased tissues, art works or cultural heritage materials. Proteome data offers great potential in terms of phylogenetic relationships, health, aging and development (Hendy 2021).

The analysis of ancient proteins starts with understanding the incorporation of the protein into a given sample. This can be obvious for endogenous proteins like collagens in bone or keratins in hair, because these proteins become incorporated while the tissue is formed (Warinner et al. 2022). In other cases, it is less clear like for dental calculus, where digestive enzymes and immune proteins from saliva and gingival fluid become part of the proteome, sometimes also supplemented by exogenous proteins like dietary or seed storage proteins (Warinner et al. 2014). Further, biomineralization also influences, because co-associated endogenous proteins, like blood proteins in bone, can become incorporated as well (Gorski 2011). And even

during the incorporation process itself, proteomes can be altered, such as through denaturation during the cooking process (Yu et al. 2017). Considerations about the incorporation are followed by taking the decay and diagenesis into account. Degradation of most organic material is particularly driven by bacteria through enzymatic digestion and factors like the environment (e.g. soil, pH, water), the characteristics of the surrounding matrix, the composition of the given protein mixture and the temperature, humidity and time the proteins were exposed to are decisive for the degradation process and yet complex to evaluate. Proteins that are generally mineralized, of high abundance, with a stable structure (e.g. triple helix of collagen) and/or have specific characteristics like stability against proteolysis, to changing pH-levels or similar are more likely to persist in the archaeological record (Warinner et al. 2022).

In general, ancient proteins benefit from limited water availability. To authenticate an ancient protein, markers of degradation can for example be used by allocating those fragmentation patterns with the detection of mass shifts that in turn result from chemical changes like hydrolysis proteins underwent while being buried. Studying those patterns helps to differentiate between ancient proteins and potential modern contaminants, although the mechanisms are not fully understood and less studied than the markers for DNA degradation (Demarchi 2020). Once the preservation status has been considered, proteins are extracted from the matrix, whereby different chemical extraction protocols can be applied depending on the sample type, size, preservation, complexity of the proteome and potential chemical modifications (Hendy et al. 2018).

Since proteomic analyses usually require small amounts of sample material, the procedure can be combined with other methods (e.g. radiocarbon dating, isotopic analysis) by using the leftover material or byproducts. This way sampling demands on irreplaceable materials can be reduced. After the extraction of the protein, it is usually enzymatically digested, because current mass spectrometers work best on peptides in the size of 6-30 amino acids followed by isolating and purifying them (Hendy 2021).

Extracted peptides can be analyzed either with PMF by MALDI-ToF or shotgun proteomics by LC-MS/MS. The analysis of the data obtained is performed with the help of specialized software, complex bioinformatic approaches and peptide marker databases, although no centralized database currently exists. Finally, the results can be interpreted and put into

context (Hendy et al. 2018). Figure 1 depicts the stages described, whereby the decrease of the black area in the pie chart indicates the loss of protein present in a fictive sample while passing through the mentioned stages.

Paleoproteomics offers in comparison to paleogenomics several advantages (Wadsworth & Buckley 2014) such as the higher abundance of proteins and their survival for much longer periods of time (Richter et al. 2022), even for millions of years under favorable conditions (Demarchi et al. 2016; Welker et al. 2019). Beyond that proteins are also found in acellular tissue like eggshells (Demarchi et al. 2016). Consequently, proteins are more valuable for studying deep time fossils and other ancient objects. Also, the analyses of proteins are more successful even in warmer environments and in general of lower costs, which is why proteomic approaches are well suited as a screening method for large sample sets (Buckley et al. 2009).

1.1.3. Collagen Fingerprinting

Collagen Fingerprinting is a form of PMF and as already mentioned better known as ZooMS. First, the main aspects of collagen are explained to provide a better understanding of the principle behind the so-called “collagen fingerprint” followed by the procedure itself.

There are almost 30 different collagen proteins known belonging to the class of structural proteins. Type I collagen is the dominant protein in bone, making up 80 % of the bone proteome and is also considered to be the most abundant protein in vertebrates (Buckley 2018). COL1 is highly abundant in the extracellular matrix of various connective tissues like in skin, tendon or ligament. Its main function lays in the bone mineral deposition. Common archaeological finds containing COL1 are for example bone, cartilage, antler, tooth dentine or cementum, parchment, leather, fish scales or artwork made with animal glues (Warinner et al. 2022). Characteristic to all collagens, not only type I, is the triple helical structure. COL1 is made up of three polypeptide α -chains, whereby in most animals the structure is composed by two α 1-chains and one α -2 chain (Brown et al. 2021). Exceptions are for example teleost fish with three different α -chains or unicellular hydra with three COL1 α 1-chains. Looking at each chain separately shows a repeating pattern of Gly-Pro-Hyp, which means glycine is typically followed by Prolin and Hydroxyprolin, the posttranslational modified version of prolin.

The latter is rarely found outside of collagens and stabilizes the structure through hydrogen bonding. Glycine fits in well into the central core due to its small size (Buckley et al. 2009).

During the course of COL1 formation, proto-COL1 α -chains are produced and with the help of the containing signal peptide transported to the endoplasmic reticulum, where the triple-helix formation is initiated. This structure is highly conserved. Following fibrillogenesis and cellular secretion the collagen triple helices form into groups of about 5 microfibrils, that again aggregate into fibrils and ultimately form into collagen fibers. These fibers serve in bone as template for biomineralization, whereby the tightness and bundling of collagen is crucial for its role as structural protein and helps to preserve collagen long-term (Richter et al. 2022). The collagen preservation status depends on the degree of degradation. Factors that enhance degradation have been mentioned in the previous chapter.

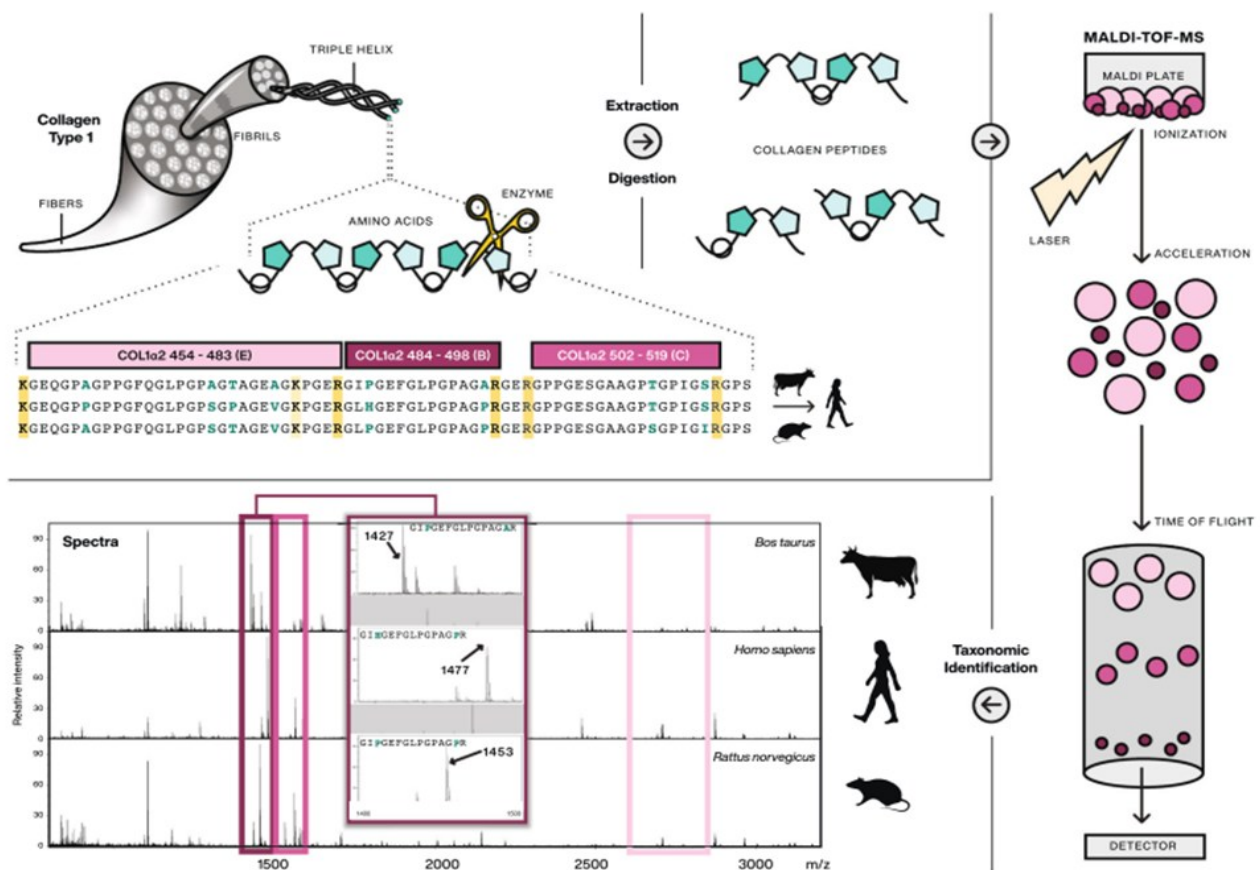


Figure 2: Schematic overview of ZooMS from the extraction and digestion of collagen to the MALDI-TOF analysis leading to the interpretation of the resulting mass spectra (Brown et al. 2021).

Collagen is specifically vulnerable to diverse fungi and soil microbes that produce collagenase, which degrades unmineralized collagen and leads to spontaneous chemical hydrolysis of mineralized collagen. Microbial growth goes along with the secretion of organic acids that further demineralize skeletal remains (Warinner et al. 2022). The collagen content within certain archaeological remains declines over time, which is why it is necessary to estimate the collagen preservation of a given sample set by either measuring the dry weight percentage (%wt) or by specifying the %N of a sample. An internal minimum standard is 1% collagen in a sample to work with, however this is often limited to radiocarbon studies where collagen loss is linked to contamination enhancement. ZooMS requires less collagen compared to radiocarbon dating or stable isotope which allows ZooMS studies to utilize more and older samples (Wang et al. 2021; Richter et al. 2022).

The first steps in obtaining ZooMS data, involve the extraction and purification of collagen. Several different protocols have been developed in the past decade, and they can be divided into the following three different categories:

- a) Non-destructive analysis of the soluble collagen fraction without acid
- b) Demineralization in acid followed by analysis of the acid insoluble fraction; and
- c) Demineralization in acid followed by analysis of the acid soluble fraction

Protocol b is most widely used by first demineralizing the bone's inorganic matrix with acid (usually HCl). In this stage it is important to monitor the samples carefully to avoid excessive protein loss. Afterwards the acid is removed remaining the acid-insoluble fraction which is washed twice or three times with an ammonium bicarbonate puffer (AmBic) to increase the pH-level. In comparison, protocol (c) utilizes the acid soluble collagen within the acid supernatant which is then filtered through a molecular weight cutoff. In the course of the extraction process COL1 undergoes gelatinization through heat, resulting in an amino acid structure available to enzymatic digestion. The latter is usually performed with trypsin that cleaves the C-terminal peptide bonds of arginine and lysine, highlighted in yellow in the sequence data in Fig. 2. As a result, several collagen peptides with difference in length and mass are produced. Those peptides are purified with C₁₈-ZipTips and spotted onto a MALDI-plate together with a matrix that cocrystalizes with the peptides (Wang et al. 2021). Within the mass spectrometer the matrix is excited with a laser leading to the vaporization and ionization

of the peptides with +1 charge. Since MALDI-MS is often combined with a Time of Flight (ToF) mass analyzer, electromagnets are then directing the ions in a time-of-flight tube where they are separated by mass. The time it takes for each peptide ion to extend across the flight tube is measured. Based on the known input energy and distance it is possible to infer the mass to charge ratio (m/z), whereby larger molecules will take longer to travel across compared to smaller ones. Afterwards the ion detector converts the ion current into an electrical current resulting in an output showing a spectrum of peaks. This mass spectrum can be referred to as collagen fingerprint (Buckley et al. 2018).

The “acid-insoluble” protocol is well suited for mineralized tissues, where destruction of part of the material is acceptable, and it can be applied to poorly preserved material. For samples that are too small and cannot be sampled due to curatorial concerns, non-destructive protocols have been developed in the past few years (e.g. van Doorn et al. 2011; Evans et al. 2023) and involve the use of erasers or even the analysis of plastic storage bags (REFs). Non-destructive approaches avoid the sample demineralization, and instead collagen is extracted directly through the incubation of the bone in an ammonium bicarbonate puffer which allows free, soluble collagen strands to come into the solution. The supernatant undergoes tryptic digestion, purified with C₁₈-ZipTips. The purified peptides are then spotted on a special plate and analyzed using MALDI-TOF- MS (Warinner et al. 2022).

The peaks detected and visualized in the mass spectrum are associated with specific peptide sequences. Although all COL1 peptides ranging from ~ 8 to 30 amino acids in length should be visible in the spectrum, in practice this is usually not the case due to different reasons. Reasons include cross-linking, incomplete digestion, glycosylation, poor ionization, unexpected PTMs or nonenzymatic digestion. Fig. 2b shows three different collagen peptide mass fingerprints and their taxonomic identifications as *Bos taurus*, *Homo sapiens* and *Rattus norvegicus*. By comparing the marker peptides, in common use are nine (Tab. 1), to reference databases conclusive taxonomic assignments can be made. The lettering system of the markers was changed from single letters to names indicating the location and sequence of the peptide that corresponds with the marker shown in Tab. 1 (Brown et al. 2021). The analysis of PMFs is also associated with some challenges such as the presence of potential contaminant peaks, matrix peaks or autodigested trypsin peaks that need to be interpreted correctly. It can also get more

complicated through *in vivo* PTMs and diagenetic forms that can induce mass shifts (Brown et al. 2021). The most important PTM for ZooMS is hydroxyproline which causes a mass shift of + 16 Da (Richter et al. 2022). In general, it is possible to go through the spectra manually or to work with automated systems, such as one recently proposed (SpecieScan) for semi-automated ZooMS identifications (Vegh & Douka 2024). The second way can also be applied as additional check of the manual identifications or to scan for contaminants.

Table 1: Commonly used markers for ZooMS (Brown et al. 2021).

Sequence	m/z	Oxidations	Gene	Nomenclature			Start Position			Proposed Full Name	Proposed "nickname"
				Letter	Tryptic		Whole Sequence	Mature Peptide	Helical Region		
GVQGPAGPAGPR	1105	1	COL1a1	Cet1 / P1	A1T47		685	524	507	COL1a1 508–519	a1 508
GLTGPAGPAGAPGDKGEAGSPAGPTGAR	2853 / 3869	2/3	COL1a1	F	A1T55/56		763	602	585	COL1a1 586–618	a1 586
GSTGEIGAGPPGPGLR	1648	2	COL1a2	Cet2 / P2	A2T26		380	301	292	COL1a2 292–309	a2 292
GEQGPAGPPGFQGLPGAGTAGEAGKPGER	2792	3	COL1a2	E	A2T41/42		542	463	454	COL1a2 454–483	a2 454
GIPGEFGLPGAGAR	1427	2	COL1a2	B	A2T43		572	493	484	COL1a2 484–498	a2 484
GPPGESGAAGPTGPIGSR	1580	1	COL1a2	C	A2T45		590	511	502	COL1a2 502–519	a2 502
GPSGEPGTAGPPGTPGPQGLLAGPGLPGSR	3017 / 3033	4/5	COL1a2	G	A2T67		845	766	757	COL1a2 757–789	a2 757
GLPGVAGSVGEPGLGIAGPPGAR	2131	3	COL1a2	D	A2T69		881	802	793	COL1a2 793–816	a2 793
IGQPGAVGPAGIR	1192 / 1208	0/1	COL1a2	A	A2T85		1066	987	978	COL1a2 978–990	a2 978

1.2. Overview of the Paleolithic period, with focus on Eurasia

The Paleolithic period of Eurasia, or the Old Stone Age when referring to sites in Africa, is the longest and oldest period of human evolution. The beginning of the Paleolithic period is associated with the first appearance of humans in a region and ends with the transition to a demonstrably different culture and way of life. This is why the respective chronological classifications vary accordingly. In Africa, for example, the oldest part of the Stone Age is referred to as the Early Stone Age, characterized by Oldowan and Acheuléen lithic industries, and dates from around 2.6 million years to 130,000 years ago. According to the Out-of-Africa model, the Palaeolithic outside Africa is to be dated with a time delay. The model postulates three waves out of Africa starting with *Homo erectus* that reached Western Asia (Dmanisi, Georgia) around 1.8 million years ago and southern Europe around 1.1 million years ago. The second wave took place about 500,000 years ago with *Homo heidelbergensis* leading mainly to Europe (Grupe et al. 2012) and during the third wave anatomically modern humans (AMH or early *Homo sapiens*) colonized Europe and East Asia via the Southern Route (70-50 ka;

Armitage et al. 2011) and later Australia (65-50 ka; Clarkson et al. 2017) and the Americas. As they arrived in Europe and northern Asia *Homo sapiens* met and admixed with other hominin groups already living in Eurasia since 250,000 years ago, namely *Homo neanderthalensis* and the Denisovans. *Homo sapiens* ultimately remained the only human species on earth, after the extinction of Neanderthals around 40,000 years ago (Higham et al. 2014) and of the Denisovans around the same time (Douka et al. 2019) or later.

Characteristic to the Paleolithic is the appropriative form of economy in groups of hunter-gatherers. Different cultures can be distinguished based on their material remains recovered in the archaeological record. For example, in the Middle Paleolithic, the Mousterian, is often associated with *Homo neanderthalensis*, whereas the Upper Paleolithic industries are normally linked to *Homo sapiens* and exhibits a broader tool diversity; with some of the earliest such cultures known as the Chatelperronian, the Proto- and Early Aurignacian and the Gravettian. As cultural transitions are fluid and based upon an incomplete archaeological record, chronological boundaries and biological constraints must be seen as a relative means of classification¹.

The Paleolithic record of Central Asia:

The present work focuses on material excavated in Mongolia; hence the Paleolithic of Central Asia is directly relevant.

The absence of faunal exchange between 800,000-170,000 years ago from the Levant in particular indicates the isolation of Asia from Africa. Hence, the archaeological record of Asia from this time is to be seen as indigenous. The Lower Paleolithic of Central Asia is for example represented by the loess site of Kul'dara in southern Tajikistan dating to around 800,000 years ago. At sites like this early stone tools made of pebble and flake implements were found. The loess offers further great potential to study paleoenvironmental conditions (Davis & Ranov 1999). Although Gesher Benot Ya'aqov (GBY) is not located in Central Asia (Israel), it is shortly mentioned because it possibly has the earliest evidence for controlled fire use, the processing of plant foods and the shaping of woods in Asia (Dennell 2008). Lower Paleolithic assemblages of Southwest and Central Asia were thought to be assignable to two lithic traditions, one group contains hand-axes and/or cleavers (Acheulean), the other not. But this classification remains

¹ <https://www.worldhistory.org/Paleolithic/> (retrieved on 15.09.24)

debatable as the absence/presence of hand-axes could also be related to the local availability of large stones suited for the tool production (Dennell 2008). The Middle-Paleolithic assemblages cannot be described by a single technocomplex as the archaeological record is variable in time (Vishnyatsky 1999). The Initial Upper Paleolithic (IUP) industries are very diverse and have persisting elements of the Middle-Paleolithic. The Middle-to-Late Pleistocene transition is dated 140-100 ka. The comparable use of technologies by Paleolithic hunter-gathers could be either related to a form of cultural transmission or to a convergent development, whereas transmission processes are according to Zwyns (2021) more suited to explain the archaeological record.

Denisova Cave is one of the key sites to study the Middle and Upper Paleolithic of different hominin groups that inhabited Eurasia during this time. There is evidence for the periodical occupation of the cave by both Neanderthals and Denisovans (Slon et al. 2017; Zavala et al. 2021). Age estimates of all Neanderthal fossils found at Denisova Cave using Bayesian age modelling date between 80,000 – 140,000 years ago, whereas the oldest Denisovan sample is dated to 195,000 and the youngest to 52,000 until 76,000 years ago (Douka et al. 2019; Brown et al. 2022). Other remains of Denisovans have been found in Baishiya Karst Cave in the Tibetan Plateau (Xia et al. 2024) and at Cobra Cave in Laos (Demeter et al. 2022).

Since Denisovans can only be studied by a few remains, the greater information pool is their DNA. Paleogenetic analyses resulted in the finding of interbreeding events between Denisovans with anatomically modern humans. High percentage is confirmed in Melanesians, Aboriginal Australians and Filipino Negritos (Reich et al. 2011). Denisovans also interbred with Neanderthals, exemplified through the discovery of “Denny,” a first-generation offspring of a Denisovan father and a Neanderthal mother (Brown et al. 2016; Slon et al. 2018). It appears that Denisovan populations were distributed across Eastern Asia, whereas Neanderthals, a traditionally European species, expanded their original European habitat region to West and Central Asia (Krause et al. 2007; Serangeli & Bolus 2008). The Teshik-Tash cave, which was discovered in 1938, yielded specimens of a child that is currently interpreted as the furthest east Neanderthal find (Weidenreich 1945). An examination of the cranium lead to equivocal results indicating features of modern humans as well (Glantz et al. 2009), but a study that

applied geometric morphometric analysis came to the previous conclusion that the Teshik-Tash child is Neanderthal (Gunz & Bulygina 2012).

The Paleolithic record of Mongolia:

The Paleolithic specifically in Mongolia can be studied at several archeological sites including the Dorolj sites, the Tolbor sites, the Orkhon sites, Salkhit and towards the south Chikhen Agui and Tsagaan Agui (Zwyns et al. 2014). The latter is the only known Middle Paleolithic site in southern Mongolia and valuable in terms of its archaeological finds that allow to reconstruct cultural habits of hominins inhabiting the Gobi Altai region (Khatsenovich et al. 2023). The locations of all sites can be seen in Fig. 3. The Tolbor sites are located in northern Mongolia and are divided into Tolbor-16 (Zwyns et al. 2014) and Tolbor-21 (Rybin et al. 2020) Both sites are assigned to the Upper Paleolithic and were occupied by early humans. There were at least two major human dispersals across Eurasia during the Late Pleistocene in which Neanderthals and Modern Humans moved eastward (Zwyns et al. 2014). Another prehistoric migration route of early humans during the Pleistocene was identified in Central Asia along the Selenga River Basin (Zwyns et al. 2019). At the Orkhon sites in Central Mongolia (Moiltyn-am, Orkhon-1, Orkhon-7) studies on the paleoenvironment were carried out, leading to the conclusion of a relatively humid climate during MIS-3 followed by aridification (Khatsenovich et al. 2021). Chikhen Agui is associated with Early Holocene hunters, archaeological findings at the site include ostrich eggshells, wooden pole and fireplaces (Derevianko et al. 2008). Currently, the skullcap from the Salkhit Valley in northeast Asia is the only Paleolithic human fossil found in Mongolia (Coppens et al. 2008), it was directly dated to about 34 cal BP and analyzed genetically in 2019. The analysis of the mtDNA yielded to the assignment of the specimen to haplogroup N, which is nowadays widespread in Eurasia (Deviese et al. 2019). The mosaic environment of Mongolia encouraged early human populations to adapt through various subsistence strategies (Khatsenovich et al. 2023). In addition, the presence of either glacial or

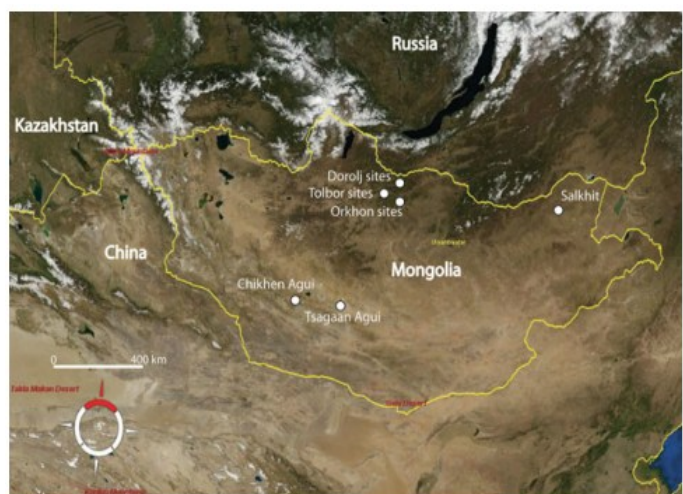


Figure 3: Map with the main stratified Paleolithic sites in Mongolia (Gunchinsuren 2014, p.5026).

interglacial oscillations affected the settlement and adaption patterns of Paleolithic hunter-gatherer groups, not only in Mongolia (Davis & Ranov 1999).

1.3. The archeological site of Tsagaan Agui

Tsagaan Agui is a Paleolithic cave site in the Gobi Altai Mountains, in southern Mongolia (Bayankhongor Province). The cave was discovered by Mongolian archaeologists in 1972. The first investigations of the site took place in the 1980s, followed by subsequent excavations between 1995 to 2000. Further excavations resumed in 2021 and 2022. (Derevianko & Petrin 1995; Khatsenovich et al. 2021; Khatsenovich et al. 2023). The cave itself can be divided into five parts. These include: the Entrance Terrace, the Entrance Grotto, the Main Chamber, the Inner Chamber and the Lower Grotto (Fig. 4). There are 14 archeological layers in the Main Chamber with at least five discrete stratigraphic units, that range from the Middle to the

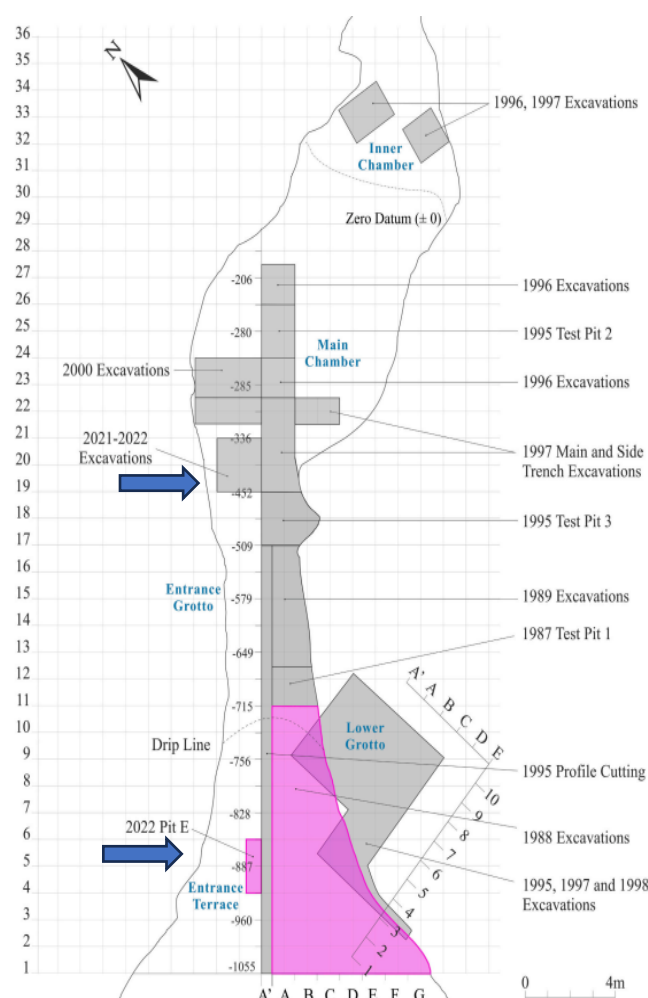


Figure 4: Plan view of Tsagaan Agui (Khatsenovich et al. 2023, edited by the author with blue arrows).

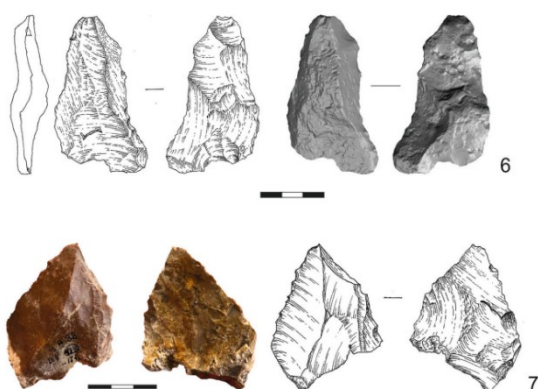


Figure 5: Lithic artefacts of the Entrance Terrace assemblage at Tsagaan Agui showing a Mousterian point with concave base (6) and a Mousterian point (7) (Khatsenovich et al. 2023).

Upper Paleolithic. The site has yielded numerous lithic artefacts, ceramics (from more recent periods) as well as floral and faunal remains (Derevianko et al. 2000; Khatsenovich et al. 2022). It is also postulated that some of the Middle Paleolithic cultural remains at Tsagaan Agui, like the lithic complex of Layers 5-7 of the Entrance Terrace (examples in Fig. 5) are possibly evidence for Denisovan presence

in the Gobi Altai region, because of close similarities to finds at Denisova Cave and Jintsai Cave, China (Khatsenovich et al. 2023). Although potential connections to a certain hominin species are tentative, it is an important consideration for this work. The bone samples for this study derived from Pit 2 (2021) and Pit E (2022) at Tsagaan Agui.

Pit 2

(Fig. 4 upper blue arrow) is located near a 1 m² sondage excavated in 2000 and was dug down to Layer 6 (stratigraphic profile of Pit 2 is shown in Fig. 6). Layer 1 has three Holocene horizons, Layer 2.1 contains a flake industry, Layer 2.2 further lithic artefacts, Layer 3 a laminar industry with evidence of Levallois point production, Layer 4 contains bidirectional blades and Layer 5-6 is characterized by core-management elements (CME). A small bone industry was found in Layers 2.1 - 4 with two

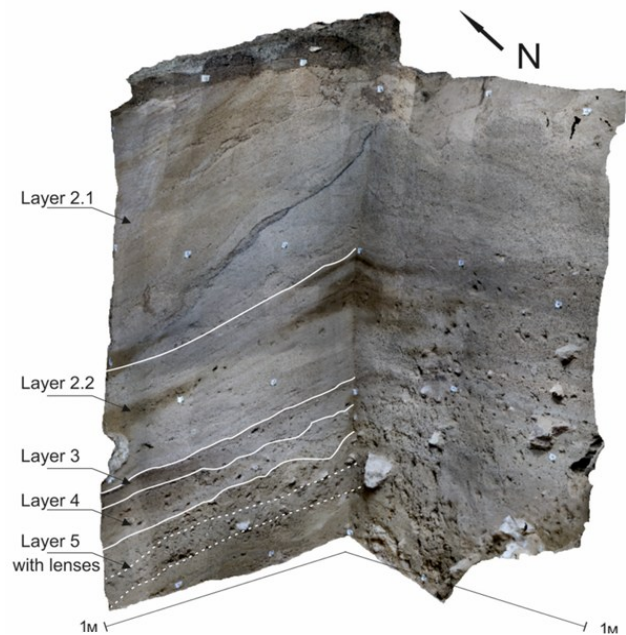


Figure 6: Stratigraphic profile of Pit 2 from Tsagaan Agui (Khatsenovich et al. 2023).

flakes

in Layer 3 showing secondary treatment, one is interpreted as perforator and the other has two drilled holes (Fig. 8). These holes were originally associated with human drilling, but in later studies it could be established that they appeared because of hyenas' gastric acid.

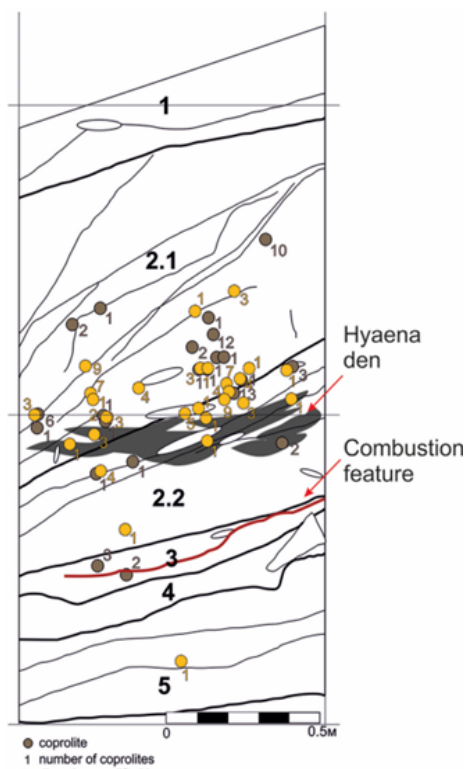


Figure 7: Hyena den in profile in Pit 2 (Khatsenovich et al. 2023).

Episodic cave hyena occupation is indicated by the discovery of 62 coprolites and 89 digestion-eroded bones in Layers 2.1 and 2.2 dated to LGM and pre-LGM, but also in a smaller amount in the lower layers (Fig. 7).



Figure 8: Bone with two holes previously interpreted as drilled by humans from Pit 2, Layer 3 from Tsagaan Agui

Pit E

is located in the Entrance Terrace (Fig. 4) and consists of two units of 1 x 0.5 m² each. The stratigraphic units in Pit E include Layer 1, 4-9, and 11-13. The layers are made up of thin sediments and decline from the northwest to the southeast. A high concentration of faunal remains were unearthed in Layer 5, which is about 20-40 cm from the modern surface. Some of the remains were linked to rodent activity which is why their position had to be determined carefully. When examining the entire Entrance Terrace distribution of finds (including the finds from 1987-1989), a concentration of the faunal remains in the central part of the Terrace becomes apparent. Lithic artefacts on the other hand are distributed more regularly. The lithic assemblage from Layers 5-7 seems to be homogenous and has been attributed to the Late Middle Paleolithic (Khatsenovich et al. 2023, Khatsenovich et al. 2021).

2. Material and Methods

This chapter focuses on the bone samples that were analyzed with the help of collagen peptide mass fingerprinting and radiocarbon dating. A short overview of the principle behind the respective method is presented as well as the experimental procedure supported by photos from the laboratory.

2.1. Material

In this work, I analyzed 566 Pleistocene-age bones from the Tsagaan Agui Cave, Mongolia. The bones fell into two categories:

- Bone fragments retrieved during excavation (hereafter “non-digested”) (N=276); and
- Bone fragments digested by hyena partly extracted from coprolites (hereafter “digested”) (N=287)

The samples were exported from Mongolia through a collaboration with the excavator Dr. Arina Khatsenovich and the Mongolian National Museum and were prepared and analyzed at the Paleoproteomics Douka Lab, University of Vienna, 2023-2024.

First, the material needed to be sorted, checked for completeness and compared to the list the excavation team made. In this process seven samples remained missing, and some sample bags had the same sample number, which is why those samples were divided into “number_1/2/3” etc. to provide a better overview and are referred to as doubles. While some samples consist only of one bone fragment, others contain a set of fragments. In those cases, one sub-sample from the bag was chosen randomly. Specific features of the bones (e.g. porous) can be found in the notes column in the result list (Appendix).

2.1.1. Non-digested bones



Figure 9: Example of one sample from Tsagaan Agui (Nr. 167), photo by the author.

In total, 279 non-digested samples were analyzed. Fig. 9 shows an example of a bone from Tsagaan Agui. The bones were hard and showed good preservation.

2.1.2. Hyena-digested bones

More than half of the sample set comprised of digested bones (N = 287) partly recovered from hyena coprolites excavated at Tsagaan Agui cave. Coprolites are fossilized animal feces and can contain valuable information provided the material (e.g. bone, plant seeds) withstands the transfer through the digestive tract.

2.2. Methods

2.2.1. Collagen peptide mass fingerprinting (ZooMS)

Experimental Procedure:

1) Sampling

First, the whole sample was weighed on a scale (Fig. 10). A small piece of bone, between 10-30 mg in weight, was removed by using a small set of pliers and tweezers. The corresponding values were noted. When dirty, some samples were cleaned with the help of a sandblaster. After this, the sub-sampled bone fragments were transferred to labeled Eppendorf tubes, and stored in a cabinet until the start of the wet lab procedure.

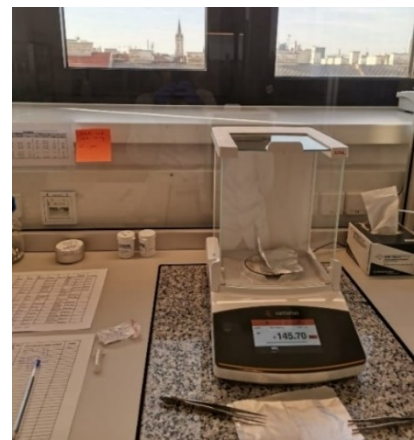


Figure 10: View on the scale in the drilling room, photo by the author.

2) Collagen extraction

Collagen extraction followed the acid-insoluble extraction protocol (Welker et al. 2015; Buckley et al. 2009). This involved:

a) Acid Demineralization:

Each sub-sample underwent demineralization using 500 μ L of 0.6 M HCl and was put into the fridge (4°C) for at least one day. Afterwards the samples were checked and their demineralization status evaluated. If they needed more time to demineralize, they were put again into the fridge. Once all of the samples reached a satisfactory degree of demineralization, the reaction was stopped either by freezing or by washing straightaway.

b) Washing:

The samples were centrifuged, and the acid supernatant was removed and transferred to a micro-well-plate and was put into the freezer for storage. The remaining sample was rinsed twice with 200 μ L of 50 mM pH 8 ammonium bicarbonate (AmBic; NH_4HCO_3). Afterwards the

pH was determined using pH indicator paper. After washing with AmBic the pH should be neutral.

c) Gelatinization:

The next step was the denaturation of the collagen structure. Therefore, 100 μL of AmBic was added to each tube which was incubated for one hour at 65°C resulting in unfolding the collagen alpha chains. Following gelatinization, the samples were centrifuged and twice 50 μL of the supernatant was put in separate micro-well-plates. The first extract was used further, whereas the second extract was retained as back-up.

d) Trypsin Digestion:

1 μL of Trypsin solution (0.4 $\mu\text{L}/\mu\text{g}$) was added to the samples followed by incubation at 37°C for 12-18 h. 1 μL of 5 % trifluoroacetic acid (TFA) was added to stop the digestion.

e) Peptide Purification:

The samples were filtered to remove non-proteinaceous material using C_{18} -ZipTips. The peptides were purified by rinsing twice with 100 μL of conditioning solution (0.1 % TFA in 50 % acetonitrile) and twice with 100 μL of washing solution (0.1 % TFA in ultrapure Milli-Q water) before being eluted with 50 μL of conditioning solution.

f) Spotting on the MALDI-plate:

First the Bruker peptide calibrant standards were spotted (0.7 $\mu\text{L}/\text{spot}$) on a ground steel 384 spot MALDI target plate, together with 0.7 μL of α -cyano-4-hydroxycinnamic acid matrix solution (Fig. 11). Each sample was spotted three times on the MALDI plate.

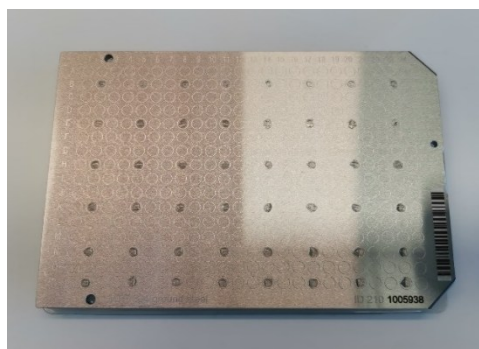


Figure 11: MALDI-plate with Calibrant and Matrix spotted on, photo by V. P.

3) MALDI-ToF-MS:

The analyses were run on a Bruker Autoflex Speed MALDI-ToF-MS (Bruker Daltonics). The generated spectra were manually analyzed using the mMass software (Niedermayer & Strohm 2012) and compared to a reference database that is specialized to Eurasian fauna and is accessible through: [BioArCh - Centres, University of York](#).

2.2.2. Radiocarbon Dating

In addition to ZooMS, a small number of samples underwent radiocarbon dating. It is a well-established technique based on the decay of the ^{14}C isotope and one of the most important ways of gaining chronometric data in the field of archaeology and anthropology. This dating method provides objective age estimates for carbon-based materials but cannot be used for samples older than about 55,000 years. The premise of the method is that the ^{14}C isotope is unstable and weakly radioactive. Plants and animals incorporate ^{14}C from the CO_2 in their immediate environment throughout their lifetimes, but this exchange stops when they die, and their ^{14}C content decreases at a specific rate following the law of radioactive decay. AMS (Accelerator Mass Spectrometry) directly measures the ^{14}C content in the sample relative to the ^{12}C and ^{13}C isotopes (Jull & Burr 2014; p. 45-53).

Experimental Procedure:

Originally nine samples from Tsagaan Agui were chosen for radiocarbon dating, but only four of them were large enough to be analyzed.

1) Collagen extraction and ultrafiltration:

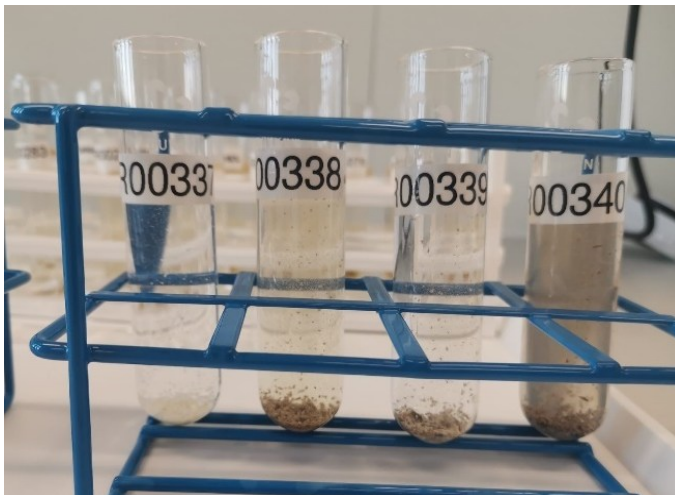


Figure 12: Samples R00337, R00338, R00339 and R00340 in Milli-Q water (photo by the author).

The bones were demineralized using 0.5 M HCl overnight. The samples were centrifuged and the acid decanted before they were washed three times with Milli-Q water. Afterwards 0.1 M NaOH was added for 30' to remove humic acids and rinsed three times with Milli-Q water. Subsequently, 0.5 M HCl was added to remove the dissolved CO_2 , followed by three rinses with Milli-Q water (Fig. 12).

2) Gelatinization:

The collagen was gelatinized in pH3 water at 75°C for 20h.

3) Ultrafiltration:

The resulting gelatin underwent ultrafiltration to remove contaminants <30 kDa. The ultrafilters and the Eze-filterers were cleaned with Milli-Q water before the samples were filtered through them. The gelatinized sample was first Eze-filtered and then passed through an ultrafilter (molecules bigger than 30 kDa are retained for dating).

4) Graphitization and AMS measurement:

The filtered gelatin was freeze-dried and then ~5 mg of dried collagen was weighed into precleaned tin capsules. These underwent combustion and graphitization using an automated system and were AMS dated at the VERA AMS facility of the University of Vienna (Fig. 13).

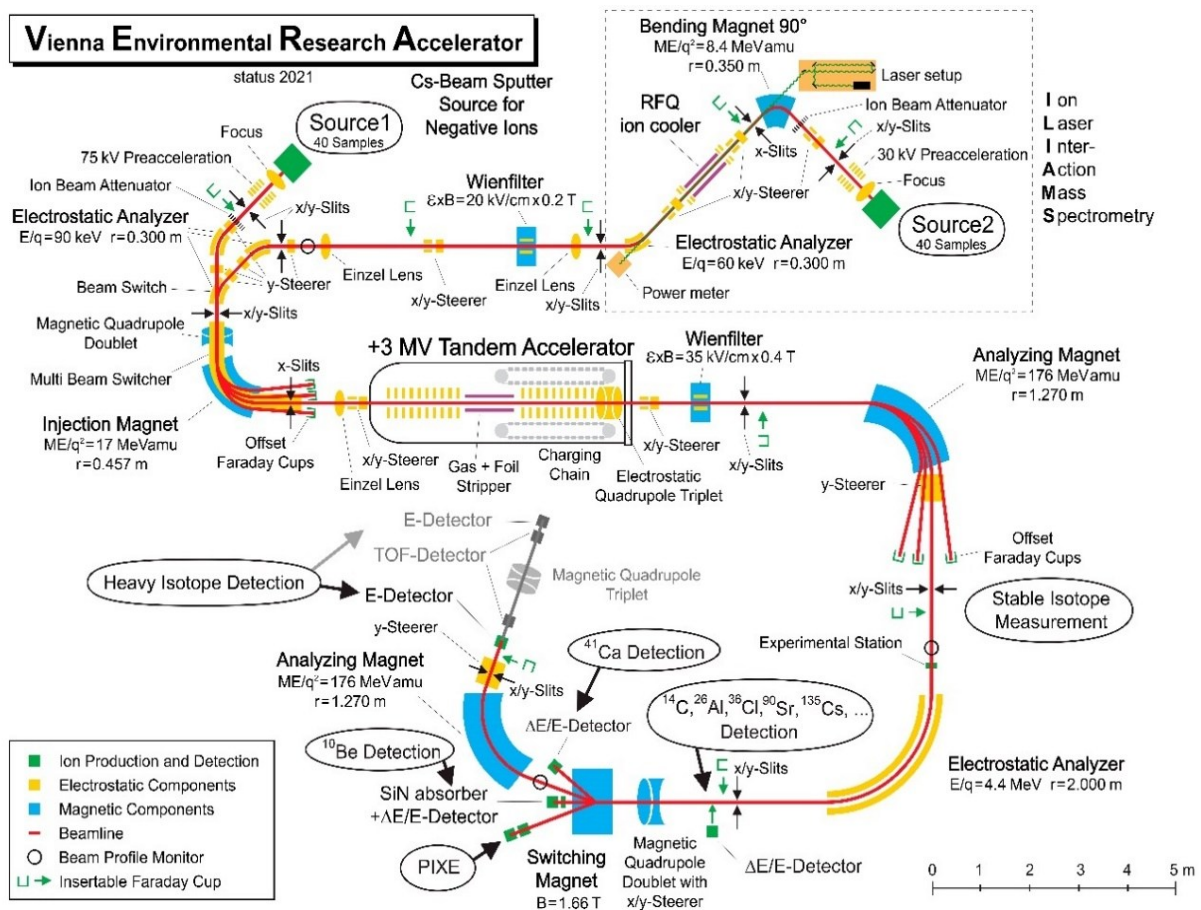


Figure 13: Overview of the upgraded VERA facility (<https://isotopenphysik.univie.ac.at/vera/> - retrieved on 4.10.2024).

3. Results

The next section presents the results from the ZooMS analysis, divided into digested and non-digested bones, followed by the AMS radiocarbon dating.

3.1. ZooMS results

ZooMS was carried out on 566 bone samples (287 digested and 279 non-digested bones). The results are presented in Fig. 14. Of these, 95% showed excellent collagen preservation and were identified.

About 43 % of the data set belongs to the order of Perissodactyla that includes for example horses, wild asses and rhinos. In addition, 29 % were identified as Artiodactyla, likely antelopes or camels. In 12 % of the cases, it was not possible to determine a ZooMS taxon, due to still incomplete reference databanks or the presence of an unknown species, which is why those samples are referred to as “indeterminable” or short “indet.”. Another 5 % were rodents, 3 % rabbits (Lagomorpha), 2 % carnivores such as cave hyena and, finally, 1 % were identified as birds.

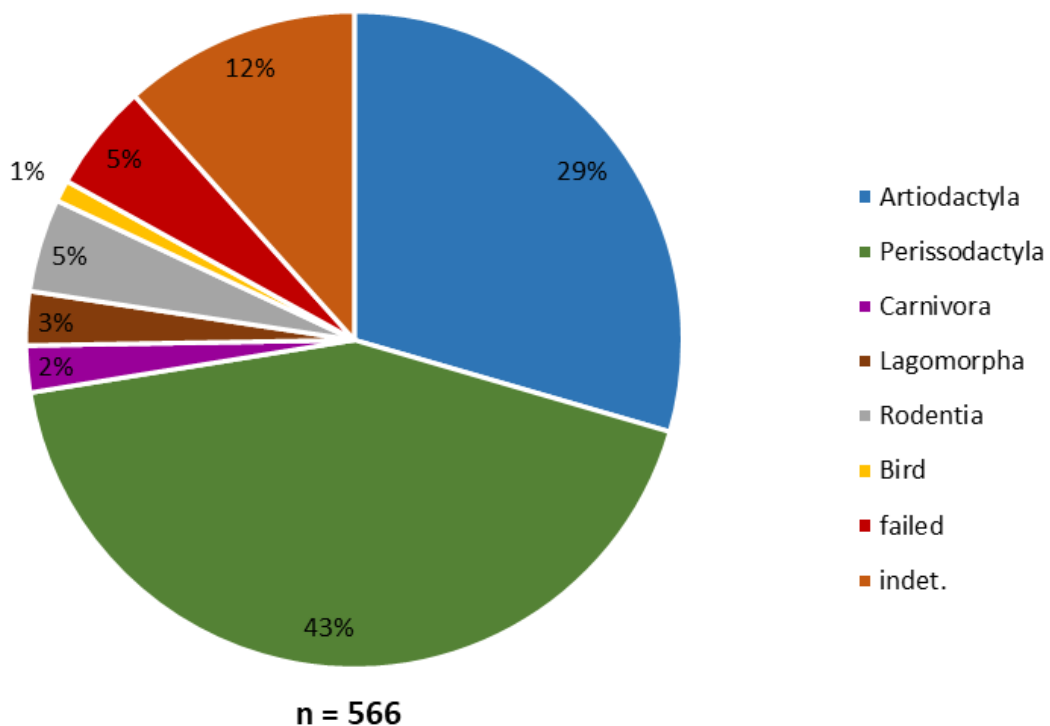


Figure 14: ZooMS results for all samples showing the distribution of the orders Artiodactyla, Perissodactyla, Carnivora, Lagomorpha, Rodentia, Bird, failed and the indeterminable (indet.) ones.

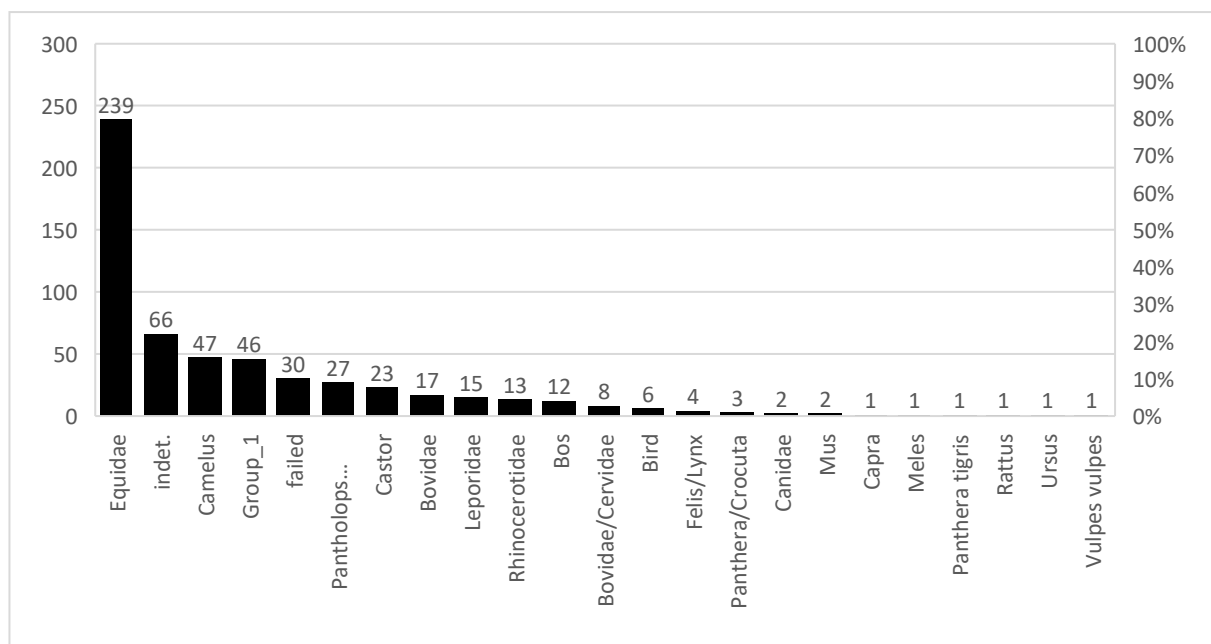


Figure 15: ZooMS results for all samples divided into their ZooMS taxa. The findings indicate the presence of Equidae, Camelus, Group_1, Pantholops hodgsonii, Castor, Bovidae, Leporidae, Rhinocerotidae, Bos, Bovidae/Cervidae, Bird, Felidae, Canidae, Mus and Panther.

Fig. 15 depicts the ZooMS results for the whole sample set (n = 566) according to their ZooMS taxa. In total, 239 samples were identified as Equids and these make up the largest fraction of the analyzed data set. The 12 % indeterminable ones (n=66) are followed by 47 camels and 46 samples that are included to an unknown taxon “Group_1”. The latter was formerly determined as *Ovis*, but after consulting Wang et al. (2023) the results matched with the described Antilopinae_2 category, also morphologically unknown there. Another 27 bones were identified as *Pantholops hodgsonii*, also known as Tibetan antelope or chiru, followed by beavers (23, *Castor*), bovids (17), lepidids (15), rhinos (13), *Bos* (12), Bovidae/Cervidae (8), birds (6), *Felis/Lynx* (4), Canidae (2), *Mus* (2), *Panthera/Crocota* (3), whereas *Capra*, *Meles*, *Panthera tigris*, *Rattus*, *Ursus* and *Vulpes vulpes* were represented by one specimen.

Since Equids are disproportionately overrepresented, Fig. 16 shows the mass spectrum of one of them, namely TSA1. In this case it was possible to determine values for all nine commonly used ZooMS markers (Table 1). COL1a1 508 – 519 (P1) at m/z 1105.6, COL1a2 978 – 990 (A/A') at m/z 1182.7/1198.7, COL1a2 484 – 498 (B) at m/z 1427.8, COL1a2 502 – 519 (C) at m/z 1550.9, COL1a2 292 – 309 (P2) a m/z 1649.8, COL1a2 793 – 816 (D) at m/z 2145.2, COL1a2

454 – 483 (E) a m/z 2820.4, COL1a1 586 – 618 (F/F') a m/z 2883.5/2899.5 and COL1a2 757 – 789 (G/G') at m/z 2983.5/2999.5.

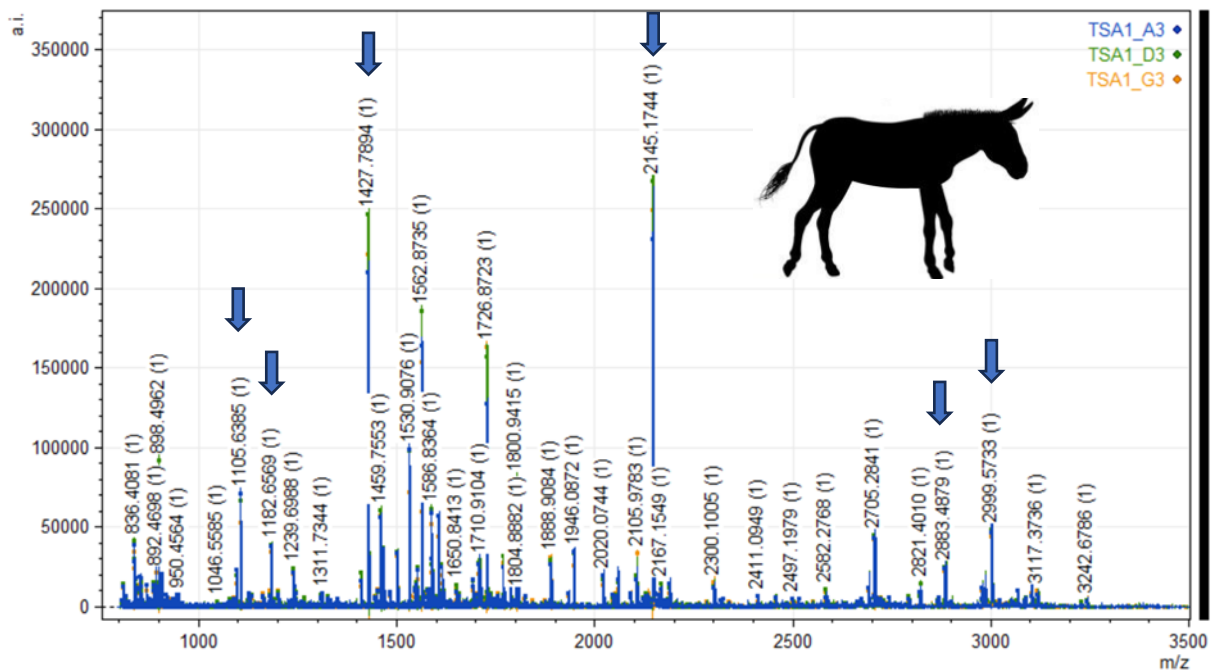


Figure 16: Example of a mass spectrum that was identified as Equid. In sample TSA1 all nine ZooMS markers were identified, six of them are marked with a blue arrow for illustration.

3.1.1. Non-Digested Samples

The ZooMS results for the 279 non-digested samples are shown in Figs. 17 and 18. Their taxonomic distribution is as follows: 34 % Perissodactyla, 23 % Artiodactyla, 17 % indeterminable, 9 % Rodentia, 4 % Lagomorpha, 2 % Carnivora and 2 % birds. The identified ZooMS taxa include in order: Equids (95), *Castor* (22), Group_1 (21), *Camelus* (18), Leporidae (10), *Pantholops hodgsonii* (10), Bovidae (8), bird (6), Bovidae/Cervidae (5), Felis/Lynx (2) and one specimen of: Canidae, Rhinocerotidae, *Meles*, *Mus*, *Panthera tigris*, *Panthera/Crocuta*, *Rattus* and *Vulpes vulpes*. 49 samples remained unidentified and another 25 failed.

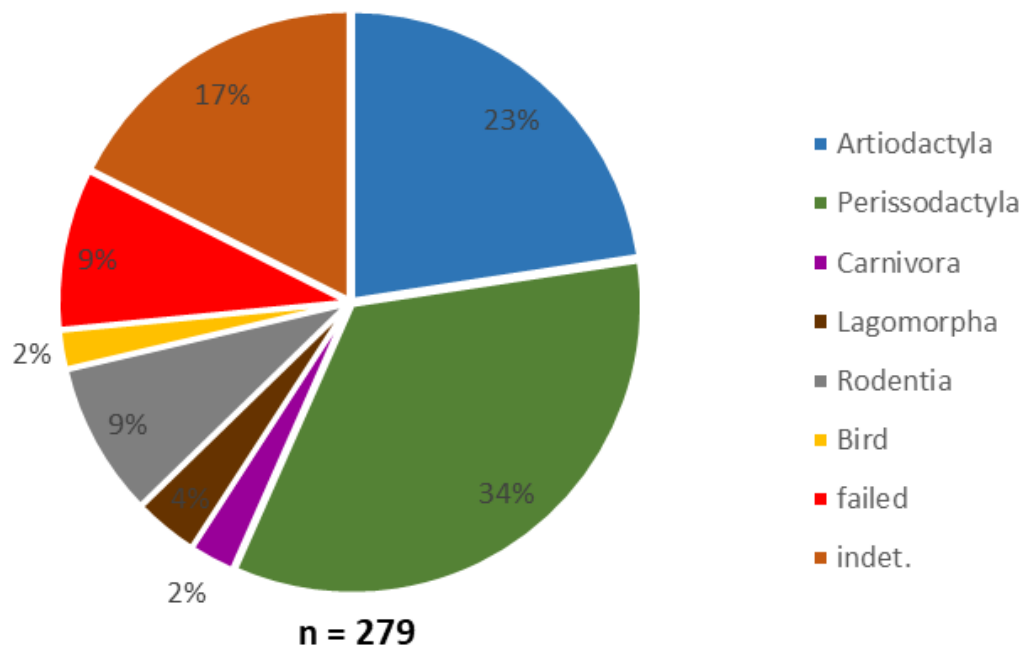


Figure 17: ZooMS results for the non-digested samples (n = 279) showing the distribution of the orders Artiodactyla, Perissodactyla, Carnivora, Lagomorpha, Rodentia, Bird, failed and indet.

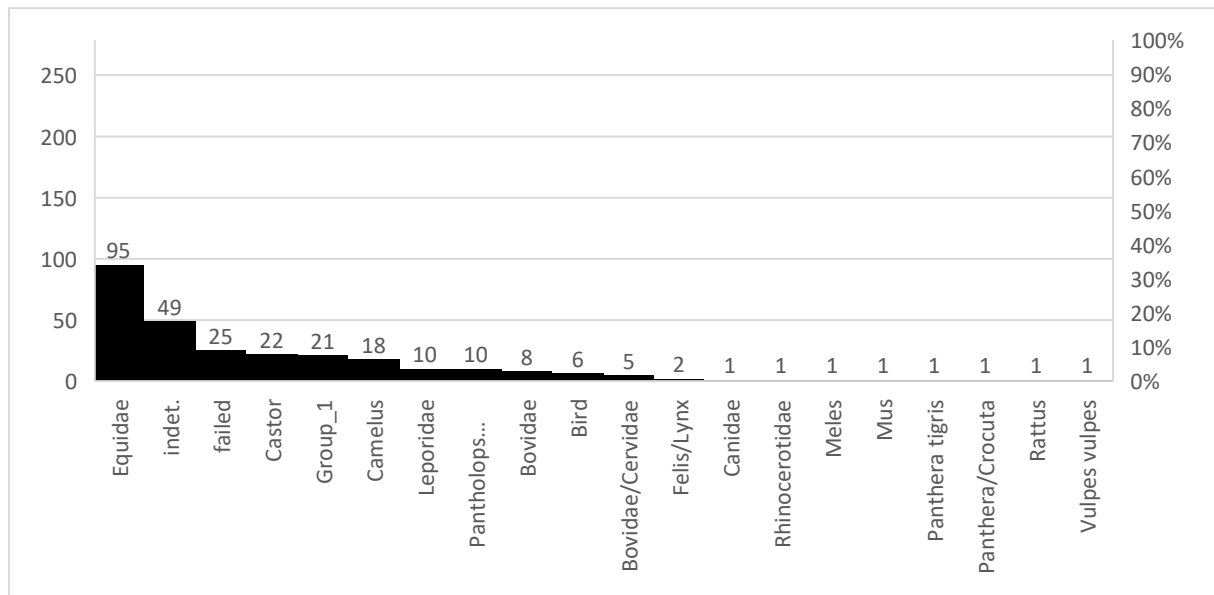


Figure 18: ZooMS results for the non-digested samples (n = 279) divided into their ZooMS taxa. The following identifications were made: Equids, Castor, Group_1, Camelus, Leporidae, Pantholops hodgsonii, Bovidae, Bos, Bovidae/Cervidae, Canidae, Rhinocerotidae, Felidae, Felis/Lynx, Meles, Mus, Panthera, Panthera/Crocota, Rattus and Vulpes vulpes, supplemented by the failed and indeterminable ones.

3.1.2. Digested Samples

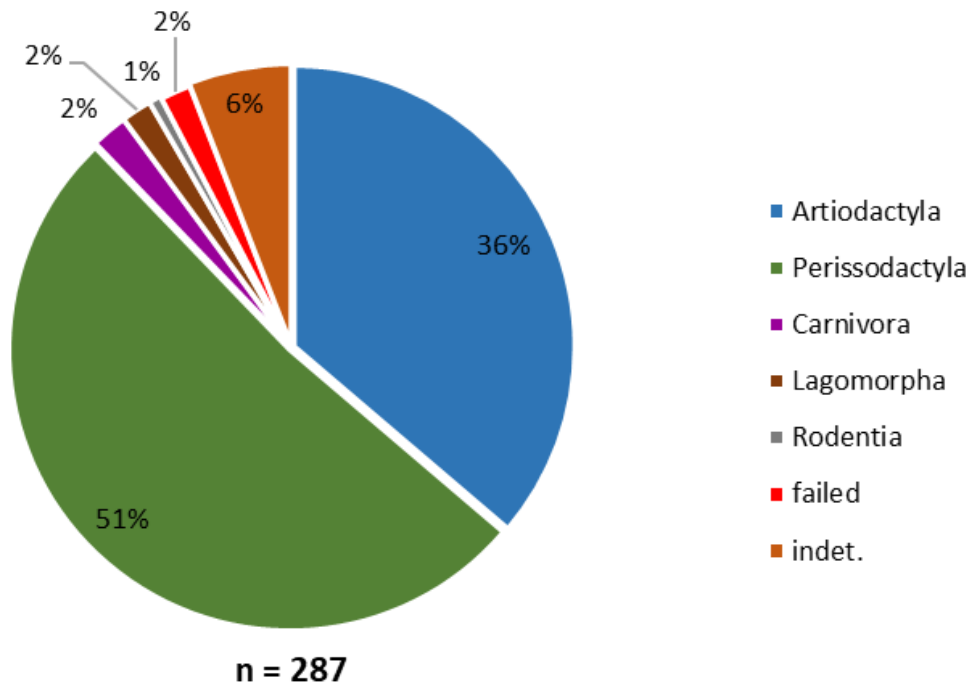


Figure 19: ZooMS results for the digested samples (n = 287) showing the distribution of the orders Artiodactyla, Perissodactyla, Carnivora, Lagomorpha, Rodentia, failed and indet.

The ZooMS analysis on the digested samples (n = 287) resulted in 51 % Perissodactylas, 36 % Artiodactylas, 6 % indeterminable ones, 2 % Carnivoras, 2 % Lagomorphas, 2 % failed and 1 % rodents (Fig. 19). The Perissodactylas are made up of 144 samples identified as Equids and 12 samples of Rhinocerotidae. Artiodactylas contain 29 samples identified as *Camelus*, 25 samples of Group_1, 17 samples of *Pantholops hodgsonii*, 12 samples of *Bos*, 9 samples of Bovidae, three samples of Bovidae/Cervidae and one sample of *Capra*. To the carnivores belong the samples identified as *Felis/Lynx* (2), Canidae (1), *Panthera/Crocuta* (2) and *Ursus sp.* (1). The Lagomorpha are made up of five samples of Leporidae and the rodents contain one sample of *Castor* and one sample of *Mus sp.*. In absolute numbers, 17 samples remained unidentified and five failed out of the whole digested data set (Fig. 20). As representative for a digested sample, the mass spectrum of TSA251 can be seen in Fig. 21. It was identified as Rhinocerotidae with the characteristic m/z values of 1105.6 (P1), 1182.7/1198.7 (A/A'), 1453.8 (B), 1550.8 (C), 2145.2 (D), 2869.5/2885.5 (F/F') and 2983.6/2999.6 8 (G/G'). Six of these markers are shown with a blue arrow in Fig. 16 for illustration.

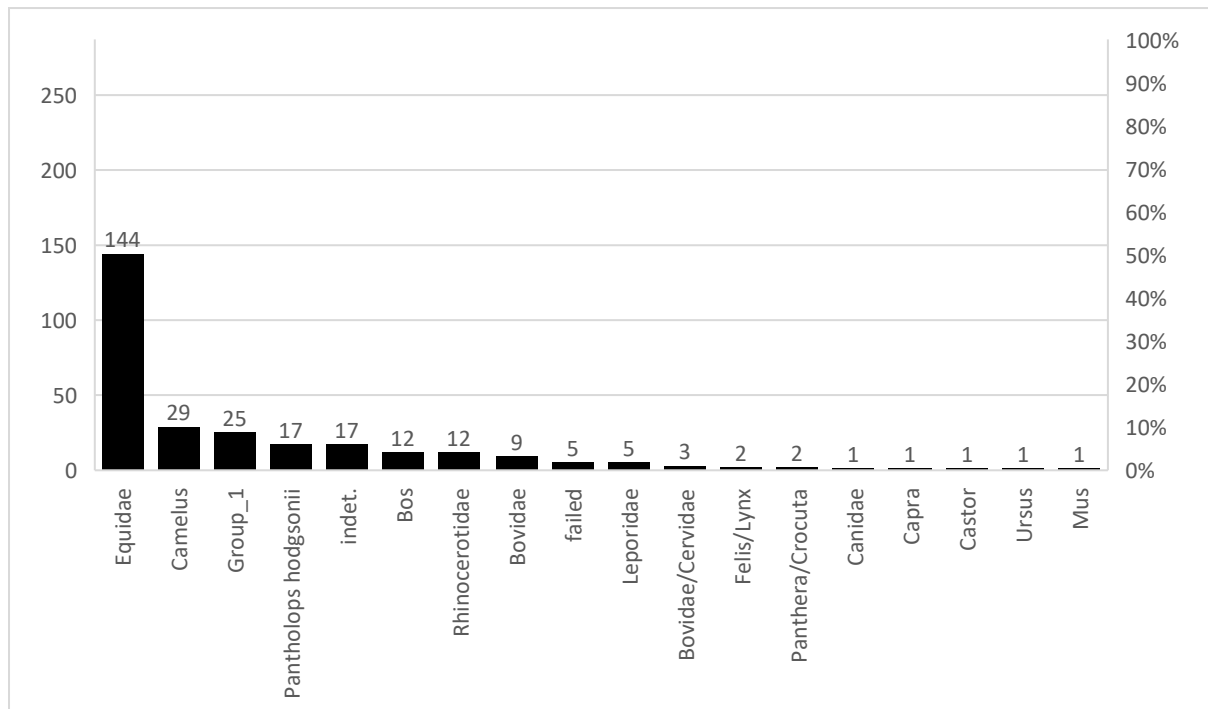


Figure 20: ZooMS results for the digested samples ($n = 287$) divided into their ZooMS taxa. The following identifications were made: Equidae, Camelus, Group_1, Pantholops hodgsonii, Rhinocerotidae, Bos, Bovidae, Leporidae, Bovidae/Cervidae, Felidae, Canidae, Capra, Castor, Hyaenidae/Felidae, Panthera/Crocuta, Ursus and Mus sp., supplemented by the failed and indet.

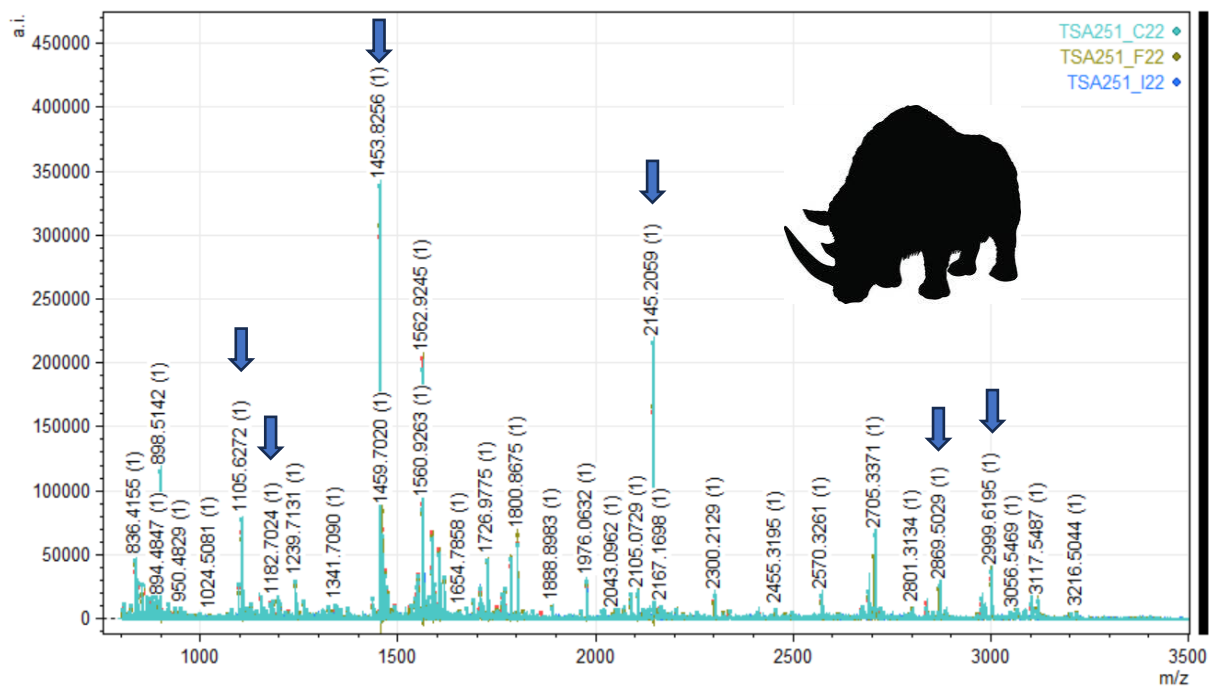


Figure 21: Example of a mass spectrum of sample TSA251 that was identified as Rhinocerotidae. It was possible to identify seven ZooMS markers except for COL1a2 292 – 309 (P2) and COL1a2 454 – 483 (E).

3.1.3. ZooMS results in context with the archaeological layers

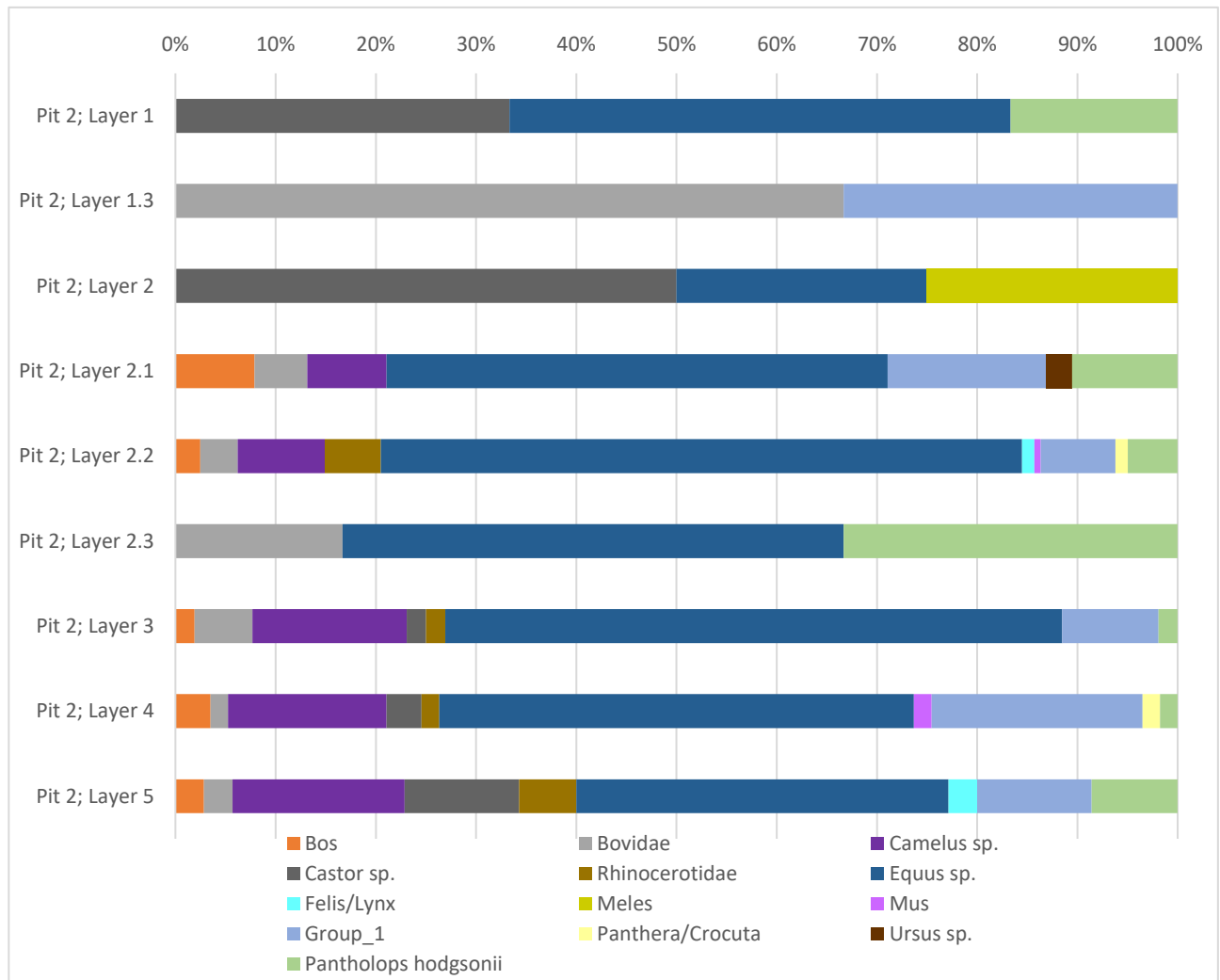


Figure 22: ZooMS identifications by layer for Pit 2/2021 ($n = 385$; after excluding samples with insufficient or unsuitable layer information and the samples that failed or remained indeterminable) showing the distribution of the identified ZooMS taxa from Layer 1 – Layer 6. Pit 2 Layer 1 ($n = 6$); Pit 2 Layer 1.3. ($n = 3$), Pit 2 Layer 2 ($n = 4$); Pit 2 Layer 2.1 ($n = 44$); Pit 2 Layer 2.2 ($n = 164$); Pit 2 Layer 2.3 ($n = 6$); Pit 2 Layer 3 ($n = 55$); Pit 2 Layer 4 ($n = 62$); Pit 2 Layer 5 ($n = 43$); Pit 2 Layer 6 ($n = 2$).

Fig. 22 above shows the ZooMS identifications per layer for Pit 2 (2021). In total, 385 samples were included into this plot. Some samples had to be excluded due to unsuitable layer information in form of missing layer association or the association of two layers to one sample (which is sometimes unavoidable when excavating). However, not all layers contain the same amount of samples, which needs to be considered. Equids were found in all layers except for Layer 1.3 which is only represented here by 3 samples. Similarly *Pantholops hodgsonii* is represented in all layers except for Layer 2 and Layer 1.3 for which only 4 and 3 bones, respectively, are analyzed. *Bos* were found in the oldest Layer 5 to Layer 2.1 except for Layer 2.3 ($n = 6$), the same applies to *Camelus* and Leporidae. Bovidae/Cervidae and Rhinocerotidae

were found from Layer 5 to Layer 2.2 except for Layer 2.3. Group_1 and Bovidae show a similar pattern found from Layer 5 to Layer 1.3. *Castor* is found both in the oldest and youngest Layer and in between. The only *Capra* sample was found in Layer 2.2. *Panthera/Crocota* was found in Layer 2.2 and Layer 4. *Felis/Lynx* appeared in Layer 5 and Layer 2.2. *Mus* is also represented in Layer 4 and beyond that in Layer 2.2. *Ursus* was only found in Layer 2.1 and *Meles* only in Layer 2.

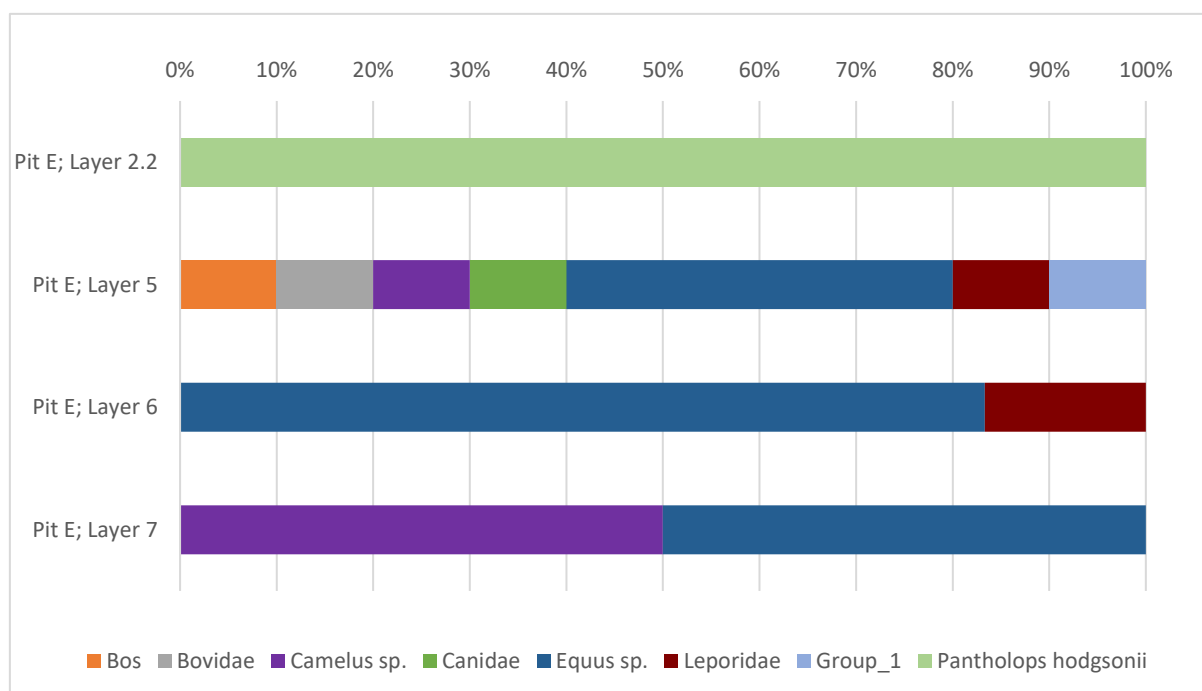


Figure 23: ZooMS identification per layer for Pit E/2022 ($n = 19$, after excluding samples with insufficient layer information and the samples that failed or remained indeterminable). Pit E Layer 2.2 ($n = 1$); Pit E Layer 5 (10); Pit E Layer 6 ($n = 6$); Pit E Layer 7

The ZooMS identification per layer for Pit E (2022) is shown in Fig. 23. The plot contains only 19 samples and has therefore only limited information value, which applies especially to Layer 2.2 that is only represented by 1 sample namely *Pantholops hodgsonii*. Equids were found in Layer 5 – 7, *Camelus* in Layer 5 and 7, Leporidae in Layer 5 and 6 and Group_1, Bovidae, *Bos* and Canidae are represented once each in Layer 5.

3.2. Radiocarbon dates

Four bone samples from Tsagaan Agui underwent radiocarbon dating. The results are shown in Tab. 2. Sample TSA 229 (Pit 2, surface) was identified using ZooMS as *Camelus* sp. and yielded a ^{14}C age of 30020 ± 250 BP. Sample TSA 720 (Pit 2, Layer 4) was identified

morphologically to the extinct giant camel, *Camelus knoblochi*, and it yielded a ^{14}C age of 41600 ± 1000 BP. Sample TSA 2290 (Pit 2, Layer 3) was determined to belong to Group_1 (an unassigned taxonomic group) and was dated to 42300 ± 1100 BP. The fourth sample TSA 2874 (Pit 2, Layer 5) was identified as *Pantholops hodgsonii* and is the oldest sample in this batch. It was dated 43200 ± 1300 BP.

Table 2: Results from the AMS radiocarbon dating, and the isotopic analysis performed for four samples from Tsagaan Agui (TSA_229; TSA_2; TSA_519_1; TSA_525_1):

Sample	ZooMS ID	Species	Context	% collagen	P Code	Lab code	F14c	Error	^{14}C Age	Error ^{14}C Age
TSA 229	TSA 229	Camelus sp.	2021 surface	8,7	UF	UCIAMS-286301	0,0228	0,0007	30020	250
TSA 720	TSA 2	Camelus knoblochi	2021 Pit 2 Layer 4 A19/1	12,6	UF	UCIAMS-286302	0,0057	0,0007	41600	1000
TSA 2290	TSA 519_1	Bovidae	2022 Pit 2 Layer 3 A18/1	10	UF	UCIAMS-286303	0,0052	0,0007	42300	1100
TSA 2874	TSA 525_1	Ungulate	2022 Pit 2 Layer 5 B19/3	1,3	ABA	UCIAMS-286511	0,0046	0,0007	43200	1300

4. Discussion

This chapter focuses first on the digested samples and their success rate in ZooMS analysis. Afterwards the identified fauna is discussed with regard to their most probable representatives in context to the site, complemented by specific features of the fauna (e.g. diet, habitat). Then, the chronological classifications of the layers are expanded and discussed in context. Finally, the paleoenvironmental situation is discussed, followed by comparing the diet of carnivores (on the example of cave hyena) and humans at Tsagaan Agui based on the zooarchaeological data from this work.

4.1. Success rate of digested samples

The preservation of the digested bone samples, i.e. bones that passed through the digestive track of a carnivore or digestion-eroded, was much better than expected with a success rate of 98 % (n=287). It appears that no harm was done to the collagen by the digestive system of the hyena, although of course the protected environment in the cave was advantageous for the good preservation. In previous studies, DNA has already successfully been extracted from coprolites (e.g. Wood et al. 2012; Bon et al. 2012) which allowed the analysis of the defecator and the dietary residues (Barnett 2019). This type of work can provide information about the diet, the producer's condition (e.g. microbiome, parasites diseases, virus infections), evolution and paleoenvironment (Yang et al. 2022). The successful application of ZooMS to bone remains from hyena coprolites at Tsagaan Agui enlarges the analyzable zooarchaeological data set and same as DNA analysis it can provide taxonomic identification but at lower costs, which offers great potential for further studies on coprolites.

4.2. Faunal Assemblage at Tsagaan Agui

The ZooMS identifications of this work will be discussed in the following summarized to the groups of equids, bovids, cervids, rodents, carnivores, rhinos, lagomorphs and birds. The probability of which members of a family or genus could be present in the sample set is discussed. In addition, the paleoenvironmental requirements and general facts about the identified fauna are mentioned to create a coherent picture of the faunal community that lived and died at Tsagaan Agui. Ultimately, the temporal occurrence is considered in context with the radiocarbon dates and the archaeological layers.

Equids

In total, 239 samples out the whole date set (n= 566) were identified as Equidae, this makes about 42 %. In Pleistocene Mongolia, Equidae would be represented by two currently extinct species, the Asiatic wild ass, *Equus hemionus*, and the sussemione *Equus ovodovi*, as well as *Equus ferus przewalskii*. The high number of equids is striking and could be related to the fact that they are large-bodied animals whose bones can split into numerous fragments. It is therefore also likely that the number of individual specimens (NISP) tends to overestimate the minimum number of individuals (MNI) present in the assemblage. Similar observations were made at Denisova Cave (Russia) or Jinsitai Cave (China). A study at the latter was able to allocate 326 equid specimens to about 25 individuals (Brown et al. 2021; Wang et al. 2023). Furthermore, equids are herd animals and occur usually in larger numbers. They are preyed upon not only by humans, but by diverse predators such as the extinct cave hyena (*Crocota crocuta spelaea*). In fact, 144 of the 239 equid samples identified in this work were digested by hyenas. Furthermore, based on evidence at adjacent sites equids were also a substantial food resource for hominins (Norton et al. 2008).

The Gobi steppe ecosystem of Mongolia is an in important habitat for migratory ungulates such as the kuhlan, Mongolian for the Asiatic wild ass *E. hemionus* (Buuveibaatar et al. 2017). It would be a very plausible identification of the equid bone samples as they were typical inhabitants of this region in former times and still today. Findings indicate that the kuhlan once ranged across Central Asia, although they are nowadays threatened (Reading et al. 2011). Other species of the genus *Equus* are also potential candidates such as *E. przewalskii*, the Mongolian wild horse or takhi. They were also originally native to the steppes of Central Asia. At Jinsitai Cave, another Paleolithic cave site, *E. hemionus* and *E. przewalskii* were morphologically identified but based on the ZooMS analysis it was not possible to distinguish those two species which is why the authors decided to combine them to one *Equus* ZooMS taxon. Since Jinsitai Cave and Tsagaan Agui Cave share distinct similarities in the form of the setting in Central Asia, Mousterian-like lithic industry, Paleolithic layers and other corresponding fauna (e.g. rhinos, antelopes, camels) it seems plausible to assume that the same Equid species could have been found at the sites. *Equus ferus* (the ancestor of today's domesticated horses *Equus ferus caballus*) and *Equus hydruntinus* were the last wild horses in Europe and became extinct during the Late Quaternary Extinction Event (Strani & DeMiguel 2023). *E. ferus* contains several subspecies and is difficult to categorize and *E. hydruntinus*

expanded in the fossil record no further than to southwest Asia (Crees & Turvey 2014). Both species would be rather atypical to be found in an archaeological site in Central Asia, therefore leaving *E. hemionus* and *E. przewalskii* still as the more probable equids for the investigated sample set. More recently, the presence of the sussemione *E. ovodovi*, has been confirmed in several locations of northern Eurasia (Pan et al. 2024) and is hence another candidate for the horse specimens in our study. It is also possible that our samples belong to an unknown extinct species of the genus *Equus*.

Bovids

Camelus sp.

In this study 47 samples (of which 29 digested bones) were identified as *Camelus*. TSA 2 (Pit 2021/2, Layer 4, Fig. 23) was already identified as *Camelus knoblochi*, an extinct giant two-humped camel species that was found in archaeological contexts in eastern Kazakhstan, south-west Russia, northern China and southern Mongolia (Fig. 24). *C. knoblochi* was the largest of the Pleistocene Eurasian Bactrian representatives of the genus *Camelus* and they form a paraphyletic group (Yuan et al. 2024). It is a proximal left metacarpal fragment and originates from a large individual. In comparison to modern Bactrian camels in the Gobi Altai region the width and transverse diameter of the proximal epiphysis is distinctly larger. These morphometric parameters

correspond well with *C. knoblochi* features (Khaveson 1954; Vangengeim & Gerbova 1962) but also with those from *Paracamelus gigas* (the assumed ancestor of members of the genus *Camelus*) except for the shape of its upper articular surface for metacarpals III and IV which is why it was identified as *C. knoblochi*). Sample TSA 2 has traces of hyena gnawing and was also cracked by humans. It was split intentionally indicated by negative conchoidal fractures on the proximal epiphysis. In addition, the other end of the bone shows signs of usage in the form of negative scars of spall removals on the narrow side of the fracture (Klementiev et al. 2022). The bone was directly dated at 41600 ± 1.000 BP which fits well in the known temporal occurrence of *C. knoblochi*. The analysis with ZooMS supported the original identification by being able to narrow it at least down to the genus *Camelus*. It is assumed that *C. knoblochi*



Figure 24: Sample TSA 2 from Pit 2021/2, Layer 4 that was identified as a proximal metacarpal fragment from *Camelus knoblochi* (Klementiev et al. 2022) and dated to 41600 ± 1000 BP.

survived until the Last Glacial Maximum, about 26,500 – 19,000 years ago (Klementiev et al. 2022). The extinction is related to climatic aridization and the corresponding change of plant communities (Titov 2008) and occurred probably about 20,000 years ago (Tang et al. 2003), although more work is required to ascertain these ages.

In addition, three more camelid bones were rediscovered from the curated faunal collections of the 1980s excavations at Tsagaan Agui and were analyzed here. Sample TSA 229 (Pit 21/2, surface) was also identified as *Camelus*, and radiocarbon dated at 30020 ± 250 BP. This suggests that camels were present at Tsagaan Agui for at least 11,000 years.

For comparison, at Denisova Cave, camel aDNA was discovered at a sediment sample dated to 140-120 ka BP (Zavala et al. 2021; Wang et al. 2023). At Jinsitai Cave, five camelid specimens were radiocarbon dated between 37-20 ka BP years ago and the authors refer to a targeted and repeated exploitation of this taxon for at least 17,000 years by Eurasian Paleolithic hunter groups (Wang et al. 2023).

If the remaining 45 *Camelus* samples found in Layers 2-5 and analyzed in this work are partly also *C. knoblochi* or a different species cannot be answered based on ZooMS alone. The current reference library used for ZooMS can only distinguish between the two extant species of *Camelus*, namely *Camelus bactrianus* and *Camelus dromedarius*. Although all investigated camelid samples resulted in *C. bactrianus*, this may be attributed to the limitation of the reference library than to the actual presence of *C. bactrianus* (the domesticated form of *Camelus ferus*). Another feasible camel species besides *C. knoblochi* would be therefore *C. ferus*. The divergence of *C. ferus* and *C. bactrianus* happened about 0.7 – 1.1 million years ago

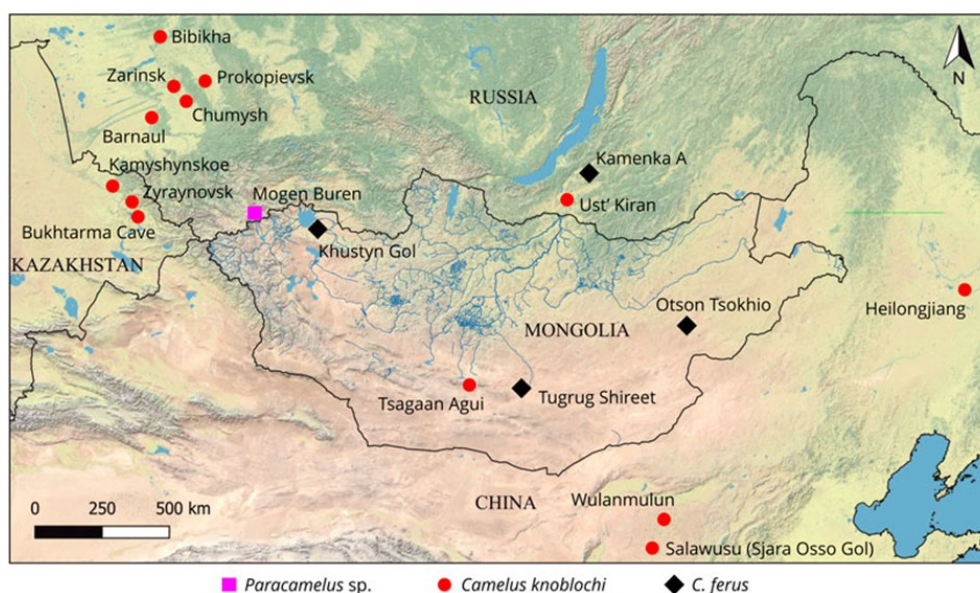


Figure 25: Map of principal finds of fossil camels in eastern Eurasia (Klementiev et al. 2022).

(Ji et al. 2009). At other Paleolithic sites in Western Asia and North Africa *Camelus thomasi* was found and dated to the Middle to Late Paleolithic (Martini & Geraads 2018). Cave arts dated to the Late Paleolithic from Russia and Mongolia depict two-humped camels which aligns well with the general occurrence of fossil camels in Central Asia (Wang et al. 2023). In general, camels are typically found in desert regions but also in cold environments like here in the Altai region. Camels are herbivores and subsist mainly on grasses. Fig. 25 shows principal finds of fossil camels in eastern Eurasia. Ultimately, only TSA 2 can rightly be described as *C. knoblochi*, the other camelid bone fragments need to be kept at the genus-level *Camelus* until further investigations.

“Group-1”

This category contains 46 samples of which 25 were digested by hyenas. Based on the Eurasian reference library for ZooMS, all samples resulted in either *Ovis* and/or *Rupicapra* which seemed to be a plausible result for the investigated site. However, Wang et al. (2023) described a group of antelopes, “Antilopinae_2” at Jinsitai Cave (China) which shows strong similarities with the *Ovis/Rupicapra* samples from Tsagaan Agui. These samples share the same markers with *Moschus berezovskii*, *Pudu pudu*, *Rupicapra rupicapra* and *Ovis aries* from the current reference library. The seven markers for the “Antilopinae_2” category and for Group_1 in this study are: COL1α1 508-519 (P1) for m/z 1105.6, COL1α2 978-990 (A) for m/z 1180.7, COL1α2 484-498 (B) for m/z 1427.7, COL1α2 502-519 (C) for m/z 1580, COL1α2 793-816 (D) for m/z 2131.1 and COL1α1 586-618 (F) for m/z 2883.4 with or without COL1α2 757-789 (G) for m/z 3017.

Consequently, ZooMS is currently not able to identify this bovid due to the absence of a larger number of reference taxa relevant to Pleistocene Mongolia, but also due to the phylogenetic closeness to other similar species. At Jinsitai it was possible to identify morphological three Antilopinae taxa based on their horn fragments: *Procapra przewalskii*, *Pachygazella* sp. (extinct) and *Spirocerus* sp. (extinct) (Wang et al. 2023). At Tsagaan Agui this is unfortunately not possible due to the high degree of fragmentation. If *Ovis* sp. is partly present in this sample set, the argali *Ovis ammon* would be a probable assumption for the taxonomic identification at species-level, because it is and was inhabiting the mountains and rocky outcrops of Mongolia and surrounding countries such as the Altai region (Reading et al. 1997).

Pantholops hodgsonii

The Tibetan antelope or chiru *Pantholops hodgsonii* (Fig. 26), could be associated with 27 bone samples (of which 17 digested). Besides the red fox *Vulpes vulpes* it is the only ZooMS taxon that could be identified to species-level. The chiru is completely endemic to the Tibetan Plateau with its high elevation, living preferably in rolling terrain at 4000-5000 m above sea level, alpine and desert steppes. Some populations are migratory, others remain local. They are herbivorous ruminants eating seasonally grasses, sedges and forbs (Leslie & Schaller 2008). The analysis of the mitochondrial genome revealed that *P. hodgsonii* is closer related to *Ovis aries* and *Capra hircus* than to other members of the Antilopinae subfamily (Xu et al. 2005). There are currently three main populations of the chiru with relatively high genetic variation (Ruan et al. 2005). The Tibetan antelope was as demonstrated also prey for the extinct cave hyena. Furthermore, the chiru was found consistently in the archaeological record highlighted by being the oldest radiocarbon dated sample with a ^{14}C age of 43.200 ± 1300 BP.



Figure 26: Picture of a mature male *Pantholops hodgsonii* in Qinghai Province, China. Photo by G. B. Schaller (Leslie & Schaller 2008).

Bos sp.

Out of all bone samples investigated, 12 were identified as *Bos* sp. and are exclusively hyena-digested bone samples. This means that these bovids ended up in the cave, because they were consumed by hyenas. The *Bos* specimens were found in five different layers (Layer 5, 4, 3, 2.2 and 2.1) which suggests that at least five individuals are present in our limited dataset. All 12 samples were identified according to the current reference library as *Bos taurus*, the domesticated cattle. It is distinguishable to other members of the genus *Bos* represented in the library (*Bos grunniens*, *Bos primigenius*) and *Bison* sp. by one peptide marker, namely COL1α2 889-906 for m/z 1532. It is not possible that the domesticated form is present so far before the Neolithic Revolution. Interestingly, the ancestor of *B. taurus* is part of the reference library, namely *B. primigenius*, but apparently not the result of the taxonomic analysis.

The question remains which *Bos* species it is, if not *B. taurus* nor *B. primigenius*? It is very likely that the *Bos* species we identified in our results is a wild bovid missing from the current ZooMS

reference library. A recent study (Janzen et al. 2021) which focused on the paleoproteomic identification of bovids in East Africa and the generation of relevant peptide markers, was able to distinguish only some of the bovid diversity present in the region. Similar work has not yet been attempted in Northern and Central Asia.

For comparison, at Denisova Cave *Bos* specimens were specified to *Bison/Yak* naming the steppe bison (*Bos priscus*) and the Baikal yak (*Poephagus mutus*) that made up the largest group out of the whole sample set with ~ 26 % (Brown et al. 2021). The Baikal yak has also been identified at the Orkhon valley in Mongolia (Khatsenovich et al. 2021)., indicating that this bovid may also be present in our data set from Tsagaan Agui.

Bovidae

In the analyzed bones, 17 samples could only be identified as belonging to Bovidae due to different reasons. One subgroup of nine bones (see Appendix) were most similar to four species (*Kobus ellipsiprymnus*, *Kobus kob*, *Madoqua kirkii* and *Pelea capreolus*) of native African bovids (unlikely to be part of the Pleistocene dataset from Tsagaan Agui). These samples belong either to an unknown/extinct bovid species or most likely to one that is currently not included in the ZooMS peptide markers library. Since they were distributed over several archaeological layers (Layer 5-2) it can be assumed that the respective species was native to the Gobi-Altai region over a long period. Three more samples (TSA 421, 436, 477) were most similar to *Nesotragus moschatus* or suni, a small antelope today endemic to eastern Africa from Kenya to KwaZulu-Natal, South Africa (Kingdon & Hoffmann 2013). Similarly to the previous group unlikely to be present in Mongolia, hence must represent an unsampled bovid species. Two bones (TSA 111, 121) could belong to either *Ovis/Group_1* or *Pantholops hodgsonii*, leaving them at the more unspecific family-level of Bovidae. Two bones (TSA 32, 46) yielded too many results to narrow it down to one species, whereas a final bone (TSA 410) appears closer to a gazelle, possibly the Mongolian gazelle *Procapra gutturosa* or dzeren.

Cervids

Bovidae/Cervidae

The analyzed data set contained eight samples that could not be assigned to either Bovidae or Cervidae, due to the missing COL1a2 502 – 519 (C) marker in all cases. The peptide markers reference library yielded four likely bovids, namely *Ovis*, *Rupicapra*, *Saiga tartarica* or *Gazella*

sp. as possible results. Some of the samples might also belong to the family of cervids with diverse members such as the red deer (*Cervus elaphus*) that was listed among others as possible result in the reference library.

Capra

One sample was identified as *Capra* sp. and it was recovered in Pit 2, Layer 2.2. Moreover, it was part of the hyena-digested samples, a typical prey. Although the current reference library lists only two different species of *Capra* (*Capra hircus*, the domesticated goat and *Capra ibex*) further species like *Capra sibirica*, *Capra caucasica*, and others, may have been present. Although no species-level identification was possible, goats were and are still typical inhabitants of the Gobi-Altai region.

Rodents

Castor sp.

In total, 23 samples were identified as belonging to *Castor* sp., out of these, one sample is part of the digested dataset, hence was consumed by hyena. As *Castor* does not belong to the typical prey of hyena (normally larger ungulates) it may be related to scavenging activities. *Castor* specimens were found throughout Layer 5-1. There are only two extant beaver species, *Castor fiber* and *Castor canadensis* both found in Eurasia. The genus *Castor* is also thought to originate in Eurasia (Horn et al. 2011). The first evidence for the presence of *C. fiber* in Mongolia and from the zooarchaeological record at Tsagaan Agui was reported recently (Klementiev et al. 2022), hence our molecular identifications finds good support in the faunal assemblage from the site.

Since beavers are semiaquatic rodents, the question arises which water source they were using in the vicinity to Tsagaan Agui? Also, the building of dams and lodges by beavers creates wetlands that are useful to other species. Because of their impact on other fauna, beavers are categorized as keystone species (Moshkin 1986). The required freshwater habitat for beavers in close vicinity to Tsagaan Agui is a rather interesting find in terms of the paleoenvironmental reconstructions and biodiversity of the site (see also 4.3.).

Mus sp.

Two bones were identified as *Mus* sp., one of them belongs to the digested samples and was found in Layer 2.2., the other specimen is from Layer 4. According to the reference library the species *Mus musculus*, house mouse is present. This species is well distinguishable from the other two *Mus* species in the library, namely from the Eurasian field mouse (*Apodemus agrarius*) and the Eurasian harvest mouse (*Micromys minutus*). Currently, the ZooMS reference database is very limited as to northern Eurasian Rodentia, hence which (sub-)species these bones belong is very tentative. Several species belong to the genus *Mus*, most likely the short-tailed house mouse, *Mus musculus musculus* is present in northern and continental Eurasia (for a review see Boursot et al. 1993)

Rattus sp.

One sample from Pit 2, Layer 5 was identified as *Rattus* with two potential species according to the current reference library, *Rattus rattus* and *Rattus norvegicus*. The first one, the black rat diverged from its closest relative *Rattus tanezumi* (Asian house rat) in Southeast Asia about 120,000 years ago (Plyusnina et al. 2009). The latter, the brown rat has its origin possibly in northern China and Mongolia. But since there are generally over 60 extant species and 4 extinct ones known it is hard to say which species is part of our dataset. In terms of their diet rats are usually omnivores and generalists eating what is available (Nowak 1999).

Carnivores

Felidae

Four bones were identified as Felidae including two possible identifications either as *Lynx* sp. or as *Felis* sp. If belonging to the genus *Lynx*, the Eurasian lynx (*Lynx lynx*) or the recently established extinct species *Lynx shansius* are likely candidates. The latter is documented in northern China during the Early Pleistocene and is so far only known from one site where a nearly complete mandible was discovered (Tong et al. 2023). Wild forms of *Felis*, such as *Felis silvestris*, the European wild cat, that expanded until the Caucasus region are possible, but other species, such as the Chinese mountain cat *Felis silvestris bieti*, a subspecies of *F. silvestris*, may be a more likely candidate (Yu et al. 2021). The manul cat *Otocolobus manul* is likely present too, as it occurs for example in Afghanistan, Armenia, China, India, Nepal, Pakistan, Russia and in Mongolia (Noonan et al. 2024).

The Felidae samples were found in Layer 5/6 and 5, as well as in Layer 2.2 in Pit 2 indicating a (temporal) presence from at least 43 ka BP (^{14}C age of TSA 2 in Layer 5) to the Last Glacial Maximum at about 23-25 ka BP (Derevianko et al. 2000, dating Layer 2). In addition, two of the four samples were digested, and one shows traces of hyena gnawing suggesting that these Felidae represent prey for the cave hyenas.

Canidae

Two samples were identified as Canidae, one from Pit 2, the other from Pit E. The one from Pit E could be narrowed down to the species level *Canis familiaris*. Although the domestic dog would be generally an unlikely candidate for a Paleolithic site, in this case it could be possible due to significant rodent activity at the Entrance Terrace (where Pit E is located). In the course of this activity, Holocene material could have been transported into Pleistocene layers. Another explanation is that this bone represents a population of wolves ancestral to the domestic dog, from which the latter was selectively bred during the Late Paleolithic (Galibert et al. 2011). Interestingly, it was possible to differentiate the samples from *Canis lupus* by the presence of COL1a2 889 – 906 with m/z 1576.8 for *Canis familiaris*. Furthermore, the *Canis* samples were found in Layer 5 that has a radiocarbon age of around 43 ka BP. The second Canidae bone sample lacks some distinctive peptide markers for further identification.

Panthera sp.

One bone was identified as tiger *Panthera tigris*, found in Pit 2 but it has unfortunately no layer information, making its chronological classification difficult to establish. It was differentiated from *Crocota* by the presence of COL1a2 292 – 309 at m/z 1609.8. Another *Panthera* species, *Panthera spelaea*, the extinct cave lion, is not present in the reference database, hence assignation of this bone fragment to *P. spelaea* is very likely. *P. spelaea* has been found at several Pleistocene sites, including at Denisova Cave in the Pleistocene layers of the Main Chamber (Brown et al. 2021).

Panthera/Crocota sp.

Three bone fragments were assigned to either belong to the genus *Panthera* or *Crocota*. The current ZooMS reference list contains two *Panthera* species, *P. tigris* and *Panthera leo*, but is missing *P. spelaea*. *P. tigris* and *P. spelaea* are native and present throughout Asia (one sample

was identified as such). At Tsagaan Agui, our two *Panthera/Crocota* bone fragments originate from Pit 2 Layer 2.2, hence are of comparable age, and should be tentatively assigned to *P. spelaea*. Another possibility is the assignment of the three bone samples to the genus *Crocota*. Since 62 hyena coprolites and 89 hyena-digested eroded bones were found at Tsagaan Agui, it would be plausible that hyena bones are part of the dataset too.

Meles sp.

One bone fragment from Pit 2, Layer 2. could be identified as *Meles*. Badgers prefer wooded and hilly terrain. According to the reference list it is *Meles meles* (European badger), but since it is the only *Meles* species listed, others like *Meles leucurus* (Asian badger) that is nowadays native in Russia, Kazakhstan, China and Mongolia and at high elevation in the Tibetan Plateau, may be considered as well (Proulx et al. 2016).

Ursus sp.

One bone was identified as *Ursus sp.*, found in Pit 2, Layer 2.1 and is hence associated with the Late Paleolithic part of the site. We may assign this to the cave bear *Ursus spelaeus* who used occasionally the caves for hibernation. *U. spelaeus* is thought to have become extinct during the Last Glacial Maximum about 24,000 years ago (Pacher & Stuart 2009). At Denisova Cave earlier zooarchaeological studies suggested the occurrence of the small cave bear, *Ursus spelaeus arctos* which offered also a possible explanation for the unusual high number of bear bones at the site (Vasiliev & Shunkov 2009). Interestingly, *U. spelaeus* preferred plant-based food which is rather untypical compared to other omnivore extant bears. Their adaptation to this type of diet went so far that they lost most of their premolars and elongated the last one which turned their chewing surface more effective for crushing plants. Yet, they did not completely abandon meat and supplemented their protein intake with insects, small mammals and fish (Probst 2015). Another likely candidate is *Ursus arctos gobiensis*, an endangered species that lives nowadays in isolated populations in southwest Mongolia (Luvsamjamba et al. 2016).

Vulpes vulpes

One of the few ZooMS identifications to species-level was the red fox, *V. vulpes*, in one case. The sample derived from Pit 2, Layer 3/4 which is dated to about 40 ka BP (according to the

new radiocarbon dates from this work). ZooMS can distinguish the red fox from the arctic fox (*Vulpes lagopus*) by COL1a2 484 – 498 (B) at either m/z 1437.7 or 1453.7. The red fox originated in Eurasia during the Middle Paleolithic (Lucenti & Madurell-Malapeira 2020). The history between foxes and humans is long, especially in former times foxes were an important source of fur and hunted for. The red fox is considered a typical representative of the Holocene fauna (Sommer & Benecke 2005).

Rhinocerotidae

In total, 13 bone samples were identified as Rhinocerotidae. Taking the temporal and local context into account, these likely belong to the woolly rhinoceros *Coelodonta antiquitatis*. This extinct species populated large parts of Eurasia during the Pleistocene, primarily in steppe regions. High-crowned teeth and a horizontal grinding of them caused by silicic acid indicates a diet mainly based on grass (Kahlke & Lacombe 2008). A correlation between their extinction about 14,000 years ago and the landscape change at the transition from the Pleistocene to the Holocene has been suggested (Stuart & Lister 2012). It is likely that forest formation in the Holocene that displaced the grasslands to which they were adapted was also a factor for the fragmentation and potential extinction of the species. A recent study on the paleoecology and phylogeography of woolly rhinoceros based on the analysis of carbon and nitrogen stable isotopes and mtDNA sequences revealed ecological flexibility and geographic variation throughout time. They detected also a stability in $\delta^{15}\text{N}$ in north-east Siberia that could reflect a long-term environmental stability which probably enabled *C. antiquitatis* to survive longer in this region (Rey-Iglesia et al. 2021). In our dataset, 12 out of the 13 samples were digested by hyena and found from Layers 2.2-5. This indicates a long hunter-prey relationship between these two species.

Lagomorphs

Leporidae

Fifteen samples were identified as Leporidae. They were found from Layer 2.1-5 indicating a relative constant presence in the Gobi-Altai region over several millennia. Ten of the fifteen samples are part of the digested sample set, fitting well into the diet patterns of hyenas. Lepids are herbivores and are native to diverse habitats from tundra to tropical forest (Chapman & Flux 2008). The reference library lists three suitable species, namely the European hare (*Lepus*

europaeus) and Arctic hare (*Lepus arcticus*) as well as *Oryctolagus cuniculus*, the European rabbit. Since the arctic hare is highly adapted to the arctic tundra, this leaves either one of the European species as the most likely candidates.

Aves

Six samples were identified as belonging to birds, found in Layer 5 and 2. The current reference library includes only three avian species (*Gallus gallus*, *Phasianus colchicus* and *Larus canus*), hence more precise, regionally appropriate identification could not be obtained. *Larus canus* was the closest candidate, however it is possible that a genus/species currently not included in the reference list could fit the same peptide markers. This could be *Larus mongolicus*, the Mongolian gull. Today, western Mongolia contains several so-called Important Bird Areas (IBAs) due to diverse natural zones from high mountains to wetlands and lakes (Purevdorj et al. 2019).

Indeterminate

In total, 66 samples yielded good data (i.e. a mass spectrum with >4 peptide markers) but taxonomic identifications could not be made. Samples with less than five peptide markers present were categorized as indeterminable. Others had significant and enough peptide markers but no corresponding taxon in the ZooMS reference list. It was possible to distinguish for example two sub-groups with repeating values for COL1α2 484 – 498 at m/z 1435 or 1453, accompanied by COL1α2 793 – 816 at m/z 2128 or 2158, which seem to represent taxonomic groups not present in the list.

Short comment on doubles and duplicate samples

Out of all analyzed samples, six sample numbers (TSA 513, 519, 520, 525, 542, 543) were (internally) listed as doubles, since there were several sample bags with the same number. Four sample numbers yielded consistent results, whereas two numbers resulted in different identifications namely TSA 513_1 as Equidae and TSA 513_2 as *Pantholops hodgsonii* as well as TSA 520_1 as Group_1 and TSA 525_2 as *Camelus*. The duplicates are made up of 11 pairs, out of which four showed different taxonomic identifications. TSA 93a/553 and TSA 108a/551 resulted in distinct ZooMS taxa. TSA 93a vs. TSA 553 (new number 93b): *Equus* vs. *Pantholops hodgsonii*; TSA 106a vs. TSA 559 (new number 106b): Group_1 vs. indeterminate; TSA 108a

vs. TSA 551 (new number 108b): *Equus* vs. *Camelus* sp.; TSA 112a vs. TSA 556 (new number 112b): failed vs. *Equus*.

Overall, our ZooMS identifications from 566 bone reflect a distinct Eurasian faunal complex consisting of megafauna, such as woolly rhino and cave bear; large ungulates, such as equids, camels and bovids; smaller ungulates such as the Tibetan antelope; diverse carnivores from cave lion, cave hyena and red fox; and smaller mammals, such as rodents and hares. The suggestion that larger animals are better represented in the ZooMS assemblage (e.g. Brown et al. 2021, Wang et al. 2023) is also the case in Tsagaan Agui as equids alone made up 42 % out of the entire dataset.

4.3. Chronological Data

Four new radiocarbon dates were produced in the course of this work. These are shown in Table 3 below in comparison to previous radiometric data from Tsagaan Agui. The older chronological determinations were based on radiocarbon and later on experimental ESR (Electron Spin Resonance) dating approaches (Derevianko et al. 2000a; Derevianko et al. 2000b; Derevianko et al. 2004). The four calibrated radiocarbon ages from Tsagaan Agui as well as the calibration curve is shown in Table 3 and Figure 27.

Table 3: Comparison of the chronological classification of some archaeological layers from Tsagaan Agui according to Derevianko et al. 2000a, Derevianko et al. 2000b, Derevianko et al. 2004 and the radiocarbon dates from this work. The radiocarbon dates were calibrated to calendar ages with IntCal2020 (Reimer et al. 2020). (^{14}C ka BP = uncalibrated thousand years BP; ka cal BP=calendar thousand years before present; ka BP=thousand years before present).

Archaeological Layer	Species	Raw ^{14}C ages uncalibrated (this work)	Calibrated ages ka cal BP (95.4 % prob)	Raw ^{14}C age & ESR (2000, 2004)
Surface	<i>Camelus knoblochi</i>	30 ± 0.25 ^{14}C ka BP	35-34 ka cal BP	No data
Layer 2		No new data		23 – 25 ka BP
Layer 3	Bovidae	42.3 ± 1.1 ^{14}C ka BP	47.4-43.1 ka cal BP	31 – 34 ka BP
Layer 4	<i>Camelus knoblochi</i>	41.6 ± 1 ka ^{14}C ka BP	42.6-42.9 ka cal BP	44 – 59 ka BP
Layer 5	Ungulate	43.2 ± 1.3 ^{14}C ka BP	49.4-43.8 ka cal BP	No data

One of the bones (TSA 229) dated here derived from the surface layer and was radiocarbon dated to about 30 ka BP or 34-35 ka cal BP. The reason that Paleolithic-age material was also found at the floor of the cave can be explained by the erosion of underlying layers as well as through human activity (tourism and pilgrims). Layer 2 was previously dated to 23-25 ka BP. For Layer 3, a series of radiocarbon dates fall to 31-34 ka BP. Bone TSA 519_1 from Layer 3 was radiocarbon dated to 47.4-43.1 ka cal BP, which is considerably older to the previous age estimates of 31-34 ka BP. A similar pattern can be observed for the chronological dates of Layer 4. Previously dated to between 44-59 ka BP, sample TSA 2 was in the course of this work dated to 42.6-42.9 ka cal BP, which is a considerably younger age estimate. Layer 5 was radiocarbon dated here between 49.4-43.8 ka cal BP, an age estimate closer to the age range of Derevianko et al. Yet, this sample may derive from Layer 4 according to the excavator, hence the dating picture of the site is far from clear.

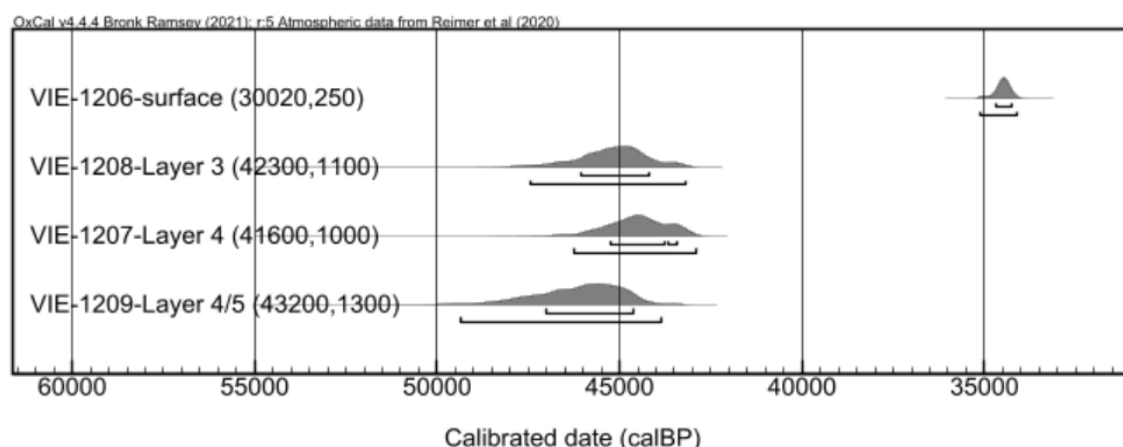


Figure 27: Calibrated radiocarbon ages, based on IntCal2020 atmospheric calibration curve (Reimer et al. 2020). The three dates from layer 3, 4 and 4/5 fall between 47-44 ka cal BP and are statistically identical. The younger date from the surface is 10 thousand years younger.

4.4. Insights into Paleoecology and Diet

The Paleolithic artefacts and bone assemblage from Tsagaan Agui cover a large but significant period of human evolution, that documents the transition from the Middle to the Upper Paleolithic period. We expect that the fossil record is incomplete, reflecting only a fraction of the past living species, which leads to a slightly distorted picture of the past. Nevertheless, the identified fauna pictures a milder climate than at present. The identification for example of migratory ungulates points to the presence of abundant grasslands (see also Khatsenovich et al. 2023). Not only the giant camel *C. knoblochi*, but also other large mammals specialized to

plants/grass, like the woolly rhino and the cave bear needed sufficiently large quantities of plant which is currently missing in the region. Some identified fauna, such as the beavers and birds, required a freshwater source in relative vicinity to the cave. A study on pollen present at Tsagaan Agui identified *Picea*, *Pinus* and *Betula* pollen, typical forested environment (Derevianko et al. 2000). Taking together, we may suggest a temperate environment for part of the period the site was occupied.

The current work gives first direct evidence of diet through the fauna exploitation at Tsagaan Agui by two top predators; the extinct cave hyena, a typical carnivore and the partly diet from humans (omnivores). The Tsagaan Agui bones show evidence of both hyena and human modifications. Humans cracked bones to access bone marrow whereas hyena do not only crack bones, but also gnaw, bite, nibble and fragment bones prior to digesting them. The presence of hyena coprolites and hyena digested bones in Layers 2 to 5 (Fig. 8) reflects a long occurrence of the cave hyena at the site. The ZooMS based taxonomic identifications (Fig. 28) and the morphological traces observed on fauna, are compared in Table 4. Human presence at Tsagaan Agui is mainly confirmed through lithic artefacts but also from traces on some bones in the form of cut-marks, cracking fractures and secondary treatment. Bones with the mentioned cracking marks were also found in Layers 2-5 indicating that the cave was used as a shelter by humans at least occasionally over millennia.

Table 4: Comparison of either traces that humans cracked a bone and/or hyena gnawed on them (internal data from the team of Dr. A.M. Khatsenovich, Institute of Archaeology and Ethnography SB RAS) complemented by the information to which genus/species the respective bone belongs to as well as the archaeological layer for chronological context.

Identified Fauna	Sample/Layer	Cracked by Humans	Hyena gnawing
Bovidae/Cervidae	TSA 524; Layer 5	✓	✗
Camelus sp.	TSA 2; Layer 4	✓	✓
Camelus sp.	TSA 522; Layer 4	✓	✗
Camelus sp.	TSA 540; Layer 4	✓	✗
Equus sp.	TSA 443; Layer 2.2	✗	✓
Equus sp.	TSA 518_1; Layer 3	✓	✗
Equus sp.	TSA 526; Layer 2.2	✓	✓
Equus sp.	TSA 530; Layer 2.2	✗	✓
Equus sp.	TSA 533; Layer 3	✓	✗
Felis/Lynx	TSA 538; Layer 2.2	✗	✓
Group_1	TSA 519_1; Layer 3	✓	✓
Group_1	TSA 520_1; Layer 2.2	✗	✓
Indet.	TSA 543; Layer 2.3	✓	✗
<i>P. hodgsonii</i>	TSA 525_1; Layer 5	✓	✗

Hyena diet at Tsagaan Agui

Tsagaan Agui was a frequented hyena den based on the presence of their stored prey and their coprolites. Hyenas used their fecal pellets to mark the den site. Prey and bone accumulation at the den is typical, as well as the finding of large amounts of fragmented bones as a result of their gnawing, nibbling (strongly chewing from one or two sides) and cracking. Like humans, hyenas crack the bones to access the marrow as nutrition. But hyenas are also able to digest small bone fragments (Diedrich & Žák 2006).

Cave hyena were the dominant scavengers in Eurasia. In the Late Paleolithic their geographical distribution ranged from the British Isles to the Pacific (Stuart & Lister 2014). A recent study on tooth microwear of *C. spelaea* and *Crocota ultima ussurica* from three different sites (Prolom 2 grotto, Ukraine; Bukhtarminskaya Cave, eastern Kazakhstan; Geographical Society Cave, Russia) came to the conclusion that microwear patterns resemble those of the extant spotted hyena, *C. crocuta*. They also found evidence that juveniles might have consumed a higher proportion of meat (Rivals et al. 2022). The extant spotted hyena is primarily a predator favoring medium-sized ungulate prey and scavenge depending on the habitat and availability of food resources different often (Gasaway et al. 1991). The spotted hyena is a cursorial predator (Stiner et al. 2009), meaning that more weak individuals are targeted such as old and young individuals. It is to be assumed that humans and hyenas competed directly on resources. Based on the bone modifications, animals that were probably targeted by both predators are camels, equids and medium-sized bovids (represented by "Group_1"). The hyena diet is more expansive and includes, based on the ZooMS identifications of this work, further bovids such as antelopes or *Bos*, cervids (e.g. *Capra*), rhinos, rodents, leopards, felids, bears and other carnivores. Cannibalism is a possibility too and is well established in other sites (Diedrich 2005f, 2006c; Cooper 1993).

The identified prey of cave hyenas at Tsagaan Agui fits well into the diet of the extant spotted hyena, as into the extinct cave hyena diet reconstructed at several sites (Bon et al. 2012; Dusseldorp 2011). A study on eight Middle to Upper Pleistocene hyena *C. crocuta spelaea* dens in the Bohemian Karst (Czech Republic) revealed *E. ferus przewalskii*, *C. antiquitatis*, *B. priscus*, *R. tarandus*, *Cervus elaphus*, *Megalocerus giganteus*, *E. hydruntinus*, *R. rupicapra*, *C. ibex*, *U. spelaeus*, *P. leo spelaea*, *C. lupus* and *M. primigenius* as main animals preyed upon on by the

extinct cave hyena (Diedrich & Žák 2006). Compared to the analyzed sample set from Tsagaan Agui, more cervids were found in the Bohemian Karst, the other results are broadly consistent with the ZooMS identifications of this work.

Human diet at Tsagaan Agui

As discussed in section 4.2, equids and camels were demonstrably exploited by humans which is also consistent with the findings depicted in Table 4. In addition, bones from medium-sized bovids like the Tibetan antelope or the species presented as “Group_1” were modified and possibly consumed by humans at Tsagaan Agui too. Furthermore, it can be assumed that the woolly rhinoceros did not end up naturally at the cave, but was rather deposited there by humans. It is likely that large animals were directly processed at the kill sites in order to minimize the weight for transport. This would also explain the absence of mammoths in the bone record of Tsagaan Agui. *M. primigenius* is confirmed as common prey for past humans, mammoths were native to Eurasia, found at other Paleolithic sites related to humans (e.g. Dusseldorp 2011) and yet, are not part of this archaeological context. One explanation could be the direct processing of these animals, and in contrast to bones, meat is not preserved in the archaeological record.

Although only one ursid specimen was found in the digested sample set, this does not necessarily mean that humans did not target cave bears. As known from several other sites (Auguste 1995, 2003; David 2002; Kindler 2007) humans, in the mentioned sites Neanderthals, systematically exploited cave bears over prolonged periods of time.

The body mass also needs to be considered in terms of dietary importance. Although large animals (megafauna) may account for a small proportion of faunal assemblages, their dietary importance can be set much higher. Hence, the dietary contribution of a certain species clearly differs. The underrepresentation of birds and the complete absence of fish is noticeable too regarding the assessment of the relative dietary composition of past humans at Tsagaan Agui. Birds have small hollow bones, fish (teleost) have small bones too and are therefore less likely to be preserved over time. Aquatic resources are generally very rare findings in Middle Paleolithic assemblages (Dusseldorp 2009). Not to forget that the current ZooMS reference library for Eurasian fauna hardly contains birds or fish. Both aspects are affecting the reconstruction of past dietary habits negatively.

Hyenas and humans competed on the same resources since both were top predators and co-existed at the cave. Hence, their niches had to be differentiated maybe in the form of temporal niche partitioning as hyenas forage usually at night and human's diurnal (Dusseldorp 2011). Another possibility is to develop different hunting strategies. As already mentioned, hyenas are cursorial predators targeting especially weak individuals, whereas humans appear to have used their knowledge of prey behavior to successfully hunt them leading to prey assemblages dominated by prime-age individuals; at least confirmed for Neanderthal associated sites (Roebroeks 2006; Stiner et al. 2009).

As mentioned previously in this chapter, large quantities of plants/grass were necessary to supply equids, camels, woolly rhinos and others. Consequently, humans may have expanded their diet by plant-based food sources too, as periods of milder climate than today would have made it possible. In times of great food scarcity however, it cannot be excluded that the inhabitants of the Tsagaan Agui cave might have also targeted and consumed carnivores or even rodents to survive. However, it is worth mentioning that without further taphonomic studies, associating several of the cave dwelling fauna identified through ZooMS with humans and predation, is tentative.

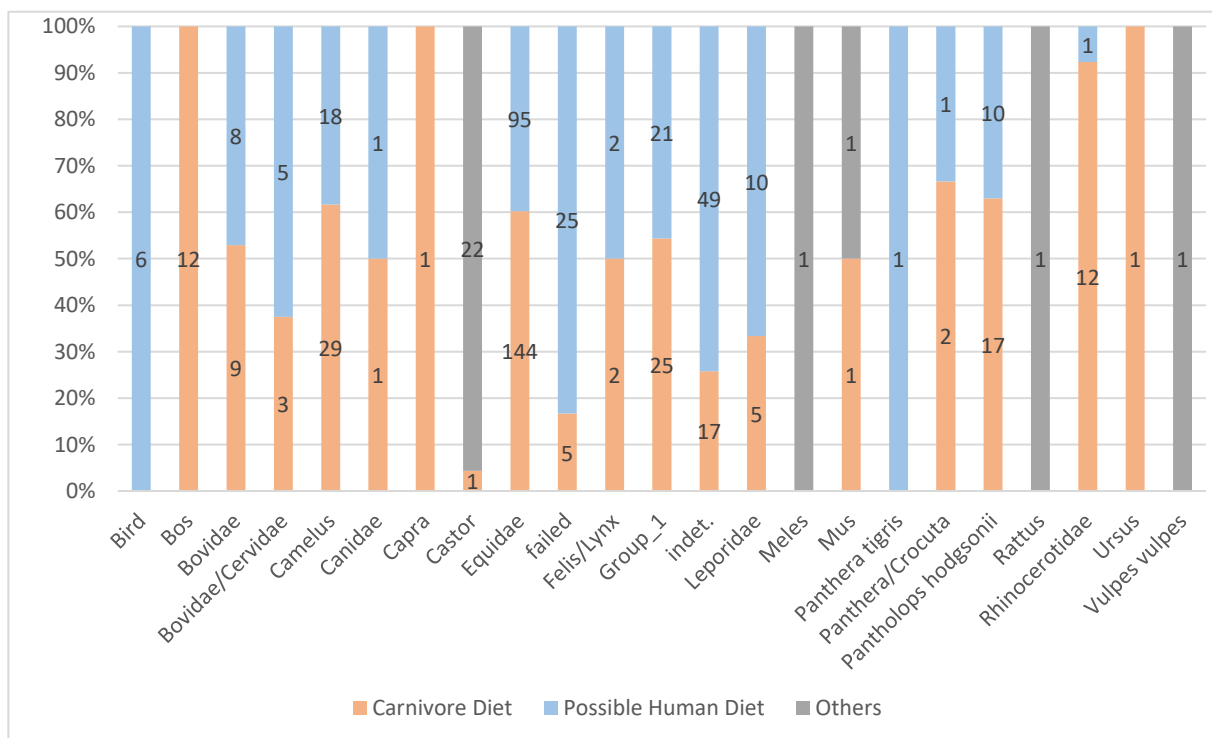


Figure 28: Overview of the hyena diet, possible human diet and other animals that ended up at Tsagaan Agui Cave. The plot is based on the ZooMS identifications of this work.

Animals that most likely ended up naturally in the cave

Only part of the non-digested bone samples found at Tsagaan Agui can be connected to human activity. There are many species, such as rats, mice, beavers, badgers, foxes, hyenas, cave lions and bears that likely ended up naturally in the cave as they are/were common cave inhabitants or were seeking temporarily for shelter. The red fox *V. vulpes* used such hyena dens also often as den or food storage, especially in the Upper Pleistocene (Diedrich & Zák 2006), which explains the finding of hares in the cave (although humans could have hunted them as well). The same applies to the badger, who moved also into caves and accumulated diverse bones from smaller mammals. Cave bears were demonstrably targeted by humans, but some individuals, young and old ones in particular, did not survive the long hibernation and died naturally in caves (Probst 2015), whereas hyenas fed on their carcasses shown at other sites (Diedrich & Zák 2006). Fig. 28 shows the distribution of the hyena diet (carnivore), possible human diet and others that lived naturally in caves or were likely deposited there by other carnivores.

5. Conclusion

In the current study, I analyzed using paleoproteomics (ZooMS) more than 500 bone fragments from the Paleolithic site Tsagaan Agui in Mongolia, with the main being their taxonomic identification. Half of the analyzed bones had been gnawed or digested by hyenas and provide a good comparison of the dietary habits of humans and hyenas.

The preservation status of the digested bone samples exceeded the expectations with a success rate of 98 %. The application of ZooMS revealed a distinct Eurasian fauna complex including equids, camels, antelopes, rhinos, beavers, felids, canids, leopards, bear, foxes, goat, mouse, rats, badger, birds and further bovids/cervids. During the Pleistocene in Mongolia, three equid species were present and are thought to be most likely represented in our data set too; namely *E. hemionus*, *E. ovodovi* and/or *E. ferus przewalskii*. These represent about 42 % of the whole data set, the proposition that large-bodied animals are overrepresented in the archaeological record could be consolidated with this work.

The giant extinct camel species *C. knoblochi* is part of the sample set too, morphologically identified as such in previous studies. The other camelid specimens from this study can be identified only the genus level *Camelus* until further work, since *C. knoblochi* is not represented in the ZooMS reference library. Other possible camelid candidates are *C. ferus* and *C. thomasi*.

The “Group-1” category includes *Ovis/Rupicapra* samples that showed strong similarities with “Antilopinae_2” from Jinsitai Cave in China. For now, it is not possible to identify these bovid samples on the basis of ZooMS. A common inhabitant of the Gobi Altai region, represented in our data set, is the Tibetan antelope that was preyed upon by cave hyenas. Another bovid hyena preyed upon on was probably the Baykal yak that is currently missing in the ZooMS library. The finding of beavers and birds at the site implicates the presence of a freshwater habitat in close vicinity to Tsagaan Agui.

C. antiquitatis is characteristic fauna in many Paleolithic sites. In our case, 12 out of 13 rhino specimens were consumed by hyenas, hence representing typical hyena prey.

Other carnivores, except for hyenas, present at the site were felids, *L. shansius*, *L. lynx*, *F. bieti* or *O. manul* were discussed as possible identifications at species level. Two Canidae specimens were also found, representing either a population of wolves ancestral to the domestic dog or

in fact, dogs as the activity of rodents could have transported younger material from the upper layers into older layers below. In addition, *P. speleae* is likely present.

Mus sp., *Rattus sp.*, *V. vulpes*, *Ursus sp.*, *Meles sp.* are interpreted as typical cave inhabitants that died naturally in the cave or were deposited there by other carnivores.

Radiocarbon dating of four samples resulted in 35-34 ka cal BP (surface, erosion), 47.4-43.1 ka cal BP (Layer 3), 42.6-42.9 ka cal BP (Layer 4) and 49.4-43.8 ka cal BP (Layer 5 or 4). The three dates from Layers 3, 4 and 4/5 fall between 47-44 ka cal BP and are statistically identical.

The new ZooMS results, in conjunction with the modification observed in the bones, allowed for direct comparison of the dietary habits of humans and hyenas at Tsagaan Agui. As both predators exploited fauna at the site, they competed directly for resources. Equids, camels and medium-sized bovids were demonstrably targeted by both. The exploitation of equids and camels by humans is well established at other sites. Since the woolly rhino would not have ended up naturally in the cave, humans may have been responsible for its deposition at the site. As for the cave bear, although it was as part of the sample group that were consumed by hyenas, other bears may have been targeted by humans too, as demonstrated at other Paleolithic sites. The underrepresentation of birds and complete absence of fish is most likely linked to the fact that they hardly preserve in the archaeological record. During interglacial oscillations, meaning periods of milder climate, plant-based food may have complemented the human diet at Tsagaan Agui. Hyenas expanded their diet with cervids, rhinos, rodents, leopards, felids, bears and other carnivores, which fit well into the diet of the extant spotted hyena. Since humans and hyenas shared the same niche, temporal niche partitioning could have been an advantageous solution for both, maybe in the form of hunting at different times (day, night) or by developing different hunting strategies.

Future work should aim at expanding the sample size in bones analyzed using ZooMS from the site, as well as include unidentified bones from contemporaneous sites in Mongolia.

6. Bibliography

- Abelson, P. H. Annual Report of the Director of the Geophysical Laboratory. Carnegie Institution of Washington Yearbook 1955, 54, 95–152.
- Armitage, S. J., Jasim, S. A., Marks, A. E., Parker, A. G., Usik, V. I., & Uerpmann, H. P. (2011). The southern route “out of Africa”: evidence for an early expansion of modern humans into Arabia. *Science*, 331(6016), 453–456.
- Auguste, P. (1995). Chasse et charognage au Paléolithique moyen: l'apport du gisement de Biache-Saint-Vaast (Pas-de-Calais). *Bulletin de la Société préhistorique française*, 155–167.
- Auguste, P. (2003). La chasse à l'ours au Paléolithique moyen: Mythes, réalités et état de la question. *BAR International Series*, 1105, 135–142.
- Barnett, R. (2025). Zooarchaeology and Ancient DNA. In *The Encyclopedia of Archaeological Sciences*, S.L. López Varela (Ed.).
- Bon, C., Berthonaud, V., Maksud, F., Labadie, K., Poulain, J., Artiguenave, F., ... & Elalouf, J. M. (2012). Coprolites as a source of information on the genome and diet of the cave hyena. *Proceedings of the Royal Society B: Biological Sciences*, 279(1739), 2825–2830.
- Boursot, P., Auffray, J. C., Britton-Davidian, J., & Bonhomme, F. (1993). The evolution of house mice. *Annual review of ecology and systematics*, 119–152.
- Brown, S., Douka, K., Collins, M. J., & Richter, K. K. (2021). On the standardization of ZooMS nomenclature. *Journal of Proteomics*, 235, 104041.
- Brown, S., Higham, T., Slon, V., Pääbo, S., Meyer, M., Douka, K., Brock, F., Comeskey, D., Procopio, N., Shunkov, M., Derevianko, A., Buckley, M. (2016). Identification of a new hominin bone from Denisova Cave, Siberia using collagen fingerprinting and mitochondrial DNA analysis. *Scientific reports*, 6(1), 23559.
- Brown, S., Massilani, D., Kozlikin, M. B., Shunkov, M. V., Derevianko, A. P., Stoessel, A., ... & Douka, K. (2022). The earliest Denisovans and their cultural adaptation. *Nature ecology & evolution*, 6(1), 28–35.
- Brownlow, S., Cabral, J. H. M., Cooper, R., Flower, D. R., Yewdall, S. J., Polikarpov, I., ... & Sawyer, L. (1997). Bovine β -lactoglobulin at 1.8 Å resolution—still an enigmatic lipocalin. *Structure*, 5(4), 481–495.
- Buckley, M., Collins, M., Thomas-Oates, J., & Wilson, J. C. (2009). Species identification by analysis of bone collagen using matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry. *Rapid Communications in Mass Spectrometry: An International Journal Devoted to the Rapid Dissemination of Up-to-the-Minute Research in Mass Spectrometry*, 23(23), 3843–3854.
- Buckley, M., Kansa, S. W., Howard, S., Campbell, S., Thomas-Oates, J., & Collins, M. (2010). Distinguishing between archaeological sheep and goat bones using a single collagen peptide. *Journal of archaeological science*, 37(1), 13–20.
- Buuveibaatar, B., Strindberg, S., Kaczensky, P., Payne, J., Chimeddorj, B., Naranbaatar, G., ... & Fuller, T. K. (2017). Mongolian Gobi supports the world's largest populations of khulan *Equus hemionus* and goitered gazelles *Gazella subgutturosa*. *Oryx*, 51(4), 639–647.
- Chapman, J. A., & Flux, J. E. (2008). Introduction to the Lagomorpha. In *Lagomorph biology: evolution, ecology, and conservation* (pp. 1–9). Berlin, Heidelberg: Springer Berlin Heidelberg.

- Clarkson, C., Jacobs, Z., Marwick, B., Fullagar, R., Wallis, L., Smith, M., ... & Pardoe, C. (2017). Human occupation of northern Australia by 65,000 years ago. *Nature*, 547(7663), 306-310.
- Collins, M., Buckley, M., Grundy, H. H., Thomas-Oates, J., Wilson, J., & van Doorn, N. (2010). ZooMS: the collagen barcode and fingerprints. *Spectrosc. Eur*, 22, 2-2.
- Cooper, S. M. (1993). Denning behaviour of spotted hyaenas (*Crocuta crocuta*) in Botswana. *African Journal of Ecology*, 31(2), 178-180.
- Coppens, Y., D. Tseveendorj, F. Demeter, T. Turbat & P.-H. Giscard. 2008. Discovery of an archaic *Homo sapiens* skullcap in northeast Mongolia. *Comptes Rendus Palevol* 7: 51-60
- Coutu, A. N., Taurozzi, A. J., Mackie, M., Jensen, T. Z. T., Collins, M. J., & Sealy, J. (2021). Palaeoproteomics confirm earliest domesticated sheep in southern Africa ca. 2000 BP. *Scientific Reports*, 11(1), 6631.
- Crees, J. J., & Turvey, S. T. (2014). Holocene extinction dynamics of *Equus hydruntinus*, a late-surviving European megafaunal mammal. *Quaternary Science Reviews*, 91, 16-29.
- David, F. (2002). Les ours du Châtelperronien de la Grotte du Renne à Arcy-sur-Cure (Yonne). In T. Tillet & L. R. Binford (Eds.), *L'ours et l'homme* (pp. 185–192). Liège: Université de Liège.
- Davis, R. S., & Ranov, V. A. (1999). Recent work on the Paleolithic of Central Asia. *Evolutionary Anthropology: Issues, News, and Reviews: Issues, News, and Reviews*, 8(5), 186-193.
- Degano, I., Biesaga, M., Colombini, M. P., & Trojanowicz, M. (2011). Historical and archaeological textiles: An insight on degradation products of wool and silk yarns. *Journal of Chromatography A*, 1218(34), 5837-5847.
- Demarchi, B. (2020). *Amino acids and proteins in fossil biominerals: an Introduction for archaeologists and palaeontologists*. John Wiley & Sons.
- Demarchi, B., Hall, S., Roncal-Herrero, T., Freeman, C. L., Woolley, J., Crisp, M. K., ... & Collins, M. J. (2016). Protein sequences bound to mineral surfaces persist into deep time. *elife*, 5, e17092.
- Demeter, F., Zanolli, C., Westaway, K. E., Joannes-Boyau, R., Düringer, P., Morley, M. W., ... & Shackelford, L. (2022). A Middle Pleistocene Denisovan molar from the Annamite chain of northern Laos. *Nature communications*, 13(1), 2557.
- Dennell, R. (2008). *The palaeolithic settlement of Asia*. Cambridge University Press.
- Derevianko, A. P., Olsen, J. W., Tseveendorj, D., Gladyshev, S. A., Nokhrina, T. I., & Tabarev, A. V. (2008). New insights into the archaeological record at Chikhen Agui Rockshelter (Mongolia). *Archaeology, Ethnology and Anthropology of Eurasia*, 34(2), 2-12.
- Derevianko, A. P., Brantingham, P. J., Olsen, J. W., and Tseveendorj, D. (2004). "Initial Upper Paleolithic Blade Industries from the North-central Gobi Desert, Mongolia," in *The Early Upper Paleolithic beyond Western Europe*. Editors P. J. Brantingham, S. L. Kuhn, and K. W. Kerry (Berkeley, California, United States: University of California Press), 207–222.
- Derevianko, A. P., Olsen, J. W., Tseveendorj, D., Krivoshapkin, A. I., Petrin, V. T., & Brantingham, P. J. (2000). The stratified cave site of Tsagaan Agui in the Gobi Altai (Mongolia). *Archaeology, Ethnology and Anthropology of Eurasia*, 1(1), 23-36.

- Derevianko, A. P., Olsen, J. W., Tseveendorzh, D., Petrin, V. T., Gladyshev, S. A., Zenin, A. N., et al. (2000a). *Archaeological Studies Carried Out by the Joint Russian-Mongolian-American Expedition in Mongolia in 1997 and 1998*. Novosibirsk: IAET SB RAS. (In Russian).
- Derevianko, A. P., Olsen, J. W., Tseveendorzh, D., Krivoshepin, A. I., Petrin, V. T., and Brantingham, P. D. (2000b). Stratified Cave Site of Tsagaan Agui in the Gobi Altai (Mongolia). (In Russian). *Archaeology, Ethnology Anthropol. Eurasia* 1, 23–36.
- Derevianko, A. P., and Petrin, V. T. (1995). *Investigation of the Tsagaan Agui Cave in the Southern Side of Gobi Altai in Mongolia*. Novosibirsk: IAET SO RAN Publ.
- Devièse, T., Massilani, D., Yi, S., Comeskey, D., Nagel, S., Nickel, B., ... & Higham, T. (2019). Compound-specific radiocarbon dating and mitochondrial DNA analysis of the Pleistocene hominin from Salkhit Mongolia. *Nature communications*, 10(1), 274.
- Diedrich, C. (2005). Eine oberpleistozäne Population von *Crocota crocuta spelaea* (Goldfuss 1823) aus dem eiszeitlichen Fleckenhyaenenhorst Perick-Höhlen von Hemer (Sauerland, NW Deutschland) und ihr Kannibalismus. *Philippia*, 12(2), 93-115.
- Diedrich, C. G. (2006). By Ice Age spotted hyenas removed, cracked, nibbled and chewed skeleton remains of *Coelodonta antiquitatis* (Blumenbach 1799) from the Lower Weichselian (Upper Pleistocene) freeland prey deposit site Bad Wildungen-Biedensteg (Hessia, NW Germany). *Journal of Taphonomy*, 4(4), 173-206.
- Diedrich, C. G., & Zák, K. (2006). Prey deposits and den sites of the Upper Pleistocene hyena *Crocota crocuta spelaea* (Goldfuss, 1823) in horizontal and vertical caves of the Bohemian Karst (Czech Republic). *Bulletin of Geosciences*, 81(4), 237-276.
- Douka, K., Slon, V., Jacobs, Z., Ramsey, C. B., Shunkov, M. V., Derevianko, A. P., ... & Higham, T. (2019). Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. *Nature*, 565(7741), 640-644.
- Dusseldorp, G. L. (2011). Studying Pleistocene Neanderthal and cave hyena dietary habits: combining isotopic and archaeozoological analyses. *Journal of Archaeological Method and Theory*, 18, 224-255.
- Dusseldorp, G. L. (2009). *A view to a kill: Investigating Middle Palaeolithic subsistence using an optimal foraging perspective*. Leiden: Sidestone Press.
- Evans, Z., Paskulin, L., Rahemtulla, F., & Speller, C. F. (2023). A comparison of minimally-invasive sampling techniques for ZooMS analysis of bone artifacts. *Journal of Archaeological Science: Reports*, 47, 103738.
- Galibert, F., Quignon, P., Hitte, C., & André, C. (2011). Toward understanding dog evolutionary and domestication history. *Comptes Rendus. Biologies*, 334(3), 190-196.
- Gasaway, W. C., Mossestad, K. T., & Standers, P. E. (1991). Food acquisition by spotted hyenas in Etosha National Park, Namibia: predation versus scavenging. *African Journal of Ecology*, 29(1), 64-75.
- Glantz, M., Athreya, S., & Ritzman, T. (2009). Is Central Asia the eastern outpost of the Neanderthal range? A reassessment of the Teshik-Tash child. *American Journal of Physical Anthropology: The Official Publication of the American Association of Physical Anthropologists*, 138(1), 45-61.
- Gorski, J. P. (2011). Biomineralization of bone: a fresh view of the roles of non-collagenous proteins. *Frontiers in bioscience (Landmark edition)*, 16, 2598.

- Grupe, G., Christiansen, K., Schröder, I., Wittwer-Backofen, U., (2012). Evolution des Menschen. *Anthropologie: Einführendes Lehrbuch*, 3-162.
- Gunz, P., & Bulygina, E. (2012). The Mousterian child from Teshik-Tash is a Neanderthal: A geometric morphometric study of the frontal bone. *American journal of physical anthropology*, 149(3), 365-379.
- Hendy, J., Welker, F., Demarchi, B., Speller, C., Warinner, C., & Collins, M. J. (2018). A guide to ancient protein studies. *Nature ecology & evolution*, 2(5), 791-799.
- Hendy, J. (2021). Ancient protein analysis in archaeology. *Science Advances*, 7(3), eabb9314.
- Higham, T., Douka, K., Wood, R., Ramsey, C. B., Brock, F., Basell, L., ... & Jacobi, R. (2014). The timing and spatiotemporal patterning of Neanderthal disappearance. *Nature*, 512(7514), 306-309.
- Horn, S., Durka, W., Wolf, R., Ermala, A., Stubbe, A., Stubbe, M., & Hofreiter, M. (2011). Mitochondrial genomes reveal slow rates of molecular evolution and the timing of speciation in beavers (*Castor*), one of the largest rodent species. *PloS one*, 6(1), e14622.
- Huq, N. L., Tseng, A., & Chapman, G. E. (1990). Partial amino acid sequence of osteocalcin from an extinct species of ratite bird. *Biochemistry International*, 21(3), 491-496.
- Janzen, A., Richter, K. K., Mwebi, O., Brown, S., Onduso, V., Gatwiri, F., ... & Boivin, N. (2021). Distinguishing African bovids using Zooarchaeology by Mass Spectrometry (ZooMS): New peptide markers and insights into Iron Age economies in Zambia. *PLoS One*, 16(5), e0251061.
- Ji, R., Cui, P., Ding, F., Geng, J., Gao, H., Zhang, H., ... & Meng, H. (2009). Monophyletic origin of domestic bactrian camel (*Camelus bactrianus*) and its evolutionary relationship with the extant wild camel (*Camelus bactrianus ferus*). *Animal genetics*, 40(4), 377-382.
- Jull, A.J.T., Burr, G.S. (2014). 14.4 – Radiocarbon: Archaeological Applications. Edited by Heinrich D. Holland & Karl K. Turekian. *Treatise on Geochemistry* (2nd Edition). Elsevier, 45-53.
- Kahlke, R. D., & Lacombe, F. (2008). The earliest immigration of woolly rhinoceros (*Coelodonta tolosiensis*, Rhinocerotidae, Mammalia) into Europe and its adaptive evolution in Palaeartic cold stage mammal faunas. *Quaternary Science Reviews*, 27(21-22), 1951-1961.
- Karas, M., & Hillenkamp, F. (1988). Laser desorption ionization of proteins with molecular masses exceeding 10,000 daltons. *Analytical chemistry*, 60(20), 2299-2301.
- Khatsenovich, A. M., Rybin, E. P., Tserendagva, Y., Bazargur, D., Margad-Erdene, G., Marchenko, D. V., ... & Derevianko, A. P. (2023). The Middle Paleolithic of Tsagaan Agui Cave in the Gobi Altai region of Mongolia and its Siberian and Central Asian links. *Archaeological Research in Asia*, 35, 100462.
- Khatsenovich, A. M., Tserendagva, Y., Bazargur, D., Marchenko, D. V., Rybin, E. P., Klementiev, A. M., ... & Derevianko, A. P. (2022). Shelter in an extreme environment: the Pleistocene occupation of Tsagaan Agui Cave in the Gobi Desert. *Antiquity*, 96(388), 989-997.
- Khatsenovich, A. M., Tserendagva, Y., Tserendagva, Y., Bazargur, D., Marchenko, D. V., & Rybin, E. P. (2021). Preliminary Results of the 2021 Excavation Campaign at Tsagaan Agui Cave in the Gobi Altai Region, Mongolia.
- Khatsenovich, A. M., Vishnevskaya, I. A., Bazargur, D., Volvakh, A. O., Klementiev, A. M., Ge, J., ... & Derevianko, A. P. (2021). Late Pleistocene paleoenvironments and episodic human occupations in the Orkhon valley of Central Mongolia. *Archaeology, Ethnology & Anthropology of Eurasia*, 49(2), 3-22.

- Khaveson, I. I. (1954). Camels from the Tertiary of the Oriental hemisphere (genus *Paracamelus*). *Trudy Paleontologičeskogo instituta*, 47, 100-162.
- Kindler, L. (2007). Die Rolle von Raubtieren in der Einnischung und Subsistenz jungpleistozäner Neandertaler- Archäozoologie und Taphonomie der mittelpaläolithischen Fauna aus der Balver Höhle (Westfalen). Mainz: Mainz University.
- Kingdon, J., & Hoffmann, M. (2013). *Nesotragus moschatus* suni. *Mammals of Africa*, 6, 214-219.
- Klementiev, A. M., Khatsenovich, A. M., Tserendagva, Y., Rybin, E. P., Bazargur, D., Marchenko, D. V., ... & Olsen, J. W. (2022). First documented *Camelus knoblochi* Nehring (1901) and fossil *Camelus ferus* Przewalski (1878) from Late Pleistocene archaeological contexts in Mongolia. *Frontiers in Earth Science*, 10, 861163.
- Krause, J., Orlando, L., Serre, D., Viola, B., Prüfer, K., Richards, M. P., ... & Pääbo, S. (2007). Neanderthals in central Asia and Siberia. *Nature*, 449(7164), 902-904.
- Leslie, D. M., & Schaller, G. B. (2008). *Pantholops hodgsonii* (Artiodactyla: Bovidae). *Mammalian Species*, (817), 1-13.
- Lucenti, S. B., & Madurell-Malapeira, J. (2020). Unraveling the fossil record of foxes: An updated review on the Plio-Pleistocene *Vulpes* spp. from Europe. *Quaternary Science Reviews*, 236, 106296.
- Luvsamjamba, A., Reynolds, H., Yansanjav, A., Tserenbataa, T., Amgalan, B., & Tumendemberel, O. (2016). Review of Gobi bear research (*Ursus arctos gobiensis*, Sokolov and Orlov, 1992). *Arid Ecosystems*, 6, 206-212.
- Mannucci, A.; Sullivan, K. M.; Ivanov, P. L.; Gill, P. Forensic Application of a Rapid and Quantitative DNA Sex Test by Amplification of the X-Y Homologous Gene Amelogenin. *Int. J. Legal Med.* 1994, 106, 190–193.
- Martini, P., & Geraads, D. (2018). *Camelus thomasi* Pomel, 1893 from the Pleistocene type-locality Tighennif (Algeria). Comparisons with modern *Camelus*. *Geodiversitas*, 40(1), 115-134.
- Massilani, D., Skov, L., Hajdinjak, M., Gunchinsuren, B., Tseveendorj, D., Yi, S., ... & Pääbo, S. (2020). Denisovan ancestry and population history of early East Asians. *Science*, 370(6516), 579-583.
- Mckittrick, J., Chen, P. Y., Bodde, S. G., Yang, W., Novitskaya, E. E., & Meyers, M. A. (2012). The structure, functions, and mechanical properties of keratin. *Jom*, 64, 449-468.
- Moshkin, V. A. (Ed.). (1986). *Castor* (p. 315pp)
- Niedermeyer, T. H., & Strohal, M. (2012). mMass as a software tool for the annotation of cyclic peptide tandem mass spectra.
- Noonan, P., Baker, Z., & Hayssen, V. (2024). *Otocolobus manul* (Carnivora: Felidae). *Mammalian Species*, 56(1038), seae004.
- Norton, C. J., & Gao, X. (2008). Hominin–carnivore interactions during the Chinese Early Paleolithic: Taphonomic perspectives from Xujiayao. *Journal of Human Evolution*, 55(1), 164-178.
- Nowak, R. M. (1999). Walker’s Mammals of the World.
- Ostrom, P. H., Schall, M., Gandhi, H., Shen, T. L., Hauschka, P. V., Strahler, J. R., & Gage, D. A. (2000). New strategies for characterizing ancient proteins using matrix-assisted laser desorption ionization mass spectrometry. *Geochimica et Cosmochimica Acta*, 64(6), 1043-1050.
- Pacher, M., & Stuart, A. J. (2009). Extinction chronology and palaeobiology of the cave bear (*Ursus spelaeus*). *Boreas*, 38(2), 189-206.

- Pan, J., Liu, X., Baca, M., Calvière-Tonasso, L., Schiavinato, S., Chauvey, L., ... & Orlando, L. (2024). Genome-wide population affinities and signatures of adaptation in hydruntines, sussemiones and Asian wild asses. *Molecular Ecology*, 33(19), e17527.
- Plyusnina, A., Ibrahim, I. N., & Plyusnin, A. (2009). A newly recognized hantavirus in the Asian house rat (*Rattus tanezumi*) in Indonesia. *Journal of General Virology*, 90(1), 205-209.
- Probst, E. (2015). *Der Höhlenbär*. Diplomica Verlag.
- Proulx, G., Abramov, A. V., Adams, I., Jennings, A. P., Khorozyan, I., Rosalino, L. M., ... & Do Linh San, E. (2016). World distribution and status of badgers—A review. *Badgers: systematics, biology, conservation and research techniques*, 31-116.
- Purevdorj, Z., Paek, W. K., Munkhbayar, M., Ganbold, O., Bing, G. C., Jargalsaikhan, A., ... & Lee, J. W. (2019). The avifaunal survey at Important Bird Areas in western Mongolia. *한국조류학회지*, 26(1), 7-15.
- Reading, R. P., Amgalanbaatar, S., Mix, H., & Lhagvasuren, B. (1997). Argali *Ovis ammon* surveys in Mongolia's south Gobi. *Oryx*, 31(4), 285-294.
- Reading, R. P., Henry, M., Lhagvasuren, B., Feh, C., Kane, D. P., Dulamtseren, S., & Enkhbold, S. (2001). Status and distribution of khulan (*Equus hemionus*) in Mongolia. *Journal of Zoology*, 254(3), 381-389.
- Reich, D., Patterson, N., Kircher, M., Delfin, F., Nandineni, M. R., Pugach, I., ... & Stoneking, M. (2011). Denisova admixture and the first modern human dispersals into Southeast Asia and Oceania. *The American Journal of Human Genetics*, 89(4), 516-528.
- Reimer, P. J., Austin, W. E., Bard, E., Bayliss, A., Blackwell, P. G., Ramsey, C. B., ... & Talamo, S. (2020). The IntCal20 Northern Hemisphere radiocarbon age calibration curve (0–55 cal kBP). *Radiocarbon*, 62(4), 725-757.
- Rey-Iglesia, A., Lister, A. M., Stuart, A. J., Bocherens, H., Szpak, P., Willerslev, E., & Lorenzen, E. D. (2021). Late Pleistocene paleoecology and phylogeography of woolly rhinoceroses. *Quaternary Science Reviews*, 263, 106993.
- Richter, K. K., Codlin, M. C., Seabrook, M., & Warinner, C. (2022). A primer for ZooMS applications in archaeology. *Proceedings of the National Academy of Sciences*, 119(20), e2109323119.
- Rivals, F., Baryshnikov, G. F., Prilepskaya, N. E., & Belyaev, R. I. (2022). Diet and ecological niches of the Late Pleistocene hyenas *Crocota spelaea* and *C. ultima ussurica* based on a study of tooth microwear. *Palaeogeography, Palaeoclimatology, Palaeoecology*, 601, 111125.
- Roebroeks, W. (2006). The human colonisation of Europe: where are we?. *Journal of Quaternary Science: Published for the Quaternary Research Association*, 21(5), 425-435.
- Ruan, X. D., He, P. J., Zhang, J. L., Wan, Q. H., & Fang, S. G. (2005). Evolutionary history and current population relationships of the chiru (*Pantholops hodgsonii*) inferred from mtDNA variation. *Journal of Mammalogy*, 86(5), 881-886.
- Rybin, E. P., Paine, C. H., Khatsenovich, A. M., Tsedendorj, B., Talamo, S., Marchenko, D. V., ... & Zwyns, N. (2020). A new Upper Paleolithic occupation at the site of Tolbor-21 (Mongolia): Site formation, human behavior and implications for the regional sequence. *Quaternary International*, 559, 133-149.
- Schweitzer, M., Hill, C.L., Asara, J.M., Lane, W.S., Pincus, S.H. (2002). Identification of Immunoreactive Material in Mammoth Fossils. *J. Mol. Evol.*, 55, 696-705.

- Serangeli, J., & Bolus, M. (2008). Out of Europe-The dispersal of a successful European hominin form: Out of Europe-Die Ausbreitung einer erfolgreichen europäischen Menschenform. *Quartär-Internationales Jahrbuch zur Erforschung des Eiszeitalters und der Steinzeit*, 55, 83-98.
- Slon, V., Hopfe, C., Weiß, C. L., Mafessoni, F., De La Rasilla, M., Lalueza-Fox, C., ... & Meyer, M. (2017). Neandertal and Denisovan DNA from Pleistocene sediments. *Science*, 356(6338), 605-608.
- Slon, V., Mafessoni, F., Vernot, B., De Filippo, C., Grote, S., Viola, B., ... & Pääbo, S. (2018). The genome of the offspring of a Neanderthal mother and a Denisovan father. *Nature*, 561(7721), 113-116.
- Sommer, R., & Benecke, N. (2005). Late-Pleistocene and early Holocene history of the canid fauna of Europe (Canidae). *Mammalian Biology*, 70(4), 227-241.
- Stiner, M. C., Barkai, R., & Gopher, A. (2009). Cooperative hunting and meat sharing 400–200 kya at Qesem Cave, Israel. *Proceedings of the National Academy of Sciences*, 106(32), 13207-13212.
- Strani, F., & DeMiguel, D. (2023). The role of climate change in the extinction of the last wild equids of Europe: Palaeoecology of *Equus ferus* and *Equus hydruntinus* during the Last Glacial Period. *Palaeogeography, Palaeoclimatology, Palaeoecology*, 620, 111564.
- Stuart, A. J., & Lister, A. M. (2012). Extinction chronology of the woolly rhinoceros *Coelodonta antiquitatis* in the context of late Quaternary megafaunal extinctions in northern Eurasia. *Quaternary Science Reviews*, 51, 1-17.
- Stuart, A. J., & Lister, A. M. (2014). New radiocarbon evidence on the extirpation of the spotted hyaena (*Crocuta crocuta* (Erxl.)) in northern Eurasia. *Quaternary Science Reviews*, 96, 108-116.
- Tanaka, K., Waki, H., Ido, Y., Akita, S., Yoshida, Y., Yoshida, T., & Matsuo, T. J. R. C. (1988). Protein and polymer analyses up to m/z 100 000 by laser ionization time-of-flight mass spectrometry. *Rapid communications in mass spectrometry*, 2(8), 151-153.
- Tong, H., Zhang, B., Chen, X., Jiangzuo, Q., Liu, J., & Wang, X. (2023). New carnivoran remains from the Early Pleistocene Shanshenmiaozui site in Nihewan Basin, northern China. *Quaternary International*, 658, 60-79.
- Titov, V. V. (2008). Habitat conditions for *Camelus knoblochi* and factors in its extinction. *Quaternary International*, 179(1), 120-125.
- Ulrich, M. M. W., Perizonius, W. R. K., Spoor, C. F., Sandberg, P., & Vermeer, C. (1987). Extraction of osteocalcin from fossil bones and teeth. *Biochemical and Biophysical Research Communications*, 149(2), 712-719.
- van Doorn, N. L., Hollund, H., & Collins, M. J. (2011). A novel and non-destructive approach for ZooMS analysis: ammonium bicarbonate buffer extraction. *Archaeological and Anthropological Sciences*, 3, 281-289.
- Vangengeim, E. A., & Gerbova, V. G. (1962). Some Data on Time and Conditions of Transbaikalian Sand Accumulation. *Bull. Comm. Study Quat*, 19, 268-274.
- Vasiliev, S. K., & Shunkov, M. V. (2009). Large Pleistocene mammals in the southern gallery of Denisova Cave. *Probl. Archaeol. Ethnogr. Anthropol. Siberia Neighboring Territories*, 25, 63-69.
- Végh, E. I., & Douka, K. (2024). SpecieScan: semi-automated taxonomic identification of bone collagen peptides from MALDI-ToF-MS. *Bioinformatics*, 40(3), btae054.
- Vishnyatsky, L. B. (1999). The paleolithic of central Asia. *Journal of World Prehistory*, 13, 69-122.

- Wadsworth, C., & Buckley, M. (2014). Proteome degradation in fossils: investigating the longevity of protein survival in ancient bone. *Rapid Communications in Mass Spectrometry*, 28(6), 605-615.
- Wang, N., Xu, Y., Tang, Z., He, C., Hu, X., Cui, Y., & Douka, K. (2023). Large-scale application of palaeoproteomics (Zooarchaeology by Mass Spectrometry; ZooMS) in two Palaeolithic faunal assemblages from China. *Proceedings of the Royal Society B*, 290(2009), 20231129.
- Warinner, C., Korzow Richter, K., & Collins, M. J. (2022). Paleoproteomics. *Chemical reviews*, 122(16), 13401-13446.
- Warinner, C., Rodrigues, J. F. M., Vyas, R., Trachsel, C., Shved, N., Grossmann, J., ... & Cappellini, E. (2014). Pathogens and host immunity in the ancient human oral cavity. *Nature genetics*, 46(4), 336-344.
- Weidenreich, F. (1945). The paleolithic child from the Teshik-Tash Cave in Southern Uzbekistan (Central Asia). *American Journal of Physical Anthropology*, 3(2), 151-163.
- Welker, F., Ramos-Madrigal, J., Kuhlwilm, M., Liao, W., Gutenbrunner, P., de Manuel, M., ... & Cappellini, E. (2019). Enamel proteome shows that Gigantopithecus was an early diverging pongine. *Nature*, 576(7786), 262-265.
- Whitford, D. (2013). *Proteins: structure and function*. John Wiley & Sons.
- Wood, J. R., Wilmshurst, J. M., Wagstaff, S. J., Worthy, T. H., Rawlence, N. J., & Cooper, A. (2012). High-resolution coproecology: using coprolites to reconstruct the habits and habitats of New Zealand's extinct upland moa (*Megalapteryx didinus*). *PloS one*, 7(6), e40025.
- Xia, H., Zhang, D., Wang, J., Fagernäs, Z., Li, T., Li, Y., ... & Welker, F. (2024). Middle and Late Pleistocene Denisovan subsistence at Baishiya Karst Cave. *Nature*, 632(8023), 108-113.
- Xu, S. Q., Yang, Y. Z., Zhou, J., Jin, G. E., Chen, Y. T., Wang, J., ... & Ge, R. L. (2005). A mitochondrial genome sequence of the Tibetan antelope (*Pantholops hodgsonii*). *Genomics, Proteomics and Bioinformatics*, 3(1), 5-17.
- Yang, L., Zhang, X., Zhao, X., & Xiang, H. (2022). The technological advance and application of coprolite analysis. *Frontiers in Ecology and Evolution*, 9, 797370.
- Yu, T. Y., Morton, J. D., Clerens, S., & Dyer, J. M. (2017). Cooking-induced protein modifications in meat. *Comprehensive Reviews in Food Science and Food Safety*, 16(1), 141-159.
- Yu, H., Xing, Y. T., Meng, H., He, B., Li, W. J., Qi, X. Z., ... & Luo, S. J. (2021). Genomic evidence for the Chinese mountain cat as a wildcat conspecific (*Felis silvestris bieti*) and its introgression to domestic cats. *Science Advances*, 7(26), eabg0221.
- Yuan, J., Hu, J., Liu, W., Chen, S., Zhang, F., Wang, S., ... & Sheng, G. (2024). Camelus knoblochi genome reveals the complex evolutionary history of Old World camels. *Current Biology*, 34(11), 2502-2508.
- Zavala, E. I., Jacobs, Z., Vernot, B., Shunkov, M. V., Kozlikin, M. B., Derevianko, A. P., ... & Meyer, M. (2021). Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. *Nature*, 595(7867), 399-403.
- Zwyns, N. (2014). Altai: Paleolithic. *Encyclopedia of Global Archaeology*, 1, 148-158.
- Zwyns, N. (2021). The Initial Upper Paleolithic in Central and East Asia: blade technology, cultural transmission, and implications for human dispersals. *Journal of Paleolithic Archaeology*, 4(3), 19.
- Zwyns, N., Gladyshev, S., Tabarev, A., & Gunchinsuren, B. (2014). Mongolia: paleolithic. *Encyclopedia of global archaeology*, 8, P5025-5032.

Zwyns, N., Paine, C. H., Tsedendorj, B., Talamo, S., Fitzsimmons, K. E., Gantumur, A., ... & Hublin, J. J. (2019). The northern route for human dispersal in Central and Northeast Asia: new evidence from the site of Tolbor-16, Mongolia. *Scientific Reports*, 9(1), 11759.

7. List of Illustrations

Figure 1: Different stages of protein incorporation and recovery in an archeological sample ranging from the ancient life to present interpretation (Warinner et al. 2022).	10
Figure 2: Schematic overview of ZooMS from the extraction and digestion of collagen to the MALDI-TOF analysis leading to the interpretation of the resulting mass spectra (Brown et al. 2021).	13
Figure 3: Map with the main stratified Paleolithic sites in Mongolia (Gunchinsuren 2014, p.5026). ...	19
Figure 4: Plan view of Tsagaan Agui (Khatsenovich et al. 2023, edited by the author with blue arrows.	20
Figure 5: Lithic artefacts of the Entrance Terrace assemblage at Tsagaan Agui showing a Mousterian point with concave base (6) and a Mousterian point (7) (Khatsenovich et al. 2023).	20
Figure 6: Stratigraphic profile of Pit 2 from Tsagaan Agui (Khatsenovich et al. 2023).	21
Figure 7: Hyena den in profile in Pit 2 (Khatsenovich et al. 2023).	21
Figure 8: Bone with two holes previously interpreted as drilled by humans from Pit 2, Layer 3 from Tsagaan Agui	21
Figure 9: Example of one sample from Tsagaan Agui (Nr. 167), photo by the author.	23
Figure 10: View on the scale in the drilling room, photo by the author.	24
Figure 11: MALDI-plate with Calibrant and Matrix spotted on, photo by the author.	25
Figure 12: Samples R00337, R00338, R00339 and R00340 in Milli-Q water (photo by the author).	26
Figure 13: Overview of the upgraded VERA facility (https://isotopenphysik.univie.ac.at/vera/ - retrieved on 4.10.2024).	27
Figure 14: ZooMS results for all samples showing the distribution of the orders Artiodactyla, Perissodactyla, Carnivora, Lagomorpha, Rodentia, Bird, failed and the indeterminable (indet.) ones.	28
Figure 15: ZooMS results for all samples divided into their ZooMS taxa. The findings indicate the presence of Equidae, Camelus, Group_1, Pantholops hodgsonii, Castor, Bovidae, Leporidae, Rhinocerotidae, Bos, Bovidae/Cervidae, Bird, Felidae, Canidae, Mus and Panther.	29
Figure 16: Example of a mass spectrum that was identified as Equid. In sample TSA1 all nine ZooMS markers were identified, six of them are marked with a blue arrow for illustration.	30
Figure 17: ZooMS results for the non-digested samples (n = 279) showing the distribution of the orders Artiodactyla, Perissodactyla, Carnivora, Lagomorpha, Rodentia, Bird, failed and indet.	31
Figure 18: ZooMS results for the non-digested samples (n = 279) divided into their ZooMS taxa. The following identifications were made: Equids, Castor, Group_1, Camelus, Leporidae, Pantholops hodgsonii, Bovidae, Bos, Bovidae/Cervidae, Canidae, Rhinocerotidae, Felidae, Felis/Lynx, Meles, Mus, Panthera, Panthera/Crocota, Rattus and Vulpes vulpes, supplemented by the failed and indeterminable ones.	31

Figure 19: ZooMS results for the digested samples (n = 287) showing the distribution of the orders Artiodactyla, Perissodactyla, Carnivora, Lagomorpha, Rodentia, failed and indet.	32
Figure 20: ZooMS results for the digested samples (n = 287) divided into their ZooMS taxa. The following identifications were made: Equidae, Camelus, Group_1, Pantholops hodgsonii, Rhinocerotidae, Bos, Bovidae, Leporidae, Bovidae/Cervidae, Felidae, Canidae, Capra, Castor, Hyaenidae/Felidae, Panthera/Crocuta, Ursus and Mus sp., supplemented by the failed and indet. ...	33
Figure 21: Example of a mass spectrum of sample TSA251 that was identified as Rhinocerotidae. It was possible to identify seven ZooMS markers except for COL1α2 292 – 309 (P2) and COL1α2 454 – 483 (E).	33
Figure 22: ZooMS identifications by layer for Pit 2/2021 (n = 385; after excluding samples with insufficient or unsuitable layer information and the samples that failed or remained indeterminable) showing the distribution of the identified ZooMS taxa from Layer 1 – Layer 6. Pit 2 Layer 1 (n = 6); Pit 2 Layer 1.3. (n = 3), Pit 2 Layer 2 (n = 4); Pit 2 Layer 2.1 (n = 44); Pit 2 Layer 2.2 (n = 164); Pit 2 Layer 2.3 (n = 6); Pit 2 Layer 3 (n = 55); Pit 2 Layer 4 (n = 62); Pit 2 Layer 5 (n = 43); Pit 2 Layer 6 (n = 2).	34
Figure 23: ZooMS identification per layer for Pit E/2022 (n = 19, after excluding samples with insufficient layer information and the samples that failed or remained indeterminable). Pit E Layer 2.2 (n = 1); Pit E Layer 5 (10); Pit E Layer 6 (n = 6); Pit E Layer7	35
Figure 24: Sample TSA 2 from Pit 2021/2, Layer 4 that was identified as a proximal metacarpal fragment from Camelus knoblochi (Klementiev et al. 2022) and dated to 41600 ± 1000 BP.	39
Figure 25: Map of principal finds of fossil camels in eastern Eurasia (Klementiev et al. 2022).	40
Figure 26: Picture of a mature male Pantholops hodgsonii in Quinghai Province, China. Photo by G. B. Schaller (Leslie & Schaller 2008).	42
Figure 27: Calibrated radiocarbon ages, based on IntCal2020 atmospheric calibration curve (Reimer et al. 2020). The three dates from layer 3, 4 and 4/5 fall between 47-44 ka cal BP and are statistically identical. The younger date from the surface is 10 thousand years younger.	51
Figure 28: Overview of the hyena diet, possible human diet and other animals that ended up at Tsagaan Agui Cave. The plot is based on the ZooMS identifications of this work.	55

8. Table Directory

Table 1: Commonly used markers for ZooMS (Brown et al. 2021).	16
Table 2: Results from the AMS radiocarbon dating, and the isotopic analysis performed for four samples from Tsagaan Agui (TSA_229; TSA_2; TSA_519_1; TSA_525_1):.....	36
Table 3: Comparison of the chronological classification of some archaeological layers from Tsagaan Agui according to Derevianko et al. 2000a, Derevianko et al. 2000b, Derevianko et al. 2004 and the radiocarbon dates from this work. The radiocarbon dates were calibrated to calendar ages with IntCal2020 (Reimer et al. 2020). (¹⁴ C ka BP = uncalibrated thousand years BP; ka cal BP=calendar thousand years before present; ka BP=thousand years before present).	50
Table 4: Comparison of either traces that humans cracked a bone and/or hyaena gnawed on them (internal data from the team of Dr. A.M. Khatsenovich, Novosibirsk State University, Russia) complemented by the information to which genus/species the respective bone belongs to as well as the archaeological layer for chronological context.	52

9. Appendix

Site	Zooms_ID	Context Information	Bone Weight [mg]	Sample Weight [mg]	Order	Family	Species/Genus	ZooMS taxon	COL1a1_5 08-519	COL1a2_978-990	COL1a2_978-990+16	COL1a2_4 84-498	COL1a2_502-519	COL1a2_2 92-309	COL1a2_7 93-816	COL1a2_4 54-483	COL1a1_5 86-618	COL1_1_5 86-618+16	COL1a2_7 57-789	COL1a2_7 57-789+16	COL1a2_8 89-906	Other peptides	Any comments regarding the sample/ID
Tsagan Agui	1	Pit 2 2022; Layer 4; A19/1	63	14	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,69	1198,7	1427,82	1550,87	1649,84	2145,21	2820,37	2883,5	2899,47	2983,55	2999,56			digested, dark, compact
Tsagan Agui	2	Pit 21/2; Layer 4; A19/1	26	16	Artiodactyla	Camelidae	<i>Camelus knoblochi</i>	Camelus sp.	1105,64	1221,7		1443,82		1634,9	2131,21	2820,45	2883,54			2991,59			cracked by human, hyaena gnawings; <i>Camelus knoblochi</i> according to previous analysis
Tsagan Agui	3	Pit 21/2; Layer 3; A19/2	108	17				failed															dark, compact
Tsagan Agui	4	Layer 3, A19/2	60	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,63	1198,64	1427,74		1649,8	2145,1	2820,26	2883,38		2983,47	2999,46			dark, compact, <i>Equus hemionus</i> ?
Tsagan Agui	5	Pit 21/2; Layer 4; A19/1	90	18	Artiodactyla	Bovidae/Cervidae		Bovidae/Cervidae	1105,6	1180,65	1196,66	1427,76		1648,85	2131,11	2793,32	2883,42	2899,43	3017,43	3033,5			could be <i>Saiga tartarica</i> , but not clear enough
Tsagan Agui	6	Pit 21/2; Layer 5; A19/3	164	14	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,57	1180,62	1196,65	1427,74	1580,79	1648,83	2131,07	2792,27	2857,34		3017,4	3033,45			
Tsagan Agui	7	Pit 21/2; Layer 5; A19/3	282	14	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,6	1221,66		1443,76		1634,83	2131,11	2820,31	2883,4		2975,47	2991,47			porous, light
Tsagan Agui	8	Pit 21/2; Layer 5/6; A19/2	293	15				failed															porous, light
Tsagan Agui	9	Pit 21/2; Layer 3; A19/2	50	16	Rodentia	Castoridae	Castor	Castor sp.	1105,59	1177,58		1427,76	1576,84		2129,12		2883,4		2983,52	2999,48			porous, light
Tsagan Agui	10	Pit 21/2; Layer 3; A19/3	127	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1199,66	1427,8		1649,87	2145,19	2820,41	2883,46		2983,55	2999,57			dark, compact
Tsagan Agui	11	Pit 21/2; Layer 2; A19/4	64	17	Artiodactyla	Bovidae	Bos sp. sp.	Bos sp.	1105,6	1192,7	1208,71	1427,77	1580,81	1648,87	2131,13	2793,31	2853,43	2870,5	3017,45	3033,51	1532		digested
Tsagan Agui	12	Pit 21/2; Layer 5; A19/2	314	20	Artiodactyla	Camelidae		Camelus sp.	1105,65	1221,72		1443,84	1550,9	1634,93	2131,24	2820,51	2883,59		2975,58	2991,6			
Tsagan Agui	13	Pit 21/2; Layer 3; A19/1	119	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,69	1427,79			2145,17	2820,37	2883,48	2899,48		2999,57			
Tsagan Agui	14	Pit 21/2; Layer 4; A19/1	229	21	Artiodactyla	Bovidae	Ovis	Group_1	1105,58	1180,64	1196,66	1427,75	1580,81	1648,84	2131,21	2792,31	2883,42		3017,44	3033,48			dark, compact

Tsagan Agui	15	Pit 21/2; Layer 2.2/3; A19/3	171	17				failed																
Tsagan Agui	16	Pit 21/2; Layer 2.2; A19/3	154	16	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,64	1427,78	1549,84	1649,85	2145,16	2820,39	2883,46		2983,55	2999,54				
Tsagan Agui	17	Pit 21/2; Layer 2.2; A19/2	99	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,63	1198,65	1427,77		1649,86	2145,16	2820,29	2883,44	2900,52	2983,58	2999,53				
Tsagan Agui	18	Pit 21/2; Layer 3/4; A19/1	492	17	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,58	1221,65		1443,75		1634,83	2131,11	2820,33	2883,41		2975,45	2991,46				hard bone
Tsagan Agui	19	Pit 21/2; Layer 5; A19/3	71	16	Artiodactyla	Bovidae	Ovis	Group_1	1105,57	1180,63	1196,64	1427,74	1580,8	1648,81	2131,08	2792,28	2883,38		3017,42	3033,48				very porous
Tsagan Agui	20	Pit 21/2; Layer 4; A19/1	37	15	Rodentia	Castoridae	Castor	Castor sp.	1105,58	1177,58		1427,74	1576,82		2129,09		2883,4	2899,34	2983,5	2999,5				very thin, red-brown
Tsagan Agui	21	Pit 21/2; Layer 3; A19/1	107	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,66	1427,78	1550,82	1649,84	2145,15	2820,35	2883,44		2983,52	2999,52				porous
Tsagan Agui	22	Pit 21/2; Layer 4; A19/1	748	17				failed															two different looking pieces (sample from broken one)	
Tsagan Agui	23	Pit 21/2; Layer 3; A19/3	244	20				failed																
Tsagan Agui	24	Pit 21/2; Layer 3; A19/1	90	17	Artiodactyla	Bovidae	Ovis	Group_1	1105,63		1196,71	1427,81	1580,86	1648,92	2131,17	2792,38	2883,48	2899,46	3017,44	3033,5				
Tsagan Agui	25	Pit 21/2; Layer 3; A19/1	313	16	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,66	1221,72		1443,85	1550,9	1634,94	2131,26	2820,51	2883,57		2975,54	2991,57				digested
Tsagan Agui	26	Pit 21/2; Layer 5/6; A19/3	193	16	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,59	1180,66	1196,67	1427,76	1580,78	1648,85	2131,09	2792,29	2857,37		3017,37					
Tsagan Agui	27	Pit 21/2; Layer 3; A19/4	333	20				failed																
Tsagan Agui	28	Pit 21/2; Layer 3; A19/2	395	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,63	1198,65	1427,76		1649,83	2145,13	2820,34	2883,41		2983,47	2999,5				fragment of rip, porous
Tsagan Agui	29	Pit 21/2; Layer 2.2; A19/4	359	14	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,64	1427,77		1649,81	2145,13	2820,34	2883,42	2899,41		2999,52				
Tsagan Agui	30	Pit 21/2; Layer 3; A19/2	388	15	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,67	1427,78		1649,84	2145,16	2821,39	2883,46		2983,55	2999,55				
Tsagan Agui	31	Pit 21/2; Layer 5/6; A19/2	323	18	Carnivora	Felidae		Felidae	1105,61	1207,65		1453,81	1566,84		2163,18	2820,44	2853,52		2999,6					cat or lynx
Tsagan Agui	32	Pit 21/2; Layer 1.3; A21/1	184	19	Artiodactyla	Bovidae		Bovidae	1105,58	1180,64	1196,65	1427,75	1550,78	1648,86	2131,11	2792,33	2883,43	2899,42	3017,39		1532			Procavia guttorosa (dzeren) as in former comments possible, but not in reference list

Tsagan Agui	33	Pit 21/2; Layer 3/4; A19/1	102	15	Rodentia	Castoridae	Castor	Castor sp.	1105,64	1177,64		1427,83	1576,91		2129,17		2883,52		2983,58	2999,6			at B1/F19 1453 higher than 1427...
Tsagan Agui	34	Pit 21/2; Layer 5; A19/3	264	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,67	1198,68	1427,81	1550,85	1649,87	2145,2	2820,41	2883,47	2899,47	2984,6	2999,65			digested
Tsagan Agui	35	Pit 21/2; Layer 3; A19/1	364	14	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,64	1221,68		1443,78		1634,87	2131,14	2821,43	2883,5		2975,61	2991,59			
Tsagan Agui	36	Pit 21/2; Layer 5; A19/1	194	16	Lagomorpha	Leporidae		Leporidae	1105,6		1221,62	1453,75	1566,8/1592,77		2129,08	2808,27	2883,52	2899,52	2957,62				Lepus europaeus ? Other: Lepus arcticus, Oryctolagus cuniculus; part of hip-bone
Tsagan Agui	37	Pit 21/2; Layer 3; A19/2	434	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,64	1198,67	1427,76	1550,8	1649,83	2145,29	2820,89	2884,01	2900		3000,18			
Tsagan Agui	38	MC; Layer 2.2	384	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,66	1427,77	1550,8	1649,85	2145,32	2820,91	2884,03	2900,02	2983,04	2999,05			hard bone
Tsagan Agui	39	Pit 21/2; Layer 2.2; A19/4	578	18				failed															
Tsagan Agui	40	Pit 21/2; Layer 3; A19/1	75	14	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,66	1199,65	1427,76		1649,81	2145,11	2820,27	2883,34			2999,45			
Tsagan Agui	41	Pit 21/2; Layer 3; A19/2	243	20	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,58	1180,63	1196,62	1427,75	1580,77	1648,83	2131,09	2792,95			3017,11	3033,12			
Tsagan Agui	42	Pit 21/2; Layer 2.2; A19/3	317	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,65	1198,64	1427,76	1550,76	1649,71	2145,04	2821,19	2883,27			2999,33			
Tsagan Agui	43	Pit 21/2; Layer 4; A19/1	302	15	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66	1198,63	1427,77	1550,78	1649,8	2145,12	2820,34	2883,42	2899,42		2999,45			
Tsagan Agui	44	Pit 21/2; Layer 4	233	16	Rodentia	Muridae	Mus musculus	Mus	1105,59	1178,58		1453,75	1592,83		2159,1	2866,62							porous
Tsagan Agui	45	Pit 21/2; Layer 4; A19/2	161	17	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,63	1198,65	1427,76	1550,78	1649,82	2145,18	2820,58	2883,66	2899,64		2999,65			porous
Tsagan Agui	46	Pit 21/2; Layer 4; A19/2	117	15	Artiodactyla	Bovidae		Bovidae	1105,61	1180,67	1196,69	1427,76			2131,1		2883,44		3017,52	3033,56	1532		dzeren?
Tsagan Agui	47	Pit 21/2; Layer 5; A19/1	328	16	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,63	1198,62	1427,73	1550,74	1649,79	2145,15	2821,56	2883,66	2899,68		2999,76			
Tsagan Agui	48	Pit 21/2; Layer 3/4; A19/2	164	14	Carnivora	Canidae	Vulpes vulpes	Vulpes vulpes	1105,61		1226,69	1437,75	1566,78		2131,17	2820,61	2853,7	2869,7		2999,92			very porous
Tsagan Agui	49	Pit 21/2; Layer 2.2/3; A19/1	287	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,62	1198,67	1427,74			2145,01	2820,1	2883,22		2983,25	2999,28			
Tsagan Agui	50	Pit 21/2; Layer 4; A19/2	172	16	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,66	1198,67	1427,8			2145,26	2821,7	2883,78		2983,81	2999,91			
Tsagan Agui	51	Pit 21/2; Layer 2.2/3; A19/1	226	20	Artiodactyla	Bovidae	Ovis	Group_1	1105,63	1180,67	1196,68	1427,78	1550,81	1648,87	2131,2	2792,61	2883,74	2899,76	3017,77	3033,84			fragment petrous bone

Tsagan Agui	52	Pit 21/2; Layer 4; A19/2	312	16	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,68	1196,7	1427,77	1580,8	1648,87	2131,11	2792,34	2883,45	2899,44	3017,43	3033,5			
Tsagan Agui	53	Pit 21/2; Layer 4; A19/3	232	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,67	1198,67	1427,78	1550,81	1649,83	2145,07	2820,2	2883,26	2899,23		2999,25			vertebra fragment
Tsagan Agui	54	Pit 21/2; Layer 2.2; A19/2	219	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65		1427,74		1649,77	2145,01	2821,11	2883,19		2984,22	2999,26			
Tsagan Agui	55	Pit 21/2; Layer 2.2; A19/3	563	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,65	1427,75	1550,76	1649,79	2145,1	2820,33	2883,41	2899,61	2983,34	2999,48			smooth surface of bone
Tsagan Agui	56	Pit 21/2; Layer4; A19/1	285	16	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,63	1198,65	1427,74	1550,77	1649,8	2145,17	2820,56	2883,66	2899,65		2999,74			
Tsagan Agui	57	Pit 21/2; Layer 4; A19/2	213	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,62		1427,74	1550,77	1649,79	2145,16	2820,54	2883,63	2899,62	2984,72	2999,74			
Tsagan Agui	58	Pit 21/2; Layer 3; A19/1	603	19				failed															
Tsagan Agui	59	Pit 21/2; Layer 3/4; A19/4	188	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,63	1198,65	1427,76			2145,19		2884,7	2899,72	2983,84	2999,86			dark, compact
Tsagan Agui	60	Pit 21/2; Layer 3; A19/1	277	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,67	1198,64	1427,74		1649,79	2145,02	2820,24	2883,21	2899,21	2984,24	2999,29			fragment tooth
Tsagan Agui	61	Pit 21/2; Layer 4; A19/4	143	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,63	1198,62	1427,75	1550,75	1649,78	2145,03	2820,14	2883,21	2899,21		2999,3			
Tsagan Agui	62	Pit 21/2; Layer 3/4; A19/4	125	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,61	1427,74			2145,03		2883,19		2983,28	2999,28			
Tsagan Agui	63	Pit 21/2; Layer 3; A19/1	183	17				indet.	1105,6			1443,73	1550,8		2131,09								digested
Tsagan Agui	64	Pit 21/2; Layer 3; A19/1	190	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,64	1198,65	1427,77			2145,14	2820,35	2883,42		2983,54	2999,55			
Tsagan Agui	65	Pit 21/2; rock cleaning; A19/4	44	17				indet.				1435											
Tsagan Agui	66	Pit 21/2; Layer 3; A19/3	147	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,65		1427,79			2145,17	2821,4	2883,5		2983,55	2999,58			
Tsagan Agui	67	Pit 21/2; Layer 2.2; A19/1	236	17	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,63	1427,75	1550,79		2145,1	2820,11	2884,24			2999,3			
Tsagan Agui	68	Pit 21/2; Layer 3; A19/3	151	20				failed															
Tsagan Agui	69	Pit 21/2; Layer 2.2; A19/4	164	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,59		1196,68	1427,8	1550,81	1649,8	2145,14	2820,38	2883,44	2899,43		2999,49			
Tsagan Agui	70	Pit 21/2; Layer 2.2; A19/3	109	18				indet.				1435											flat bone fragment
Tsagan Agui	71	Pit 21/2; Layer 2.2/3; A19/1	151	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,63	1199,66	1427,75			2145,19	2820,27	2883,41		2983,53	2999,53			
Tsagan Agui	72	Pit 21/2; Layer 2.2; A19/4	208	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,64		1427,74		1649,76	2145,11	2820,1	2883,15	2899,12		2999,28			digested

Tsagan Agui	73	Pit 21/2; Layer 2.1; A19/4	36	17	Artiodactyla	Bovidae	Ovis	Group_1	1105,64		1196,69	1427,79	1580,83	1648,89	2131,22	2792,63	2883,77	2899,76	3017,78	3033,81			
Tsagan Agui	74	Pit 21/2; Layer 2.2; A19/3	335	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,65		1427,77			2145,2	2821,66	2883,72		2983,85	2999,88			porous
Tsagan Agui	75	Pit 21/2; Layer 2.2; A19/1	775	21	Artiodactyla	Bovidae/Cervidae		Bovidae/Cervidae	1105,61	1180,68	1196,62	1427,78		1648,86	2131,13	2793,38	2883,44		3017,5	3033,58			fragment femur; gazelle, saiga, sheep, deer...
Tsagan Agui	76	Pit 21/2; Layer 2.2; A19/1	68	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66		1427,76			2145,06		2883,21		2984,29	2999,31			
Tsagan Agui	77	Pit 21/2; Layer 2.1; A21/1	191	22	Lagomorpha	Leporidae		Leporidae	1105,63		1221,7	1453,75			2129,06								
Tsagan Agui	78	Pit 21/2; Layer 2.1; A21/4	177	20	Artiodactyla	Bovidae	Ovis	Group_1	1105,65	1180,72	1196,7	1427,79		1648,87	2131,1	2792,29	2883,31	2900,37	3017,26	3033,41			
Tsagan Agui	79	Pit 21/2; Layer 2.1; A21/3	186	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,67	1198,68	1427,79		1649,85	2145,26	2820,77	2883,88	2899,9		2999,85			
Tsagan Agui	80	Pit 21/2; Layer 2.2; A19/3	122	18	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,61	1180,66	1196,73	1427,76		1648,86	2131,18				3017,82	3033,95			digested; flat bone fragment
Tsagan Agui	81	Pit 21/2; Layer 2.1; A19/4	144	21				indet.				1435											
Tsagan Agui	82	Pit 21/2; Layer 2.2; A19/2	211	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,67	1198,71	1427,81		1650,84	2145,23		2883,6		2983,73	2999,74			
Tsagan Agui	83	Pit 21/2; Layer 2.1; A20/1	985	17				failed															old test pit; hard bone, hole in the middle
Tsagan Agui	84	Pit 21/2; Layer 2.2; A19/2	226	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,67	1198,67	1427,81		1649,83	2145,38		2884,14		2984,2	3000,28			
Tsagan Agui	85	Pit 21/2; Layer 2.1; A 19/3	408	15	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,66	1198,68	1427,79	1550,87	1649,83	2145,36	2821,92	2884,04	2899,13					
Tsagan Agui	86	Pit 21/2; Layer 2.1; A 19/2	232	21	Carnivora	Ursidae	Ursus	Ursus sp.	1105,6	1218,56	1234,62	1453,78	1566,8		2163,03								digested; porous, <i>Ursus arctos</i> ?
Tsagan Agui	87	Pit 21/2; Layer 2.2; A19/4	152	18	Artiodactyla	Equidae	Equus	Equus sp.	1105,59	1182,62	1198,62	1427,76	1550,79	1649,79	2145,08	2820,32	2883,37	2899,35					
Tsagan Agui	88	Pit 21/2; Layer 2.2; A19/1	281	22	Carnivora	Felidae		Felidae	1105,59	1207,64		1453,74	1566,78	1610,79	2163,25	2820,6	2853,7	2869,71		2999,84			digested; cat or lynx
Tsagan Agui	89	Pit 21/2; Layer 2.2; A19/1	282	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,66	1198,65	1427,77	1551,78	1649,78	2145,04	2820,15	2883,24		2983,21	2999,25			
Tsagan Agui	90	Pit 21/2; Layer 2.2; A19/2	210	23	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,63	1221,68		1443,78	1550,82	1634,82	2131,09	2820,24	2883,29		2975,29	2991,32			
Tsagan Agui	91	Pit 21/2; Layer 2.2; A19/3	473	23	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,61	1221,67		1443,76	1550,79	1634,84	2131,08	2820,41	2883,49	2899,4					COL1a2_6 04-618: 1235
Tsagan Agui	92	Pit 21/2; Layer 2.2; A19/2	227	20	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,69	1196,68	1427,79	1580,83	1648,88	2131,14		2883,44		3017,51	3033,57			
Tsagan Agui	94	Pit 21/2; Layer 2.2; A19/2	111	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,67	1198,66	1427,79		1649,87	2145,18	2821,44	2883,49		2983,63	2999,65			

Tsagan Agui	95	Pit 21/2; Layer 2.1; A19/1	212	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,63		1427,74	1550,76		2145,01	2820,1	2883,17	2899,18	2983,29	2999,26			porous
Tsagan Agui	96	Pit 21/2; Layer 2.1; A19/1	184	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66		1427,8	1550,85	1650,83	2145,19	2820,42	2883,44	2899,45	2983,52	2999,55			porous
Tsagan Agui	97	Pit 21/2; Layer 2.2; A19/1	304	24				indet.				1435											
Tsagan Agui	98	Pit 21/2; Layer 2.1; A19/4	456	17				indet.				1435											digested
Tsagan Agui	99	Pit 21/2; Layer 2.2; A19/1	129	17	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,67	1427,79	1550,84	1649,88	2145,23	2820,61	2883,68	2899,67		2999,76			
Tsagan Agui	100	Pit 21/2; Layer 2.1; A19/4	398	18				failed															humerus epiphysis; embryon?
Tsagan Agui	101	Pit 21/2; Layer 2.1; A19/1	131	18				indet.				1435											
Tsagan Agui	102	Pit 21/2; Layer 2.1; A19/3	307	18	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,62	1221,68		1443,77	1550,8	1634,83	2131,05	2821,2	2883,23	2900,16	2975,33	2991,29		COL1a2_6 04-618: 1235	digested
Tsagan Agui	103	Pit 21/2; Layer 2.1; A19/3	67	14				indet.				1435											
Tsagan Agui	104	Pit 21/2; Layer 2.2; A19/2	355	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,67	1427,8	1550,85	1650,87	2145,33	2820,92	2884,03	2900,06		3000,24			fragment tooth
Tsagan Agui	105	Pit 21/2; Layer 2.2; A19/2	615	16	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,62	1180,69	1196,7	1427,79	1580,82	1648,87	2131,14	2792,38	2857,45		3017,44	3033,67			
Tsagan Agui	107	Pit 21/2; Layer 2.2; A19/1	167	17	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,58	1221,63		1443,72		1634,77	2131,09	2820,36	2883,43		2975,42	2991,54			digested
Tsagan Agui	109	Pit 21/2; Layer 2.1; A19/3	163	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,67	1427,81	1550,84	1649,88	2145,2	2820,41	2883,51		2983,59	2999,58			digested
Tsagan Agui	110	Pit 21/2; Layer 2.1; A19/1	68	20	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,61	1180,68	1196,67	1427,75	1580,79	1648,82	2131,1		2857,23		3017,7	3034,8			thin bone fragment
Tsagan Agui	111	Pit 21/2; Layer 2.1; A19/2	373	19	Artiodactyla	Bovidae		Bovidae	1105,63	1180,69	1196,7	1427,78	1580,82	1648,87	2131,2	2792,58			3018,75	3033,85			porous/parts powder, sheep or tibetan antelope
Tsagan Agui	113	Pit 21/2; Layer 1; G29/4	265	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,69	1198,68	1427,81	1550,84	1649,87	2145,25	2820,65	2883,75	2899,7		2999,8			
Tsagan Agui	114	Pit 21/2; barrow; D29/2	275	15	Artiodactyla	Bovidae	Ovis	Group_1	1105,64	1180,71	1196,7	1427,79	1580,84	1648,9	2131,24	2792,54	2883,71		3017,71	3033,89			
Tsagan Agui	115	Pit 21/2; G29/1	402	19				failed															
Tsagan Agui	116	Pit 21/2; Layer 1; D29/2	546	22				indet.				1435/1453			2134/2150								
Tsagan Agui	117	Pit 21/2; Layer 1; D29/2	363	14	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,43	1198,72	1427,83	1550,85	1649,84	2145,22	2820,47	2883,55			2999,68			
Tsagan Agui	118	Pit 21/2	119	18	Carnivora	Canidae		Canidae	1105,62	1210,67	1226,7	1453,74	1566,79		2131,04		2853,311						probably Vulpes
Tsagan Agui	119	Pit 21/2; Layer 1; G29/2	151	15				indet.				1435/1459			2134/2150								fragment vertebra

[illegible]

																								bone powder
Tsagan Agui	140	Pit 21/2; G29/3	128	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,62	1198,67	1427,69	1550,66	1649,58										I ph, right hind leg; bone powder
Tsagan Agui	141	Pit 21/2; G29/4	170	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,68	1427,71	1550,64	1649,58										II ph, right leg; bone powder
Tsagan Agui	142	Pit 21/2; G29/4	476	22	Rodentia	Castoridae	Castor	Castor sp.	1105,65	1177,65	1193,67	1427,74	1576,67		2130,2									
Tsagan Agui		Pit 21/2; G29/1	708	20				indet.	1105,61	1177,59		1427,69			2130,11									could be Castor (but not enough marker)
Tsagan Agui	143																							
Tsagan Agui	144	Pit 21/2; D29/4	310	16				indet.				1453			2128									metatarsal
Tsagan Agui	145	Pit 21/2; G29/2	252	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,67	1198,66	1427,71	1550,66	1649,56							2958,1			
Tsagan Agui	146	Pit 21/2; D29/2	293	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,68	1427,7	1550,64	1649,54		2821,51					2957,16			hip bone juv., porous
Tsagan Agui		Pit 21/2; G29/1	292	18				indet.				1453			2128									
Tsagan Agui	147																							
Tsagan Agui	148	Pit 21/2; G29/4	577	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,65	1427,67	1550,61	1649,52										metatarsal
Tsagan Agui	149	Pit 21/2; G29/2	133	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,69	1427,72	1550,65	1649,58										fragment rib
Tsagan Agui	150	Pit 21/2; D29/3	524	25	Rodentia	Castoridae	Castor	Castor sp.	1105,59	1177,59	1193,68	1427,66			2130,1									
Tsagan Agui		Pit 21/2; G29/4	446	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,68	1198,68	1427,75	1550,65	1649,58										fragment rib
Tsagan Agui	151																							
Tsagan Agui	152	Pit 21/2; G29/1	680	24	Rodentia	Castoridae	Castor	Castor sp.	1105,64	1177,64		1427,73	1576,69		2130,18									
Tsagan Agui	153	Pit 21/2; depth 234	165	25	Rodentia	Castoridae	Castor	Castor sp.	1105,61	1177,61	1193,6	1427,69	1577,66		2129,16						2999,99			wall Entrance Grotto
Tsagan Agui	154	Pit 21/2; Layer 4; A19/2						not found																fragment III ph with hyaena gnwanings ; sample is missing
Tsagan Agui		Pit 21/2; G29/1	565	25	Rodentia	Castoridae	Castor	Castor sp.	1105,63	1177,63		1427,72	1577,69		2130,18									
Tsagan Agui	155																							
Tsagan Agui	156	Pit 21/2; G29/1	348	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,68	1182,78	1198,78	1427,99	1551,02	1650,05	2145,02									fragment rib
Tsagan Agui	157	Pit 21/2; G29/3	221	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,68	1182,77	1198,79	1427,99	1551,02	1650,04	2145,01						2983,92			fragment rib
Tsagan Agui	158	Pit 21/2; G29/1	185	20	Rodentia	Castoridae	Castor	Castor sp.	1105,64	1177,61	1193,58	1427,71	1576,65		2130,14						2999,03			
Tsagan Agui		Pit 21/2; G29/3	92	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,66	1427,69	1550,62	1649,56										fragment rib juv.,

[illegible]

Tsagan Agui		Pit 21/2; Layer 5/6; A19/1	254	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67		1427,71			2146,12							
Tsagan Agui	180	Pit 21/2; Layer 5; A19/3	297	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,65	1198,64	1427,73	1550,64	1649,55								
Tsagan Agui	181	Pit 21/2; Layer 5/6; A19/1	394	25				indet.		1221,64		1444,67			2132,08						COL1a2_6 04-618: 1235	could be Camelus (but not enough marker)
Tsagan Agui	182	Pit 21/2; Layer 1.3; A19/4	866	19				failed														hard, porous
Tsagan Agui		Pit 21/2; Layer 5; A19/3	220	22				indet.				1453			2128							
Tsagan Agui	183																					
Tsagan Agui	184	Pit 21/2; Layer 6; A19/4	297	23				failed														
Tsagan Agui	185	Pit 21/2; Layer 5; A19/3	1543	20				indet.				1453			2128							fragment upper mandible and teeth
Tsagan Agui	186	Pit 21/2; Layer 5; A19/3	1271	19	Charadriiformes	Laridae	Bird	Bird	1162,67	1221,69		1463,72			2149,93						COL1a1 238-318: 1306,66 COL1a1 295-309: 1393,68 COL1a1 688-704: 1459,68 COL1a1 220-237: 1572,67	
Tsagan Agui		Pit 21/2; Layer 5; A19/3	1696	19				indet.				1453			2158							
Tsagan Agui	187																					
Tsagan Agui	188	Pit 21/2; Layer 5; A19/3	194	23				indet.														fragment os sacrum
Tsagan Agui	189	Pit 21/2; Layer 5; A19/1	637	22				indet.				1453			2128							
Tsagan Agui	190	Pit 21/2; Layer 2.2; A19/4	187	23				failed														
Tsagan Agui		Pit 21/2; Layer 5; A19/2	57	17	Rodentia	Castoridae	Castor	Castor sp.	1105,62	1177,66		1427,7	1576,64									fragments mandible
Tsagan Agui	191																					
Tsagan Agui	192	Pit 21/2; Layer 5; A19/2	698	24				indet.				1453			2158							
Tsagan Agui	193	Pit 21/2; Layer 5; A19/4	710	19				failed														
Tsagan Agui	194	Pit 21/2; Layer 5; A19/2	751	25				indet.				1453			2128							
Tsagan Agui		Pit 21/2; Layer 5; A19/3	739	18				indet.				1453			2128							cleaning
Tsagan Agui	195																					
Tsagan Agui	196	Pit 21/2; Layer 5; A19/3	464	25	Rodentia	Castoridae	Castor	Castor sp.	1105,62	1177,62		1427,71	1576,68		2130,16							

Tsagan Agui	197	Pit 21/2; Layer 5; A19/4	1461	24				indet.					1453			2158							
Tsagan Agui	198	Pit 21/2; Layer 5; A19/3	1198	23				indet.					1453			2158							
Tsagan Agui	199	Pit 21/2; Layer 4; A19/1	2142	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,71	1198,68	1427,72										digested	
Tsagan Agui	200	Pit 21/2; Layer 5; A19/2	223	18	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,69	1221,82		1443,99	1550,06		2131,01	2820,03							
Tsagan Agui	201	Pit 21/2; Layer 5/6; A19/3	598	23	Charadriiformes	Laridae	Bird	Bird	1162,67	1221,73		1463,71									COL1a1 295-309: 1393,94 COL1a1 688 - 704: 1459,97 COL1a1 220 - 237: 1573,03		
Tsagan Agui	202	Pit 21/2; Layer 5; A19/2	262	23				failed														cleaning; fragment ph	
Tsagan Agui	203	Pit 21/2; Layer 5; A19/3	774	19				indet.	1105,62	1177,6		1427,69			2130,11							not enough marker for identification, but maybe Castor sp.	
Tsagan Agui	204	Pit 21/2; Layer 5; A19/2	2684	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,65	1198,67	1427,7	1649,65										
Tsagan Agui	205	Pit 21/2; Layer 5/6; A19/1	1438	19				indet.				1453			2158								
Tsagan Agui	206	Pit 21/2; Layer 5/7; A19/4	67	17	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,63	1221,7		1443,71	1634,65								COL1a2_6 04-618: 1235		
Tsagan Agui	207	Pit 21/2; Layer 5; A19/3	663	24	Charadriiformes	Laridae	Bird	Bird	1162,65	1221,71											COL1a1 238-318: 1306,61 COL1a1 295-309: 1393,67 COL1a1 688 - 704: 1459,66 COL1a1 220 - 237: 1572,64 COL1a2 10 - 42: 3113,81		
Tsagan Agui	208	Pit 21/2; Layer 5/6; A19/1	205	26				indet.				1453			2128								
Tsagan Agui	209	Pit 21/2; Layer 5; A19/1	607	18				indet.				1453			2142								
Tsagan Agui	210	Pit 21/2; Layer 5; A19/3	122	25				indet.	1105,63	1177,64		1427,72			2130,17							not enough marker for identification, but	

																						maybe Castor sp.
Tsagan Agui	211	Pit 21/2; Layer 5; A19/3	1260	22				indet.														
Tsagan Agui	212	Pit 21/2; Layer 2.1; A20/1	3008	26	Charadriiformes	Laridae	Bird	Bird	1162,72	1221,82		1463,68			2149,82						COL1a1 238-318: 1306,61 COL1a1 295-309: 1393,65 COL1a1 688-704: 1459,64 COL1a1 220-237: 1572,62	old test pit
Tsagan Agui	213	Pit 21/2; Layer 5; A19/3	202	26				indet.	1105,64			1427,71			2130,12							not enough marker for identification, but maybe Castor sp.
Tsagan Agui	214	Pit 21/2; Layer 5; A19/1	2167	23				failed														
Tsagan Agui	215	Pit 21/2; Layer 5/6; A19/4	118	24				failed														
Tsagan Agui	216	Pit 21/2; Layer 4; A19/3	1710	24				failed														
Tsagan Agui	217	Pit 21/2; Layer 4; A19/1	1019	21	Lagomorpha	Leporidae		Leporidae	1105,62		1221,67	1453,81			2129,25		2883,74	2900,8	2957,88			
Tsagan Agui	218	Pit 21/2; Layer 5; A19/3	84	19	Lagomorpha	Leporidae		Leporidae	1105,61		1221,69	1453,71			2129,17	2809,49	2883,68		2957,75			
Tsagan Agui	219	Pit 21/2; Layer 5; A19/4	1602	23				indet.				1453			2158							
Tsagan Agui	220	Pit 21/2; Layer 5; A19/1	106	20	Rodentia	Muridae	Rattus	Rattus sp.	1105,6			1453,77	1593,82		2143,17		2883,52	2899,56				<i>Rattus rattus</i> or <i>Rattus norvegicus</i>
Tsagan Agui	221	Pit 21/2; Layer 5; A19/1	661	26	Lagomorpha	Leporidae		Leporidae	1105,63		1221,69	1453,8	1566,86/159 2,86		2129,2	2808,47	2883,64	2899,63	2957,73			COL1a2 604 - 618: 1235
Tsagan Agui	222	Pit 21/2; Layer 5; A19/1	651	22	Lagomorpha	Leporidae		Leporidae	1105,64		1221,71	1453,82			2129,23	2809	2883,62	2899,67	2957,76			vertebra; <i>Lepus</i> sp. or <i>Oryctolagus cuniculus</i>
Tsagan Agui	223	Pit 21/2; Layer 4; A19/1	/	/				not found														empty tube
Tsagan Agui	224	Pit 21/2; Layer 4; A19/2	11	11	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,62	1199,64	1427,72		1649,79	2145,11	2820,46	2883,52		2984,64	2999,65		bone powder
Tsagan Agui	225	Pit 21/2; Layer 2.2; A19/4	12	12	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,71	1427,82	1550,85	1649,83	2145,21	2820,49	2883,59		2983,69	2999,7		bone powder

Tsagan Agui	226	Pit 21/2; Layer 4; A19/2	21	11	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,63	1198,63	1427,75	1550,79	1649,8	2145,13	2820,44	2883,53	2900,53	2983,65	2999,65			bone powder
Tsagan Agui	227	Pit 21/2; Layer 2.1; A19/4	17	17	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,63	1427,75	1550,8	1649,78	2145,17	2820,47	2883,57	2899,58		3000,8			bone powder
Tsagan Agui	228	Pit 21/2; Layer 5; A19/1	12	12	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,6	1221,67		1443,75	1550,79	1634,83	2131,12	2820,45	2883,55	2899,55	2975,61	2991,64		COL1a2 604 - 618: 1235	digested; bone powder
Tsagan Agui	229	Pit 21/2; surface	211	19	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,59	1221,66		1443,74	1550,79	1634,81	2131,12	2820,47	2883,57	2900,55		2991,69		COL1a2 604 - 618: 1235	
Tsagan Agui	230	Pit 21/2; Layer 3; A19/3	165	21				indet.	1105,6			1443,77			2131,13								could be Camelus (but not enough marker)
Tsagan Agui	231	Pit 2; Layer 5; A18/4	224	24				indet.															
Tsagan Agui	232	Pit 2; Layer 5; B19/3	118	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,67	1198,68	1427,81		1649,85	2145,23	2820,51	2883,62	2900,62	2983,66	2999,73			digested splint bone MTIV dex
Tsagan Agui	233	Pit 2; Layer 5; B19/4	381	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,66	1182,7	1198,69	1427,83	1550,88	1649,88	2145,26		2883,69		2983,82	2999,84			
Tsagan Agui	234	Pit 2; Layer 5; A18/1	185	24	Artiodactyla	Bovidae	Ovis	Group_1	1105,61	1180,61	1196,66	1427,77	1580,81	1648,86	2131,16	2792,51	2883,58		3017,64	3033,7			epiphysis of vertebra; chamois or sheep
Tsagan Agui	235	Pit 2; Layer 5; B19/3	303	25				failed															
Tsagan Agui	236	Pit 2; Layer 5; B18/1	280	24	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,69	1196,71	1427,79	1580,82		2131,16	2793,41	2883,53	2899,53	3017,58	3033,64			
Tsagan Agui	237	Pit 2; Layer 3; A18/1	208	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,65	1427,77	1551,82	1649,83	2145,16		2883,54		2983,56	2999,64			
Tsagan Agui	238	Pit 2; Layer 3; B19/4	280	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,62		1427,74		1649,79	2145,13		2883,54			2999,64			
Tsagan Agui	239	Pit 2; Layer 3; B19/1	322	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,65	1427,77		1649,81	2145,15		2884,52		2983,66	2999,69			teeth
Tsagan Agui	240	Pit 2; Layer 3; B19/4	114	22	Artiodactyla	Bovidae		Bovidae	1105,62	1150/1166	1166/1182	1427,78	1550,81	1648,86	2131,16	2793,42	2883,58		3017,62	3033,68	1532		just animals native in africa as result: waterbuck, kob, kirk's dik-dik and grey rhebok?
Tsagan Agui	241	Pit 2; Layer 4; B19/1	341	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,67	1427,8		1649,86	2145,17	2821,36	2883,46		2983,55	2999,57			digested
Tsagan Agui	242	Pit 2; Layer 5; B19/1	349	23				failed															digested
Tsagan Agui	243	Pit 2; Layer 5; B19/1	938	16	Carnivora	Felidae		Felidae	1105,59	1207,63		1453,76	1566,79		2163,08		2853,39	2869,42		2999,48			digested; Felis catus or Lynx sp.
Tsagan Agui	244	Pit 2; Layer 4; B19/3	6309	23	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,66	1196,69	1427,79	1580,85	1648,88	2131,13	2792,36	2883,44	2899,42	3017,42	3033,51			digested

Tsagan Agui	245	Pit 2; Layer 5; B19/2	359	26	Rodentia	Castoridae	Castor	Castor sp.	1105,63	1177,64		1427,81	1576,87		2129,26		2883,5		2983,55	2999,58			digested
Tsagan Agui	246	Pit 2; Layer 4; B19/4	3266	26	Artiodactyla	Bovidae	Ovis	Group_1	1105,65	1180,71	1196,73	1427,84	1580,89	1648,93	2131,23		2883,54		3017,47	3033,57			digested
Tsagan Agui		Pit 2; Layer 5; B19/1	1296	21	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,62	1182,66	1198,71	1453,81			2145,17		2869,43		2983,53	2999,59			digested
Tsagan Agui	247																						
Tsagan Agui	248	Pit 2; Layer 4; B18/1	344	22	Artiodactyla	Bovidae	Ovis	Group_1	1105,59	1180,66	1196,67	1427,76	1580,83	1648,87	2131,14	2792,36	2883,46	2899,41	3017,45	3033,53			digested
Tsagan Agui	249	Pit 2; Layer 4; A18/1	182	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66	1198,68	1427,8	1550,85	1649,88	2145,2	2820,44	2883,53	2899,52	2983,62	2999,63			digested
Tsagan Agui	250	Pit 2; Layer 5; B19/2	616	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,7	1198,72	1427,84	1550,89	1649,89	2145,23	2820,45	2883,57	2899,55	2983,57	2999,62			digested
Tsagan Agui		Pit 2; Layer 4; B19/2	1798	22	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,63	1182,7	1198,68	1453,83	1550,86		2145,21		2869,5	2885,48	2983,62	2999,62			digested; Coelodont a antiquitatis?
Tsagan Agui	251																						
Tsagan Agui	252	Pit 2; Layer 5; B18/1	548	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,67	1427,81		1649,86	2145,2	2820,4	2883,52	2899,45	2983,58	2999,6			digested
Tsagan Agui	253	Pit 2; Layer 5; A18/1	1938	20	Artiodactyla	Bovidae	Ovis	Group_1	1105,58	1180,65	1196,66	1427,73	1580,77	1648,83	2131,1	2793,42	2883,56	2899,52	3018,58	3033,69			digested
Tsagan Agui	254	Pit 2; Layer 4; B19/1	1094	18	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,61	1221,67		1443,77	1550,82	1634,85	2131,13	2820,43	2883,51	2900,46	2975,61	2991,58		COL1a2 604 - 618: 1235	digested
Tsagan Agui		Pit 2; Layer 5; B19/3	380	25				failed															digested
Tsagan Agui	255																						
Tsagan Agui	256	Pit 2; Layer 5; B19/1	891	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,72	1199,65	1427,83	1550,87	1649,9	2145,21	2820,49	2883,57		2983,67	2999,69			digested
Tsagan Agui	257	Pit 2; Layer 5; B19/4	629	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,64	1427,76		1649,83	2145,17	2820,51	2883,59	2899,59	2983,7	2999,73			digested
Tsagan Agui	258	Pit 2; Layer 5; B18/1	523	22	Artiodactyla	Bovidae	Bos sp. sp.	Bos sp.	1105,63	1192,74	1208,74	1427,8	1580,84	1648,91	2131,2	2793,54	2853,6	2870,59	3018,66	3033,77	1532		digested
Tsagan Agui		Pit 2; Layer 4; B19	741	19	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,67	1196,69	1427,78	1580,83		2131,16	2792,46	2883,58	2899,57	3017,63	3033,72			digested
Tsagan Agui	259																						
Tsagan Agui	260	Pit 2; Layer 5; A18/1	1285	26	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,65	1221,72		1443,83		1634,93	2131,24	2820,54	2883,65	2899,61	2975,77	2991,73			digested
Tsagan Agui	261	Pit 2; Layer 5; A18/4	1176	23	Artiodactyla	Bovidae		Bovidae	1105,61	1150/1166	1166/1182	1427,77		1648,86	2131,16	2793,45	2883,59	2899,58	3017,64	3033,71	1532		digested; just animals native in africa as result: waterbuck, kob, kirk's dik-dik and grey rhebok?
Tsagan Agui	262	Pit 2; Layer 4; B19/1	1150	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,65	1427,77		1649,83	2145,18	2821,51	2883,59		2983,65	2999,71			digested
Tsagan Agui		Pit 2; Layer 5; B19/2	1919	26				failed															digested
Tsagan Agui	263																						
Tsagan Agui	264	Pit 2; Layer 5; B19/2	241	20	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,62	1221,67		1443,76		1634,85	2131,15	2820,49	2883,58		2975,68	2991,68			digested

Tsagan Agui	265	Pit 2; Layer 2.1/2.2; B18/2	1881	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,67	1427,78		1649,85	2145,18	2820,51	2883,59	2899,62	2983,71	2999,72			digested; wall crash
Tsagan Agui	266	Pit 2; Layer 4; B18/1	2754	22	Artiodactyla	Bovidae	<i>Bos sp.</i>	Bos sp.	1105,61	1180,62	1208,72	1427,79	1580,81	1648,89	2131,17	2792,4	2853,52		3017,53	3033,66	1532		digested
Tsagan Agui	267	Pit 2; Layer 4; A18/1	781	23				indet.															digested
Tsagan Agui	268	Pit 2; Layer 4; B19/2	1972	24	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,65	1180,73	1196,72	1427,83	1580,88	1648,94	2131,26			3017,8	3033,84				digested
Tsagan Agui	269	Pit 2; Layer 4; B18/1	1732	26				indet.															digested
Tsagan Agui	270	Pit 2; Layer 4; B19/3	3117	26	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,65	1221,71		1443,81	1550,85	1634,9	2131,23		2883,66		2975,76	2991,77		COL1a2 604 - 618: 1235	digested
Tsagan Agui	271	Pit 2; Layer 4; B19/3	904	25	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,65	1221,72		1443,82		1634,91	2131,22	2820,53	2883,58		2975,69	2991,71			digested
Tsagan Agui	272	Pit 2; Layer 4; B19/3	1385	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,67	1182,72	1198,7	1427,86		1649,91	2145,28	2820,57	2883,65	2899,67	2983,74	2999,76			digested
Tsagan Agui	273	Pit 2; Layer 4; B19/3	1389	26	Carnivora	Hyaenidae/Felidae		Hyaenidae/Felidae	1105,6	1207,65		1453,77			2147,14		2853,56	2869,58	2983,7	2999,7			digested; lion, tiger or hyaena
Tsagan Agui	274	Pit 2; Layer 4; B19/2	1008	20	Artiodactyla	Bovidae	Ovis	Group_1	1105,64	1180,7	1196,7	1427,81	1580,88	1648,9	2131,2	2792,47	2883,63	2899,65	3017,7	3033,76			digested
Tsagan Agui	275	Pit 2; Layer 4; B19/2	8464	24	Artiodactyla	Bovidae	Ovis	Group_1	1105,64	1180,69	1196,72	1427,79	1580,86	1648,89	2131,18	2793,46	2883,58	2899,57	3017,73	3033,73			digested
Tsagan Agui	276	Pit 2; Layer 4; B18/3	741	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,68	1427,79		1649,85	2145,19	2820,52	2883,63		2983,7	2999,72			digested
Tsagan Agui	277	Pit 2; Layer 4; B19/1	1968	22	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,68	1196,7	1427,79	1580,85	1648,88	2131,18	2792,48	2883,56		3017,6	3033,64			digested
Tsagan Agui	278	Pit 2; Layer 4; B19/1	4190	20	Artiodactyla	Bovidae/Cervidae		Bovidae/Cervidae	1105,65	1180,71	1196,72	1427,82		1648,93	2131,24	2792,56	2883,69	2899,71	3017,7	3033,84			digested
Tsagan Agui	279	Pit 2; Layer 4; B19/3	1012	22	Artiodactyla	Bovidae	Ovis	Group_1	1105,61	1180,66	1196,67	1427,76	1580,81	1648,85	2131,12	2793,4	2883,51	2899,51	3017,57	3033,65			digested
Tsagan Agui	280	Pit 2; Layer 4; B19/2	258	24	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,66	1221,72		1443,83		1634,91	2131,24	2820,58	2883,67			2991,77			digested
Tsagan Agui	281	Pit 2; Layer 5; B19/2	553	21	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,67	1182,71	1198,7	1453,84	1550,88		2145,27		2869,67	2885,73	2983,8	2999,81			digested; <i>Coeladonta antiquitatis</i> ?
Tsagan Agui	282	Pit 2; Layer 5; B18/2	914	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,67	1182,73	1198,69	1427,85		1649,92	2145,28	2821,48	2883,71		2983,79	2999,82			digested
Tsagan Agui	283	Pit 2; Layer 4; B19/4	3516	22	Artiodactyla	Bovidae	<i>Bos sp.</i>	Bos sp.	1105,64	1192,74	1208,75	1427,81	1580,84		2131,2	2793,49	2853,59		3017,68	3033,72			digested
Tsagan Agui	284	Pit 2; Layer 4; A18/1	336	26	Artiodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,65	1427,77	1550,81	1649,84	2145,19	2820,53	2883,62		2983,73	2999,76			digested
Tsagan Agui	285	Pit 2; Layer 2.1; B18/1	462	19	Artiodactyla	Equidae	Equus	Equus sp.	1105,63	1182,67	1198,69	1427,8		1649,87	2145,22	2820,6	2883,68	2899,62	2983,8	2999,8			digested

Tsagan Agui	286	Pit 2; Layer 2.1; B18/1	1509	23	Artiodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,64	1427,78	1550,81	1649,82	2145,16	2821,46	2883,55		2983,65	2999,66			digested
Tsagan Agui	287	Pit 2; Layer 2.2; B19/3	388	22	Artiodactyla	Equidae	Equus	Equus sp.	1105,63	1182,69	1198,68	1427,79		1649,84	2145,16	2821,47	2883,54		2983,66	2999,66			digested
Tsagan Agui	288	Pit 2; Layer 2.1; B19/4	474	23	Artiodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,66	1427,77	1550,84	1649,84	2145,18	2820,49	2883,59		2983,7	2999,71			digested
Tsagan Agui	289	Pit 2; Layer 2.1; B19/3	961	25	Artiodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66	1198,66	1427,78	1550,82	1649,82	2145,19	2820,54	2883,6		2983,72	2999,74			digested
Tsagan Agui	290	Pit 2; Layer 2.1; B18/1	893	21	Artiodactyla	Equidae	Equus	Equus sp.	1105,59	1182,63	1198,61	1427,73	1550,76	1649,8	2145,13	2820,44	2883,53	2899,52	2983,67	2999,67			digested
Tsagan Agui	291	Pit 2; Layer 2.1; B19/4	144	21	Artiodactyla	Equidae	Equus	Equus sp.	1105,66	1182,72	1198,72	1427,85	1550,91	1649,92	2145,29	2820,66	2883,74		2983,59	2999,65			digested
Tsagan Agui	292	Pit 2; Layer 2.1; A18/2	548	21				indet.															digested
Tsagan Agui	293	Pit 2; Layer 2.1; B19/1	266	23	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,66	1221,71		1443,83	1550,86	1634,9	2131,24	2820,64	2883,7		2975,81	2991,79		COL1a2 604 - 618: 1235	digested
Tsagan Agui	294	Pit 2; Layer 2.1; B19/3	128	22	Artiodactyla	Bovidae	Bos sp.	Bos sp.	1105,6	1192,7	1208,71	1427,76	1580,81	1648,86	2131,13	2792,41	2853,52	2869,5	3017,57	3033,66	1532		digested
Tsagan Agui	295	Pit 2; Layer 2.1; B19/4	183	21	Artiodactyla	Bovidae	Bos sp.	Bos sp.	1105,61	1192,7	1208,7	1427,76	1580,8	1648,85	2131,13	2792,43	2853,51	2869,49	3017,56	3033,65	1532		digested
Tsagan Agui	296	Pit 2; Layer 2.1; A18/2	1086	21	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,62	1221,67		1443,76	1550,79	1634,83	2131,14	2820,47	2883,58	2899,6	2975,66	2991,69			digested
Tsagan Agui	297	Pit 2; Layer 2.1; B19/4	143	21	Artiodactyla	Bovidae	Bos sp.	Bos sp.	1105,6	1192,7	1208,7	1427,75	1580,79	1648,84	2131,12	2792,43	2853,53	2869,33	3017,64	3033,68	1532		digested
Tsagan Agui	298	Pit 2; Layer 2.1; B19/1	82	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,64	1198,64	1427,76	1550,79	1649,81	2145,17	2820,49	2883,59	2899,56	2983,7	2999,7			digested
Tsagan Agui	299	Pit 2; Layer 2.1; A18/2	420	21				indet.															digested
Tsagan Agui	300	Pit 2; Layer 2.1; B19/2	433	24				indet.															digested
Tsagan Agui	301	Pit 2; Layer 2.1; B19/1	566	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,66	1427,7	1550,86	1649,84	2145,17	2820,44	2883,53	2899,53	2983,62	2999,64			digested
Tsagan Agui	302	Pit 2; Layer 5; B18/1	712	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,67	1198,69	1427,79			2145,21	2820,54	2883,65	2899,64	2983,76	2999,78			digested
Tsagan Agui	303	Pit 2; Layer 3; A18/1	1025	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,62	1198,64	1427,72		1649,78	2145,09	2821,4	2883,5		2983,64	2999,62			digested
Tsagan Agui	304	Pit 2; Layer 3; B19/4	2079	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,7	1198,69	1427,82		1649,87	2145,23	2820,54	2883,65		2983,76	2999,77			3 different ziplock bags
Tsagan Agui	305	Pit 2; Layer 3; B19/2	251	21				indet.															digested
Tsagan Agui	306	Pit 2; Layer 4; B19/1	1805	22	Lagomorpha	Leporidae		Leporidae	1105,6		1221,68	1453,77	1567/1593		2129,17		2883,55	2899,58	2957,69			COL1a2 604 - 618: 1235	digested; Lepus sp. or <i>Oryctolagus cuniculus</i>
Tsagan Agui	307	Pit 2; Layer 3; B19/2	1419	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,69	1427,8		1649,85	2145,2	2820,54	2883,57		2983,72	2999,7			digested

Tsagan Agui	308	Pit 2; Layer 3; B19/4	249	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66	1198,67	1427,78		1649,87	2145,16	2820,47	2883,52	2899,53	2983,59	2999,66			digested
Tsagan Agui	309	Pit 2; Layer 3; B19/4	607	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,69	1198,7	1427,8	1550,85	1649,86	2145,2	2820,52	2883,55	2899,61	2983,69	2999,69			digested
Tsagan Agui	310	Pit 2; Layer 3; B19/3	3515	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,65	1427,78		1649,85	2145,17	2820,47	2883,56	2899,53	2983,68	2999,68			digested
Tsagan Agui	311	Pit 2; Layer 3; B19/1	2485	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,65	1427,78		1649,84	2145,17	2820,45	2883,54	2899,53	2983,64	2999,66			digested
Tsagan Agui	312	Pit 2; Layer 3; B19/3	2759	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,68	1427,8		1649,87	2145,2	2820,52	2883,6		2983,74	2999,72			digested
Tsagan Agui	313	Pit 2; Layer 3; B19/4	1775	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,66	1427,79		1649,85	2145,18	2820,48	2883,56		2983,67	2999,68			digested
Tsagan Agui	314	Pit 2; Layer 3; B19/1	2116	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,63	1198,69	1427,74		1649,81	2145,13	2820,44	2883,54		2983,68	2999,67			digested
Tsagan Agui	315	Pit 2; Layer 3; A18/1	911	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,66	1182,71	1198,71	1427,83		1649,91	2145,26	2820,59	2883,7	2900,71	2983,79	2999,82			digested
Tsagan Agui	316	Pit 2; Layer 3; A18/1	799	24	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,6	1221,67		1443,76		1634,85	2131,15	2820,48	2883,57	2899,53	2975,62	2991,67			digested
Tsagan Agui	317	Pit 2; Layer 3; A18/1	967	20	Artiodactyla	Bovidae	Bos sp. sp.	Bos sp.	1105,62	1192,7	1208,71	1427,77	1580,83	1648,86	2131,15	2792,43	2853,57	2869,59	3017,66	3033,72			digested
Tsagan Agui	318	Pit 2; Layer 3; B19/4	1817	25	Lagomorpha	Leporidae		Leporidae	1105,62		1221,68	1453,8	1592,85		2129,2		2883,57	2899,57	2957,67				digested; Lepus sp. or Oryctolagus cuniculus
Tsagan Agui	319	Pit 2; Layer 3; B19/3	411	23	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,61	1182,65	1198,66	1453,79			2145,17		2869,55	2885,54	2983,7	2999,7			digested
Tsagan Agui	320	Pit 2; Layer 3; B19/1	642	24	Artiodactyla	Bovidae		Bovidae	1105,62	1150/1166	1166/1182	1427,75	1550,79	1648,84	2131,14	2792,45	2883,59	2899,57	3017,7	3033,74	1532		digested; just animals native in africa as result: waterbuck, kob, kirk's dik-dik and grey rhebok?
Tsagan Agui	321	Pit 2; Layer 3; B19/2	863	20	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,61	1221,66		1443,75	1550,8	1634,84	2131,14	2820,47	2883,57	2899,51	2975,73	2991,68			digested
Tsagan Agui	322	Pit 2; Layer 3; B19/4	4433	24	Artiodactyla	Bovidae	Ovis	Group_1	1105,63	1180,7	1196,72	1427,79	1580,84		2131,18	2792,47	2883,58	2899,63	3017,64	3033,7			digested
Tsagan Agui	323	Pit 2; Layer 3; B19/4	205	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66	1198,68	1427,78		1649,84	2145,18	2820,5	2883,57	2899,55	2983,65	2999,7			digested
Tsagan Agui	324	Pit 2; Layer 3; B19/4	191	25	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,59	1221,65		1443,74		1634,82	2131,1	2820,36	2883,46	2899,47	2975,53	2991,55		COL1a2 604 - 618: 1235	digested
Tsagan Agui	325	Pit 2; Layer 3; A19/3	203	22	Artiodactyla	Bovidae	Ovis	Group_1	1105,61	1180,67	1196,69	1427,78	1580,8	1648,86	2131,14	2793,39	2883,49	2899,46	3017,52	3033,59			digested
Tsagan Agui	326	Pit 2; Layer 3; B19/4	282	20				indet.															digested
Tsagan Agui	327	Pit 2; Layer 3; B19/2	1113	26	Artiodactyla	Bovidae/Cervidae		Bovidae/Cervidae	1105,63	1180,69	1196,72	1427,81		1648,9	2131,2	2792,47	2883,59	2899,6	3017,62	3033,69			digested

Tsaga an Agui	328	Pit 2; Layer 3; B19/3	2416	23	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,61	1221,67		1443,77	1550,8	1634,84	2131,14	2820,45	2883,52		2991,61			COL1a2 604 - 618: 1235	digested
Tsaga an Agui	329	Pit 2; Layer 3; A18/1	2258	27	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,64	1221,69		1443,79		1634,88	2131,17	2820,39	2883,52		2975,56	2991,6			digested
Tsaga an Agui	330	Pit 2; Layer 3; A18/1	402	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,68	1427,79		1649,85	2145,17	2820,46	2883,54		2983,66	2999,66			digested
Tsaga an Agui		Pit 2; Layer 3; B19/4	1333	27	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,64	1198,62	1427,77	1550,82	1649,79	2145,13	2820,43	2883,46		2983,58	2999,6			digested
Tsaga an Agui	332	Pit 2; Layer 3; A18/1	1509	24				indet.														digested	
Tsaga an Agui	333	Pit 2; Layer 3; A18/1	161	17	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,62	1198,6	1427,74		1649,77	2145,11	2820,41	2883,52		2983,61	2999,62			digested
Tsaga an Agui	334	Pit 2; Layer 3; B19/3	290	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,64	1427,76	1550,8	1649,82	2145,14	2820,44	2883,52	2899,56	2983,62	2999,65			digested
Tsaga an Agui		Pit 2; Layer 2.2; B19/2	336	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66	1198,67	1427,79	1550,82	1649,86	2145,18	2820,44	2883,52	2900,47	2983,62	2999,62			digested
Tsaga an Agui	336	Pit 2; Layer 2.2; B19/2	556	19	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,64	1221,71		1443,81		1634,9	2131,2	2820,52	2883,6	2899,65	2975,67	2991,68			digested
Tsaga an Agui	337	Pit 2; Layer 2.2; B19/2	887	21	Artiodactyla	Bovidae	Bos sp. sp.	Bos sp.	1105,64	1192,73	1208,75	1427,81	1580,84	1648,9	2131,19	2792,42	2853,52	2869,38	3017,59	3033,67	1532		digested
Tsaga an Agui	338	Pit 2; Layer 2.2; B19/3	838	24	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,6	1221,66		1443,75	1551,82	1634,82	2131,11	2820,38	2883,48		2975,56	2991,58			digested
Tsaga an Agui		Pit 2; Layer 2.2; B19/2	516	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,66	1182,69	1198,7	1427,85	1550,89	1649,89	2145,27	2820,59	2883,69	2899,7	2983,67	2999,77			digested
Tsaga an Agui	340	Pit 2; Layer 2.2; B19/3	355	28	Artiodactyla	Bovidae	Bos sp. sp.	Bos sp.	1105,65	1192,71	1208,75	1427,82	1580,86	1648,92	2131,23	2792,43	2853,58		3017,61	3033,67	1532		digested
Tsaga an Agui	341	Pit 2; Layer 2.2; A18/2	636	22	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,59	1182,64	1198,62	1453,77	1550,83		2145,13		2869,47		2983,59	2999,58			digested
Tsaga an Agui	342	Pit 2; Layer 2.2; B19/2	554	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,65	1198,65	1427,78	1550,81	1649,81	2145,15	2820,43	2883,5	2899,49					digested
Tsaga an Agui		Pit 2; Layer 2.2; B19/2	873	24	Artiodactyla	Bovidae/Cervidae		Bovidae/Cervidae	1105,62	1180,67	1196,68	1427,78		1648,87	2131,12		2883,46	2899,46	3017,5	3033,57			digested
Tsaga an Agui	344	Pit 2; Layer 2.2; B19/3	554	24	Artiodactyla	Bovidae	Ovis	Group_1	1105,57	1180,63	1196,65	1427,73	1580,75	1648,82	2131,07	2792,28	2883,4	2899,39	3017,37	3033,5			digested
Tsaga an Agui	345	Pit 2; Layer 2.2; B19/2	171	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,64	1427,77	1550,8	1649,79	2145,16	2820,46	2883,55	2899,61	2983,66	2999,65			digested
Tsaga an Agui	346	Pit 2; Layer 2.2; A18/4	946	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,64		1427,77		1649,82	2145,14	2821,44	2883,48		2983,52	2999,59			digested
Tsaga an Agui		Pit 2; Layer 2.2; B19/3	727	23	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,62	1180,65	1196,68	1427,8	1580,83	1648,89	2131,17	2792,41	2857,54		3017,55	3033,62			digested
Tsaga an Agui	348	Pit 2; Layer 2.2; A18/4	1476	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,68	1427,8	1550,85	1649,84	2145,17	2820,45	2883,5	2899,5		2999,63			digested
Tsaga an Agui	349	Pit 2; Layer 2.2; B19/1	393	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,71	1182,74	1198,73	1427,89	1550,92	1649,96	2145,31	2820,7	2883,73	2900,72	2983,78	2999,85			digested
Tsaga an Agui	350	Pit 2; Layer 2.2; B19/1	281	19				indet.														digested	

Tsagan Agui	351	Pit 2; Layer 2.2; B19/4						not found																digested
Tsagan Agui	352	Pit 2	3803	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,67	1198,68	1427,8	1550,83	1649,87	2145,19	2820,49	2883,55		2983,64	2999,68				digested
Tsagan Agui	353	Pit 2; Layer 2.2; B19/2	1162	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,71	1198,7	1427,84	1550,88	1649,91	2145,26		2883,56	2899,58		2999,69				digested
Tsagan Agui	354	Pit 2; Layer 2.2; B19/3	764	25	Artiodactyla	Bovidae		Bovidae	1105,66	1150,74/1166,73	1166,73/1182,71	1427,84	1550,86	1648,93	2131,22	2792,51	2883,62	2899,63	3017,68	3033,75	1532		digested; just animals native in africa as result: waterbuck, kob, kirk's dik-dik and grey rhebok?	
Tsagan Agui	355	Pit 2; Layer 2.2; A18/1	695	25	Artiodactyla	Bovidae	Ovis	Group_1	1105,65	1180,68	1196,72	1427,79	1580,83	1648,89	2131,16	2792,47	2883,54	2900,58	3017,62	3033,66				digested
Tsagan Agui	356	Pit 2; Layer 2.2; B19/4	1308	23	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,67	1182,65		1453,85			2145,25	2869,61		2983,73	2999,74					digested
Tsagan Agui	357	Pit 2; Layer 2.2; A18/2	868	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,69	1198,7	1427,8	1550,85	1649,88	2145,2	2820,58	2883,65		2983,75	2999,76				digested
Tsagan Agui	358	Pit 2; Layer 2.1ora; B19/3	290	27	Artiodactyla	Bovidae	Ovis	Group_1	1105,65	1180,65	1196,72	1427,82	1580,85	1648,91	2131,21	2792,45	2883,61	2899,61	3017,64	3033,73				digested
Tsagan Agui	359	Pit 2; Layer 2.2; B19/4	785	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,66	1182,7	1198,72	1427,84	1550,88	1649,87	2145,25	2883,63		2983,72	2999,76					digested
Tsagan Agui	360	Pit 2; Layer 2.1; A18/2	281	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,68	1427,81		1649,84	2145,22	2820,49	2883,55	2899,62	2983,66	2999,67				digested
Tsagan Agui	361	Pit 2; Layer 2.1ora; B19/3	2690	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,67	1182,71		1427,86	1550,93	1649,91	2145,29	2820,63	2883,7		2983,79	2999,82				digested
Tsagan Agui	362	Pit 2; Layer 2.1/2.2; A19/2	425	20	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,65	1180,71	1196,71	1427,82	1580,87	1648,92	2131,21	2792,5	2857,54		3017,6	3033,66				digested
Tsagan Agui	363	Pit 2; Layer 2.2; B19/4	1642	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,69	1427,82	1550,89	1649,86	2145,22	2820,48	2883,56	2899,56	2983,66	2999,68				digested
Tsagan Agui	364	Pit 2; Layer 2.2; A19/4	715	26	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,64	1180,68	1196,71	1427,83	1580,86	1648,93	2131,23	2792,49	2857,61		3017,61	3033,7				digested
Tsagan Agui	365	Pit 2; Layer 2.2; B19/2	1921	27	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65		1427,79	1550,86		2145,18	2820,46	2883,54			2999,67				digested
Tsagan Agui	366	Pit 2; Layer 2.2; B19/1	436	22	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,69	1180,76	1196,76	1427,88	1580,93	1648,97	2131,27	2793,49	2857,64		3017,65	3033,74				digested
Tsagan Agui	367	Pit 2; Layer 2.2; B19/4	271	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,67	1182,71		1427,84	1550,89	1649,91	2145,26	2820,56	2883,64		2983,83	2999,77				digested
Tsagan Agui	368	Pit 2; Layer 2.2; B19/2	390	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,69	1198,67	1427,82	1550,87	1649,88	2145,21	2820,47	2883,55		2983,68	2999,69				digested
Tsagan Agui	369	Pit 2; Layer 2.2; B19/2	1501	26	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,65	1221,7		1443,81	1550,88	1634,9	2131,2	2820,53	2883,63		2975,7	2991,74				digested
Tsagan Agui	370	Pit 2; Layer 2.2; B19/4	623	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,66	1182,71	1198,7	1427,83	1550,87	1649,89	2145,22	2820,51	2883,6	2899,58	2983,67	2999,7				digested

Tsagan Agui		Pit 2; Layer 2.2; B19/2	1562	25	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,69	1182,7		1453,86	1550,93		2145,31		2869,65		2983,76	2999,77			digested
Tsagan Agui	372	Pit 2; Layer 2.2; B19/1	679	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66	1198,68	1427,8	1550,86	1649,85	2145,17	2820,44	2883,5	2899,43	2983,51	2999,62			digested
Tsagan Agui	373	Pit 2; Layer 2.2; B19/4	448	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,7	1427,8	1550,84	1649,86	2145,2	2820,52	2883,61	2899,58	2983,72	2999,73			digested
Tsagan Agui	374	Pit 2; Layer 2.2; B19/4	551	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,64	1198,63	1427,75	1550,79	1649,82	2145,13	2820,42	2883,49	2899,49		2999,61			digested
Tsagan Agui	375	Pit 2; Layer 2.2; B19/4	540	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,66	1198,67	1427,78	1550,82	1649,84	2145,17	2820,46	2883,53	2899,53	2983,61	2999,64			digested
Tsagan Agui	376	Pit 2; Layer 2.1; B18/4	109	24	Lagomorpha	Leporidae		Leporidae	1105,61		1221,67	1453,78	1566/1592		2129,15	2808,36	2883,5	2899,5	2957,6			COL1a2 604 - 618: 1235	digested
Tsagan Agui	377	Pit 2						not found															
Tsagan Agui	378	Pit 2; Layer 1; B19/1	784	28	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,63	1180,67	1196,7	1427,78	1580,83	1648,87	2131,15	2792,43	2857,52		3017,59	3033,64			digested; lower 1ph
Tsagan Agui	379	Pit 2; Layer 2.2; B19/2	242	20	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,62	1180,68	1196,67	1427,79	1580,84	1648,87	2131,14	2792,36	2857,5		3017,54	3033,63			digested
Tsagan Agui	380	Pit 2; Layer 2.2; B19/2	1148	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,69	1198,71	1427,82	1550,87	1649,85	2145,2	2820,45	2883,55	2899,56	2983,62	2999,66			digested
Tsagan Agui	381	Pit 2; Layer 2.2; B19/1	360	28	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,69	1198,7	1427,81	1550,85	1649,88	2145,2	2820,45	2883,54		2983,61	2999,66			digested with holes
Tsagan Agui	382	Pit 2; Layer 2.2; A18/1	368	20	Artiodactyla	Bovidae	Ovis	Group_1	1105,65	1180,71	1196,72	1427,81	1580,86	1648,91	2131,2	2793,49	2883,59	2899,58	3017,64	3033,69			digested
Tsagan Agui	383	Pit 2; Layer 2.2; B19/2	836	23	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,64	1221,7		1443,8	1550,84	1634,89	2131,17	2820,48	2883,54	2899,47	2975,69	2991,64			COL1a2 604 - 618: 1235
Tsagan Agui	384	Pit 2; Layer 2.2; B19/2	1012	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,65	1198,66	1427,78	1550,83	1649,83	2145,16	2820,42	2883,49	2899,5	2983,61	2999,62			digested
Tsagan Agui	385	Pit 2; Layer 2.2; B19/1	563	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67		1427,78		1649,86	2145,17	2820,44	2883,53	2899,52	2983,64	2999,66			digested
Tsagan Agui	386	Pit 2; Layer 2.2; B19/4	859	22	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,6	1182,62	1198,65	1453,76			2145,12	2869,43	2885,41	2983,56	2999,56				digested
Tsagan Agui	387	Layer 2.2; B19/1	691	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,65	1198,65	1427,78		1649,83	2145,14	2820,43	2883,47	2899,47	2983,62	2999,58			digested
Tsagan Agui	388	Pit 2; Layer 2.2; B19/2	106	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,69	1427,8	1550,84	1649,86	2145,2	2820,5	288357	2899,57		2999,69			digested tooth fragment
Tsagan Agui	389	Pit 2; Layer 2.2; A18/1	793	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,64	1427,77	1550,82	1649,82	2145,15	2820,43	2883,52	2899,52	2983,62	2999,63			digested vertebra fragment
Tsagan Agui	390	Pit 2; Layer 2.2; B19/2	1369	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,65	1427,77	1550,81	1649,82	2145,15	2820,42	2883,5	2899,52	2983,61	2999,63			digested
Tsagan Agui	391	Pit 2; Layer 2.2; B19/2	2815	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,66	1427,76		1649,82	2145,15	2820,44	2883,53	2899,54	2983,64	2999,65			digested
Tsagan Agui	392	Pit 2; Layer 2.2; B19/2	325	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,62	1427,76	1550,81	1649,81	2145,14	2820,44	2883,53	2899,52	2983,64	2999,65			digested

Tsagan Agui	393	Pit 2; Layer 2.2; B19/1	983	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,64	1427,75	1550,78	1649,82	2145,13	2820,41	2883,47	2899,47	2983,58	2999,6			digested
Tsagan Agui	394	Pit 2; Layer 2.2; B19/2	504	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,66	1427,77	1550,8	1649,79	2145,15	2820,42	2883,5	2899,5	2983,6	2999,63			digested
Tsagan Agui	395	Pit 2; Layer 2.2; B19/3	1526	19	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,6	1221,66		1443,77	1550,8	1634,84	2131,14	2820,42	2883,51	2899,51	2975,68	2991,61			digested
Tsagan Agui	396	Pit 2; Layer 2.2; B19/2	895	30	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,69	1198,67	1427,81	1550,85	1649,86	2145,2	2820,45	2883,54	2899,51	2983,66	2999,66			digested
Tsagan Agui	397	Pit 2; Layer 2.2; B19/4	1214	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,66	1427,75		1649,81	2145,11	2820,34	2883,44		2983,54	2999,55			digested
Tsagan Agui	398	Pit 2; Layer 2.2; A18/1	2262	20	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,6	1221,66		1443,75	1550,79	1634,82	2131,12	2820,4	2883,48	2899,46	2975,61	2991,59			Mn lens
Tsagan Agui	399	Pit 2; Layer 2.2; B19/4	1074	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,68	1427,8	1550,85	1649,84	2145,18	2820,45	2883,51	2899,53	2983,6	2999,62			digested
Tsagan Agui	400	Pit 2; Layer 2.2; B19/4	691	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,65	1427,78	1550,81	1649,84	2145,15	2820,4	2883,49	2899,48		2999,59			digested
Tsagan Agui	401	Pit 2; Layer 2.2; B19/4	534	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,68	1427,79		1649,86	2145,18	2820,47	2883,55	2899,53	2983,66	2999,67			digested
Tsagan Agui	402	Pit 2; Layer 2.2; B19/4	1403	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,66	1427,81	1550,84	1649,85	2145,21	2820,48	2883,57	2899,57	2983,69	2999,69			digested
Tsagan Agui	403	Pit 2; Layer 2.2; B19/2	465	27	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,62	1180,71	1196,67	1427,79	1580,8	1648,88	2131,16	2792,41	2857,52		3017,6	3033,66			digested
Tsagan Agui	404	Pit 2; Layer 2.2; B19/1	157	28	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,71	1427,8	1550,84	1649,85	2145,21	2820,53	2883,6	2899,55	2983,72	2999,72			digested
Tsagan Agui	405	Pit 2; Layer 2.2; B19/4	1837	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,67	1198,68	1427,78	1550,82	1649,83	2145,17	2820,46	2883,53	2899,5	2983,63	2999,63			digested
Tsagan Agui	406	Pit 2; Layer 2.2; B19/3	1233	29	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,65	1221,69		1443,82	1550,85	1634,9	2131,21	2820,51	2883,59	2899,63	2975,66	2991,68			digested
Tsagan Agui	407	Pit 2; Layer 2.2; A18/1	1658	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68	1198,68	1427,81	1550,84	1649,87	2145,22	2820,52	2883,62	2899,63	2983,69	2999,73			digested
Tsagan Agui	408	Pit 2; Layer 2.2; B19/4	1054	19	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,64	1182,71	1198,7	1453,82			2145,21		2869,51	2885,54	2983,6	2999,63			digested
Tsagan Agui	409	Pit 2; Layer 2.2; B19/2	1751	29	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,66	1198,66	1427,79	1550,82	1649,83	2145,18	2820,46	2883,54	2899,53	2983,64	2999,66			digested
Tsagan Agui	410	Pit 2; Layer 2.2; B19/2	918	27	Artiodactyla	Bovidae		Bovidae	1105,6	1180,64	1196,67	1427,75	1550,76	1648,83	2131,11	2792,35	2883,48	2899,48	3017,48	3033,58	1532		digested; Springbok, Thomson's Gazelle, Grant's Gazelle or Oribi according ZooMS Database
Tsagan Agui	411	Pit 2; Layer 2.2; A19/2	1931	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,67	1427,78	1550,81	1649,84	2145,15	2820,41	2883,48	2899,46	2983,58	2999,59			digested
Tsagan Agui	412	Pit 2; Layer 2.2; B19/2	428	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,67	1182,72	1198,74	1427,85		1649,93	2145,27	2820,6	2883,69	2899,65	2983,81	2999,81			digested
Tsagan Agui	413	Pit 2; Layer 2.2; B19/2	382	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,68	1198,67	1427,8	1550,85	1649,85	2145,19	2820,47	2883,54	2899,51	2983,67	2999,67			digested

Tsagan Agui	414	Pit 2; Layer 2.2; A18/2	498	25	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,64	1221,71		1443,83		1634,9	2131,23	2820,47	2883,58		2975,64	2991,67			digested
Tsagan Agui	415	Pit 2; Layer 2.2; B19/1	781	27	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,68	1198,73	1427,79	1550,82	1649,82	2145,19	2820,51	2883,59	2899,62	2983,73	2999,66			digested fragment epiphysis of vertebra
Tsagan Agui	416	Pit 2; Layer 2.2; A18/2	1881	24	Perissodactyla	Rhinocerotidae		Rhinocerotidae	1105,64	1182,67	1198,68	1453,83	1550,85		2145,22		2869,6	2885,59		2999,75			digested
Tsagan Agui	417	Pit 2; Layer 2.2; A18/4	295	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,68		1427,82	1550,86	1649,87	2145,22	2820,54	2883,61	2983,76	2999,74				digested
Tsagan Agui	418	Pit 2; Layer 2.2; B19/1	650	26	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,62	1180,66	1196,66	1427,78	1580,8	1648,88	2131,15	2792,42	2857,47		3017,56	3033,64			digested
Tsagan Agui	419	Pit 2; Layer 2.2; B19/1	769	25	Artiodactyla	Bovidae		Bovidae	1105,56	1150,6		1427,75	1550,82	1648,84	2131,15	2793,35	2883,47		3017,49	3033,59			digested; just animals native in africa as result: waterbuck, kob, kirk's dik-dik and grey rhebok?
Tsagan Agui	420	Pit 2; Layer 2.2; B19/1	1724	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,57	1182,6	1198,6	1427,71	1550,72		2145,09					2999,48			digested
Tsagan Agui	421	Pit 2; Layer 2.2; B19/2	189	20	Artiodactyla	Bovidae		Bovidae	1105,56		1182,58	1427,76		1648,85	2131,14		2883,42		3017,44	3033,52	1532		digested; as result suni (unlikely) - > unknown species?
Tsagan Agui	422	Pit 2; Layer 2.2; B19/1	515	27	Artiodactyla	Bovidae	Ovis	Group_1	1105,59	1180,66	1196,68	1427,72	1580,78	1648,8	2131,12		2883,43		3018,42	3033,47			digested
Tsagan Agui	423	Pit 2; Layer 2.2; B19/3	598	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,6	1198,64	1427,75	1550,8	1649,81	2145,15	2820,4	2883,48	2899,46	2983,59	2999,58			digested
Tsagan Agui	424	Pit 2; Layer 2.2; B19/1	3354	29	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,66	1198,65	1427,79	1550,84	1649,84	2145,19	2820,41	2883,48	2899,49	2983,52	2999,61			digested sin magnum
Tsagan Agui	425	Pit 2; Layer 2.2; A18/1	1715	19	Artiodactyla	Bovidae	Bos sp. sp.	Bos sp.	1105,59	1192,7	1208,69	1427,76	1580,8	1648,85	2131,15	2792,35	2853,44	2869,43	3017,42	3033,57	1532		digested
Tsagan Agui	426	Pit 2; Layer 2.2; B18/2	3779	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,64	1198,63	1427,76	1550,81	1649,82	2145,14	2820,37	2883,44	2899,43	2983,52	2999,55			digested
Tsagan Agui	427	Pit 2; Layer 2.2; B18/2	740	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,63	1198,61	1427,75	1550,78	1649,8	2145,12	2820,36	2883,43	2899,42		2999,53			digested
Tsagan Agui	428	Pit 2; Layer 2.1rea; B19/1	1721	26	Artiodactyla	Bovidae	Ovis	Group_1	1105,6	1180,65	1196,67	1427,77	1580,81	1648,87	2131,14	2792,37	2883,47	2899,46	3017,45	3033,58			digested
Tsagan Agui	429	Pit 2; Layer 2.2; B19/4	1573	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,63	1198,62	1427,76	1550,78	1649,81	2145,14	2820,39	2883,45	2899,43	2983,47	2999,5			digested
Tsagan Agui	430	Pit 2; Layer 2.2; B19/4	366	24	Artiodactyla	Bovidae		Bovidae	1105,59	1150/1166	1166/1182	1427,76	1550,8	1648,87	2131,15	2792,39	2883,49	2899,45	3017,53	3033,59	1532		digested; just animals native in africa as result: waterbuck, kob, kirk's dik-dik and grey rhebok?

Tsaga an Agui	431	Pit 2; Layer 2.1; B19/1	1096	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,62	1198,61	1427,73	1550,77	1649,78	2145,09	2820,4	2883,49	2899,5	2983,56	2999,59			digested
Tsaga an Agui	432	Pit 2; Layer 2.2; B19/2	854	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,63	1427,75	1550,78	1649,8	2145,11	2820,38	2883,48	2899,44	2983,58	2999,59			digested
Tsaga an Agui	433	Pit 2; Layer 2.3; B18/2	150	25				indet.															
Tsaga an Agui	434	Pit 2; Layer 2.3; B18/1	2213	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,66	1427,78			2145,17	2820,41	2883,47		2983,59	2999,58			digested
Tsaga an Agui	435	Pit 2; Layer 2.3; B19/3	417	19	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,6	1180,62	1196,65	1427,77	1580,83	1648,86	2131,13	2792,39	2857,52		3017,45	3033,59			digested
Tsaga an Agui	436	Pit 2; Layer 2.3; B19/3	476	25	Artiodactyla	Bovidae		Bovidae	1105,6	1180,65	1196,64	1427,77	1580,83	1648,87	2131,15	2792,34	2883,45	2899,44	3017,46	3033,56	1532		digested; suni (unlikely) - > unknown species?
Tsaga an Agui	437	Pit 2; Layer 2.3; B19/3	1437	28	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,65	1427,78		1649,82	2145,17	2820,38	2883,48	2899,46	2983,54	2999,58			digested
Tsaga an Agui	438	Pit 2; Layer 2.3; B19/3	776	23	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,59	1180,64	1196,66	1427,76	1580,79	1648,85	2131,11	2793,3	2857,37		3017,47	3033,5			digested
Tsaga an Agui	439	Pit 2; Layer 2.3; B19/1	1448	26				indet.															digested
Tsaga an Agui	440	Pit 2; Layer 2.2; B19/2	1961	22	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,62	1221,67		1443,8	1550,82	1634,87	2131,16	2820,39	2883,48	2899,48	2975,55	2991,55		COL1a2 604 - 618: 1235	digested
Tsaga an Agui	441	Pit 2; Layer 2.2; B19/2	1561	17	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,64	1198,63	1427,76	1550,81	1649,81	2145,13	2820,34	2883,42	2899,38	2983,53	2999,5			digested
Tsaga an Agui	442	Pit 2; Layer 2.1; A18/2	37	16	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,6	1180,66	1196,67	1427,79	1580,83	1648,9	2131,19	2792,42	2857,5		3017,52	3033,62			digested
Tsaga an Agui	443	Pit 2; Layer 2.2; B19/2	1566	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,68	1427,77	1550,82	1649,83	2145,16	2820,47	2883,55	2899,51	2983,67	2999,67			hyaena gnawings
Tsaga an Agui	444	Pit 2; Layer 2.2; B19/1	937	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,67	1427,81	1550,85	1649,89	2145,22	2820,48	2883,55	2899,55	2983,59	2999,67			digested
Tsaga an Agui	445	Pit 2; Layer 2.2; B19/3	113	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,67	1427,79		1649,86	2145,2	2820,43	2883,49	2899,48	2983,65	2999,6			digested
Tsaga an Agui	446	Pit 2; Layer 4; B18/4	1607	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,65	1427,77	1550,81	1649,83	2145,17	2820,39	2883,48	2899,47	2983,6	2999,58			digested
Tsaga an Agui	447	Pit 2; Layer 2.1; A18/2	364	27	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,67	1427,82		1649,85	2145,24	2820,46	2883,54	2899,5	2983,62	2999,66			digested tooth, upper part Pd3-4 sin
Tsaga an Agui	448	Pit 2; Layer 2.2; B19/4	875	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,68	1427,78	1550,82	1649,84	2145,19	2820,41	2883,48	2899,49	2983,52	2999,6			digested
Tsaga an Agui	449	Pit 2; Layer 2.2; B19/4	1748	20				indet.															digested
Tsaga an Agui	450	Pit 2; Layer 2.2; A18/3	1419	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,68	1427,8	1550,85	1649,86	2145,19	2820,42	2883,5	2899,45	2983,61	2999,6			digested
Tsaga an Agui	451	Pit 2; Layer 2.2; B19/2	978	24	Artiodactyla	Bovidae	Ovis	Group_1	1105,61	1180,66	1196,68	1427,78	1580,83	1648,88	2131,16	2792,39	2883,48	2899,46	3017,46	3033,57			digested
Tsaga an Agui	452	Pit 2; Layer 2.2; B19/3	693	27	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,66	1198,67	1427,8		1649,85	2145,2	2820,42	2883,5	2899,52	2983,63	2999,62			digested

Tsagan Agui	453	Pit 2; Layer 2.1; B19/4	921	21	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,59	1182,65	1196,69	1427,78	1580,82	1648,89	2131,17	2792,4	2857,49		3017,54	3033,62			digested
Tsagan Agui	454	Pit E; Layer 2.2; B19/1	848	27	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,59	1180,63	1196,66	1427,74	1580,77	1648,82	2131,09	2792,34	2857,45		3017,48	3033,58			digested
Tsagan Agui	455	Pit E; Layer 5; A5/4	2487	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,63	1427,75	1550,78	1649,8	2145,12	2820,39	2883,48	2899,48	2983,58	2999,6			digested; grey on the outside
Tsagan Agui	456	Pit E; Layer 6/1; A5/4	928	20	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	Pantholops hodgsonii	1105,61	1180,63	1196,66	1427,81	1580,84	1648,9	2131,18	2792,41	2857,47		3017,45	3033,61			digested
Tsagan Agui	457	Pit E; Layer 7; A4/4	689	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,63	1427,79	1550,82	1649,84	2145,18	2820,42	2883,5	2899,45	2983,59	2999,61			digested
Tsagan Agui	458	Pit E; Layer 5; A5/2	171	20	Carnivora	Canidae	<i>Canis familiaris</i>	Canidae	1105,61		1226,66	1453,79	1566,83		2131,15	2821,37	2853,45	2869,44		2999,57		COL1a2 889 - 906: 1576,85	digested
Tsagan Agui	459	Pit E; Layer 5; A5/2	1176	27	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,66	1427,8	1550,85	1649,94	2145,2	2820,44	2883,49	2899,48	2983,6	2999,61			digested
Tsagan Agui	460	Pit E; Layer 7; A4/4	4349	24	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,64	1221,73		1443,82	1550,88	1634,91	2131,2	2820,45	2883,51		2975,56	2991,6		COL1a2 604 - 618: 1235	digested
Tsagan Agui	461	Pit E; Layer 5; A5/2	1201	27	Lagomorpha	Leporidae		Leporidae	1105,6		1221,66	1453,79	1566,81/159 2,85		2129,16		2883,46	2899,46	2957,55	2973,51			digested
Tsagan Agui	462	Pit E; Layer 5; A5/4	606	26	Artiodactyla	Bovidae	<i>Bos sp. sp.</i>	Bos sp.	1105,62	1192,71	1208,72	1427,79	1580,86	1648,87	2131,16	2792,31	2853,46	2869,49	3017,51	3033,57	1532		digested
Tsagan Agui	463	Pit E; Layer 6; A5/4	2159	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,7		1427,84	1550,88	1649,91	2145,25	2820,46	2883,54	2899,5	2983,59	2999,67			digested
Tsagan Agui	464	Pit E; Layer 6; A5/4	3554	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65		1427,78	1550,82	1649,84	2145,16	2820,38	2883,44	2899,46	2983,55	2999,54			digested
Tsagan Agui	465	Pit E; Layer 5; A5/2	624	27	Artiodactyla	Bovidae		Bovidae	1105,61	1150,65/116 6,65	1166,65/118 2,65	1427,78	1550,84	1648,87	2131,15	2792,34	2883,48	2899,56	3017,41	3033,55	1532		digested; just animals native in africa as result: waterbuck, kob, kirk's dik-dik and grey rhebok?
Tsagan Agui	466	Pit E; Layer 5; A4/2	395	28	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66		1427,79	1550,83	1649,84	2145,18	2820,42	2883,5	2899,48		2999,59			digested
Tsagan Agui	467	Pit E; Layer 5; A5/2	8577	23	Artiodactyla	Bovidae	Ovis	Group_1	1105,61	1180,67	1196,66	1427,78	1580,84	1648,88	2131,15	2792,35	2883,47	2899,47	3017,51	3033,58			very hard bone
Tsagan Agui	468	Pit E; Layer 6; A5/2	6738	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,66	1427,81	1550,84	1649,86	2145,22	2820,42	2883,55		2983,53	2999,63			digested
Tsagan Agui	469	Pit E; Layer 5; A4/2	1449	26	Artiodactyla	Camelidae	<i>Camelus</i>	Camelus sp.	1105,59	1221,64		1443,77	1550,81	1634,85	2131,15	2820,39	2883,47		2975,51	2991,53		COL1a2 604 - 618: 1235	digested
Tsagan Agui	470	Pit E; Layer 6; A5/2	709	23	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,67	1427,8	1550,82	1649,84	2145,19	2820,43	2883,5	2899,47	2983,63	2999,59			digested

Tsagan Agui	471	Pit E; Layer 6; A4/4	352	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,65	1198,66	1427,77	1550,8	1649,82	2145,16	2820,38	2883,47		2983,56	2999,56			
Tsagan Agui	472	Pit E; Layer 5; A5/4	1359	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,64	1427,78	1550,81	1649,84	2145,17	2820,4	2883,49	2899,48		2999,58			digested
Tsagan Agui	473	Pit E; Layer 6; A5/2	173	24	Lagomorpha	Leporidae		Leporidae	1105,59		1221,65	1453,78	1566,8/1592,82		2129,16	2808	2883,47	2899,46	2957,54			COL1a2 604 - 618: 1235	digested
Tsagan Agui	474	Pit 2; Layer 2.2; B18/2	313	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,62	1182,67	1198,68	1427,8		1649,87	2145,19	2820,45	2883,54	2899,48		2999,62			digested
Tsagan Agui	475	Pit 2; Layer 2.2; B19/3	819	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,68		1427,82	1550,81		2145,19	2820,36	2883,44	2899,42		2999,54			digested
Tsagan Agui	476	Pit 2; Layer 2.2; B19/2	254	26	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,66	1427,79	1550,83	1649,87	2145,17	2820,41	2883,46		2983,53	2999,56			digested with holes
Tsagan Agui	477	Pit 2; Layer 2.2; B19/3	227	23	Artiodactyla	Bovidae		Bovidae	1105,6	1180,65	1196,67	1427,78	1580,83	1648,88	2131,14	2792,34	2883,42	2899,47	3017,45	3033,5	1532		sun (unlikely) - > unknown species
Tsagan Agui	478	Pit 2; Layer 2.2; B19/4	3311	28	Perissodactyla	Rhinocerotidae	<i>Coelodonta antiquitatis</i>	Rhinocerotidae	1105,6	1182,68	1198,67	1453,8			2145,16		2869,44	2885,45	2983,55	2999,56			digested
Tsagan Agui	479	Pit 2; Layer 2.2; B19/3	270	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,65	1427,79	1550,81	1649,83	2145,18	2820,43	2883,49	2899,41	2983,57	2999,6			digested
Tsagan Agui	480	Pit 2; Layer 2.2; B19/4	1383	25				indet.															digested
Tsagan Agui	481	Pit 2; Layer 2.2; B19/2	626	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,66	1427,77	1550,82	1649,83	2145,15	2883,46	2899,42	2983,53	2999,56				digested
Tsagan Agui	482	Pit 2; Layer 2.2; B19/2	321	22				failed															digested
Tsagan Agui	483	Pit 2; Layer 2.2; A18/4	400	27	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65		1427,78		1649,83	2145,17	2820,43	2883,49		2983,53	2999,59			digested
Tsagan Agui	484	Pit 2; Layer 2.2; B19/1	221	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,62	1427,77	1550,78	1649,86	2145,15	2820,38	2883,45	2899,42	2983,54	2999,55			digested
Tsagan Agui	485	Pit 2; Layer 2.2; B19/4	2190	19	Artiodactyla	Bovidae	Ovis	Group_1	1105,6	1180,67	1196,69	1427,79	1580,83	1648,88	2131,16	2792,39	2883,5	2899,5	3017,41	3033,55			digested
Tsagan Agui	486	Pit 2; Layer 2.2; B19/3	4201	26	Artiodactyla	Bovidae	Ovis	Group_1	1105,6	1180,66	1196,69	1427,77	1580,81	1648,87	2131,14	2792,51	2883,45	2899,44	3017,44	3033,55			digested
Tsagan Agui	487	Pit 2; Layer 2.2; B19/1	1375	27	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,65	1198,64	1427,79	1550,8	1649,86	2145,19	2820,44	2883,49		2983,59	2999,6			digested
Tsagan Agui	488	Pit 2; Layer 2.2; A18/1	581	18	Perissodactyla	Equidae	Equus	Equus sp.	1105,59	1182,63	1198,68	1427,76	1550,8	1649,79	2145,15	2820,36	2883,45		2983,54	2999,54			digested
Tsagan Agui	489	Pit 2; Layer 2.2; B19/4	2631	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,66	1198,66	1427,8	1550,78	1649,9	2145,17	2820,39	2883,49		2983,53	2999,59			digested
Tsagan Agui	490	Pit 2; Layer 2.2; B19/2	432	20	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,65	1427,77	1550,81	1649,8	2145,12	2820,32	2883,38			2999,48			digested
Tsagan Agui	492	Pit 2; Layer 2.2; B18/4	457	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,64	1198,63	1427,76	1550,8	1649,81	2145,15	2820,37	2883,45	2899,42	2983,55	2999,56			digested
Tsagan Agui	493	Pit 2; Layer 2.2; B19/2	256	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,64	1427,78	1550,83	1649,84	2145,16	2820,38	2883,47		2983,54	2999,59			digested
Tsagan Agui	494	Pit 2; Layer 2.2; B19/4	1334	17	Perissodactyla	Equidae	Equus	Equus sp.	1105,6	1182,64	1198,64	1427,78		1649,83	2145,16	2820,38	2883,46	2899,44		2999,57			digested

Tsagan Agui	495	Pit 2; Layer 2.2; B19/3	161	21	Perissodactyla	Rhinocerotidae	<i>Coelodonta antiquitatis</i>	Rhinocerotidae	1105,59	1182,66	1198,63	1453,79	1550,81		2145,17		2869,45	2885,45	2983,5	2999,56			digested
Tsagan Agui	496	Pit 2; Layer 2.2; B19/2	620	28	Artiodactyla	Camelidae	<i>Camelus</i>	<i>Camelus</i> sp.	1105,62	1221,68		1443,81		1634,9	2131,2	2820,44	2883,55		2975,56	2991,58		COL1a2 604 - 618: 1235	digested
Tsagan Agui	497	Pit 2; Layer 2.2; B19/1	633	26	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,61	1182,64	1198,65	1427,78	1550,81	1649,84	2145,17	2820,39	2883,46	2899,43	2983,56	2999,56			digested
Tsagan Agui	498	Pit 2; Layer 2.2; A18/1	892	20	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,62	1182,67	1198,67	1427,81		1649,88	2145,21	2820,46	2883,52	2899,47	2983,62	2999,61			digested
Tsagan Agui	499	Pit 2	561	21	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,6	1182,65	1198,65	1427,78	1550,81	1649,84	2145,15	2820,4	2883,45	2899,42	2983,52	2999,56			digested
Tsagan Agui	500	Pit 2; Layer 2.2; A18/2	640	23	Artiodactyla	Bovidae	<i>Capra</i>	<i>Capra</i> sp.	1105,6	1180,66	1196,69	1427,8	1580,78	1648,87	2131,15	2793,3	2883,39		3077,47	3093,5			digested
Tsagan Agui	501	Pit 2; Layer 4; B18/3	163	20	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,59	1182,64	1198,61	1427,77	1550,81	1649,83	2145,14	2821,39	2883,42	2899,4		2999,52			digested
Tsagan Agui	502	Pit 2; Layer 4; B18/2	318	18	Artiodactyla	Bovidae	<i>Ovis</i>	Group_1	1105,59	1180,62	1196,64	1427,75	1580,8	1648,85	2131,12	2792,29	2883,45	2899,46	3017,54	3033,54			digested
Tsagan Agui	503	Pit 2; Layer 4; B18/3	271	20	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,64	1182,67	1198,68	1427,82	1550,84	1649,85	2145,19		2883,51		2983,55	2999,59			digested
Tsagan Agui	504	Pit 2; Layer 4; B19/4	1358	26				indet.															digested
Tsagan Agui	505	Pit 2; Layer 4; B19/2	375	28	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,6	1182,64	1198,65	1427,77	1550,82	1649,83	2145,17	2820,38	2883,45	2899,47	2983,56	2999,58			digested
Tsagan Agui	506	Pit 2; Layer 4; B19/2	2481	21	Artiodactyla	Bovidae	<i>Ovis</i>	Group_1	1105,61	1180,67	1196,68	1427,79	1580,84	1648,89	2131,17	2793,39	2883,49	2899,48	3017,53	3033,58			digested
Tsagan Agui	507	Pit 2; Layer 4; B18/1	1522	28	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,57	1182,62	1198,62	1427,74	1550,79	1649,79	2145,12	2820,34	2883,42	2899,41	2983,48	2999,52			digested
Tsagan Agui	508	Pit 2; Layer 4; B18/2	2215	25				indet.															digested
Tsagan Agui	509	Pit 2; Layer 4; B18/3	1055	23	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,6	1182,64	1198,67	1427,78	1550,82	1649,84	2145,17	2820,4	2883,48	2900,43	2983,57	2999,57			digested
Tsagan Agui	510	Pit 2; Layer 4; B18/1						not found															digested
Tsagan Agui	511	Pit 2; Layer 4; B18/2	562	23	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,59	1182,62	1198,64	1427,77	1550,79	1649,82	2145,17	2820,52	2883,62	2899,63		2999,73			digested
Tsagan Agui	512	Pit 2; Layer 4; B18/1	829	22	Artiodactyla	Camelidae	<i>Camelus</i>	<i>Camelus</i> sp.	1105,6	1221,66		1443,75	1550,8	1634,83	2131,11	2820,42	2883,51	2899,52		2991,6			digested
Tsagan Agui	514	Pit 2; Layer 2.2; B19/4	298	20	Perissodactyla	Rhinocerotidae	<i>Coelodonta antiquitatis</i>	Rhinocerotidae	1105,61	1182,64	1198,63	1453,78	1550,8		2145,15		2869,52	2886,47		2999,63			
Tsagan Agui	515	Pit 2; Layer 2.2; B19/1	579	21	Carnivora	Felidae/Hyaenidae	<i>Panthera/Crocuta</i>	<i>Panthera/Crocuta</i>	1105,6	1207,66		1453,77	1566,76		2147,13		2853,54	2869,54		2999,67			digested
Tsagan Agui	516	Pit 2; Layer 2.2; A18/2	237	22	Artiodactyla	Camelidae	<i>Camelus</i>	<i>Camelus</i> sp.	1105,62	1221,69		1443,77	1550,79	1634,86	2131,14	2820,51	2883,56	2899,57		2991,66			fragment vertebra

[illegible]

Tsagan Agui	535	Pit 2; Layer 4; B19/4	23	23	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,61	1221,68		1443,77		1634,83	2131,13	2820,48	2883,55	2899,59		2991,65			bone flake
Tsagan Agui	536	Pit 2; Layer 2.3; B19/1	233	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,65	1182,69	1198,71	1427,83		1649,9	2145,24	2820,56	2883,64	2899,61	2983,69	2999,75			
Tsagan Agui	538	Pit 2; Layer 2.2; A18/1	1474	30	Carnivora	Felidae	Felis/Lynx	Felis/Lynx	1105,61	1207,67		1453,79			2163,14	2820,6	2853,55		2983,7	2999,7			hyaena gnawings
Tsagan Agui	539	Pit 2; Layer 2.2; B19/2	69	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,68		1427,8	1550,83	1649,86	2145,2	2820,54	2883,63	2899,63		2999,75			bone blank?
Tsagan Agui	540	Pit 2; Layer 4; B19/4	20	20	Artiodactyla	Camelidae	Camelus	Camelus sp.	1105,63	1221,69		1443,78	1550,84	1634,86	2131,16	2820,47	2883,59	2899,54		2991,67			cracked by human
Tsagan Agui	541	Pit 2; Layer 4; B19/4	42	24	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,67	1198,63	1427,8	1550,84	1649,87	2145,2	2820,5	2883,58	2899,58		2999,74			
Tsagan Agui	543	Pit 2; Layer 2.3; B19/1	181	24				indet.															cracked by human
Tsagan Agui	546	Pit 2; Layer 4; A19/2	2068	25	Perissodactyla	Equidae	Equus	Equus sp.	1105,64	1182,71		1427,8	1550,84	1649,86	2145,19	2820,6	2883,6		2983,68	2999,71			
Tsagan Agui	548	Pit 2; Layer 4; A19/2	230	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,63	1182,67		1427,79	1550,82	1649,84	2145,17	2820,49	2883,57	2899,56		2999,68			
Tsagan Agui	555	Pit 2; Layer 2.2; A19/1	896	21	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,64	1198,66	1427,77	1550,8	1649,84	2145,16	2820,46	2883,53	2899,54		2999,64			
Tsagan Agui	557	Pit 2; Layer 2.2; A19/1	73	19	Perissodactyla	Equidae	Equus	Equus sp.	1105,58	1182,61		1427,73	1550,76	1649,81	2145,25	2820,91	2884,03	2900,05	2984,23	3000,23			
Tsagan Agui	558	Pit 2; Layer 2.2; A19/2	4096	22	Charadriiformes	Laridae	Bird	Bird	1162,62	1221,71		1463,78			2149,08		2879,52						COL1a1 295-309: 1393,7; COL1a1 220 - 237: 1572; COL1a1 688 - 704: 1459,75; COL1a1 934-963: 2705,32; COL1a2 10 - 42: 3113,59
Tsagan Agui	560		436	29	Artiodactyla	Bovidae	Pantholops hodgsonii	Pantholops hodgsonii	1105,62	1180,69	1196,68	1427,78	1580,82	1648,88	2131,17	2792,48	2857,59		3017,58	3033,7			
Tsagan Agui	561	Pit 2; Layer 2.2; B19/4	676	19	Artiodactyla	Bovidae	Ovis	Group_1	1105,62		1196,72	1427,78	1580,8	1648,88	2131,17	2792,52	2883,64	2899,6	3017,66	3033,78			digested
Tsagan Agui	562	Pit 2; Layer 2.2; B19/1	557	29	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,66		1427,78	1580,8	1648,87	2131,17	2792,5	2883,59	2899,56	3017,68	3033,73			bone from copro (digested)
Tsagan Agui	563	Pit 2; Layer 2.1; A18/2	334	22	Perissodactyla	Equidae	Equus	Equus sp.	1105,61	1182,65	1198,62	1427,77		1649,79	2145,17	2820,49	2883,62		2983,72	2999,75			copro + bone
Tsagan Agui	564	Pit 21/2; Layer 5; B19/4	1595	26	Lagomorpha	Leporidae		Leporidae	1105,63		1221,69	1453,79	1566,83/1592,86		2129,22	2808	2883,7	2899,7	2957,81				
Tsagan Agui	565	Pit 2; Layer 3; B19/2	322	28	Artiodactyla	Bovidae/Cervidae		Bovidae/Cervidae	1105,6			1427,75		1648,83	2131,12	2792,46	2883,57	2899,58	3017,63	3033,71			

Tsagan Agui	519_2		25	25	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,67	1196,7	1427,78	1580,82	1648,88	2131,18	2792,53	2883,67	2899,66	3017,72	3033,81			
Tsagan Agui	520_1	Pit 2; Layer 2.2; B19/4	150	25	Artiodactyla	Bovidae	Ovis	Group_1	1105,62	1180,68	1196,67	1427,77	1580,82	1648,88	2131,15	2792,47	2883,57	2899,53	3017,57	3033,67			fragment dex metatarsal with hyaena gnawings
Tsagan Agui	520_2		144	23	Artiodactyla	Camelidae	<i>Camelus</i>	<i>Camelus</i> sp.	1105,62	1221,67		1443,77	1550,81	1634,85	2131,17	2820,56	2883,65	2899,63		2991,68			
Tsagan Agui	520_3		61	20	Artiodactyla	Bovidae	Ovis	Group_1	1105,61	1180,67	1196,68	1427,77	1580,81	1648,87	2131,17	2792,54	2883,66	2899,63	3017,67	3033,7			
Tsagan Agui	525_1	Pit 2; Layer 5; B19/1	31	16	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	<i>Pantholops hodgsonii</i>	1105,61	1180,66	1196,67	1427,78	1580,78	1648,86	2131,13	2793,39	2857,5		3017,52	3033,61			cracked by human
Tsagan Agui	525_2		50	19	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	<i>Pantholops hodgsonii</i>	1105,62	1180,68	1196,7	1427,79	1580,84	1648,9	2131,2	2792,58	2857,69		3017,73	3033,86			
Tsagan Agui	537_1	Pit 2; Layer 5; B19/4	26	14	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	<i>Pantholops hodgsonii</i>	1105,61	1180,65	1196,66	1427,76	1580,8	1648,86	2131,13	2792,42	2857,51		3017,5	3033,64			bone flake
Tsagan Agui	537_2	Pit 3; Layer 5; B19/4						not found															
Tsagan Agui	542_2		111	28				indet.															
Tsagan Agui	542_1	Pit 2; Layer 4; B18/2	72	26				indet.															cracked or gnwanings
Tsagan Agui	543_3		51	23				indet.															
Tsagan Agui	544=227	Pit 2	939	22	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,61	1182,66	1198,64	1427,79	1550,82	1649,85	2145,18	2820,48	2883,55			2999,62			
Tsagan Agui	545=226	Pit 2	1224	22	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,61	1182,68	1198,67	1427,77	1550,81	1649,85	2145,3	2820,87	2884	2900	2984,15	3000,22			
Tsagan Agui	547=228	Pit 2	3009	22	Artiodactyla	Camelidae	<i>Camelus</i>	<i>Camelus</i> sp.	1105,6	1221,64		1443,74	1550,79	1634,82	2131,09	2820,41	2883,5	2899,47	2975,57	2991,58			flat
Tsagan Agui	549=225	Pit 2	3792	30	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,63	1182,67		1427,79	1550,85	1649,83	2145,19	2820,51	2883,6	2899,58		2999,71			
Tsagan Agui	550=224	Pit 2	2016	23	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,62	1182,64		1427,78	1550,85	1649,85	2145,17	2820,51	2883,59	2899,55	2983,71	2999,74			
Tsagan Agui	553=81	Pit 2	237	30				indet.															
Tsagan Agui	554=102	Pit 2	737	26	Artiodactyla	Camelidae	<i>Camelus</i>	<i>Camelus</i> sp.	1105,63	1221,7		1443,8	1550,82	1634,89	2131,18	2820,51	2883,61	2899,61		2991,7			
Tsagan Agui	93a	Pit 21/2; Layer 2.2; A19/2	455	24	Perissodactyla	Equidae	<i>Equus</i>	<i>Equus</i> sp.	1105,64	1182,69	1198,71	1427,81	1550,84	1649,85	2145,21	2820,49	2883,56	2899,57		2999,65			digested
Tsagan Agui	93b	Pit 2	448	27	Artiodactyla	Bovidae	<i>Pantholops hodgsonii</i>	<i>Pantholops hodgsonii</i>	1105,63	1180,69	1196,67	1427,79	1580,85	1648,86	2131,15		2857,56		3017,65	3033,73			digested, former 552 (duplicate)

Abstract:

ZooMS ist eine paläoproteomische Methode, die auf der Analyse von Kollagen und keratinhaltigem Material aus archäologischen Stätten beruht und ist besonders nützlich für die schnelle taxonomische Identifizierung fragmentierter Knochenansammlungen. Die Proben für diese Arbeit stammen aus der paläolithischen Höhlenstätte Tsagaan Agui in der südlichen Mongolei. Die Stätte hat eine große lithische Industrie (Mittelpaläolithikum), zahlreiche Knochen, einige mit Schnittspuren, Rissfrakturen und sekundärer Behandlung durch den Menschen, sowie Hyänenkoprolithe und durch Verdauung erodierte Knochen hervorgebracht. In dieser Arbeit wurden 566 Knochen aus dem Pleistozän mit ZooMS analysiert, wovon 276 Knochen während den Ausgrabungen geborgen wurden und 287 Knochenfragmente wiesen Anzeichen dafür auf, dass sie von Hyänen angeknabbert oder verdaut wurden, manche Knochen wurden direkt aus ihren Koprolithen entnommen. Insgesamt wiesen 95 % der Knochen eine ausgezeichnete Kollagenerhaltung auf; die verdauten Proben zeigten eine Erfolgsquote von 98 % bei der Kollagenerhaltung. Zu den identifizierten ZooMS-Taxa gehören Equiden (die größte Fraktion mit 42 %), Kamele, Antilopen, Nashörner, Biber, Feliden, Caniden, Lepiden, Bären, Füchse, Ziege, Mäuse, Ratten, Dachs, Vögel und einige weniger gut definierte Boviden/Cerviden, die zusammen auf einen ausgeprägten eurasischen Faunakomplex hindeuten. Vier Knochenproben wurden mit Radiokarbon datiert, die älteste auf 49,4-43,8 ka cal BP und wurde taxonomisch als *Panthalops hodgsonii* identifiziert. Sowohl Menschen als auch Hyänen ernährten sich von Kamelen, Equiden und mittelgroßen Boviden. Hyänen erweiterten ihren Speiseplan mit Cerviden, Nashörnern, Nagetieren, Lepiden, Feliden, Bären und anderen Carnivoren. Die identifizierte Fauna, die hauptsächlich aus wandernden Huftieren besteht, deutet auf ein reichliches Vorkommen von Gras/Pflanzen sowie auf Wasserquellen hin, die heute nicht mehr deutlich sichtbar sind. Dies lässt auf ein gemäßigtes Klima während der Zeit schließen, in der die Stätte bewohnt war. Letztlich wird in dieser Arbeit die prähistorische Fauna, die in und um einen wichtigen paläolithischen menschlichen Unterschlupf in Zentralasien lebte und von Raubtieren wie Menschen und Hyänen getötet wurde, genauer identifiziert, was wichtige neue Erkenntnisse liefert.

Schlüsselwörter: ZooMS, Paläoproteomik, Paläolithikum, Radiokarbondatierung, Tsagaan Agui, Zentralasien, eurasische Fauna, Höhlenhyäne