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# A FAUNAL ASSEMBLAGE FROM THE IRON-AGE SITE OF NICULIȚEL (BABADAG CULTURE): ARCHAEOZOOLOGIC AND ARCHAEOGENETIC DATA*

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**Keywords**: archaeozoology, archaeogenetic, Early Iron Age, Niculițel, Babadag culture, quantification, osteometric data.

**Abstract**. *The faunal remains were collected during the archaeological researches carried out in 1988 and 2000. The analysed assemblage consists of 902 remains, out of which four are human (Homo sapiens). The remains originate from fish, birds and mammals. The mammalian bones number 615 remains, out of which 397 were identified by species. The list of identified domestic mammal comprise cattle (Bos taurus), sheep (Ovis aries), goat (Capra hircus), horse (Equus caballus), and pig (Sus domesticus), with domestic cattle prevailing. Only three species of wild mammals were identified: red deer (Cervus elaphus), wild boar (Sus scrofa) and roe deer (Capreolus capreolus); the largest number of remains belongs to red deer. There is a single fragment coming from birds and six fragments from reptiles (Testudo graeca and Emys orbicularis). Fish bones are numerous (276), and the identified species are pike (Esox lucius), common carp (Cyprinus carpio), tench (Tinca tinca), wels catfish (Silurus glanis), and zander (Sander lucioperca); the highest share is represented by the common carp. Archaeogenetic analyses were carried out for some swine remains from Romanian territory, dating from the Iron Age, in order to identify their genetic profile. The analysed samples presented two different ancient haplotypes, previously described in the literature, haplotypes that sustained the pattern of spread for the domestic pigs on the European continent.*

**Rezumat**. *Resturile faunistice au fost colectate în timpul cercetărilor arheologice desfășurate în anii 1988 și 2000. Eșantionul analizat cuprinde 902 resturi faunistice, dintre care patru provin de la om (Homo sapiens). Resturile aparțin la trei grupe*

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*faunistice: pești, păsări și mamifere. De la mamifere provin 615 resturi, dintre care 397 au fost identificate până la nivel de specie. Lista mamiferelor domestice identificate cuprinde: vita (Bos taurus), oaia (Ovis aries), capra (Capra hircus), calul (Equus caballus) și porcul (Sus domesticus). Numai trei specii de mamifere sălbatice au fost identificate: cerb (Cervus elaphus), mistreț (Sus scrofa) și căprior (Capreolus capreolus); cel mai mare număr de resturi aparține cerbului. Un singur fragment provine de la păsări și șase resturi de la reptile (Testudo graeca și Emys orbicularis). Oasele de pește sunt numeroase (276), iar speciile identificate sunt: știucă (Esox lucius), crap (Cyprinus carpio), lin (Tinca tinca), somn (Silurus glanis) și șalău (Sander lucioperca); cea mai mare parte a resturilor de pește provine de la crap. Pentru identificarea profilului genetic al unor resturi de suine de pe teritoriul României din Epoca Fierului s-a realizat o serie de analize moleculare. Probele analizate au prezentat două haplotipuri ancestrale, decrise în prealabil în literatura de specialitate, haplotipuri care au confirmat modelul de răspândire a porcilor domestici pe continentul european.*

## Introduction

The archaeological site Babadag–*Cornet* is located at ca. 5 km north of the Niculițel commune, Tulcea County, Romania, in the area of the Danube ponds near Lake Gorgonel. The site witnessed rescue excavations on area of ca. 2000 m$^2$ in the years 1988 and in 2000, on the occasion of gas adduction works.

The majority of discoveries belong to a Babadag-culture settlement. From a spatial-chronological point of view, this culture was traced to the regions of Dobrudja, South-eastern Moldavia and Eastern Muntenia from the end of the 9th century to the first half of 8th century BC[3].

## Material and methods

The faunal remains analysed come from two archaeological campaigns carried out in 1988 and in 2000 at Babadag–*Cornet*. The assemblage contains 902 remains, out of which four are human (*Homo sapiens*).

The method of osteological determination (qualitative analysis) was supplemented by quantitative (establishing the number of remains for each species, and the minimum number of individuals) and

[3] MORINTZ 1987; JUGĂNARU 2005.

osteometric ones (some data are used to assess the sex and the withers height of the slaughtered individuals).

**Results**

The identified remains belong to four taxonomic groups: fish, reptiles, birds, and mammals. The largest share is taken by mammalian remains (68%), followed by fish (30%) (Figure 1).

*Fish*

Fishing was a relatively important food-producing activity of the Early Iron ages communities from Niculițel; the 276 fish remains represent 30.7% of the entire assemblage. The remains belong to the following species: pike (*Esox lucius*), common carp (*Cyprinus carpio*), tench (*Tinca tinca*), wels catfish (*Silurus glanis*), and zander (*Sander lucioperca*). Common carp has the highest share (67% of the identified fish remains), followed by catfish (23.9%) and pike (4.3%) (Figure 2).

*Reconstituting the capture size for fish.* The sizes of the species present in this assemblage were reconstituted after the minimum number of individuals and was calculated using the combinatory method[4].

Pike (*Esox Lucius*). The minimum number of individuals for this species is limited to two. Both are of large size, measuring 621 mm and, respectively, 715 mm (total length), and belong to the category of reproducers.

Common carp (*Cyprinus carpio*). Size was reconstituted for 13 individuals, calculated on the basis of the left opercular bone. The dimensions are large, ranging between 590 mm to 780 mm TL (mass between 3 and 7 kg) (Figures 3 and 5); the entire series consists of reproducing specimens. The total mass for the 13 individuals was ca. 60 kg.

Tench (*Tinca tinca*). A single tench individual was estimated in the assemblage; its total length was 350 mm (ca. 0.4 kg).

Wels catfish (*Silurus glanis*). The sizes of 14 individuals were reconstituted. Only three of them are small, the remaining 11 being large

[4] POPLIN 1976.

and very large (Figure 4). Five specimens were over 2 m in length, with the largest reaching 2.7 m TL and 135 kg in mass (Figure 5).

Zander (*Sander lucioperca*). Two individuals were identified, for which the following sizes were estimated: a large specimen of 569 mm TL (1.6 kg), and a very large specimen of 903 mm TL (6.8 kg) (Figure 5). The total mass for the 14 specimens was ca. 660 kg.

The sizes of the fish individuals from this assemblage are conspicuously large and very large. The total mass for the 32 individuals was over 700 kg, with the largest share provided by zander (90%) and carp (7.2%). Overall, fish provided a quite large portion of the animal protein consumed by the human community from Niculițel.

*Birds and reptiles*

Birds yielded a single remain, while from reptile come six dermal plates from carapace, belonging to two tortoise species (*Testudo graeca* and *Emys orbicularis*).

*Mammals*

The large share of the assemblage is represented by mammalian bones, from which come 615 remains, of which 397 were identified up to the level of species. Most of the mammalian remains belong to domestic ones (88.4%): cattle (*Bos taurus*), sheep (*Ovis aries*), goat (*Capra hircus*), horse (*Equus caballus*), and pig (*Sus domesticus*). In the group of domestic mammals, the largest share is constituted by cattle, with 46.6% of the total mammalian remains. Cattle are followed by ovicaprids (19%) and horse (10.5%) of the total identified mammalian remains (Figures 6 and 7). The ratios are similar in terms of the minimum number of individuals, with a preponderance of cattle (28%), followed by ovicaprids (18%) and pig (12%).

*Bos taurus.* Most of the remains attributed to cattle belong to the appendicular skeleton (64%) vs. the axial skeleton (36%) (Figure 8). Two upper molars were measured (28 mm and, respectively, 32 mm in length) (Figure 9). From the wide bones, three fragments of the coxal bone were measured (Figure 10). More numerous are the metrical data

for the long and short bones (Figure 11), for example the astragalus (average length of 66.2 mm), 1st phalanx (average length of 59.4 mm) and metapodials. The withers height was estimated at 123.7 cm, calculated on the basis of a metatarsal originating from a castrated individual.

*Ovis aries/Capra hircus*. For ovicaprids too, remains from the appendicular skeleton predominate (59%) over those from the axial skeleton (41%). The distribution of these remains according to the skeletal segment is found in Figure 8. Few ovicaprid remains have been measured. The average length of the lower M3 molar is 22.6 mm. From the long and short bones, only three fragments were measurable (Figure 11). On the basis of a sheep astragalus, the withers height was estimated at 74.8 cm.

*Sus domesticus*. For pig, most of the remains belong to the axial skeleton (65%), and the rest (35%) to the appendicular one. The distribution of the 20 remains according to the skeletal segments is found in Figure 8. It was possible to measure a fragment of a maxillary, one of a mandible (Figure 9), and a distal fragment of a humerus (Figure 11).

*Equus caballus*. The ratio between the two groups is balanced, with 52% of the remains belonging to the appendicular skeleton, and 48% to the axial one. An M3 molar from a mandible was measured, as well as five fragments of long bones (Figures 9 and 11). The lateral length of a metacarpus (212 mm) and the lateral length of a metatarsus were used for estimating the withers height. The resulting values are 136 cm and 134 cm.

*Canis familiaris*. Two scapulae and of a coxal bone were measured (Figure 10). Nine of the long bones, some complete, were measurable (Figure 11).

There are few remains of wild mammals, and the identified species are: red deer (*Cervus elaphus*), wild boar (*Sus scrofa*) and roe deer (*Capreolus capreolus*); the majority of remains belong to red deer (8% of the total identified mammalian remains, respectively 9% of the total number of estimated individuals) (Figure 7). The metrical data for red deer and wild boar are found in Figures 9 and 11.

**Archaeogenetic analysis**

Pigs—a significant part of daily meat consumption—have been a topic of great interest for scientists, not only for their economic value today, but also for what they meant in the past, in the dawn of the domestication. From the very beginning, their omnivorous diet made the tamest wild individuals of *Sus scrofa* come closer to the human environment and later adapt to it more easily. This determined one of the most solid and widespread connections between humans and animals. Therefore, different biologic and behavioural particularities of pigs can help us understand better the domestication process and, indirectly, some important aspects of human history, like the influence on human religion[5]. Although the interpretation of these influences relies especially on archaeological evidence, the archaeogenetic analysis for *Sus scrofa* individuals—as for the rest of the livestock—is a great help for explaining the evolution history for the entire set of elements that build the human society.

Previous studies have established the main directions for the spread of economic and cultural elements during Neolithic, and among these, the spread of pig domestication placed the Romanian territory in a geographical key-position for a long period, throughout the entire domestication process. One of the reasons for this is that, according to data collected so far, European pigs were first domesticated in the Near East, about 10,000 years ago[6] and later introduced into Europe along two different pathways: to the South, respectively the North of the Danube[7]. Therefore, the Romanian territory represented a gate for the dissemination of domestication. As this process continued and developed throughout the millennia, the same territory was also a path in the way back of the spread of domestic European stocks in the Near East[8]. Except for this aspect, the emergence of domestic pigs on the European continent was significantly influenced by a strong cultural context, described by the

[5] ALBARELLA *et al*. 2007, 1–13.
[6] ALBARELLA *et al*. 2007, 1–13.
[7] LARSON *et al*. 2007.
[8] LARSON *et al*. 2007.

existence of several highly developed Neolithic cultures, like Gumelnița, Criș, Boian-Giulești, Zau, Precucuteni and Cucuteni.

The first samples analysed so far from Romanian territory were collected from the few archaeological sites in the South and South-East of Romania[9]. They were part of a broader study, counting hundreds of archaeozoological samples from the entire European continent. The Romanian samples covered a long period, from the early stages of domestication in the Neolithic to the Roman period. This study focuses on a later period from the European domestication process, describing the genetic signature for both wild and domestic individuals of *Sus scrofa* from the Babadag Culture (Iron Age). The findings will contribute to tracking the genetic changes appeared throughout the domestication process on the Romanian territory.

For the present study, were considered two different archaeological sites from the South-eastern part of Romania, out of which from Niculițel were collected samples belonging to the Babadag Culture (three samples) and to the Roman period (four samples), while from the Babadag archaeological site, all five samples collected belonged to the Babadag Culture. Thus, twelve samples represented by bone remains and teeth were subjected to morphometric and DNA analyses.

The genetic analysis comprised more steps: the first ones—including the DNA extraction, the spectrophotometric quantification of the extract and the PCR set-up—were carried out in a laboratory specialised in ancient DNA (aDNA) analysis.

First of all, a small quantity of bone tissue was sampled to be subjected to DNA extraction protocol. To this end, the grinding step was performed in order to eliminate the contaminated surface of a small bone fragment that was cut afterwards and powdered with a micro-dismembrator. The powder was incubated over night with a lysis buffer; the following day, the extraction protocol continued with the centrifugation of samples, to separate the liquid layer from the non-dissolved tissue. Then, the extract was concentrated using the Amicon Ultra 30K MWCO tubes and purified according to the protocol offered by

[9] BORONEANȚ *et al*. 2006.

the Qiaquick kit, from Qiagen. After the DNA extraction, the extract concentration was quantified using a spectrophotometer and the blank purity was checked.

In the next step, the polymerase chain reaction was performed, in order to obtain a high number of copies of a very small fragment from the D-loop region of the mitochondrial DNA. According to previous studies, this small fragment of only 120 base pairs in length was able to differentiate seven ancient haplotypes identified for the *Sus scrofa* individuals from the European continent. A certain concentration of magnesium chloride and bovine serum albumin was used to enhance the quality of the PCR products. After the polymerase chain reaction, the PCR products were tested through the agarose gel electrophoresis and later purified to be sequenced.

The last step was DNA sequencing, which was performed using certain DNA quantities, previously calculated according to the DNA concentration of the purified PCR products. Each DNA strand was sequenced with the forward, respectively the reverse primer through Sanger sequencing. The results were processed in the Geneious (Biomatters Ltd.) and the MEGA6[10] software in order to obtain the complete sequences.

To investigate the frequency of each haplotype within the entire set of samples as well as the differences between haplotypes, the haplotypes network was constructed by using the median-joining algorithm in Network[11] and the DNA-SP 5 software[12].

Most *Sus scrofa* individuals subjected to DNA analysis in this study were identified as domestic, except for one individual from the Roman period and two individuals from the Babadag Culture.

The samples from the Babadag Culture seemed to hold more damaged DNA than the samples from the Roman period. While the DNA of the four samples from the Roman period, from Niculițel, was successfully amplified through the PCR and the genetic signature for

[10] TAMURA *et al.* 2013.
[11] BANDELT *et al.* 1999.
[12] LIBRADO, ROZAS 2009.

these samples was further identified, only some of the samples belonging to the Babadag Culture held positive PCR results and could be successfully sequenced. Therefore, the DNA of the two wild individuals from the Babadag archaeological site and the DNA of one domestic individual from Niculițel could not be amplified and sequenced.

Out of the seven ancient haplotypes previously described for the European continent, only two were identified within the entire set of samples, comprising both the Babadag Culture and the subsequent Roman period: the haplotypes ANC-Aside and ANC-Cside. A new haplotype was also identified for a sample from the Babadag site; most likely, this new genetic signature is only a consequence of the aDNA damage. Two different mutations describe the three identified haplotypes: a transversion in the 62 situs and one transition in the 82 situs (Figure 12).
All pigs from the Babadag Culture which genetic profile could be identified were domestic and had the ANC-Aside haplotype; only one wild individual from the Roman period featured the ANC-Cside haplotype.

Considering the absence of any genetic profile for the wild individuals in the Babadag Culture and the presence of only one haplotype for all of the successfully sequenced samples from this period, no genetic changes could be traced in time between wild and domestic pigs, and the haplotypes network was drawn for the entire set of samples (Figure 13).

A previous study on samples from the South-eastern part of the Romanian territory[13] emphasized on the prevalence of the Near-Eastern ANC-Y1-6A haplotype for domestic pigs in the early stages of domestication process (in Chalcolithic), and its change into the ANC-Aside haplotype during the later stages, starting with the Bronze Age.
The samples analysed in this study pinpointed only a later stage in the domestication process, since they belonged to two different and yet very close periods of time (the Babadag Culture and the Roman period). As it was also previously shown[14], the Near-Eastern genetic signature of

[13] LARSON *et al*. 2007.
[14] OTTONI *et al*. 2013.

domestic pigs from the early stages of domestication in Europe was replaced, by the fifth century A.D., with a European one. The presence of the European ANC-Aside haplotype in the domestic pigs from the Babadag Culture and Roman period in the South-eastern part of Romanian territory confirms this theory.

The genetic profile identified for the domestic pigs in this study was identical for both Babadag Culture and the Roman period, which proves two things. First, that the main genetic changes had occurred before and that the proportion of the genetic signature had already changed. Secondly, that the time frame between the two periods sampled in this study was too narrow for any further genetic changes to appear.

**Conclusions**

The analysed assemblage comprises remains from fish, reptiles, birds and mammals, with the latter taxon predominating. In the osteological assemblage, mammals have a share of 88% of the total, suggesting that the main food source for the Iron-Age communities from Niculițel was animal husbandry. The remaining 12% of identified mammalian remains originate from wild species, pointing to a relatively reduced importance of hunting in the food economy of this settlement.

In terms of the identified remains numbers, cattle predominate in the domestic mammals group, followed by ovicaprids, horse and pig.

Three wild mammalian species were identified, dominated by the red deer. From the ecological standpoint, the list of hunted species suggest, foremost, an exploitation of forest (*Sus scrofa*, *Cervus elaphus*) as well as forest edge fauna (*Capreolus capreolus*). Today the red deer has disappeared from the area, being restricted to the Carpathian range.

Fishing is a relatively important activity of food acquisition at Niculițel: fish remains constitute 30.7% of the entire assemblage, originating from pike, common carp, wels catfish, and zander. The fish are generally large and very large. The total mass obtained for the 32 individuals is over 700 kg, which is illustrative for the degree to which fish provided an important input of animal protein into the diet of the Niculițel communities.

Two of the described ancient haplotypes of *Sus scrofa and Sus domesticus* were identified for the samples analysed in this study and their prevalence was strictly related to the number of domestic, respectively wild individuals.

By the time of the Babadag Culture, the European signature of *Sus scrofa* was already prevalent in the livestock from the Romanian territory and no further changes occurred until the Roman period.

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| **Taxonomic group** | **NISP** | **%** |
|---|---|---|
| Fish | 276 | 30.73 |
| Reptiles | 6 | 0.67 |
| Birds | 1 | 0.11 |
| Mammals | 615 | 68.49 |
| **Total** | **898** | **100** |
| *Homo sapiens* | 4 | - |

Figure 1. Faunal groups identified in the assemblage (NISP — number of identified specimens).

| **Taxon** | **NISP** | **%** |
|---|---|---|
| *Esox lucius* | 9 | 4.39 |
| *Cyprinus carpio* | 139 | 67.8 |
| *Tinca tinca* | 1 | 0.49 |
| *Silurus glanis* | 49 | 23.9 |
| *Sander lucioperca* | 7 | 3.42 |
| **Total identified remains** | **205** | **100** |

| | | |
|---|---|---|
| Unidentified remains | 71 | – |
| Total | 276 | – |

Figure 2. Fish remains quantification.

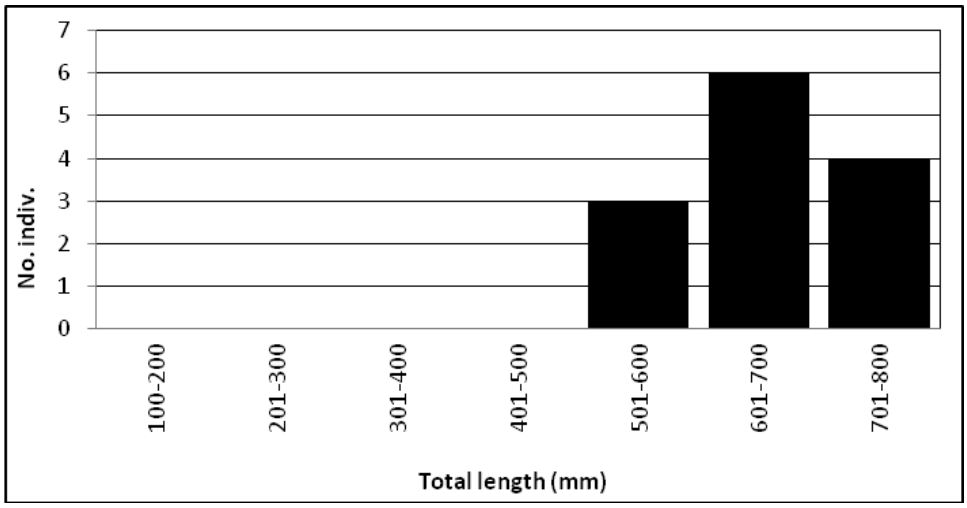


Figure 3. Reconstituted sizes of the common carp (*Cyprinus carpio*) individuals (n=13).

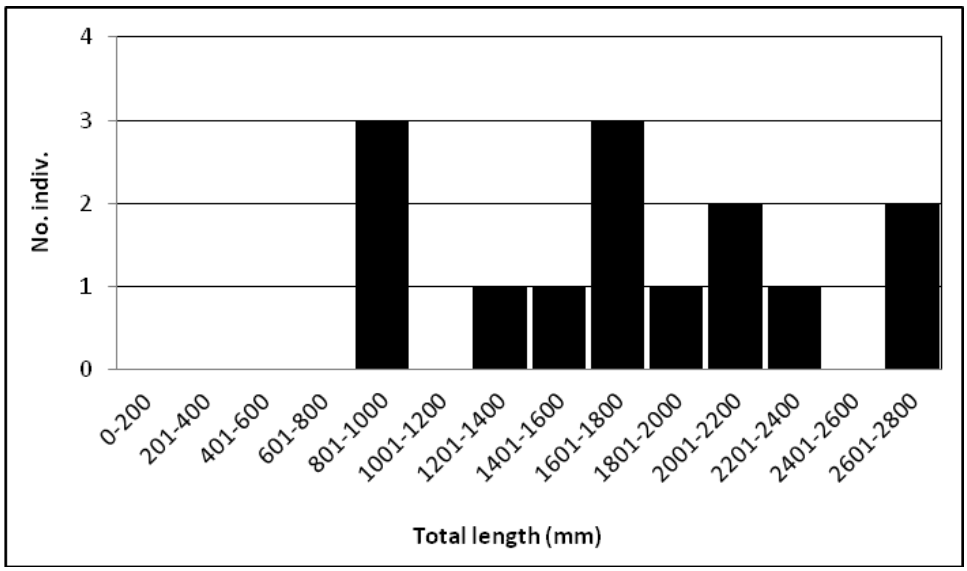


Figure 4. Reconstituted sizes of the wels catfish (*Silurus glanis*) individuals (n=14).

| Taxa | Total length (mm) | Mass (kg) |
|---|---|---|
| *Esox lucius* | 715 | 2.764 |
| | 621 | 1.768 |
| *Cyprinus carpio* | 589 | 3.060 |
| | 593 | 3.122 |
| | 597 | 3.186 |
| | 605 | 3.315 |
| | 613 | 3.448 |
| | 661 | 4.319 |
| | 673 | 4.557 |
| | 675 | 4.590 |
| | 698 | 5.060 |
| | 730 | 5.785 |
| | 742 | 6.074 |
| | 762 | 6.577 |
| | 783 | 7.106 |
| *Tinca tinca* | 350 | 0.400 |
| *Sander lucioperca* | 903 | 6.882 |
| | 569 | 1.608 |
| *Silurus glanis* | 800 | 3.270 |
| | 885 | 4.443 |
| | 892 | 4.550 |
| | 1206 | 11.371 |
| | 1591 | 26.373 |
| | 1644 | 29.132 |
| | 1742 | 34.733 |
| | 1785 | 37.402 |
| | 1829 | 40.272 |
| | 2127 | 63.690 |
| | 2197 | 70.270 |
| | 2327 | 83.673 |
| | 2600 | 117.187 |
| | 2729 | 135.750 |

Figure 5. The reconstituted sizes for the identified fish species.

| Species | NISP | MNI |
|---|---|---|
| *Bos taurus* | 185 | 9 |
| *Canis familiaris* | 28 | 3 |
| *Equus caballus* | 42 | 4 |
| *Ovis aries/Capra hircus* | 76 | 6 |
| *Sus domesticus* | 20 | 4 |
| **Total domestic mammals** | **351** | **26** |
| *Cervus elaphus* | 33 | 3 |
| *Capreolus capreolus* | 5 | 1 |
| *Sus scrofa* | 8 | 2 |
| **Total wild mammals** | **46** | **6** |
| Total identified mammals | 397 | 32 |
| Unidentified mammals | 218 | - |

Figure 6. Mammalian remains quantification (NISP — number of identified specimens; MNI — minimum number of individuals).

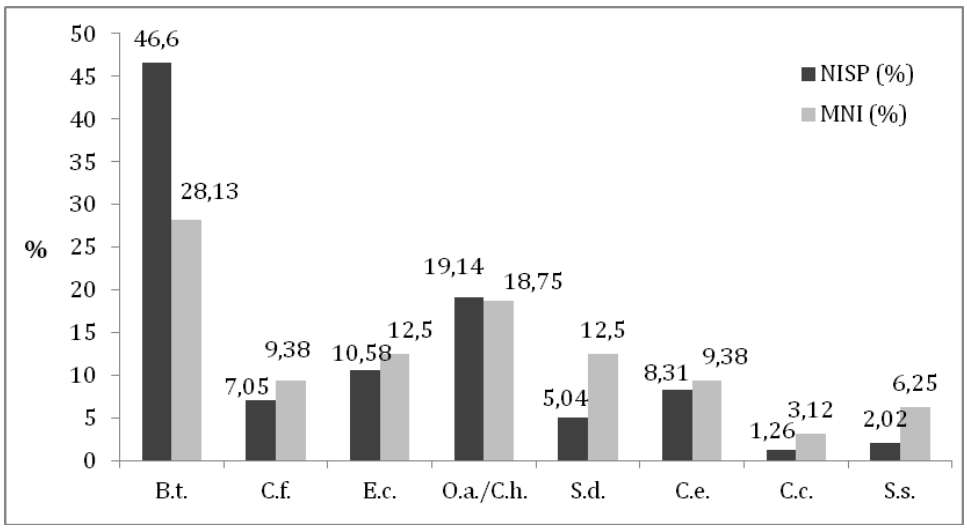


Figure 7. Shares of identified mammalian remains. B.t. – *Bos taurus*, C.f. – *Canis familiaris*, E.c. – *Equus caballus*, O.a. – *Ovis aries*, C.h. – *Capra hircus*, S.d. – *Sus domesticus*, C.e. – *Cervus elaphus*, C.c. – *Capreolus capreolus*, S.s. – *Sus scrofa*.

| **Anatomical region** | *Bos taurus* | *Ovis aries/ Capra hircus* | *Sus domesticus* | *Equus caballus* | *Canis familiaris* |
|---|---|---|---|---|---|
| skull | 47 | 19 | 13 | 19 | 11 |
| vertebrae | 19 | 12 | 0 | 1 | 1 |
| girdle | 20 | 2 | 0 | 4 | 5 |
| stylopod | 20 | 10 | 4 | 5 | 7 |
| zeugopod | 20 | 19 | 3 | 6 | 4 |
| autopod | 59 | 14 | 0 | 7 | 0 |
| **TOTAL** | **185** | **76** | **20** | **42** | **28** |

Figure 8. Distribution of domestic mammal remains according to the anatomical region.

| **Species** | **Anatomical element** | **L M1-M3** | **L P2-P4** | **L M3** | **B M3** | **L P2-M3** |
|---|---|---|---|---|---|---|
| *Bos taurus* | maxilla | 77 | - | 28 | 25 | - |
| | upper M3 molar | - | - | 32 | 20.5 | - |
| *Ovis aries / Capra hircus* | lower M3 molar | - | - | 24 | 9 | - |
| | mandible | 47.5 | 19 | 23 | 8.5 | 68 |
| | mandible | - | - | 21 | 8 | - |
| | mandible | 52 | - | 25 | 8 | - |
| | mandible | (47) | 23 | (20) | 7 | (68) |
| | mandible | (49) | 25 | 23 | 7.5 | (71) |
| *Sus domesticus* | mandible | - | - | 40 | 15 | - |
| | maxilla | - | - | 28.5 | 16 | - |
| *Equus caballus* | mandible | - | - | 32 | 14 | - |
| *Cervus elaphus* | mandible | 85.5 | - | 36 | - | - |

Figure 9. Metrical data (in mm) for mammalian dentition (L P2-M3 – length of the cheektooth row, L P2-P4 – length of the premolar row, L M1-M3 – length of the molar row, L M3 – length of the third molar, B M3 – breadth of the third molar).

| Species | Anatomical element | GLP | LG | BG | SLC | LAR | BAR |
|---|---|---|---|---|---|---|---|
| *Bos taurus* | pelvis | - | - | - | - | 58 | 54 |
| | pelvis | - | - | - | - | 65 | 55 |
| | pelvis | - | - | - | - | 69 | 64 |
| *Canis familiaris* | pelvis | - | - | - | - | 21 | 19 |
| | scapula | 27 | 23 | 16 | 23 | - | - |
| | scapula | 26.5 | 23 | 16.5 | 23 | - | - |

Figure 10. Metrical data (in mm) for the mammalian wide bones (GLP — Greatest length of the Processus articularis (glenoid process), SLC — Smallest length of the Collum scapulae (neck of the scapula), LG — Length of the glenoid cavity, BG - Breadth of the glenoid cavity, LAR — Length of the acetabulum on the rim, BAR – Breadth of the acetabulum on the rim).

| Species | Anatomical element | GL | Bp | Bd | SD | BFp | BFd | Dd | GB |
|---|---|---|---|---|---|---|---|---|---|
| *Bos taurus* | astragalus | 64 | - | 42 | - | - | - | - | - |
| | astragalus | 70.5 | - | 43.5 | - | - | - | - | - |
| | astragalus | 63 | - | 41.5 | - | - | - | - | - |
| | astragalus | 61.5 | - | 38 | - | - | - | - | - |
| | astragalus | 72 | - | 46 | - | - | - | - | - |
| | centrotarsus | - | - | - | - | - | - | - | 56.5 |
| | phalanx 1 | 63.5 | 31 | 29 | 27 | - | | - | - |
| | phalanx 1 | 55 | 28 | 25.5 | 23 | - | | - | - |
| | phalanx 1 | 57.5 | 30.5 | 29.5 | 27 | - | | - | - |
| | phalanx 1 | 66 | 37 | | 31.5 | - | | - | - |
| | phalanx 1 | 55 | 27 | 26 | 24 | - | | - | - |
| | femur | - | - | 80 | - | - | 74 | - | - |
| | humerus | - | - | 84 | - | - | 72.5 | | - |
| | humerus | - | - | 86 | - | - | 82 | | - |
| | metacarpus | - | - | 70 | - | - | - | 36 | - |
| | metacarpus | - | 66.5 | - | - | - | - | | - |
| | metatarsus | - | 42 | - | - | - | - | | - |
| | metatarsus | - | - | 67 | - | - | - | 39 | - |
| | metatarsus | - | - | 59 | - | - | - | 34 | - |
| | metatarsus | - | 46.5 | - | - | - | - | | - |

| Species | Anatomical element | GL | Bp | Bd | SD | BFp | BFd | Dd | GB |
|---|---|---|---|---|---|---|---|---|---|
| | metatarsus | 227 | 49 | 57 | 29 | - | - | 31 | - |
| | radius | - | - | 61.5 | - | - | 56 | - | - |
| | radius | - | - | 77 | - | - | 74 | - | - |
| | radius | - | 89 | - | - | 76 | - | - | - |
| | radius | - | 95 | - | - | 87 | - | - | |
| | patella | 65 | - | - | - | - | - | - | 52 |
| | tibia | - | - | 72 | - | - | 62 | - | - |
| *Ovis aries / Capra hircus* | radius | - | 27.5 | - | - | 24.5 | - | - | - |
| | astragalus | 33 | | 21 | - | - | - | - | - |
| | humerus | | | 30.5 | | - | 29.5 | - | - |
| *Sus domesticus* | humerus | | | 40 | | - | | - | - |
| *Equus caballus* | radius | | | 69 | | - | 58 | - | - |
| | metacarpus | | 56 | | | - | | - | - |
| | metacarpus | 215 | 49 | | 33 | - | | - | - |
| | tibia | | | 74 | | - | 53 | - | - |
| | metatarsus | 256 | 49 | 45 | 32 | | | - | - |
| *Canis familiaris* | humerus | 157.5 | 37 | 30 | 12 | | 21.5 | - | - |
| | humerus | 157 | 37 | 30 | 12 | | 20.5 | - | - |
| | femur | 176 | 35.5 | 29.5 | 11 | 18 | 29 | - | - |
| | femur | 160 | 37 | 28 | 12 | 18 | 28 | - | - |
| | femur | 177 | 35.5 | 30 | 11.5 | 18 | 30 | - | - |
| | tibia | 181 | 32 | 21.5 | 11 | 31 | 19 | - | - |
| | tibia | 180 | 32 | 21.5 | 11.5 | 31.5 | 18 | - | - |
| | radius | - | - | 23 | - | - | 18.5 | - | - |
| | humerus | - | - | 28 | 14 | - | 22 | - | - |
| *Cervus elaphus* | radius | - | - | 56.5 | 32 | - | - | - | - |
| | radius | - | - | 57.5 | - | - | - | - | - |
| | humerus | - | - | - | - | - | 60 | - | |
| | centrotarsus | - | - | - | - | - | - | - | 53 |
| | radius | - | - | 64 | - | - | 61 | - | - |
| | phalanx 2 | 52 | 25.5 | 22.5 | 19 | - | - | - | - |
| | phalanx 2 | 48.5 | 22.5 | 20 | 18 | - | - | - | - |
| *Sus scrofa* | tibia | - | - | 43 | 30 | - | 33 | - | - |

| Species | Anatomical element | GL | Bp | Bd | SD | BFp | BFd | Dd | GB |
|---|---|---|---|---|---|---|---|---|---|
| | humerus | - | - | 54 | - | - | 42 | - | - |
| | metacarpus 2 | 80 | 7 | 13 | 6 | - | - | - | - |

Figure 11. Metrical data (in mm) for the long and short bones of the identified mammals (GL — Greatest length, GB — Greatest breadth, Bp — (Greatest) breadth of the proximal end, BFp — (Greatest) breadth of the Facies articularis proximalis, Bd — (Greatest) breadth of the distal end, BFd — Breadth of the Facies articularis distalis, Dd — (Greatest) depth of the distal end, SD — Smallest breadth of diaphysis).

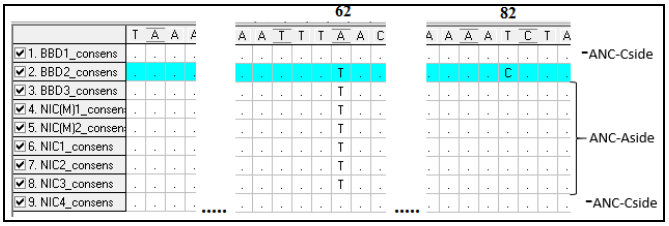


Figure 12. Sites of mutations that differentiate the three haplotypes identified within the analysed samples.

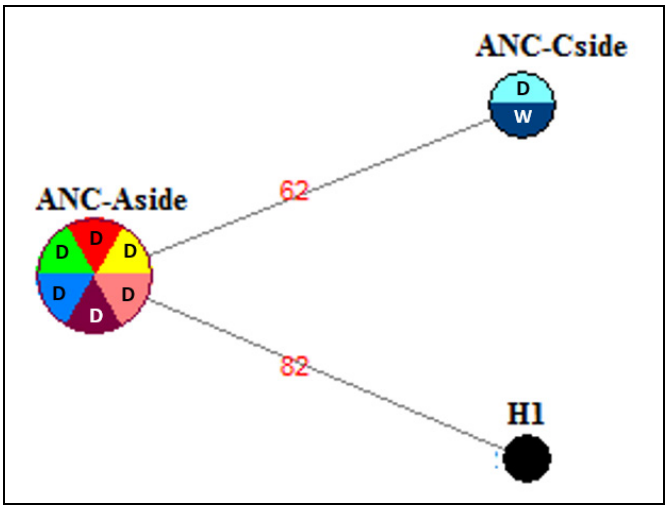


Figure 13. Haplotypes network for the samples analysed; the size of circles is proportional with the number of samples presenting that specific haplotype and each colour represents a different individual (D=domestic; W=wild).