SAMPLE SIZE AND TAXONOMIC RICHNESS IN MAMMALIAN AND AVIAN BONE ASSEMBLAGES FROM ARCHAEOLOGICAL SITES

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'Sampling is a ghost which has come to haunt the corridors of archaeology'

A. J. Ammerman et al. (1978: 123)

Abstract

It has been well known in archaeozoology that the number of animal species recognized in an assemblage increases along with the number of identifiable bone specimens. It is for this reason that comparisons between faunal assemblages of radically different sizes can be heavily biased, since the number of species would rather reflect the number of bones available for study than the number of animal taxa exploited by ancient peoples. In this study, parameters of 35 prehistoric mammalian and 29 avian bone assemblages are compared from this point of view for the first time. The numbers of identifiable bird bones result in a more intensive increase in the number of species than is the case with larger mammals (domesticates and game), most commonly encountered in prehistoric archaeozoological assemblages. The reasons behind this phenomenon include the greater number of bird species in nature, the smaller number of bones in the avian skeleton, and the differential taphonomic processes that affect selectively the remains of mammals and birds. These should all be considered during the analysis and interpretation of archaeozoological assemblages.

Kivonat

A régészeti állattanban is ismert összefüggés, hogy a leletegyüttesek nagyságával az adott lelőhelyről ismert állatfajok száma - bizonyos határig - növekszik. Emiatt a különböző méretű minták összehasonlítását objektív hiba terheli. Az utóbbi évek régészeti madártani kutatásainak köszönhetően számos lelőhely emlős- (35) és madár- (29) csontanyagát ekként összehasonlítva kiderült, a madármaradványok számbeli növekedését az újabb fajok megjelenése lényegesen gyorsabban követi, mint azt eddig a nagyobb testű emlősállatok esetében tapasztaltuk. Ennek természetes és kultúrtörténeti okai összetettek. A Kárpát-medencében több madárfaj fordul elő, mint élelmezési vagy más szempontból vadászatra méltó emlősfaj. A régészeti ásatásokról ismert madárfajok száma emiatt nagyobb az emlősökénél. Ugyanakkor a madárcsontváz a repülő életmód következtében egyszerűsödött, kevesebb csontot tartalmaz. Végül az emlősök csontjainak töredezettségi foka általában nagyobb. E jelenségek figyelembe vétele a régészeti kutatás szempontjából azért fontos, mert kihat az állatmaradványok értelmezésére. Alaposabb ismerete segíti a korabeli életmód jobb megértését, az állattartás, a vadászat és a madarászat egymáshoz viszonyított szerepének pontosabb tisztázását.

KEYWORDS: ARCHAEOZOOLOGY, ARCHAEO-ORNITHOLOGY, SAMPLE SIZE, TAXONOMIC RICHNESS, QUANTITATIVE METHODS, REGRESSION ANALYSIS

KULCSSZAVAK: RÉGÉSZETI ÁLLATTAN, RÉGÉSZETI MADÁRTAN, MINTANAGYSÁG, FAJGAZDAGSÁG, MENNYISÉGI MÓDSZEREK, REGRESSZIÓ ANALÍZIS

Introduction

Archaeozoology is a discipline aimed at understanding the relationship between people and animals in ancient times. It would be therefore of vital interest to be able to reconstruct the number of animal species exploited by human communities throughout history. This short paper is devoted to comparing the various sources of bias that may distort the comparison between the representation of two vertebrate classes, mammals and birds, in the archaeological record.

The diversity of the animal kingdom has fascinated people since at least Biblical times. Creationism reckoned with a set inventory of animal species (**Figure 1**), actually reflected in the ingenious seven-tier, hierarchical taxonomic system by Karl Linné (**Figure 2**) whose logic withstood 250 years of advancement in biology (Bartosiewicz 2006). In his ever meticulously expanded book, *Systema Naturae* (1735-1758) 20,000 plant and animal species were described (today we know approximately 1 413 000 species). Recent concern about the rapid loss of this richesse owing to environmental deterioration is a clear, post-Enlightenment, rational manifestation of the same importance we place on diversity.

In spite of their diachronically increasing interference with nature, humans have exploited only a fraction of the animals available in their environments. It is poorly understood why only some two dozen of these were domesticated (Gentry et al. 2004), and even the repertoire of hunted creatures tends to be relatively limited. Moreover, archaeozoological assemblages are understood to have been decimated by the taphonomic process and represent, therefore, only a fraction of the animal remains originally accumulated by prehistoric human activity. This fact further reduces the number of species left of the formidable richness of the original fauna.

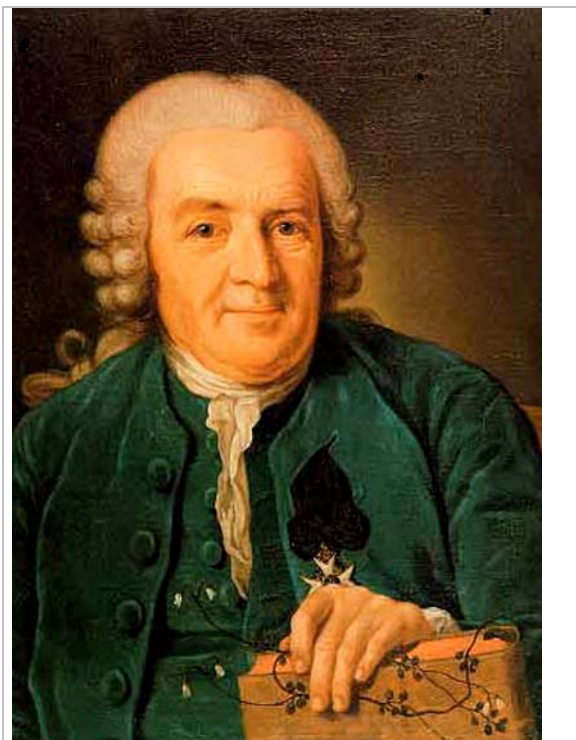**Figure 1.**

Noah's Ark by Edward Hicks (1846)

Figure 2.

Portrait of Karl Linné by Per Krafft the Elder (1774)

Materials and method

Archaeo-ornithological research during recent years in Hungary has offered a unique opportunity to compare several avian and mammalian bone assemblages from the viewpoint of taxonomic richness. Thirty-five of the 53 mammalian assemblages from Neolithic and Copper Age sites reviewed recently (Bartosiewicz 2005: Table 6.1, 61-63) have been selected in this study to be compared to 29 prehistoric sites that yielded bird remains, ranging from the Early Neolithic to the Bronze Age. Part of the avian assemblages had already been available in the literature (Bökönyi & Jánossy 1965, Jánossy 1985, Bökönyi 1992), however, eight were identified by the junior author of this paper (Gál 2004, Pike-Tay et al. 2004) and will be published in reports in progress (Gál in press/a-b, Gál 2007). Newly identified, unpublished materials used in this paper include assemblages from Balatonkeresztúr-Réti-dűlő (Copper and Bronze Ages), Balatonszemes-Bagódomb (Copper and Bronze Ages), Felsővadász-Várdomb (Neolithic and Bronze Age), Ordacsehi-Kistöltés (Bronze Age-Iron Age transition).

A notable cultural difference between the archaeological representation of the two vertebrate classes is that while one may reckon with the presence of at least five domesticates among mammals (the "Neolithic package" of dog, sheep, goat, cattle, pig and possibly even horse by the Bronze Age), prehistoric bird bone assemblages represent exclusively wild species.

Comparing relative frequencies in terms of percentages is a widely practiced method in the quantitative analysis of archaeological assemblages of all sorts. It is well known, however, that in the absence of sufficiently large samples of representative value no reliable conclusions can be drawn. Rare finds occur in small samples with negligible probability, and when they do, they tend to be disproportionately overrepresented in percentual terms: the chance discovery of a single bone representing an exotic species in an assemblage of 50 bones would yield a relatively high contribution of 2%.

It has been well known in archaeozoology that - until a certain point - the number of animal species recognized in an assemblage (R: taxonomic richness) increases along with the number of identifiable bone specimens (NISP). It is for this reason that comparisons between faunal assemblages of radically different sizes can be heavily biased, since the number of species would rather reflect the number of bones available for study than the culturally idiosyncratic number of animal taxa exploited by an ancient community (Grayson 1984: 136-137).

The interpretation of this quantitative tendency, however, is further complicated by the fact that in the archaeozoological literature animal species from all vertebrate classes (and sometimes even molluscs) tend to be pooled in such calculations, and little attention is paid to fundamental taxonomic and taphonomic differences that may affect the results. In the current study, statistical parameters for prehistoric mammalian and avian bone assemblages are compared for the first time from this point of view.

Results

The relationship between assemblage size (NISP) and taxonomic richness (R) may be studied in a rather straightforward manner using regression analyses easily illustrated in bivariate plots. Although there is a usually high, positive correlation between the number of identifiable bones and taxonomic richness, this relationship is not linear: the number of species follows increasing sample size in a degressive manner and is "exhausted" when new species are no longer encountered. In the theoretical case of truly random sampling, the least common species would be the last to occur. The degressive trend is illustrated using our sample of prehistoric mammalian bone assemblages in **Figure 3**.
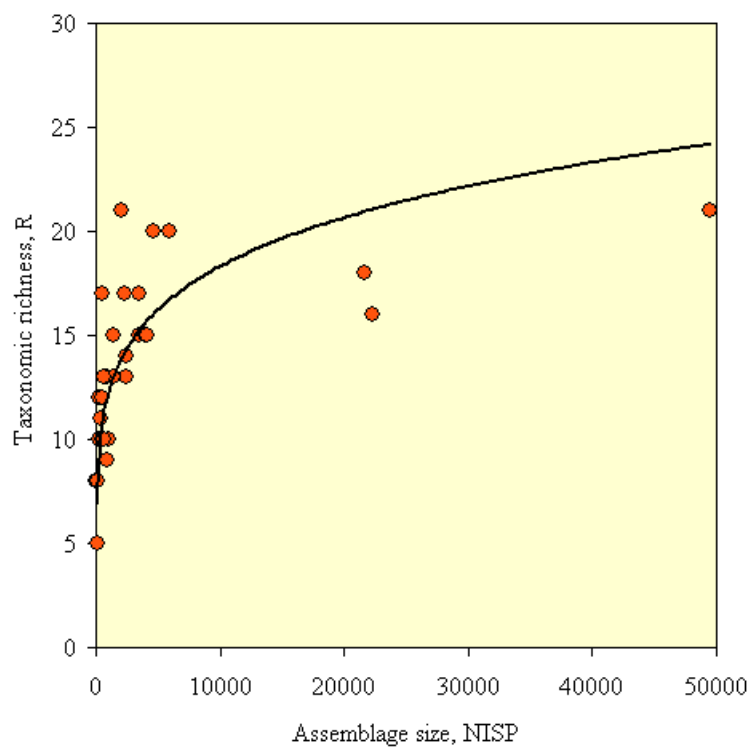
Figure 3. Plot of raw data for mammalian remains illustrating the degressive increase in taxonomic richness (R) along with increasing assemblage size (NISP)
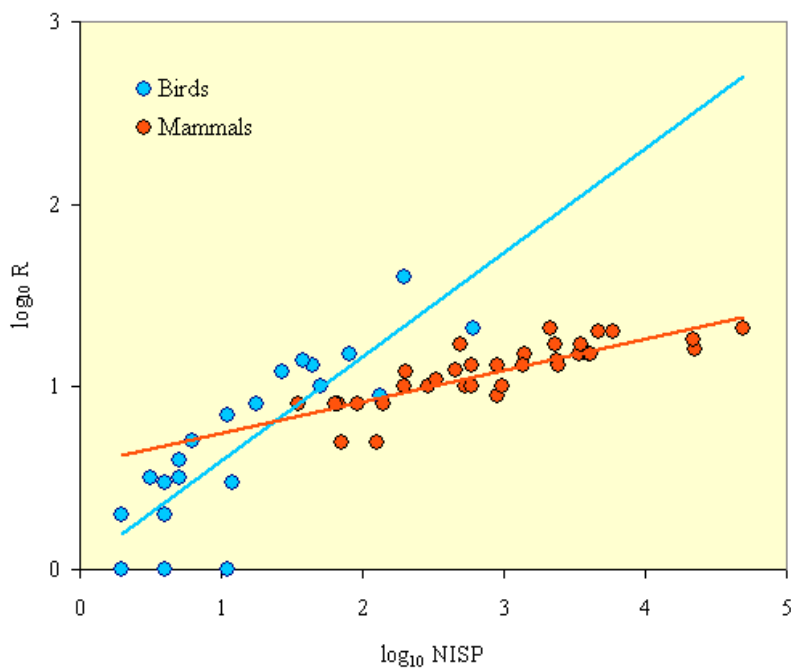

Figure 4. Differences between prehistoric mammalian and avian assemblages

This relationship can be conventionally described using exponential equations, in this case:

$$y = 3.696x^{0.174}$$

(x standing for the number of identifiable specimens and y for taxonomic richness). This equation is supported by a $R^2 = 0.692$ coefficient of determination, showing that in almost 70% of the cases the number of species recognized is indeed a function of assemblage size.

Aside from the fact that the best represented smaller assemblages dominate the left hand side of this graph, exponential equations are also difficult to compare. The heteroscedasticity of our data, i. e. taxonomic variability increasing by absolute assemblage size has been reduced by using decimal logarithms of both NISP and R (**Figure 4**). In the resulting graph the distribution of data points is more even and the trends characteristic of mammalian and bird bone assemblages may be compared more conveniently. One can see that the slope is clearly steeper with the blue data points for birds than with the red dots for mammals, but the relationship between assemblage size and taxonomic richness is similarly close in both sets of data. We can predict taxonomic richness equally well in both groups, but it increases much more rapidly along with assemblage size in the case of birds, marked in blue.

An additional advantage of this method is that the logarithmic transformation results in linear regression equations that lend themselves to easier interpretation. A summary of parameters for the two regression lines shown in **Figure 4** is given in **Table 1**.

The most striking difference between the two vertebrate classes is shown between the coefficients of regression obtained. These values describe the slope of the linear relationship that is also immediately visible in Figure 4. The more than threefold value characteristic of bird bone assemblages reveals that significantly fewer bones from birds result in the occurrence of new species. In other words, the trend of increasing taxonomic richness is less degressive in the case of avian remains, i. e. sample size is worth increasing. Differences in the coefficient of integration (intersection point with the y axis representing taxonomic richness) indicate that there is a smaller rate of increase to be reckoned with in mammalian bone assemblages. Coefficients of determination show the aforementioned close relationship between the two variables in both assemblages, that are significant on a high level of statistical probability.

Discussion

The striking difference between the parameters obtained for mammals and birds respectively, is

rooted in a complex of natural and culture-historical causes whose effects would be impossible to separate. Three aspects are definitely worth considering:

Taxonomy

To begin with, the number of bird species known from archaeological excavations is much greater than the number of mammals systematically exploited in antiquity. It has to be mentioned, however, that this is a reflection of proportions visible in the modern fauna: the variety of birds living in natural conditions is also much greater than that of medium-sized and large mammals, whose bones are most commonly encountered in archaeozoological assemblages (**Figure 5**).
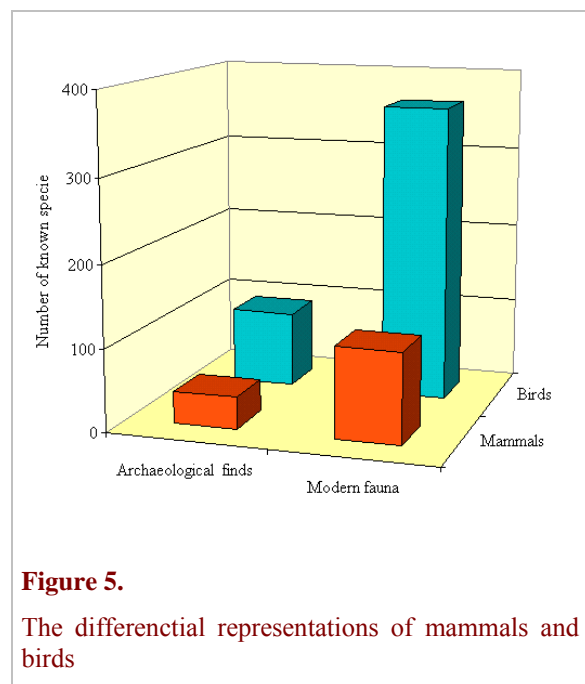

Figure 5.

The differencial representations of mammals and birds

Archaeo-ornithological data first summarized in this study are compared to the numbers of mammals (excluding "microfauna", i. e. small rodents, bats, etc.) known from archaeological excavations in Hungary (Vörös 2003: 73-74) and a modern-day census for both vertebrate classes (Rakonczay ed. 1990) in **Table 2.**

This tabulated summary shows that the mammals under discussion here tend to be somewhat better represented in excavated assemblages than birds. On the other hand, the number of known bird species is significantly higher both in nature and archaeozoological samples. Although to some extent it may be coincidental, the 3.3 rate calculated between modern bird and mammalian species corresponds exactly to the ratio between the coefficients of regression listed in Table 1 (0.571/0.174=3.3).
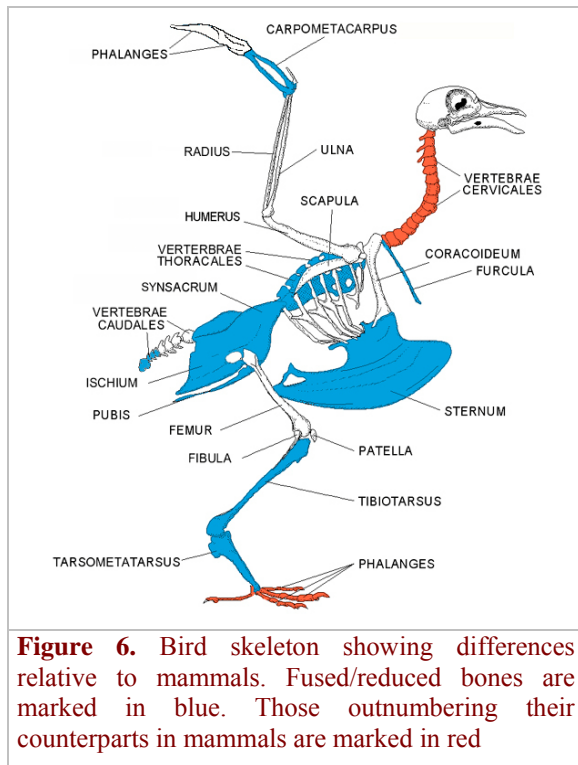
Figure 6. Bird skeleton showing differences relative to mammals. Fused/reduced bones are marked in blue. Those outnumbering their counterparts in mammals are marked in red

Anatomy

In addition to the indubitably greater number of species available to prehistoric hunters, anatomical differences between the skeletons of birds and mammals may also impact on the differential representation of these two vertebrate classes in archaeozoological assemblages.

Owing to the mechanical requirements of flying, the bird skeleton has been reduced to significantly fewer bones during evolution (**Figure 6**).

The resulting structures increase stability mid-air and the lack of relatively robust articulations saves some weight. One may count 75-100 bones in an avian skeleton, depending on the number of cervical vertebrae and ribs, if the skull and pelvis are taken as single bones.

Mammalian skeletons, on the other hand, are composed of approximately 200 elements on average, when the skull and pelvis are counted as single bones. While the number of cervical vertebrae is constant (7) complex articulations that aid locomotion on ground (especially between vertebrae and in the carpal and tarsal joints), increase the weight of mammals in comparison with birds (**Figure 7**).

Taphonomy

Both the number of species available to prehistoric people and the aforementioned quantitative traits of the skeleton influence the archaeological representation of mammals and birds through a filter of various stages in the taphonomic process

that determine the final composition of archaeozoological assemblages.

Animal exploitation in prehistory involved a number of decisions, beginning with the choice of animals to be culled or hunted. Evidently, access to various taxa differed broadly between animal keeping, terrestrial hunting, fowling, fishing and gathering molluscs. The fauna of the habitat within which humans settled, therefore, is reflected but selectively in archaeological assemblages (Bartosiewicz 2001).

Even the animals exploited may have been processed differently not only in light of their natural anatomy, but also by cultural tradition. Body parts of larger mammals were exposed to more intensive butchery but possibly less transport than the more "portable" carcasses of birds. However, cultural difference may be hypothesized even in this regard (Gál 2007).

Finally, the larger bones of mammals tend to be more heavily fragmented in archaeological deposits, while the delicate bones of birds disintegrate at a different rate. Therefore the methods of recovery (especially the use of water-sieving or lack thereof) further increase the gap between the representation of mammalian and avian remains. It is exactly the few bones that are more numerous in the avian skeleton than in mammals (cervical vertebrae and phalanges; c. f. Figure 6) that will hardly ever be recovered by hand-collection only.
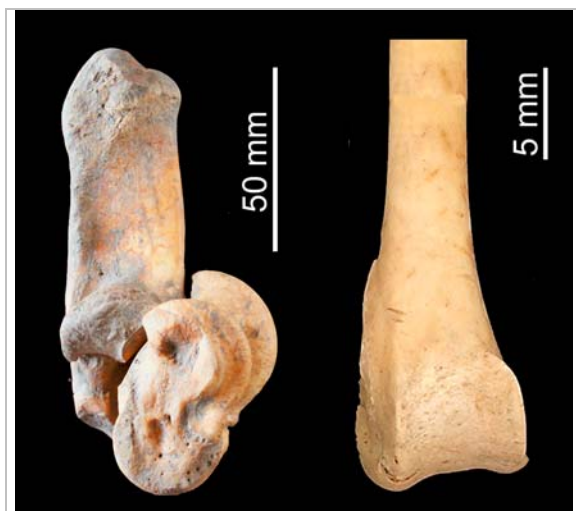

Figure 7.

Difference in the complexity and robusticity of tarsal bones in red deer (left) and mallard (right). The separate calcaneus and astragalus of mammals correspond to the lower, rounded half of the tibiotarsus in mallard. They are both reduced and fused in birds (Sajópetri 46).

Table 1
Parameters of linear equations for mammalian and avian assemblages shown in Figure 4.

Vertebrate class	Number of sites	Coefficient of			Level of probability
		regression	integration	determination	
Mammal	35	0.174	0.568	0.692	0.010
Bird	29	0.571	0.020	0.750	0.000

Table 2.
The number of mammalian and avian species

	Mammals	Birds	Bird / Mammal rate
Known modern fauna	110	363*	3.3
Archaeological evidence	39	93	2.4
Percent of representation	38 %	26 %	

*Herman (1901) listed 337 species from "historical" Hungary incl. the Carpathians

Conclusions

Sampling affects mammalian and bird remains differently. Our study has shown that the numerical representation of identifiable bird bones results in a lot more intensive increase in the number of species than is the case with larger mammals, domesticates and game, most commonly encountered in prehistoric archaeozoological assemblages. This trend could be traced back to an inseparable complex of taxonomic, anatomical and taphonomic differences.

The importance of considering these differences from an archaeological point of view is that through sample size, they have a direct impact on the interpretation of animal remains. The use of large assemblages as well as familiarity with such qualitative detail may help better understanding ancient lifeways and shed light on the relationships between animal keeping, hunting and fowling, whose studies require different methods and can therefore be integrated only within a relatively loose interpretational framework.

Acknowledgements

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