ARCHAEOZOOLOGY OF THE NEAR EAST
VI

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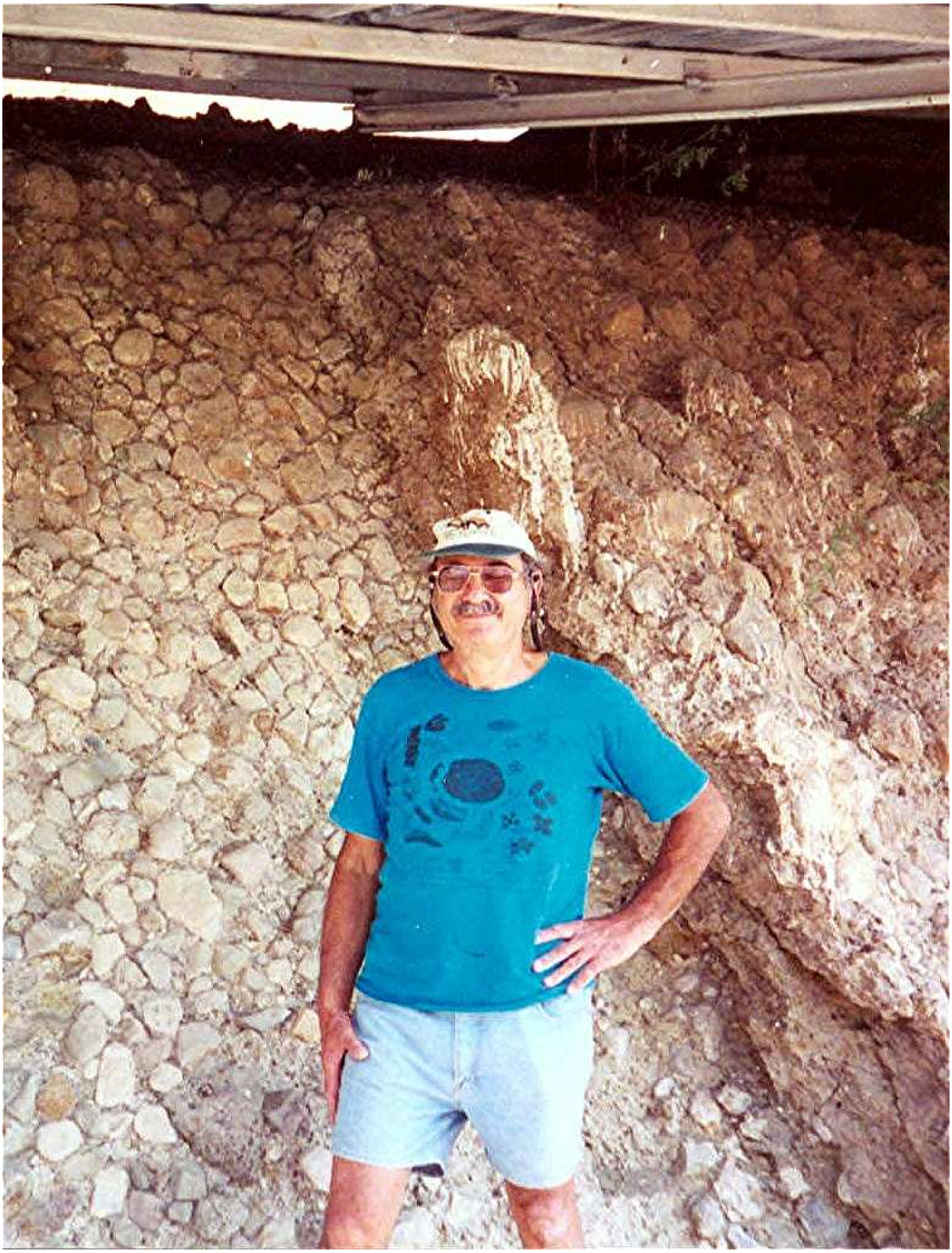

Prof.Dr. Eitan Tchernov

This volume is dedicated to the memory of Prof. Dr. Eitan Tchernov, in fond memory of his enthusiasm and support to many in the field of archaeozoology**.**

Preface

The ASWA VI meeting was held at the Institute of Archaeology, University College London, from 30th August-1st September 2002, timetabled to follow on the heels of the ICAZ meeting in Durham, UK. Over 55 participants attended the meeting, travelling from 13 countries, bringing the latest research results from our field. As usual, it was a pleasure to see so many doctoral students presenting their research – a sign for a very healthy future for zooarchaeology in south west Asia. It is still unfortunate, however, that colleagues from some Middle Eastern countries were unable to attend due to financial and political constraints.

Presentations were organized into the following six themes, which highlight the scope of the ASWA membership: Animals in Palaeolithic and Epipalaeolithic Levant; Neolithic Patterns of Animal Use; Animals in Neolithic Anatolia; Animals in the Chalcolithic and Bronze Ages; Iron Age, Nabatean and Roman Patterns of Animal Use; Animals in Ancient Egypt. There was also a poster session, and contributors were invited to submit papers to this volume.

As always with the ASWA forum, the meeting served to welcome new scholars to the group, but was also very much a reunion of old friends and colleagues who have been sharing new information and discussing issues of joint interest for many years now. In this vein, it is a great sadness that ASWA VI was the last international meeting attended by Prof. Eitan Tchernov, an original founder of the group and mentor and inspiration to so many. For many of us, it was the last time we saw Eitan, and experienced his usual incisive comment, unstoppable enthusiasm for the subject, and warm friendship. He will be greatly missed.

ASWA VI was supported by the Institute of Archaeology, UCL, who provided facilities and financial and administrative help. In particular, the organizing team was aided greatly by the administrative assistance of Jo Dullaghan at the Institute. ARC bv (Archaeological Research and Consultancy, Groningen, The Netherlands) once again shouldered the finances of the publication of the proceedings, and we are extremely grateful for their continuing support. Many thanks are also due to the postgraduate student helpers from the Institute of Archaeology who made the meeting run so smoothly: Banu Aydinoğlugil, Jenny Bredenberg, Chiori Kitagawa, Peter Popkin, and Chris Mosseri-Marlio (who also produced the logo reproduced on the frontispiece of this volume).

Many thanks to all the participants for making the meeting such a success!

Louise Martin
London 2005

Participants of the 6th ASWA Conference, held at the Institute of Archaeology, University College London.

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Contents

Preface

HOW LOW SHOULD WE GO? USING HIGHER-LEVEL TAXONOMY AND TAPHONOMY IN PALEOECOLOGY

Miriam Belmaker[1]

Abstract

There have been two trends in paleocological research. The first concentrated on the identification of specimens to species and genus level. This methodology enabled precise paleocological reconstruction based on modern analogues. On the down side, this type of analysis left out many animal bone fragments that were not identifiable. The second trend incorporated higher-level taxonomy. Since many tribes and families are similar in their habitat requirements, the analysis of the unidentified fragments has the potential to alter previous conclusions (based on specimens identified to species alone), providing a more comprehensive picture of the environment.

This paper addresses the question of whether identification to higher-level taxonomy may change previous paleoecological inferences from prior analyses of Stratum I 26 from the site of ‘Ubeidiya. Two databases are compared. The first is the published database (Tchernov 1986a and b), which includes only specimens identified to species and genus; the second includes all fragments identified at higher taxonomic levels. Different paleoecological models are applied to both databases.

Results indicate that NISP increased from ca. 60 to 2300 with inclusion of the fragments. Species richness, based on morphotyping, increased ~3 fold. The paleoecological reconstruction shifted from a habitat dominated by woodland and woodland-bushland to one which included grassland environments.

These results suggest that using higher-level taxonomy is of great importance in paleoecological reconstruction (as opposed to Bar Oz and Dayan, 2002). The discrepancy arises from the fact that a low diversity site (such as those from Levanite Epipalaeolithic) may be heavily dominated by a single species (e.g. gazelle) while the high richness and diversity in ‘Ubeidiya make palaeolenvironmental reconstructions much more susceptible to a change in analytical methodology. One cannot *a priori* conclude that using higher level taxonomy will or will not change the biodiversity of a site, and each site is a case on its own.

Résumé

Il y eu deux tendances dans les études paléoécologieques. La première se focalise sur l’identification de spécimens jusqu’au rang de genre et d’espèce. Cette méthodologie a permis les reconstitutions paléoécologiques fondées sur les analogies modernes. De l’autre côté cette approche analytique a délaissé beaucoup de fragments non identifiés. La seconde tendance incorpore des niveaux taxinomiques plus élevés. Du fait que beaucoup de tribus et de familles sont similaires dans les exigences de type d’habitats, l’analyse des fragments non identifiés peut altérer les conclusions précédentes (fondées sur les identifications spécifiques seulement), et fournissant une image plus exacte de l’environnement.

Cet article cherche à examiner si une identification de plus haut niveau taxinomique va changer les précédentes conclusions paléoécologiques issues des précédentes analyses du strate I 26 du site d’‘Ubeidiya. Deux bases de données sont comparées. La première est celle publié par Tchernov (1986), qui n’inclue que les spécimens identifiés jusqu’au rang de genre et d’espèce; le second comprend tous les fragments identifiés à un niveau taxinomique plus élevé. Des modèles paléoécologiques différents ont été appliqué aux deux bases de données.

Les résultats indiquent qu’avec l’addition des fragments les NISP augmente de ~60 à ~2300. La richesse spécifique basé sur la typo morphologie a augmenté d’environ trois fois.La reconstitution paléoécologique a glissé d’un habitat dominé par un paysage boisé, à boisé et buissons vers un pâturage.

Ces résultats suggèrent qu’utiliser un niveau taxinomique plus élevé est très important dans les reconstitutions paléoécologies (contra Bar Oz, ASWA 2000). Le désaccord est soulevé par le fait qu’un site à faible diversité (comme ceux de l’épipaléolithique Levantin) pourrait être très fortement dominés par une seule espèce (e.g. Gazelle) alors que la forte diversité et richesse à ‘Ubeidiya entraîne un changement d’approche analytique pour les reconstitutions paléoenvironnementales. On ne peu pas conclure a priori qu’utiliser un niveau taxinomique plus élevé peut ou ne peut pas changer l’image de la biodiversité d’un site et chaque site est un cas singulier.

Key Words: Paleoecology, methodology, biodiversity, taxonomy, ‘Ubeidiya.

Mots Clés: paléoécologie, méthodologie, biodiversité, taxonomie, ‘Ubeidiya.

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Introduction

Evolutionary processes have resulted in the morphological adaptation of organisms to their habitat. Hence, the presence of a mammalian species obligatory to a specific environment, and its relative abundance has been used as evidence for climatic change e.g. the presence of reindeer, today in northern latitudes, in the southern latitudes of Europe served to indicate the limits of glaciations during the Pleistocene (Delpech and Heintz 1976). The main premise underlying this method is the unique niche requirements of the species. In order to estimate habitat change, fossil taxa are assigned a preferred habitat based on the habitat preference of the nearest living relative. The relative frequency of an indicative species is then used as a proxy of the preferred habitat within the total environment. For example, if the extinct species *Parameriones obeidiensis* is assigned a grassland habitat similar to its living descendant *Meriones tristrami* (Tchernov 1986a), and it comprises 18% of the fossil assemblage in question, then grasslands are equally assumed to comprise 18% of the total paleoenvironment of the site in question. It is important to note that percentages are cumulative so that the total percent of all grassland species are taken together.

Despite being widely used, this method, called the Modern Analogue Relative Frequency (MARF), has several shortcomings (Andrews 1995). First, relative species frequencies are highly sensitive to taphonomic biases. These may be concerned with the time and space averaging, depositional milieu, differential preservation, random effects or anthropogenic bias (Behrensmeyer 1978, 1982, 1984, 1992; Behrensmeyer *et al* 1986, 1992; Behrensmeyer and Hill 1980; Hanson 1980; Lyman 1984, 1994; Voorhies 1969). Second, when using single species adaptations there is a strong dependency on precise taxonomic identification. The habitat associated with extinct species is usually based on morphological similarities to extant related species. This premise, of resemblance in paleo and modern habitats between phylogentically close species, although probably true for most cases, should not be taken as an *a priori* assumption (Andrews 1995). Moreover, since the identification is restricted to body elements that can be identified to species with a known phylogeny, the proportion of assemblage that can be identified represents a mere fragment of the total assemblage available to the researcher.

To overcome these problems, "taxon free" or "phylogeny free" methods have been developed. The methods associate different ecomorphological characters with a species regardless of its taxonomic identification. This allows for comparison of assemblages that differ in species composition due to spatial and temporal distances, but that have similar ecomorphological diversities. The widely used methods are the ecomorphological distribution and the cenogram graph. The ecomorphological distribution was developed by Andrews *et al* (1979) and later refined by Reed (Reed 1995, 1996, 1998). Andrews *et al* (1979) compared four African modern communities from various localities; lowland forest, montane forest, flood plain and woodland-bushland. These environments were found to differ significantly from one another on scales of percentage of different taxonomic orders (taxonomy), size distribution, locomotion and feeding adaptation (Andrews *et al* 1979). Moreover, when fossil assemblages were studied in a similar manner, they were statistically assigned to modern communities. Such analyses have since been done for many Neogene and Quaternary sites (Andrews 1989, 1992, 1995, 1996; Andrews *et al* 1979; Andrews and Nesbit Evans 1978; Cerling *et al* 1992; Fernández-Jalvo *et al* 1998; Gagnon 1997; Gunnell 1995; Kay and Madden 1997; Nesbit Evans *et al* 1981; Reed 1995, 1996, 1998).

The second method developed by Legendre is the cenogram graph (Legendre 1986, 1987; Valverde 1967). This method correlates the rank species by size (on the x axis) with log body weight (on the y axis). The mammalian species fall on a regression slope. Carnivores and bats fall above and beneath the slope respectively and hence are removed from the analysis. The angle of the slope produced correlates with open *versus* closed and humid *versus* dry environments. This method has been applied to paleontological sites worldwide (Gunnell 1990; Legendre *et al* 1991; Montuire 1994, 1998, 1999; Montuire and Desclaux 1997; Montuire and Girard 1998; Morgan *et al* 1995; Spencer 1991; Wilf *et al* 1998).

The advantages of the ecomorphological methods are that assumptions are based on actual data rather than *a priori* assumption, and since the phylogentic relationship does not need to be determined, a higher proportion of the assemblage may be included in the analysis. On the down side, the habitat reconstructions are more generalized that in the MARF method and since obtaining body size is dependant on morphometric measurements, they are confined to complete specimens which still restricts the size of the assemblage available.

A third alternative method is presented here. This method of using higher-level taxonomy with taphonomic considerations is based on the working hypothesis that congeners, members of the same family and the same tribe often share similar environments. For example, all three member of the genus *Apodemus* (*A. sylvaticus*, *A. flavicollis* and *A. mystacinus*), although they differ in specific habitat preferences, can be characterized as generalized forest dwellers (Harrison and Bates 1991).

Using this method, all fragments in the assemblage are identified to the lowest taxonomic unit possible but, if due to the high level of fragmentation, abrasion and/or weathering, identifications are not possible, higher taxonomic levels are used. Ecological preferences are assigned to the taxon based on the living members of the same taxon. The difference from the modern analogue method is that we do not need to assume the *nearest* living member, which may or may not have similar habitat requirements. Since we are using extant family or tribe levels, which share generalized habitat preferences, we can compare them to actual members of the modern family. While not all fossil taxa belong to extant families, it is commonly the case with the overwhelming majority of Plio-Pleistocene taxa. While the advantage of this method is that it is the most inclusive of all methods due to the proportion of the assemblage which it analyzed, the reconstructions are very generalized, but serve to give a broad view of overall landscape changes rather than detailed ones.

Many faunal assemblages were analyzed in the past with a paleontological orientation, which emphasizes taxonomic identification. Paleoecological reconstructions that stem from such studies were usually based on the MARF method. Reanalysis of old assemblages in light of new taphonomic models, and the inclusion of fragments previously unidentified, raises questions of the cost benefit value of such studies. An analogous issue is the identification of shaft fragments and the implication of their inclusion on subsequent interpretations of the data. This has been widely addressed with regards to the question of human procurement of meat and the question of hunting *versus* scavenging in the Middle Paleolithic (Marean and Kim 1998; Stiner 1991, 1994, 2002). Contrary to the extensive discussion in the literature concerning anthropological questions, the methods have been mostly ignored as far as paleoecology has been concerned, although results for the Epipaleolithic site for Nahal Hadera V indicate that a revised study including the previously unidentified small fragments did not change the paleoecological reconstruction obtained from the fauna (Bar-Oz and Dayan 2002).

The aim of this paper is to test a paleoecological reconstruction obtained using the higher-level taxonomy method compared to one obtained using the MARF method. Stratum I 26 of the Lower Pleistocene site of ’Ubeidiya will be used as a case study.

The site

‘Ubeidiya is situated in the Central Jordan Valley (Fig. 1) (Bar-Yosef and Goren-Inbar 1993). The geological deposits of the ‘Ubeidiya Formation are primarily shoreline lake sediments. Post-depositional tectonics caused the sediments to fold and fault resulting in two anticlines separated by a small syncline. The faulting resulted in the dip of the layers, at times to nearly 80 degrees (Bar-Yosef and Goren-Inbar 1993; Bar-Yosef and Tchernov 1972). Excavation was conducted by opening four geological trenches, transverse to the strike of the strata (Picard and Baida 1966), which were numbered with Roman numerals I - IV. Within each trench, the strata were given Arabic numerals, from oldest to youngest, thus, I 26 is the 26th stratum of trench I (Fig. 2).

The overall reconstruction of the site is of a delta of an ephemeral stream entering into a fresh-water lake (Picard and Baida 1966). Four cycles have been identified at the site within the ‘Ubeidiya Formation corresponding to four cycles of depositional environments (Picard and Baida 1966). The four cycles are Limnic Inferior (LI), Fluviatile Inferior (FI), Limnic Upper (LU) and Fluviatile Upper (FU). Each cycle represents several strata of similar deposit type. Low-energy lacustrine sediments of silt, clay and oolithic limestone dominate the limnic cycles while High-energy clastic sediments of conglomerates; chalks, marls and basaltic sands dominated the fluviatile cycles (Fig. 3).

Stratum I 26 is situated within the FI cycle and comprises of sand and conglomerates of flint, limestone and basalt. It has a maximum thickness of ca. 80 cm, and thickens along its strike (in a northeast direction).

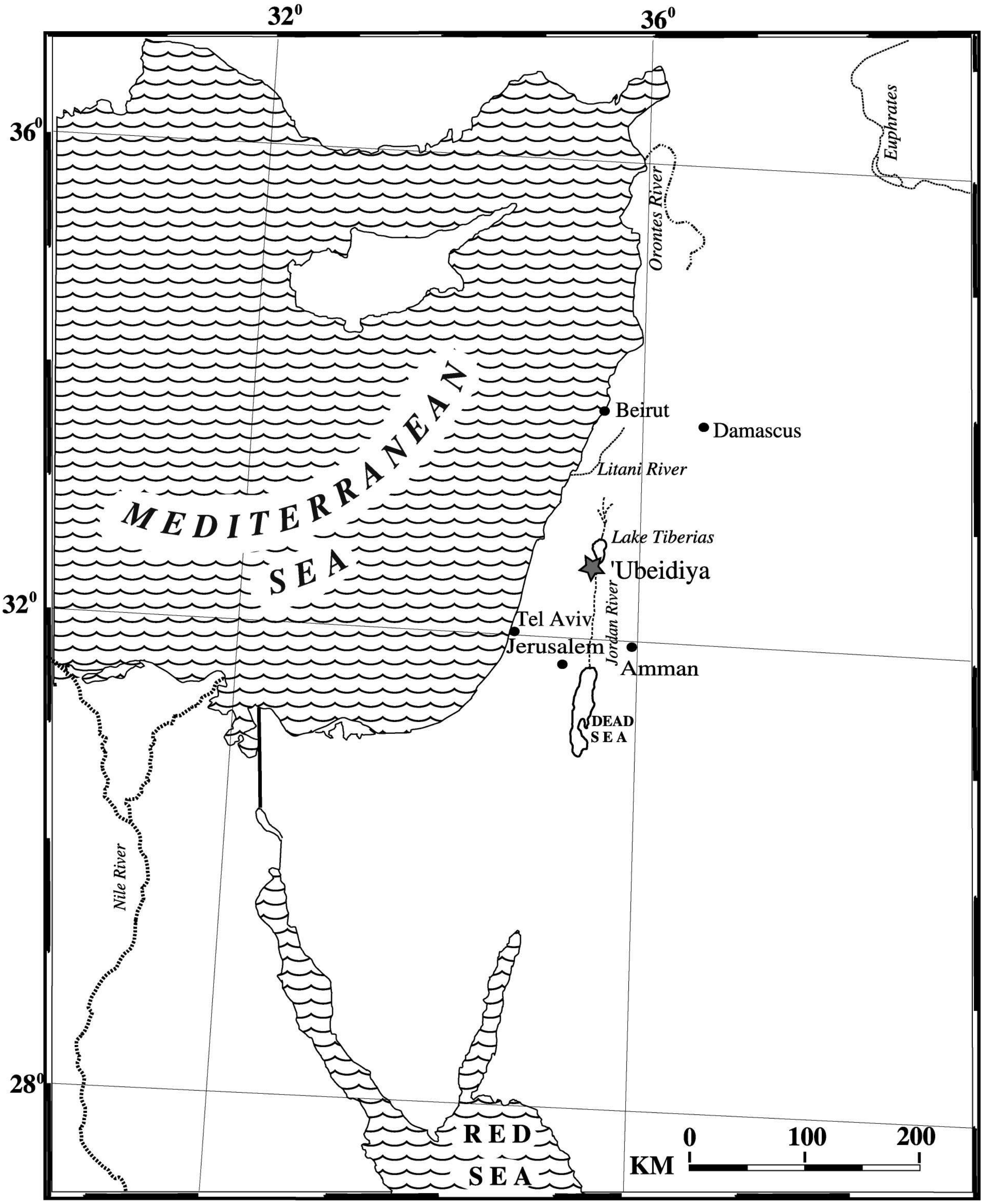

Fig. 1. Location of the site of ‘Ubeidiya.

The stratum was originally subdivided into 4 substrata: I 26a through d. Both I 26a and I 26d, were originally called "living floors". This identification has since been abandoned as sedimentological analyses, degree of preservation of the artifacts and lack of refitted pieces indicated that there were a series of palimpsests accumulated within a gravelly beach deposit. The artifact densities did not differ significantly enough between the levelled pebbled horizon "living floors" and the interspersed clayey sub-layers to warrant a separate analysis for the sub-strata (Bar-Yosef and Goren-Inbar 1993). An area of 121 square meters was exposed for sub-stratum I 26a and a somewhat smaller area for three addi-

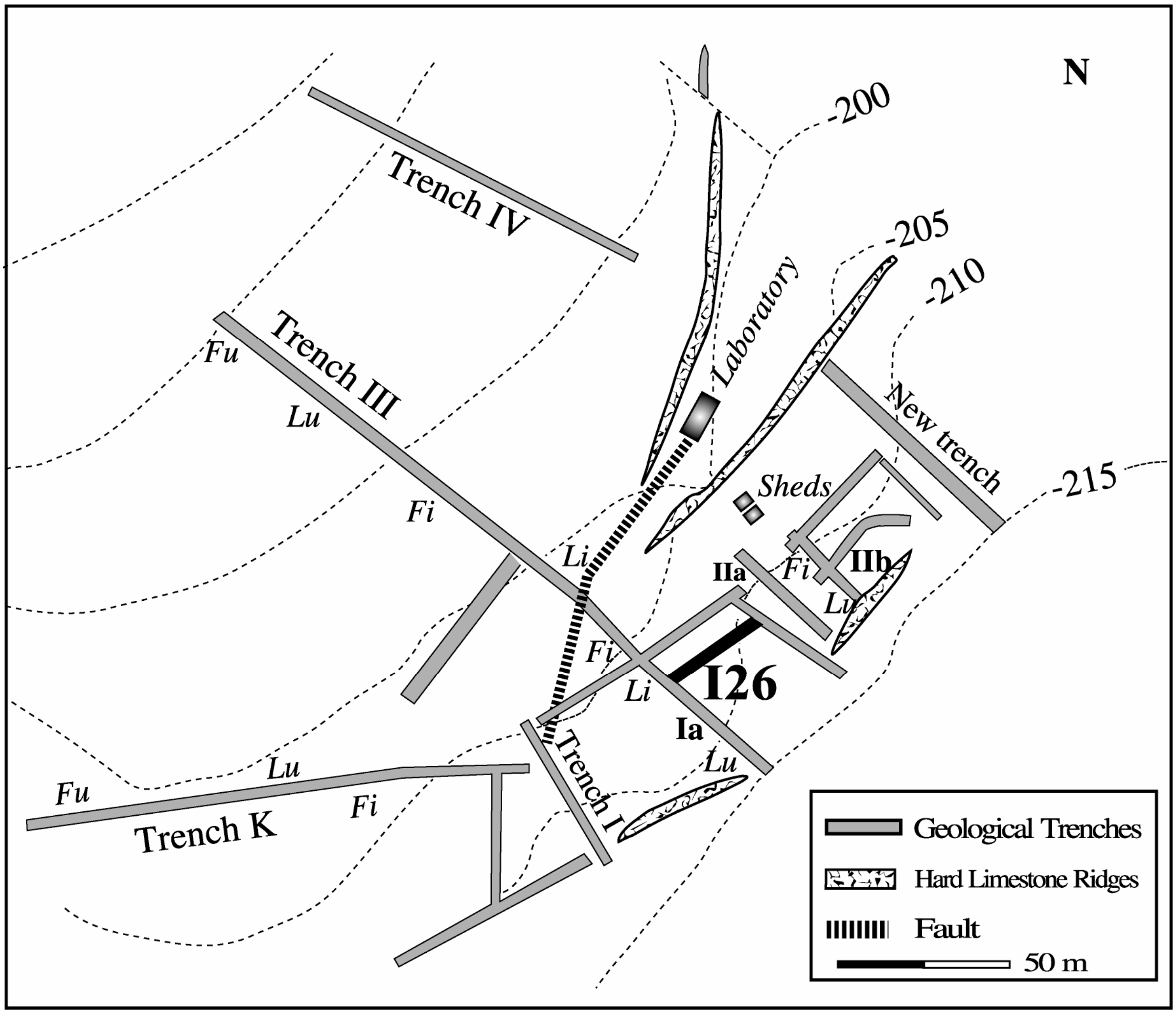

Fig. 2. Map of ‘Ubeidiya excavation denoting the location of stratum I 26.

tional sub-strata I 26b-d (Bar-Yosef and Goren-Inbar 1993). Following the results from the lithic analysis, faunal analysis in this study was combined for all sub-strata.

The dating of the site relies primarily on biochronology and on the position of the formation within the stratigraphic sequence of the Central Jordan Valley. The Cover Basalt lava flows were K/Ar dated around the Sea of Galilee to 5 -3.3 million years ago (Heinmann and Braun 2000; Mor 1993). The ‘Erq el Ahmar Formation overlies the Cover Basalt and underlies the ‘Ubeidiya Formation. It is assigned to the Pliocene. Paleomagnetic studies have shown that the ‘Erq el Ahmar Formation includes both normal and reverse sequences (Braun *et al* 1991; Verosub and Tchernov 1991). A detailed study has indicated that the normal polarity sequence is correlated with the normal zone within the Olduvai sub-chron dated from 1.96-1.78 million years ago (Ron and Levi 2001). Paleomagnetic studies of the ‘Ubeidiya Formation itself, have indicated reversed polarity indicating that the formation predates the Brunhes/Matuyama boundary at 0.78 million years ago (Braun *et al* 1991; Opdyke *et al* 1983; Verosub and Tchernov 1991). The Yarmouk Basalt lava flow, which overlays the ‘Ubeidiya Formation, and has been radiometrically dated to 0.79 ± 0.17 million years (Braun *et al* 1991; Heinmann and Braun 2000), serves as an upper limit for the formation.

To date, the only way to estimate within which part of the Matuyama chron ‘Ubeidiya is deposited in is to rely on the biostratigraphy and cultural evidence. Haas suggested affinities to the European Villanfranchian fauna, which places the formation within the Lower Pleistocene (Haas 1961, 1963, 1966, 1968; Stekelis *et al* 1960). Despite suggestions for an older date (Repenning and Fejfar 1982), a revision of the fauna validated the original estimation (Tchernov 1987, 1988). Correlation with European fauna identified three taxa groups corresponding to Mammalian Neogene zones (MN) 20

West		Geological Trenches		East	
Cycle	**K**	**III**	**I**	**II**	**Type of Environment**
FU		**Fault** **92** **86**	**Naharayim Formation** **erosion**		**Fossil, soils, screes and fluviatile deposits**
LU		**85** **56**	**42** **~|** **33**	**51** **~|** **43**	**Marshy to open, turbid like, with some fluviatile penetration**
FI		**48-55**	**28-32**	**41-42**	**Screes in the west and fossil soils**
		47	**26-27**	**37-40**	**Shoreline deposit**
			25 **~|** **21**	**36** **|** **33**	**West: fossil soils and fluviatile deposit** **East: muddy to non-marshy littoral**
		26	**20**	**32**	**Shoreline deposits**
	29-30	**23-25**			**Wadi beds, gravel laid by floods**
		22	**17-19**	**28-31**	**Muddy littoral to fossil soils**
			top 15-16	**26-27**	**Fine shoreline conglom. covers living floor**
			main 15	**22-25**	**Swampy, muddy littoral**
			13-14	**21**	**Shoreline deposits**
	20	**20**	**6-12**		**Swampy, muddy littoral**
LI	**19**	**19**	**(layers missing due to fault)**	**19-20**	**Quiet, shallow water with water plants**
		18		**17-18**	
		14-17		**11-16**	**Deep water to littoral**
		13		**9 c,d-10**	
		12			**Muddy, shallow littoral**
		10-11		**9 a,b**	
		9	**1**	**8**	**Deep water lake**
		4-8	**2-5**	**2-7**	**Swampy and littoral to deep water**
		Base of 'Ubeidiya not exposed			

Fig. 3. ‘Ubeidiya stratigraphic sequence. Large type denotes the location of stratum I 26.

through 16. The most indicative species corresponding to absolute dating in Europe are *Lagurodon* cf. *arnakae* and *Stephanorhinus etrucus etruscus*. The presence of both younger and archaic species in the same locality suggested a date ca. 1.4 – 1.5 million years ago. This observation is corroborated by similarities of the lithic assemblage to Olduvai Upper Bed II where the Early Acheulian was dated to ca. 1.3 million years ago (Bar-Yosef and Goren-Inbar 1993).

Methods and Materials

All mammal remains were identified to the lowest taxonomic level possible depending on the state of fragmentation, abrasion and weathering. If identification to species was not possible, higher-level taxonomy was applied i.e. genus, tribe and family. Identification was done by comparison to the comparative mammalian collection of the Hebrew University of Jerusalem. The data obtained was compared with the published faunal analysis by Tchernov using the MARF method of paleoecological reconstruction (Tchernov 1986a).

Each taxon (for this study as well as the taxa published by Tchernov (Tchernov 1986a)) was assigned a preferred habitat based on the preferred habitats of living genera, tribes and families. The working hypothesis is that during the Pleistocene, 'Ubeidiya was already situated with the Mediterranean region, as today (Suc 1987), and hence all types of environments reflect those present in the Mediterranean climate. A wet cold winter and hot dry summer characterize the Mediterranean region. Within the circummediterranean, several different subhabitats within the general Mediterranean region can be discerned. Thus, while the vegetation in the low temperature areas is usually forest with 90-100% tree coverage, the higher temperatures exhibit batha or garigue with less than 40% tree coverage (Rabinovich-Vin 1986). The limiting factors that influence the type of vegetation are climatic - precipitation and temperature (Waisel *et al* 1982).
Five habitat types were identified:

1. Aquatic habitats include all persistent water sources and the immediate adjacent banks around them
2. Grassland habitats include areas with high precipitation but no woody vegetation types
3. Woodland-bushland habitats include all areas with woody vegetation types with densities low enough so that treetops do not touch (trees are defined as woody plants taller than 1 meter)
4. Woodland habitats included all areas with woody vegetation types with densities high enough so that treetops touch
5. Arid environments include sparse vegetation.

Analysis was based on Number of Identified Specimens (NISP) relative frequency. The Brillouin index was used as a diversity index. Although the Shannon-Wiener index of diversity (H') has been commonly applied to archaeofaunal analyses it depends on a set of underlying assumptions that must be taken into consideration. Shannon-Wiener (H') assumes random sampling from an infinitely large population and that all species in the population are represented in the sample (Magurran 1988). Therefore, this index by its very nature should not be applied to archaeofaunal assemblages. The Brillouin index (HB) assumes a non-random sampling in which the sample is completely analyzed, while the total number of species in the population in unknown (Magurran 1988). These conditions are met in archaeofaunal assemblages, which are characterized by a non-random, finite sample size. Therefore, the appropriate index for archaeofaunal analysis is the Brillouin index. The results were compared to sites from a various periods in the region. Statistical analysis used StatView 5.1, MS Excel 2001 and Kovatch MVSP 3.13d. Differences between the distributions were tested using chi-square and adjusted g test and UPGMA Cluster analysis based on the chord distance index.

Results

The re-analysis of Stratum I 26 included 2663 fragments. Of those, 350 fragments were identified to family level or lower as opposed to 63 in the published list by Tchernov (Tchernov 1986a). The inclusion of previously unidentified fragments increased species richness (S) from 8 to 29. The Brillouin index (HB) increased from 1.453 to 2.251, while evenness (HB') decreased from 0.774 to 0.704 (Table 1).

Comparison of habitat distribution for stratum I 26 using higher level taxonomy (this study) and MARF (Tchernov 1986a) is presented in Figure 4. The use of higher-level taxonomy reversed the paleoecological interpretation from a woodland and woodland-bushland dominated one (together ca. 70%) in the MARF analysis to a mixture of woodland and grassland in which grassland habitats occupy ca. 20% of the total in the higher-level taxonomy analysis. In both reconstructions, the aquatic habitat is ca. 35% of the total area. Since the relative frequency of the aquatic fauna did not change, the data was recalculated with the exclusion of the aquatic fauna. Results presented in Figure 5 indicate that the shift is even more dramatic and the increase in grassland habitat using the higher-taxonomy method is ca. 30%. The distribution for both types of analyses differ statistically for both the distribution with aquatic fauna (χ^2=19.783 df=4 p value=0.0006 N=439) and without the aquatic fauna (χ^2=20.047 df=3 p value=0.002 N=284).

Table 1. Distribution of taxa in ‘Ubeidiya I 26 NISP (percent) and diversity indices for MARF method (Tchernov, 1986a, b) and higher-taxonomy method (this study)
The presence of hominids is evident by the lithic remains although no actual human remains were found and hence cannot be quantified.

Taxa	**This study NISP (%)**	**Tchernov 1986a, b NISP (%)**	**Habitat preference**
Crocidura ssp. (*C. leucodon*/ *C. russula*)	5 (1.43)	0 (0)	Woodland-Bushland
Macaca sylvana	2 (0.57)	0 (0)	Woodland
Homo ergaster	1 (0.29)	0* (0)	Woodland-Bushland
Ursus etruscus	2 (0.57)	0 (0)	Woodland
Canis cf. *etruscus*	1 (0.29)	0 (0)	Woodland-Bushland
Canis arnensis	4 (1.14)	6 (9.52)	Woodland-Bushland
Lutra sp.	3 (0.86)	1 (1.59)	Aquatic
Felidae sp. size of *Felis silvestris*	1 (0.29)	0 (0)	Woodland-Bushland
Felidae sp. size of *Felis chaus*	1 (0.29)	0 (0)	Woodland-Bushland
Crocuta crocuta	1 (0.29)	0 (0)	Woodland-Bushland
Sus strozzi	4 (1.14)	3 (4.76)	Woodland
Kolpochoerus olduvaiensis	2 (0.57)	0 (0)	Woodland
Hippopotamus ssp. (*H.behemoth*/*H. gorgops*)	123 (35.14)	0 (0)	Aquatic
Hippopotamus behemoth	0 (0)	22 (34.92)	Aquatic
Camelus sp.	1 (0.29)	0 (0)	Arid
Cervidae gen. indet.	0 (0)	20 (31.75)	Woodland
Cervidae A. (size of *Croizetoceros ramosus*)	22 (6.29)	0 (0)	Woodland
Cervidae B. (size of *Cervus perreri*)	38 (10.86)	0 (0)	Woodland
Cervidae C. (size of *Cervus perolensis*)	3 (0.86)	0 (0)	Woodland
Praemegaceros verticornis	8 (2.29)	3 (4.76)	Woodland-Bushland
Pelorovis oldowayensis	2 (0.57)	0 (0)	Woodland-Bushland
Gazella cf. *gazella*	14 (4)	7 (11.11)	Woodland-Bushland
Bovini gen. indet. (size of *Bos* sp.)	2 (0.57)	0 (0)	Woodland
Stephanorhinus etruscus etruscus	5 (1.43)	0 (0)	Woodland-Bushland
Equus ssp. (*Equus tabeti*/ *Equus caballus*)	25 (7.14)	0 (0)	Grassland
Mammuthus merdionalis tamenensis	4 (1.14)	1 (1.59)	Woodland-Bushland
Allocricetus bursae	2 (0.57)	0 (0)	Grassland
Apodemus ssp. (*A. sylvaticus*/ *A.flavicollis*/ *A.mystacinus*)	14 (4)	0 (0)	Woodland
Parameriones obeidiensis	8 (2.29)	0 (0)	Grassland
Gerbillus dasyurus	2 (0.57)	0 (0)	Arid
Lagurodon cf. *arankae*	44 (12.57)	0 (0)	Grassland
Tibericola jordanica	6 (1.71)	0 (0)	Aquatic
TOTAL	350 (100)	63 (100)	
Unidentified fragments	1980	n.a	
Species richness	29	8	
Brillouin diversity index (HB)	2.259	1.453	
Evenness	0.706	0.774	

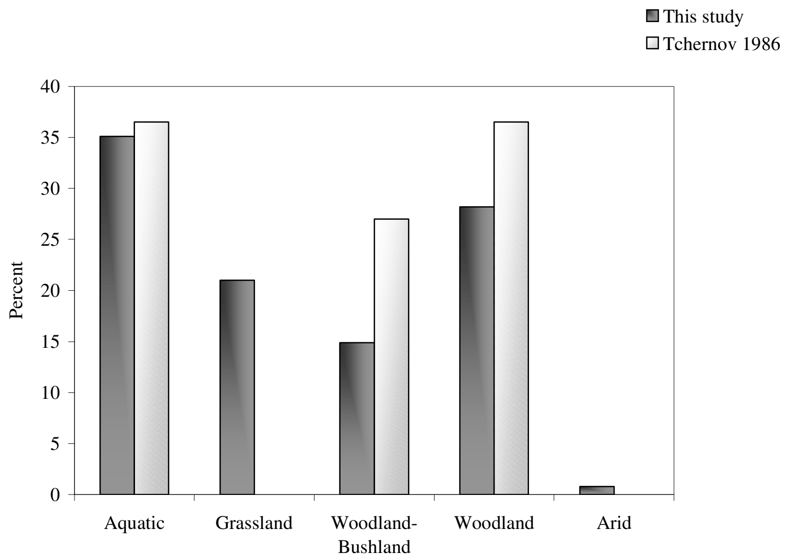

Fig. 4. Distribution of habitats in 'Ubeidiya I 26 (Percent NISP) for MARF method N =63 and S=8 (Tchernov, 1986a, b) and higher-taxonomy method N=350 and S=29 (this study).

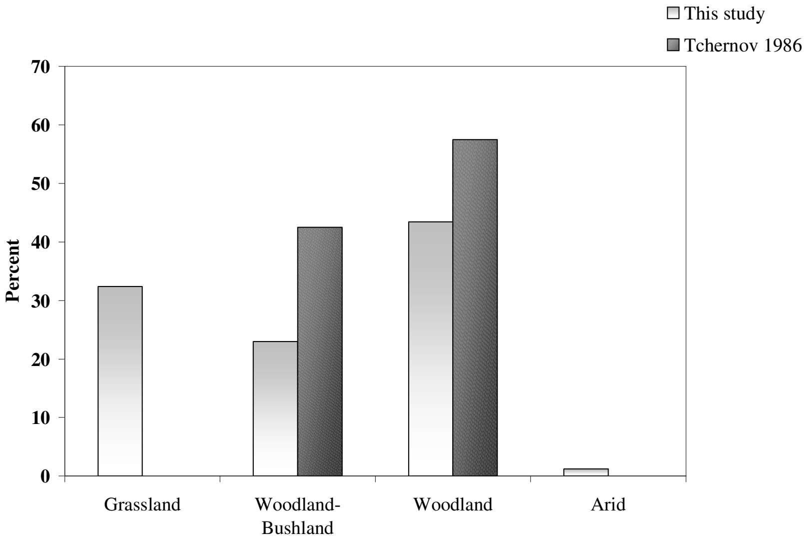

Fig. 5. Distribution of habitats in 'Ubeidiya I 26 (Percent NISP) for MARF method (Tchernov, 1986a, b) and higher-taxonomy method (this study) not incuding aquatic habitat.

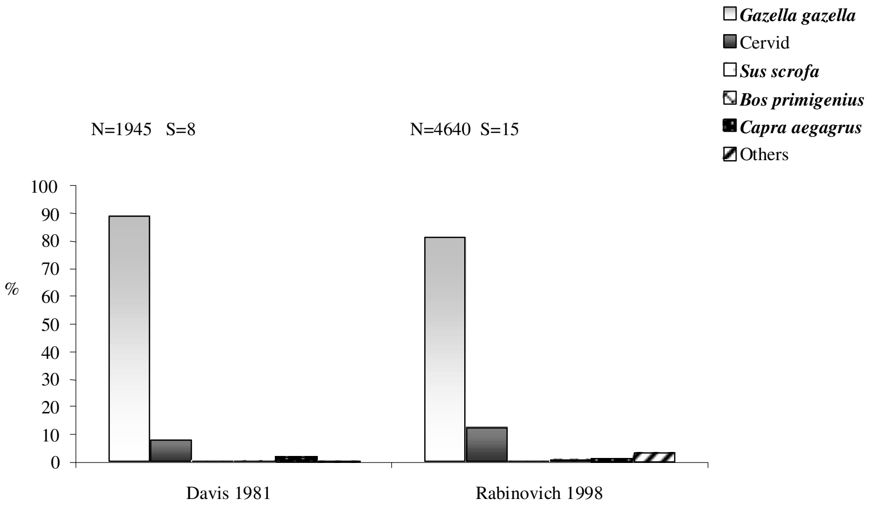

Fig. 6. Distribution of taxa in Hayonim D (Percent NISP) for MARF method (Davis 1981) and higher-taxonomy method (Rabinovich 1998).

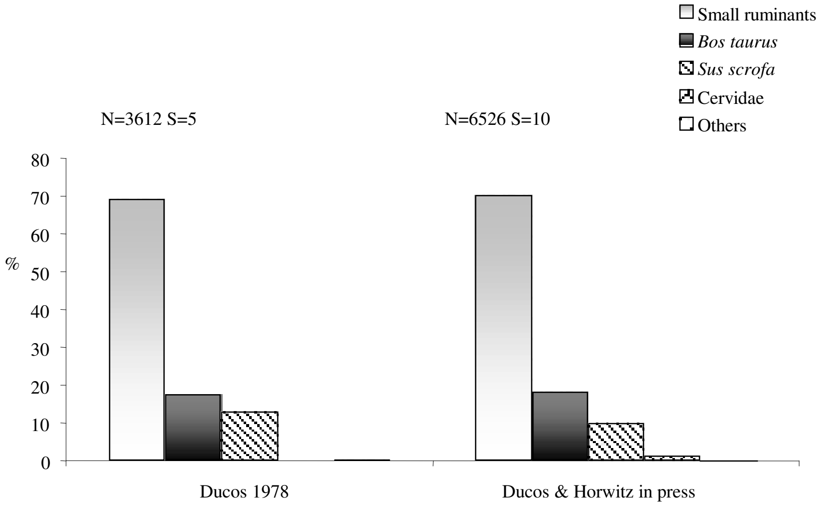

Fig. 7. Distribution of taxa in Abu Gosh (Percent NISP) for MARF method (Ducos 1978) and higher-taxonomy method (Ducos and Horwitz in press).

Discussion

Results indicate that the use of high level taxonomy and the incorporation of previously unidentified fragments shifts the paleoecological reconstruction obtained. Two question arise from the results presented:

1. Which of the two reconstructions is more accurate and a better representation of the Lower Pleistocene environment?
2. Is the case study presented for stratum I 26 in ‘Ubeidiya true for all assemblages and or a unique case, which cannot and should not be applied to other sites?

Close observation of the results obtained for ‘Ubeidiya reveals that the shift in paleoecological habitats resulted in the identification of grassland species such as *Equus* ssp. and *Lagurodon* ssp., which were previously absent from the assemblage. The species were identified based on diagnostic body elements such as teeth, although these were very fragmented so that species identification and/or any type of measurement was impossible. Hence, any attempt to use these specimens in more accurate paleoecological reconstruction (i.e. relative frequency of MARF) and ecomorphology would have excluded them from the analysis despite their positive presence in the stratum. This suggests that the high-level taxonomy method provides the most accurate general reconstruction, albeit at the cost of identification of the microhabitats within the woodland and woodland-bushland environment.

The issue of the applicability of the results obtained for ‘Ubeidiya to other archaeozoological and paleontological assemblages is paramount because of the cost benefit of both time and money invested in the process of reanalysis of large assemblages. In order to assess whether the results are applicable to other sites, data were obtained from the literature from two sites, which were analyzed twice, the second analysis including similar higher-level taxonomy identification similar to the one performed in this analysis. The sites are Hayonim D, an Upper Paleolithic site in the Galilee, Israel, and the PPNB site of Abu Gosh, near Jerusalem. Hayonim D was analyzed by Davis (Davis 1981) using diagnostic specimens that were identified to species level, and reanalyzed by Rabinovich (Rabinovich 1998) using higher-level taxonomy. Abu Gosh was analysed by Ducos (Ducos 1978) using only species level identification and reanalyzed by Ducos and Horwitz (Ducos and Horwitz in press), using higher-level taxonomy. Due to the small number of species, data are presented for taxa rather than habitats (Fig. 6 and 7). Overall distributions for both pairs of analyses in the two sites were very similar despite the high increase in total number of identified specimens and increase in total species richness. Hayonim D NISP increased from 1945 to 4640 and species richness increased from 8 to 15. At Abu Gosh, NISP increased from 3612 to 6526 and species richness increased from 5 to 10.

Despite similar distributions, results differed statistically using the commonly used chi-square test for independence. Although we advocate the use of statistical testing, it is of utmost importance that we understand the accurate null hypotheses and underlying assumptions for each test and choose the appropriate test for the case at hand. In the case presented here, a comparisonis made between two discrete distributions; the chi-square test for independence or g-adjusted is commonly applied, and the null hypothesis for both tests is that the distributions are *equal* (Hays 1988).

In very large sample sizes, such as the ones available in zooarchaeological assemblages, equal distributions are in all probability impossible. The null hypothesis is not that two distributions are equal but that they are similar enough to one another so that they are no longer significantly different. If we are asking what is the dominant game animal or domesticated stock, a difference between 78 and 79% has little bearing on the understanding of the economy despite being statistically significantly with very large sample sizes (in the order of thousands).

In order not to throw the baby out with the bath water, or to abandon all form of statistical testing, ordination methods such as cluster analysis or Principal Component Analysis (PCA) should be used in lieu of hypothesis testing (Pielou 1975; Sneath and Sokal 1973). Although ordination would not result in a p-value for similarity it does allow determination of how close different distributions are to one another. If we obtain similar dendograms using a wide variety of clustering methods, we have reason to feel confident that the clustering is more robust.

I applied a cluster analysis using UPGMA cluster method with a chord distance index using six analyses (Fig. 8). These included two analyses for each of the sites described above: ‘Ubeidiya I 26, Hayonim D and Abu Gosh. Results indicate that analyses from the same site are more similar to one another than to any other analysis but the distance between the analyses differ. While the distance between Hayonim D and Abu Gosh analyses is relatively short (2.183 for Hayonim D and 5.787 for Abu Gosh), the distance between the two 'Ubeidiya analyses is almost double (12.798), which suggests that the two 'Ubeidiya analyses are very different from one another. Similar results (not shown here) were obtained using different clustering method and distance indices suggests that the results obtained are robust.

These results beg the question of whether one can *a priori* determine which site will benefit from a reanalysis of the faunal assemblage and which will not. Table 2 presents a summary of the diversity indices for each of the sites analyzed with the chord distance index between the two analyses for each site. Results suggest that rich and even assemblages will be susceptible to an increased sample size and/or the inclusion of higher taxonomic levels, which may alter the paleoecological inference. Poor and uneven assemblages are more robust to an increase in sample size and/or inclusion of higher taxonomic levels, which may not alter the paleoecological reconstruction.

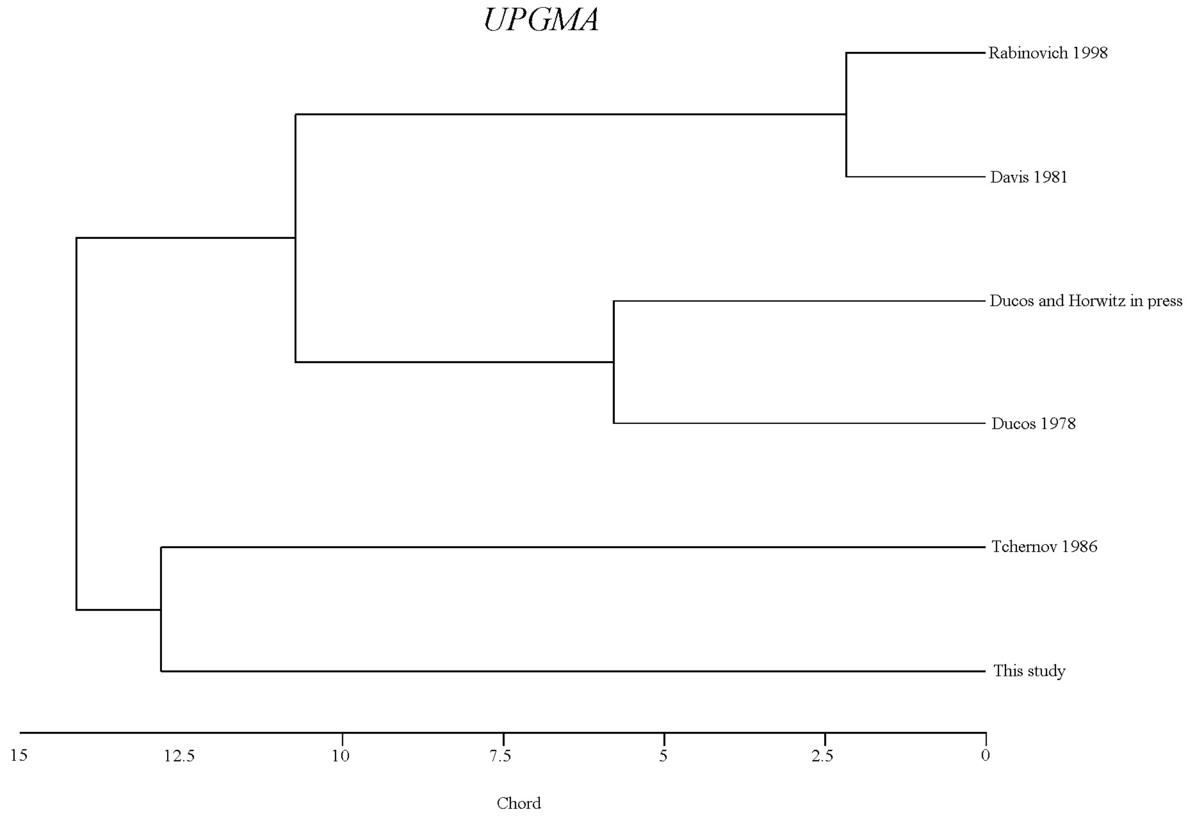

Fig. 8. Dendogram representing cluster analysis using UPGMA cluster method and chord distance index for three pairs of sites. Each site has two types of analyses: MARF and higher level taxonomy.

Conclusions

The use of higher-level taxonomy and the inclusion of all fragments in paleoecological analyses have the potential to reverse the environmental reconstruction obtained from the mammalian fauna. The extent of the effect of the increase in sample size on community richness and paleoecological reconstruction depends on the underlying structure of the original assemblage and cannot be *a priori* determined.

Table 2. Comparison between the chord distances obtained for the pairs of analysis (MARF vs. higher-taxonomy) for different sites and the diversity indices obtained for the higher taxonomy sample.

Site	**N for higher taxonomy analysis**	**S for higher taxonomy analysis**	**Richness (Brillouin) for higher taxonomy analysis**	**Evenness for higher taxonomy analysis**	**Chord distance between analyses for same site**
‘Ubeidiya	350 (2330)	29	2.259	0.706	12.798
Hayonim D	6526	10	1.584	0.689	5.787
Abu Gosh	4640	15	0.804	0.298	2.183

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