

Paleoecologic and taphonomic patterns derived from correspondence analysis of zooarcheological and paleontological faunal samples, a case study from the North American prairie/forest ecotone

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Abstract. Mammalian faunal lists from 34 late Holocene archeological and paleontological sites from Iowa have been analyzed by correspondence analysis to evaluate taphonomic and paleoenvironmental signals in fossil vertebrate accumulations. The Iowa database was selected for this evaluation because of a relatively dense record of suitable late Holocene localities, a location which transects the modern ecotone between the eastern deciduous forest and the prairies of the Great Plains, and relatively diverse fossil faunas (66 taxa) collectively represented in these sites. Correspondence analysis suggested that the major factors influencing faunal similarities were (1) size of screen mesh used in sample collection, (2) cultural vs. non-cultural associations, (3) taxonomic confidence of the identifier (generic vs. specific designation), (4) research interests of individual taxonomists, and (5) taxonomic philosophy of each analyst. Paleoenvironmental signals can be derived within site complexes but in this region they are almost completely masked by the taphonomic attributes of the individual sites.

Key words: Mammalia, late Holocene, taphonomy, paleoecology, zooarcheology, ordination, correspondence analysis, Iowa.

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I. INTRODUCTION

The State of Iowa (USA), located at about 42°N latitude has eastern and western borders that are defined by the Mississippi and Missouri Rivers, respectively. This 485 km (308 miles) east/west transect is situated on the ecotone separating the Eastern Deciduous Forest Biome from the Prairie Biome of North America (BAILEY 1981). Based on land surveys conducted prior to, and during, European settlement (1832-1859), forests were extensively developed along river valleys in the eastern part of the state and occasionally extended onto the uplands, especially in northeastern Iowa (THOMPSON 1987). Oak savanna was characteristic of eastern Iowa uplands (BAKER et al. 1993) and prairies dominated the western landscape. The gallery forests were poorly developed in the western part of the state but they were present to varying degrees (TIFFANY 1982), especially along the Missouri River (Iowa State Planning Board 1935). There clearly is a modern environmental gradient between western Iowa Prairies and eastern Iowa forests.

Iowa's location on the ecotone between the Great Plains and eastern forests makes the state an ideal location to investigate an east/west faunal gradient during the late Holocene (< 4000 yr. B.P.). Assuming that climate was controlled by similar meteorological patterns over the past 10 000 years (WENDLAND 1978; WENDLAND et al. 1987), changes in precipitation should alter floral composition in ecotonal associations (e.g. relative abundance of prairie and forest habitat); there would be an immediate response in the relative abundance of prairie and forest mammal species within the ecotone (SEMKEN 1983). Because of this ecological relationship and the number and variety of late Holocene vertebrate local faunas, the Iowa data base appeared most suitable to examine changes in species composition across a major ecotone during the late Holocene. Most of the known archeological sites are located near rivers (Fig. 1) and therefore the presence of gallery forests in prairie dominated regions could mute the faunal differences between eastern and western sites in the state. The occurrence of all known paleontological sites in fluvial deposits along streams would also subject non-cultural sites to the same gallery forest affect. Nonetheless, an apparent distinctive change in the nature of the uplands across Iowa during the late Holocene has been interpreted from a number of sites. Specifically, the predominance of prairie micromammal species recovered from western Iowa sites (RHODES & SEMKEN 1976) is distinctly different from the relatively few prairie species from sites representative of the eastern part of the state (JENKINS & SEMKEN 1972; BENN 1980). Mesic late Holocene conditions are also recorded for eastern Iowa where the pollen record documents an invasion of mesic trees into the prairie after 3500 yr B.P. (BAKER et al 1990, 1993).

However, before any paleoecological signals can be deciphered from the prehistoric record, it is essential to examine the effects of different taphonomic biases, as recognized by KOWALSKI (1990), as a fundamental part of any paleoecological analyses. To this end, we have subjected the Iowa faunal data to an ordination analysis which groups sites and species by similarities. Resulting clusters were then examined for different taphonomic variables to see if they were important in forming the clusters.

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II. METHODS

Ordination is a term used to describe a set of techniques which arrange sampling units in relation to one or more coordinate axes such that their positions relative to the axes and to each other provides maximum information about their similarities or dissimilarities (LUDWIG & REYNOLDS 1988). Interestingly, GOODALL (1954) introduced the term ordination to identify techniques used to arrange botanical samples in order to quantify the concept of a vegetational continuum along environmental gradients. In this study, we are using ordination to examine prehistoric faunal samples along a geographic/environmental gradient in Iowa.

The goal of ordination is to simplify and condense data sets in the hope of elucidating, by inference, relationships between variables. As indicated by WHITTAKER & GAUCH (1973), ordination techniques have the following properties: (1) relative freedom from distortion, (2) lucidity or clarity of results, (3) efficient use of data, and (4) heuristic value for revealing otherwise unrecognized patterns and relationships. There are several different methods of ordination. Among them are principal components analysis (PCA), factor analysis (FA), and correspondence analysis (CA) (LUDWIG & REYNOLDS 1988). CA was originally developed by the French for application

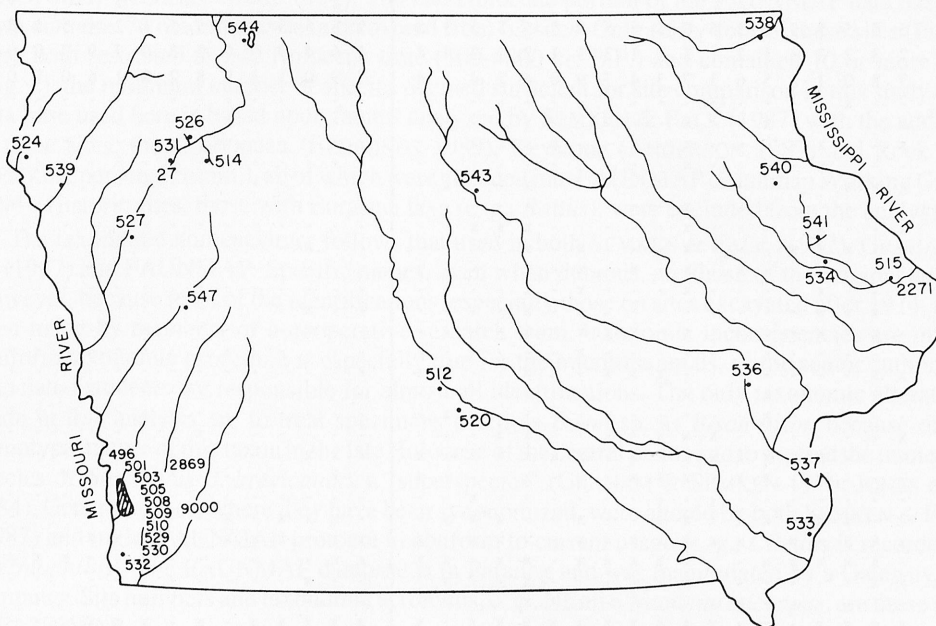


Fig. 1. Location of late Holocene sites in Iowa with ten or more identified mammals: 27 – Phipps, 108 – Rock Run, 496 – State School, 501 – Johnson-3, 503 – Johnson-1, 505 – Kuhl-4, 508 – Kuhl-1, 509 – Gamble, 510 – Lincoln I, 512 – Christenson, 513 – Clarkson, 514 – Chan-ya-ta, 515 – Robert Battey, 520 – Cribb's Crib, 524 – Broken Kettle West, 526 – Wittrock, 527 – Dixon, 529 – Garrett Farm, 530 – Pleasant Ridge, 531 – Brewster, 532 – Thurman, 533 – Kingston, 534 – Hadfield's Cave, 536 – Woodpecker Cave, 537 – McKinney, 538 – Lane Enclosure, 539 – Rainbow, 540 – Willard Cave, 541 – Schmitt, 544 – Arthur, 547 – M.A.D., 2271 – Keystone Rockshelter, 2869 – Wall Ridge, 9000 – Chabneau.

to contingency table problems with nominal data (e. g., presence/absence data), the format of the Iowa faunal samples. CA is a method of displaying entities from both the rows and columns of a contingency table (Fig. 2) as variables on the same graph (RINGROSE 1992). In other words, it combines Q- and R-mode FA (ROCK 1988). This property differentiates CA from the other ordination techniques of PCA and FA. For the Iowa data set, both sites and species are shown on the same graph.

CA is an extension of the method of weighted reciprocal averaging used in direct gradient analysis developed by WHITTAKER (1967). Conceptually for the Iowa faunal data set, CA computes species (R-mode) and site (Q-mode) resemblance matrices. These are then converted to eigenvalues and eigenvectors, which are scaled to provide CA scores (LUDWIG & REYNOLDS 1988). The scores can then be plotted on axes. The first CA axis (Fig. 3, horizontal line) has the largest eigenvalue and hence the greatest importance in differentiating the variables and the second axis (vertical) has the second largest eigenvalue. For CA, the second axis is not correlated with the first one; this ensures that different information is conveyed by the second axis. Although additional axes are available, it is best in practice to have only two axes which represent most of the variation in the matrix (TER BRAAK 1987b).

For our analysis of the Iowa data, we specifically used the CANOCO computer program (TER BRAAK 1987a) to do the CA. Data for this analysis was derived from the FAUNMAP data base

(FAUNMAP Working Group 1994). The late Holocene portion of the FAUNMAP data base for Iowa contains 76 mammalian taxa recovered from 63 sites. Only thirty-four of these sites (Fig. 1) were both restricted to late Holocene time (500-4000 yr. B.P.) and contained 10 or more taxa (Fig. 2), the minimum number of species deemed sufficient for site comparison in this study. The data base used here is based upon faunas analyzed by SEMKEN & FALK (1987) with the addition of three sites, the Chaboneau (BEHREND 1989), Keystone (ANDERSON 1987) and Rock Run (SEMKEN, personal comm.), all of which were encoded into FAUNMAP (Faunmap Working Group 1994). Historic sites, those with Eurasian taxa (e. g., *Rattus*), were excluded from the analysis.

The taxonomic nomenclature follows that used in both SEMKEN & FALK (1987), GRAHAM et al. (1987) and FAUNMAP. Specific names, even when dubious, are those of the original author. However, because most of the identifications, especially those on sites excavated after 1974, have been made by members of a cooperative research team, taxonomic inconsistencies are minor. Uniform taxonomic procedure is especially true for the micromammals, as the senior author and associated students are responsible for almost all identifications. The only taxonomic alterations made in this analysis are to treat specimens listed as *Bison* sp. as *Bison bison* because of the monotypic nature of this taxon in the late Holocene of the central plains and to present the numerous species of *Blarina* as *B. brevicauda*, a "superspecies" (GRAHAM & SEMKEN 1976; JONES et al. 1984). Generic names, where they have been synonymized, were altered by both SEMKEN & FALK (1987) and in the FAUNMAP protocol to conform to current usage (e. g., *Citellus* is recorded as *Spermophilus*). The FAUNMAP database is in Paradox and was manipulated by a Gateway 486 computer. Site numbers and taxonomic acronyms, e. g., NEmi = *Neotoma micropus*, are those used in FAUNMAP.

III. RESULTS OF CORRESPONDENCE ANALYSIS

T a x o n o m i c I n c i d e n c e M a t r i x. Fig. 2 represents an incidence matrix in which the species and sites are arranged in order of their score on the first CA axis. This matrix presents a striking diagonal pattern with taxonomic composition varying gradually across the matrix and, at the same time, demonstrating that the species composition of the sites at either margin of the matrix are distinctively different. For example, *Neotoma micropus* (NEmi), *Cynomys ludovicianus* (CYlu), and *Onychomys leucogaster* (ONle) are either unique to a site or common only to sites on the right margin; *Spermophilus* sp. (SP), *Urocyon cinereoargenteus* (UYci) and *Canis latrans* (CAla) are identified only from those sites situated on the left margin. Sites with the greatest number of shared taxa with either or both margins are located in the more central columns.

Fig. 2. Taxonomic Incidence Matrix of sites and taxa used in the Correspondence Analysis of late Holocene sites in Iowa. Site numbers are identified in Fig. 1. The taxonomic abbreviations are: ACam – *Antilocapra americana*, BIbi – *Bison bison*, BLba – *Blarina brevicauda*, CA – *Canis* sp., CAfa – *Canis familiaris*, CAla – *Canis latrans*, CAlu – *Canis lupus*, CLga – *Clethrionomys gapperi*, CRca – *Castor canadensis*, CSpa – *Cryptotis parva*, CVca – *Cervus canadensis*, CYlu – *Cynomys ludovicianus*, DEva – *Didelphis virginianus*, EPfs – *Eptesicus fuscus*, ERdo – *Erethizon dorsatum*, FSru – *Felis rufus*, GEbu – *Geomys bursarius*, GLvo – *Glaucomys volans*, LS – *Lepus* sp., LUca – *Lutra canadensis*, MAam – *Martes americana*, MApe – *Martes pennanti*, MEme – *Mephitis mephitis*, MI – *Microtus* sp., MIoc – *Microtus ochrogaster*, MIpe – *Microtus pennsylvanicus*, MIpi – *Microtus pinetorum*, MTmx – *Marmota monax*, MUvn – *Mustela nivalis*, MUvi – *Mustela vison*, MY – *Myotis* sp., MYke – *Myotis keenii*, NEfl – *Neotoma floridana*, NEmi – *Neotoma micropus*, OD – *Odocoileus* sp., ODva – *Odocoileus virginianus*, ONle – *Onychomys leucogaster*, ORpa – *Oryzomys palustris*, OTzi – *Ondatra zibethicus*, PE – *Peromyscus* sp., PEle – *Peromyscus leucopus*, PEma – *Peromyscus maniculatus*, PGfl – *Perognathus flavescens*, PIst – *Pipistrellus subflavus*, PRLr – *Procyon lotor*, RY – *Reithrodontomys* sp., RYme – *Reithrodontomys megalotis*, SAAq – *Scalopus aquaticus*, SC – *Sciurus* sp., SCca – *Sciurus carolinensis*, SCni – *Sciurus niger*, SNco – *Synaptomys cooperi*, SP – *Spermophilus* sp., SPfr – *Spermophilus franklini*, SPtr – *Spermophilus tridecemlineatus*, SXcs – *Sorex cinereus*, SY – *Sylvilagus* sp., SYfl – *Sylvilagus floridanus*, TAs – *Tamias striatus*, TShu – *Tamiasciurus hudsonicus*, TXta – *Taxidea taxus*, URam – *Ursus americanus*, UYci – *Urocyon cinereoargenteus*, VUve – *Vulpes velox*, VUVu – *Vulpes vulpes*, ZPhu – *Zapus hudsonius*.

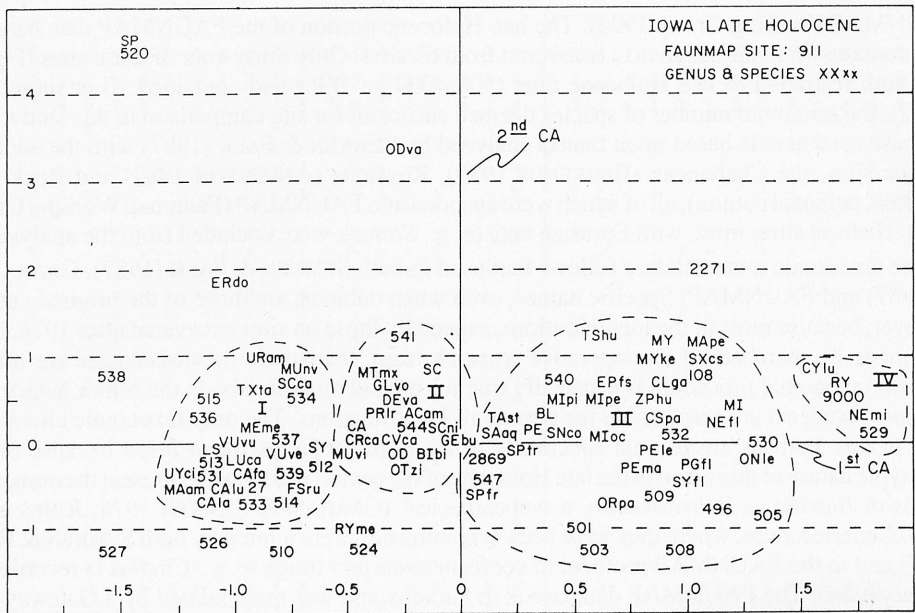


Fig. 3. Correspondence Analysis of the late Holocene sites in Iowa with ten or more species. Site numbers are identified in Fig. 1, taxa in Fig. 2. Clusters I and II are tighter than they appear because these clusters have been expanded so that symbols do not overlap.

These sites also tend to be the ones with the greatest number of identified taxa (e. g., Hadfield's cave, $N = 34$, Site # 534) but this observation is not absolute. Lincoln I (510), which lies next to Hadfield's cave, has only ten identified mammals; most of these are represented at other sites.

When the matrix is examined taxonomically, rare species [e. g., *Neotoma micropus* (NEmi) and *Spermophilus* sp. (SP)] are situated at either the top or the bottom of the species list and the most frequently identified taxa appear toward the middle. *Geomys bursarius* (GEbu), plains pocket gopher; *Odocoileus* sp. (OD), deer, and *Bison bison* (BIbi), American bison, are present in all but five sites. Again, there are exceptions because the single late Holocene record of *Antilocapra americana* (ACam), pronghorn, is positioned next to *B. bison* in the taxonomic column, its location being a function the overall "common" nature of associated species in the Arthur (544) site.

Upon first inspection, the matrix appears to represent a distinct late Holocene east/west cline representative of the ecotone across Iowa with prairie species [*Neotoma micropus* (NEmi), southern plains woodrat; *Cynomys ludovicianus* (CYlu), blacktail prairie dog; and *Onychomys leucogaster* (ONle), northern grasshopper mouse] concentrated to the lower right (Fig. 2). Woodland species [*Urocyon cinereoargenteus* (UYci), grey fox; *Erethizon dorsatum* (ERdo), porcupine; and *Martes americana* (MAam), marten] appear to be located on the upper left side of Fig. 2. However, the "woodland" grouping contains some taxa like the badger (*Taxidea taxus*, TXta), that although widespread, are most common in the prairie. This mixture is a characteristic of any ecotonal situation including that in Iowa.

The geography of the sites (Fig. 1) invalidates the ecocline interpretation; the Dixon (527) and Lane Enclosure (538) sites, which are juxtaposed on the left margin of Fig. 2, are located at geographic extremes in the state; the Lane Enclosure is in the northeasternmost county of Iowa (Allamakee) and Dixon is in the westernmost tier of Iowa counties (Woodbury). Geographic discontinuity is further documented by the Kingston (east) and Phipps (west) sites (533 and 27), McKinney (east) and Rainbow (west) sites (537 and 539), and Willard Cave (east) and Wall Ridge

(west) sites (540 and 2869), each a juxtaposed pair in the matrix (Fig. 2). Each of these site pairs is widely separated geographically between western and eastern Iowa. Thus, an environmental transect across the ecotone can not be the major factor controlling faunal composition of late Holocene sites in this analysis (Fig. 2). Other factors must strongly influence the matrix.

Subjective examination of Fig. 2 suggests several alternative explanations for both faunal differences and similarities. First, the 32 taxa recorded below *Bison bison* (BIbi) in the taxonomic column on the incidence matrix (Fig. 2) are micromammals (rodents, insectivores and bats), species that are only recovered by intensive use of fine mesh (1.6 mm) waterscreens. These micromammals represent exactly half of the taxa on the faunal list (Fig. 2). Those recorded above *Bison bison* (BIbi) include deer (OD), two fox genera (VU and UY), badger (TXta), marmot (MTmx) and muskrat (OTzi), all of which are large enough to be recovered by trowel or in excavations in which coarse screens (7.0 mm; 0.25 in) were used primarily for secondary recovery. Thus, recovery technique apparently is the major factor influencing the micromammal/large mammal dichotomy that strongly affects the matrix. Some micromammals are recorded above the *Bison* row [e. g., *Reithrodontomys megalotis* (RYme) harvest mouse, *Sciurus carolinensis* (SCca) gray squirrel and *Glaucomys volans* (GLvo) southern flying squirrel] but none of the latter are known from more than three sites. Moreover, these specimens may have been recovered from one-liter matrix samples collected in varying quantities for flotation to recover seeds and mollusks from many sites beginning in the 1970's (BAERREIS 1980). The tendency for the species recovered from cultural sites to be toward the left and those from non-cultural (paleontological) local faunas to be toward the right is also apparent from Fig. 2.

Taxonomic Composition and Site Correspondence. In order to examine the relationships between these late Holocene sites and their faunal composition, the sites and taxa were displayed as a biplot of the first two CA axes (Fig. 3). The location of acronyms on the biviates (Figs. 3, 4, 5 & 6) have been slightly expanded in drafting so that overlapping positions within clusters of sites and taxa are separated for clarity.

The relationship between the faunal incidence matrix (Fig. 2) and the plot of CA scores on the first two CA axes (Fig. 3) is evident. Taxa that are common to most sites (e. g., *Ondatra zibethicus* (OTzi), *Geomys bursarius* (GEbu), *Bison bison* (BIbi), *Odocoileus* sp. (OD), *Sciurus niger* (SCni), and *Cervus canadensis* (CVca) occur in a cluster, identified here as Cluster II, near the center of the first axis. These taxa also occur in the center of the incidence matrix (Fig. 2). Many of these animals were either basic subsistence or economic (pelts) species that are common in prehistoric North American archeological sites and their "commonplaceness" in the zooarcheological assemblages reflects human selection, the cultural filter. Sites like Arthur (544) MAD (547), Schmitt (541), and Wall Ridge (2869) either fall in or near Cluster II. None of these sites contain the rarer species (Fig 2).

Taxa and sites toward either end of the incidence matrix (Fig. 2), generally occur in either Clusters I or IV of Fig. 3. For example, Cluster IV represents three taxa and two sites which occur in the lowermost right end members of the incidence matrix. In other words, the four clusters defined in Fig. 3 reflect the same apparent gradient discussed above for the incidence matrix (Fig. 2). This is not surprising since both have been ordered by scores of the first CA axis.

There are seven sites and four taxa that fall outside of these four clusters. *Odocoileus virginianus* (ODva), the whitetailed deer, is an outlier because of taxonomic inconsistencies in the identification of deer remains from other sites in Iowa. Both *O. virginianus* and *O. hemionus*, the blacktailed deer, were present in Iowa historically (BOWLES 1975), but these two taxa are difficult to differentiate on osteological elements other than relatively complete antlers (PURDUE 1989) or lower jaws (LIVINGSTON 1987). For this reason, most analysts from the northern plains have referred any deer remains to generic level only. This makes the specific identification of *O. virginianus* in Cribb's Crib (520) almost unique (one other site, Fig. 2) for this faunal matrix, and is part of the reason that this site is offset. The identification of *Spermophilus* to generic level only is another unique feature of Cribb's Crib taxonomy. Many elements of *Spermophilus* can be readily identified to species in Iowa and for this reason numerous *Spermophilus* remains from all other

sites have been assigned to a species. These two taxonomic anomalies at Cribb's Crib are reinforced by the presence of a rare taxon (porcupine, ERdo) in association with a small faunal list; together they create an anomaly of this magnitude. The Cribb's Crib example underscores the significance of differences in taxonomic approach to identify faunal remains (analyst bias), the varying potential for osteological elements of different taxa to be differentiated (identification bias), as well as the degree of processing needed for the recovery of microfauna.

Normally, in a CA, taxonomic units would be standardized to a certain level (e. g., all *O. virginianus* would have been converted to *Odocoileus* sp.). However, these examples were not revised to show the value of not standardizing taxonomy or eliminating sites on the first CA analysis, since it is useful in identifying both analyst and identification bias. These biases can be corrected in further analyses.

The species of Cluster I also are distinctive. The taxa in this cluster are *Ursus americanus* (URam) black bear, *Mustela nivalis* (MUnv) least weasel, *Taxidea taxus* (TXta) badger, *Urocyon cinereoargenteus* (UYci) grey fox, *Canis latrans* (CALa) coyote, *C. lupus* (CALu) wolf, *C. familiaris* (CAfa) dog, *Felis rufus* (FSru) bobcat, *Martes americana* (MAam) martin, *Lutra canadensis* (LUca) otter, *Mephitis mephitis* (MEme) striped skunk, *Vulpes vulpes* (VUvu) red fox, *V. velox* (VUve) swift fox as well as *Sciurus carolinensis* (SCca), grey squirrel, *Lepus* sp. (LS) jackrabbit and *Sylvilagus* sp. (SY) rabbit. All but the last three are carnivores; the latter also are commonly regarded as subsistence species. This "carnivore" cluster may represent either local faunas in which taxonomic effort was directed not only toward "common" subsistence species (inc. bison, rabbit and deer) but also toward all large mammals, especially carnivores (taxonomic bias), or special selection by prehistoric people of furbearers (cultural filter).

Seven sites (Broken Kettle West [524], Lincoln I [510], Wittrock [526], Dixon [527], Lane Enclosure [538], Schmitt [541] as well as Arthur [544], which is also within the "common" cluster), appear to both fall near to, and surround, this "carnivore" cluster (Cluster I); fewer carnivores are present in these sites. The sites within the "carnivore" cluster also can be subdivided, somewhat arbitrarily, into two groups, by the second (vertical) axis. Those centered below the first CA axis represent Native American lodge sites in northwestern Iowa (except Lincoln I, 510, in southwestern Iowa); those above the first CA axis are eastern Iowa long-house villages or habitated rock shelters. Two sites (Christensen, 512 and Clarkson, 513) lying between these two subclusters, just below the first axis, are located in central Iowa. The environmental potential of this distinction is discussed in the following section.

A third cluster (III) is composed of 23 species with 15 local faunas and a fourth (IV) comprises three taxa with two local faunas. The local faunas, as well as the center of distribution for a majority of their component species in Clusters III and IV, are dispersed in comparison to those in either the "carnivore" (Cluster I) or "common mammal" (Cluster II) clusters. Clusters III and IV are primarily composed of micromammals (small rodents and insectivores). However, Cluster III also contains a small carnivore, (*Martes pennanti* (MApe), and a medium-sized rabbit, (*Sylvilagus floridanus* (SYfl). The division between Clusters II and III is graphically most obvious in the area where the first and second order axes intersect. However, if statistical distance from the origin (O/O) is considered, the "common" cluster would include the chipmunk (TAst) and the mole (SAaq), as well as the thirteen-lined (SPtr) and Franklin's (SPfr) ground squirrels. Thus, the primary division of the late Holocene local faunas seem to be related to nearly mutually exclusive faunal packages, those composed largely of megamammals in either a "common" or "carnivore" cluster and those composed largely of rodents, insectivores and bats in one of two "micromammal" clusters (III and IV). Subjective evaluation of the first CA in Fig. 3 suggests that the Iowa data be further investigated with respect to (1) faunal recovery procedures, e. g., screen size, and (2) site type, e.g., earth lodge village vs. shelter cave vs. paleontological, etc.

F a u n a l R e c o v e r y B i a s . The presence of a "micromammal" and a "megamammal" division is apparent from the species distribution in Fig. 3. Cluster I and Cluster II are primarily composed of "megamammals," whereas with two exceptions Clusters III and IV

are composed of "micromammals." This pattern undoubtedly relates to the methods used in the recovery of faunal remains. STYLES (1981) has shown that the screen mesh-size and methods of screening (dry vs. flotation) can significantly affect the composition of faunal samples. To this end the authors reconfigured the data with respect to screening techniques used in recovering the Iowa faunas (Fig. 4).

All of the sites used in this study (those with 10 or more species), with one possible exception (Woodpecker Cave, 536, screen-mesh size was not recorded), employed a screen mesh of 7.0 mm (0.25 inch) or less. General use of screens of this or finer mesh has been common in Iowa since the 1960's and this, in part, is the reason for the high quality of the faunal data base (Fig. 2). An initial correspondence plot (not figured) using fine (1.6 mm) vs. coarse (>1.6 mm, ~ 7.0 mm) indicated that four sites had not been fine screened. Three of these sites (Dixon, 527; Lane, 538; Cribbs' Crib, 520) are located outside of Cluster I, and Schmitt (541), is located at the edge of Cluster II. The finescreen category for the remainder of the sites on the negative side of the first CA axis did not correspond logically with the paucity of micromammals identified. Either the micromammals were not present, not identified, or not recovered. We have divided sites into three categories based upon the screen-size used in faunal recovery (Fig. 4): "Fine" screened sites are those in which fine screened matrix was processed in bulk with waterscreens and volumes would be measured in cubic meters, "flotation" sites are those in which flotation samples are measured in liters, and "coarse" screened sites are those where all of the matrix was processed without water through 7 mm mesh screens. Unlike the following analysis (Fig. 5) where the sites were categorized by site type, two of the divisions in this correspondence (Fig. 4 – flotation and fine screen) are subjective because of extensive processing of one-liter samples at Hadfields and Author. Moreover, the number of flotation samples collected and the number actually processed are not always clear in the literature.

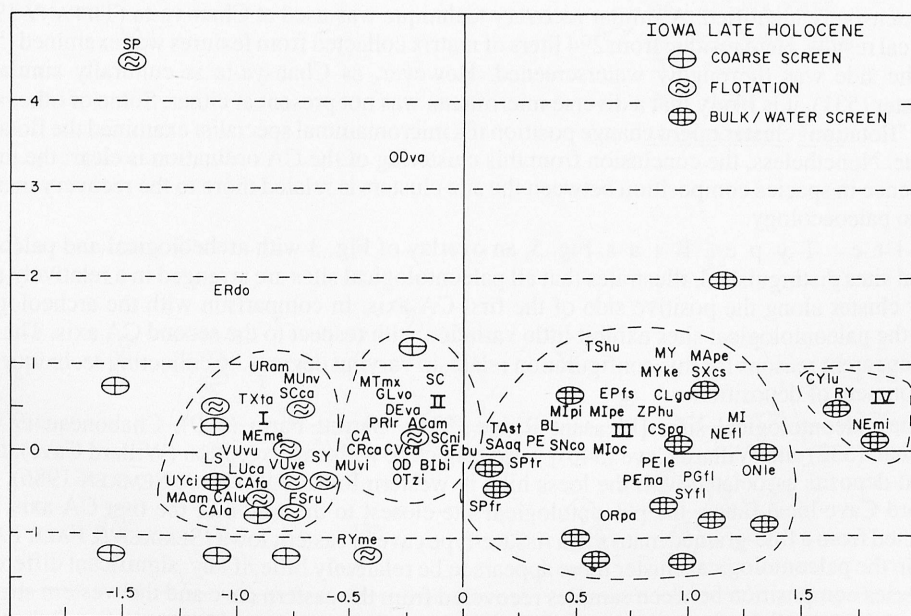


Fig. 4. Correspondence Analysis of the sites depicted by recovery technique. Coarse screens are 7 mm (0.25 in) in mesh, waterscreen recovery at < 1.6 mm mesh, and flotation reflects material picked from residue of the flotation process. Sites screened with greater than 7 mm mesh screen did not produce a sufficient number of taxa for inclusion in this study.

A review of the original site reports indicated that the amount of matrix processed through 1.6 mm or finer screens varied considerably between sites. Without exception, the site reports that indicated "bulk" processing of matrix through 1.6 mm water screen are those sites on the positive side of the first axis; volumes of matrix processed for these sites vary but, if totaled, would be measured in cubic meters. Conversely, the "fine screen" excavation strategy used for most of those sites to the left of the prime ordinate consisted only of liter-size samples collected for flotation from selected units. Total volumes processed in these were in tens of liters except for Author (544) and Hadfields' Cave (534), where 591 and 550 liters of matrix, respectively, were processed, by flotation. The faunal list from these sites, because of volume, cannot be reasonably compared to Cribb's Crib in which the residue from only 13 liters of matrix was examined for vertebrates. Cribb's Crib (DE VORE 1990) is significant in that it was the first site in Iowa (1966 excavation), known to the authors, that employed floatation. The heavy fraction from 13 of 21 samples (liters?) was picked: only four contained bone and none of the bones were identifiable. Technically, the sites were sampled for their microbiological component and the samples were adequate for molluscs and seeds (e. g. Cribb's). However, the volume processed clearly was insufficient for recovery of a representative sample of microvertebrates in comparison to bulk screened techniques.

Examination of Fig. 4, in which the sites and species location are the same as in Fig. 3, presents a relatively clear dichotomy along the first CA axis. Sites on the positive side of the axis were extensively waterscreened through 1.6 mm mesh screen, those to the left employed 7 mm screens in conjunction with varying degrees of floatation. These two clusters are strongly correlated with the "megamammal" (negative axis) and "micromammal" (positive axis) clusters that were discussed above. There is an exception to this pattern. One fine-screened site (Brewster, 531) falls well within the "coarse" cluster.

The excavator (DALLMAN 1983) illustrates and carefully describes the bulk processing technique used. However, his report does not contain as many micromammals in the faunal list as expected, despite this intense effort for secondary recovery via fine-mesh waterscreens. This may result from either the fact that micromammals were not preserved at this site or their remains were not extensively identified. A similar recovery technique was used at Chan-ya-ta (TIFFANY 1982) identical results. Here residue from 294 liters of matrix collected from features was examined (515) and the side was thoroughly waterscreened. However, as Chan-ya-ta is culturally similar to Brewster (531), it is likely that a diverse microfauna was not present at either. Some of other sites in the "flotation" cluster might change position if a micromammal specialist examined the flotation residue. Nonetheless, the conclusion from this clustering of the CA ordination is clear: the major difference in species composition between the site clusters is related more to the recovery method than to paleoecology.

Site Type Bias. Fig. 5, an overlay of Fig. 3 with archeological and paleontological sites distinguished, illustrates that all paleontological sites are arranged in a relatively tight linear cluster along the positive side of the first CA axis. In comparison with the archeological sites, the paleontological sites exhibit little variation with respect to the second CA axis. The two most apparent reasons for this configuration relate, in varying degrees, to collecting technique and environment of deposition.

The paleontological sites [Pleasant Ridge (530), Garrett Farm (529), Chaboneau (9000), Thurman (532) and Willard Cave (540)] were collected, with one exception (Willard Cave), from fluvial deposits associated with the loess hills in western Iowa (RHODES & SEMKEN 1986). The Willard Cave local fauna, the paleontological site closest to the origin of the first CA axis, was collected from a fine-grained matrix in a fissure-type cave in eastern Iowa (SEMKEN & FALK 1987). Within the paleontological cluster there appears to be relatively little, if any, significant difference in species composition between samples recovered from the eastern cave and the western stream-channel deposits. Selective sorting undoubtedly enhanced micromammal concentration in the loess hills sites as did owl pellet accumulation in Willard Cave. Moreover, all of the paleontological sites were selected for excavation because bulk waterscreen recovery would produce large micromammal samples. Larger mammals, while present in all of these sites, would more likely be recovered from localities with coarser-grained sediments. Willard Cave, which also served as a natural trap,

produced a more extensive megamammal sample than the sites from western Iowa, but the narrow cave entrance would exclude the larger species; most of the deer remains are from fawns.

Four of the archaeological sites also were recovered from fluvial deposits [MAD (547), Rainbow (539), Christenson (512), and Clarkson (513)]. These, however, were situated in very fine-grained floodplain or terrace deposits in which micromammals could be excluded by fluvial sorting. Any micromammal remains, along with the megamammals, in these sites would result from cultural procurement for either subsistence or as pests attracted to the site. Moreover, these sites were not waterscreened except for liter-sized floatation samples. Thus, the abundance of micromammal remains collected resulted from both intense waterscreening of sediments and depositional environments that they represented. On the other hand, many of the zooarcheological samples were not processed through fine screens (compare Figs. 4 and 5) and therefore have a poor representation of microfauna. Depositional environments at these sites may have also been important by selectively preserving certain taxa and skeletal elements.

Archeological sites can produce zooarcheological samples comparable in micromammal species density to paleontological sites. The Glenwood earthlodge sites (496, 501, 503, 505, 508, 509 and 2869) are incorporated with three of the paleontological sites in Cluster III of the bivariate (Fig. 5). The culturally associated Rock Run shelter (108) is also closely nested with this cluster; Keystone (2271), also a cultural shelter cave, lies well above Cluster III, but has greater affinity to paleontological associations than to those from archeological sites. Thus, the paleontological sites are surrounded on three sides by micromammal-rich zooarcheological samples. While these culturally associated faunas are distinct, they clearly approach the paleontological samples in species density and can provide a comparable paleoecological signal. Waterscreen recovery and micromammal, as well as megamammal, identification was a major part of the research design in all of the sites in Clusters III and IV.

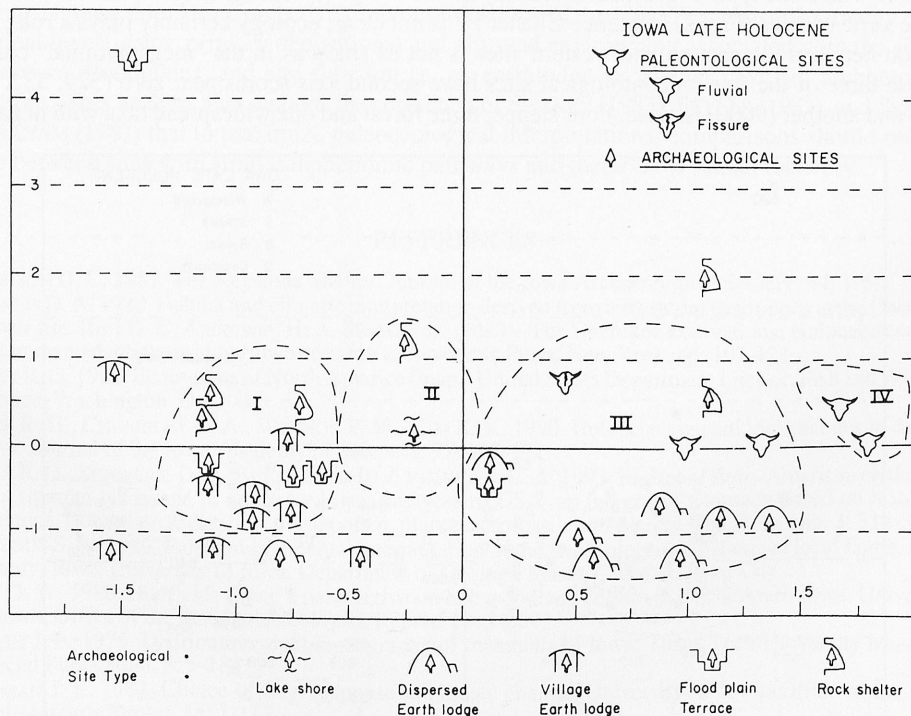


Fig. 5. Correspondence Analysis with sites identified by site type.

Most of the taxa with a positive second axis CA score in the "subsistence" cluster (Cluster II) have centers of distribution (Fig. 6) in either the boreal or deciduous forests of North America (BOWLES 1975; JONES et al. 1983). This distribution, however, is in contrast to the "carnivore" cluster (Cluster I) with a largely widespread composition. If the widespread animals (16 taxa) are eliminated from consideration in the combined "megamammal" clusters, four steppe and two forest (boreal and deciduous) taxa with negative scores would be in contrast to seven forest and two steppe species with positive scores. We interpret this trend as an environmental distinction. The "micromammal" cluster (Cluster III) supports the same paleoenvironmental interpretation. Cluster IV is distinct from III because of the relatively high density of prairie forms identified in the Chaboneau (9000) and Garrett Farm (529) sites. These two sites, along with the Pleasant Ridge (530) and Turman (532), produced similar but unique (for Iowa) sympatries (area where all living taxa presently coexist) to the southwest of the state (SEMKEN & FALK 1987; RHODES & SEMKEN 1986). Thus, the pulling power of relatively rare species appears to equally influence both the correspondence and sympatry techniques. The compatibility of the two techniques emphasizes the southwestern character of these local faunas. Each of these sites is paleontological (Fig. 5) and the degree to which site type (Fig. 5), data recovery method (Fig. 4), ecology (Fig. 6), and the presence of rare xeric species (Fig. 2) influence Cluster IV is not clear; ecology certainly plays a role. The division between the eastern and western sites is not as sharp as in the "megamammal" cluster because three of the five paleontological sites have second axis scores near zero (529, 532, and 2869) and another (9000) is close. Four steppe, three forest and one widespread taxa with negative

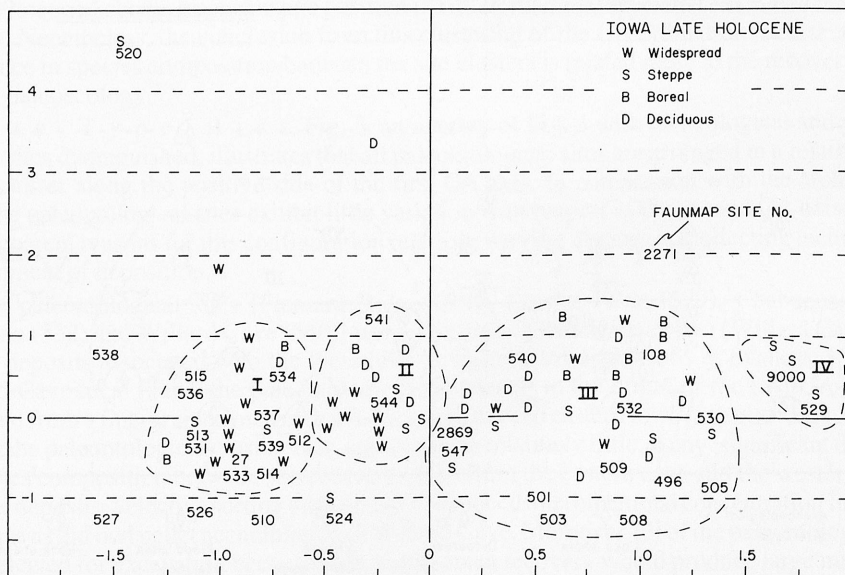


Fig. 6. Correspondence Analysis with species identified by primary ecological associations.

scores in the "micromammal" clusters are in sharp contrast to 14 forest (boreal and deciduous), three steppe, and one widespread species with positive scores. Intense bulk waterscreening as well as lack of cultural disturbance probably is responsible for the recovery of potentially rare forest species in the western localities and for prairie species in the eastern paleontological sites. However, methods of faunal accumulation (owl pellets vs. human foraging strategies) are also important in determining faunal composition. In any case, the paleontological sites provide a better mix of forest and prairie species than the zooarcheological samples. In all, the combined "mega-mammal and micromammal" distributions suggest that the east/west, forest/prairie transition that is present in Iowa today was present during the late Holocene as well. Details on the relative abundance of all component species, then and now, probably would be required to evaluate any changes in the strength of the ecotone.

IV. SUMMARY

Correspondence analysis of late Holocene mammal-bearing sites in Iowa, which transect the modern prairie/forest ecotone, revealed a subtle difference in taxonomic composition between sites within the eastern and western parts of the state. The close association of the western Iowa sites to rivers with proximal gallery forests is partially responsible for this similarity. Identified paleoecological differences, however, were almost completely masked by taphonomic factors. The strongest taphonomic influence identified in this study is related to recovery method, primarily screen-mesh size and volume of matrix processed in bulk through waterscreens. There also is a taxonomic distinction between non-cultural (paleontological) and both between and within culturally (archaeological) associated faunas. This difference can be minimized by increased use of bulk processing of matrix through fine-mesh waterscreens. As noted by GRAHAM & SEMKEN (1987, p. 6) "it is critical that future paleoecological and zooarcheological samples be collected by comparable methodologies." Other differences in species composition can be attributed to, in varying degrees, taxonomic objectives and/or philosophy of the identifier, research strategy of the principal investigator, primary depositional and physical environment associated with the site (e. g., cave vs. floodplain), and site function (e. g., earthlodge vs. shelter cave) in archeological situations. This analysis also supports the contention of SEMKEN (1983), STYLES (1981), and SEMKEN & GRAHAM (1987) that to maximize paleoecological interpretations, comparisons should only be made between sites with similar taphonomic pathways and methods of faunal recovery.

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