

Analysis of Plant and Animal Remains from 44RN220

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INTRODUCTION

Archaeological plant and animal assemblages represent only a small fraction of what was originally used and deposited by humans in open-air settings. Natural and cultural factors can significantly modify organic remains, resulting in recovered assemblages that differ dramatically from the original deposits. As archaeologists, we examine collections that have undergone a series of processes—from the original selection of plants and animals by humans, to food preparation, cooking, discard, animal and insect scavenging, burial, decay, and weathering, to the recovery of food residues by archaeologists. Using standard methodological procedures for sampling, quantification, and analysis allows us to make sense of our assemblages in spite of the deleterious effects of these processes.

Here I report on the identification and analysis of the archaeobotanical and zooarchaeological assemblages from 44RN220. I treat the plant data first, followed by the animal data. In each section, I present a basic discussion of recovery/ preservation issues, quantitative methods, and laboratory procedures. This is followed by the results and analysis of the data. Finally, I discuss the patterns identified in each assemblage as a means to reconstruct more general subsistence practices at the site. Analysis of the plant and animal data both point to a special-purpose seasonal occupation of the site oriented around the hunting and butchering of white-tailed deer and the collection of medicinal plant resources.

THE ARCHAEOBOTANICAL ASSEMBLAGE

Recovery and Preservation Bias

The circumstances under which plants preserve best archaeologically involve extreme conditions (e.g., exceptionally wet, dry, or cold environments) that prohibit decomposition of organic matter (Miksicek 1987). Plants can also preserve through exposure to fire, which can transform plant material from organic matter into carbon (Miksicek 1987). The likelihood that a plant will become carbonized varies according to the type of plant, how it is prepared and used, and whether it has a dense or fragile structure (Scarry 1986). Plants that are eaten whole are less likely to produce discarded portions that may find their way into a fire. Plants that require the removal of inedible portions (e.g., hickory nutshell, corn cobs) are more likely to find their way into a fire, and thus into the archaeological record. Inedible plant parts represent intentional discard that is often burned as fuel. Moreover, because inedible portions tend to be dense and fibrous, they are more likely to survive the process of carbonization than the edible parts (e.g., hickory nutshell vs. nutmeats). Physical characteristics are also important for determining whether or not a plant will survive a fire. Thick, dense nutshells are more likely to survive a fire than smaller, more fragile grass seeds. Food preparation activities also affect potential plant carbonization. The simple process of cooking provides the opportunity for carbonization through cooking accidents. Foods that are conventionally eaten raw, however, are less likely to be deposited in fires than cooked foods.

Some plants that find their way into the archaeological record in carbonized form were not eaten at all. Wood fuel is the most obvious example. Burned house structures can also yield carbonized plant deposits, and these deposits often differ dramatically from refuse deposits (Scarry 1986). Other non-food plants that become carbonized are incidental inclusions, such as

seeds blown by wind dispersal (Miksicek 1987; Minnis 1981; Scarry 1986). Indeed, most secondary invaders are weedy species with lots of seeds (e.g., cheno/am plants) (Minnis 1981).

While we cannot ever hope to know the absolute quantities or importance of different plants in any past subsistence economy, the preservation and recovery biases discussed above do not prohibit quantitative analyses of archaeobotanical assemblages. The most commonly used plant resources in any subsistence economy are more likely to be subject to activities that result in carbonization (e.g., through fuel use and accidental burning) and ultimately, deposition (Scarry 1986; Yarnell 1982). Thus, we can quantitatively examine the relative importance of commonly-used plant resources through time and across space.

Methods of Quantification

Quantitative methods in archaeobotany have developed significantly over the past several decades, and as a result, have been a subject of much critical discussion (Hastorf and Popper 1988). The most common methods for recording and quantifying plant remains are counts and weights. Because of problems with comparability between different types of plant taxa, however, raw (or absolute) counts and weights are not appropriate comparative measures (Scarry 1986). For example, denser taxa yield higher weights than more fragile taxa, and some taxa yield higher seed counts than others (e.g., grasses versus fruits) (Scarry 1986). Thus, using absolute counts or weights to summarize plant data is highly problematic. Most archaeobotanists agree that absolute counts are inadequate for assessing past people-plant interactions in that they do not control for biases related to preservation and sampling error (Kandane 1988; Miller 1988; Popper 1988; Scarry 1986). Absolute counts and weights are simply raw, unstandardized data.

One way to avoid the problems of absolute counts/weights is through the use of ubiquity measures (Godwin 1956; Hubbard 1975, 1976, 1980; Popper 1988, Willcox 1974). This type of analysis is essentially a presence/absence analysis that sidesteps the problems of counts and weights by measuring the frequency of occurrence instead of abundance. In other words, ubiquity analysis measures the number of samples in which a taxon was identified, as opposed to the number of specimens represented by that taxon. The researcher first records the presence of a specific taxon in each sample, and then computes the percentage of all samples in which the taxon is present (Popper 1988). For example, if hickory shell is present in four out of ten samples, then its ubiquity value is 40%. Thus, each taxon is evaluated independently (Hubbard 1980). Because different types of plants are disposed of differently, direct comparisons of ubiquity values between taxa are problematic (Hubbard 1980:53). For example, a 70% ubiquity value for hickory nutshell would not be equivalent to a 70% ubiquity value for beans as these categories have different preservation opportunities—hickory nutshell represents a processing by-product often used as fuel, while beans represent edible portions.

As with any quantitative measure, ubiquity analysis has its disadvantages. A sufficient number of samples is necessary to provide meaningful results as using too few samples creates a high likelihood of sampling error. Hubbard (1976:60) suggests a minimum of 10 samples. Moreover, although ubiquity analysis may mitigate for preservation biases, it is not immune to them (Hubbard 1980:53; Scarry 1986:193). Most importantly, because ubiquity deals with occurrence frequency and not abundance, it can potentially obscure patterns where occurrence frequency does not change but abundance does (Scarry 1986). As Scarry (1986:193) notes: “the frequency with which a resource is used may remain constant, while the quantity used varies.” For example, a family may consistently eat corn on a daily basis, but the quantity they consume

may vary from day to day. Despite these weaknesses, ubiquity analysis is a good starting point and can provide meaningful results when used alongside other measures.

While ubiquity measures may sidestep the problems inherent in absolute counts, it does not provide a means for calculating relative abundances of different plant taxa. Using comparative ratios is one way of determining the relative abundances of different plants. For the purposes of this analysis, I use dependent ratios to calculate relative abundances of different categories of plants. While it might be preferable to use independent ratios and standardize data to soil volume or plant weight, sample sizes are simply too low to yield meaningful results.

Laboratory Procedures

Flotation samples from 44RN220 were collected at variable volumes, ranging from 4-14 L samples. Both the light and heavy fractions of the flotation samples were analyzed. Although the materials from the light and heavy fractions were processed and sorted separately, data from the two fractions were combined for analysis. According to standard practice, the light fractions were weighed and then sifted through 2.0 mm, 1.4 mm, and 0.7 mm standard geological sieves. Carbonized plant remains from both fractions were sorted in entirety down to the 2.0 mm sieve size with the aid of a stereoscopic microscope (10–40 X). Residue less than 2.0 mm in size was scanned for seeds, which were removed and counted; in addition, taxa encountered in the 1.4 mm sieve that were not identified from the 2.0 mm sieve were also removed, counted, and weighed.

Botanical materials were identified with reference to a seed identification manual (Martin and Barkley 1961) and the author's archaeobotanical comparative collection. All plant specimens were identified to the lowest possible taxonomic level. Taxonomic identification was not always possible—some plant specimens lacked diagnostic features altogether or were too highly fragmented. As a result, these specimens were classified as “unidentified” or “unidentified seed.” In other cases, probable identifications were made—for example, if a specimen closely resembled a corn kernel, but a clear taxonomic distinction was not possible (e.g., the specimen was highly fragmented), then the specimen was identified as a probable corn cupule and recorded as “corn kernel cf.”

Once the plant specimens were sorted and identified, I recorded counts, weights (in grams), portion of plant (e.g., corn kernels versus cupules), and provenience information. Wood was weighed but not counted, and no wood identification was conducted. Generally, most of the seeds identified in the samples were too small to weigh, and thus only counts were recorded. Hickory nutshell and corn remains were identified only as fragments, and were both counted and weighed. Other than counts and weights, no other measurements were taken on any specimens.

Basic Results

This section presents the results of the identification of the carbonized plant remains from 44RN220, which forms the basis for the quantitative analysis that follows. Plant data from flotation samples are summarized for the site in Table 1. Raw counts and weights are provided for each taxon (except for the “other seeds” category in which only counts are provided); plant weight, wood weight, and soil volume are also provided. Seasonality data are provided in Table 2. Macrobotanical data recovered through ¼-inch screening are listed according to feature/unit contexts in Table 3. Plant data are also reported by individual contexts (e.g., test units & features) in Appendix A.

A total of 34 flotation samples from 10 test units and 9 features were collected and analyzed, representing a total of 345 liters of soil with a total plant weight of 175.57 grams.

Combined, these samples yielded 12 plant taxa, including corn, hickory, walnut, and several different types of seeds (Table 1). Corn (*Zea mays*) was the only definitive field cultigen present in the samples, although a possible sumpweed seed (*Iva annua*) was also identified. Nutshell recovered from the flotation samples includes hickory (*Carya* sp.) and walnut (*Juglans* sp.). While the nutmeats of walnuts can be easily extracted from the shell, hickory nuts require extensive processing before they are rendered palatable. The hickory kernels are so tightly enmeshed in the interior shell that picking the nutshells from the cracked shell casing is a time-consuming task. Instead, hickory nuts were generally pounded into pieces and boiled to extract the oil (Ulmer and Beck 1951). The process of boiling the pounded hickory nuts separates the pieces of shell, which sink to the bottom of the pot, from the oil, which rises to the top as the nutmeats dissolve and can be skimmed off or decanted. This oil or milk would then be used as an added ingredient in soups and stews, as a condiment for vegetables, or as a general sauce or beverage (Scarry 2003; Talalay et al. 1984).

Table 1. Summary of plant taxa for 44RN220 flotation samples

N of Samples	34		
Total Volume (liters)	345		
Plant Weight (grams)	175.57		
Wood Weight (grams)	174.18		
		count/weight	
Common Name	<i>Taxonomic Name</i>	(n)	(g)
<u>CROPS</u>			
Corn cupule	<i>Zea mays</i>	6	0.00
Corn kernel	<i>Zea mays</i>	31	1.16
Corn kernel cf.	<i>Zea mays</i> cf.	1	0.00
Sumpweed cf.	<i>Iva annua</i> cf.	1	0.00
<u>NUTS</u>			
Hickory	<i>Carya</i> sp.	70	1.11
Walnut	<i>Juglans</i> sp.	2	0.07
<u>FRUITS</u>			
Hawthorn cf.	<i>Crataegus</i> sp.	1	0.00
<u>OTHER SEEDS</u>			
Bearsfoot	<i>Polymnia uvedalia</i>	78	
Bedstraw	<i>Galium</i> sp.	5	
Chenopod	<i>Chenopodium</i> sp.	3	
Grass family	Poaceae	6	
Holly	<i>Ilex</i> sp.	1	
Holly cf.	<i>Ilex</i> sp. cf.	1	
Knotweed cf.	<i>Polygonum</i> sp. cf.	1	
Wax myrtle	<i>Myrica</i> sp.	1	
<u>UNIDENTIFIED</u>		1	
<u>UNIDENTIFIED SEED</u>		3	

The only fruit seed identified was a possible hawthorn seed (*Crataegus* sp.). The remaining taxa identified in the assemblage include of variety of seed types. These include bearsfoot (*Polymnia uvedalia*), bedstraw (*Galium* sp.), chenopod (*Chenopodium* sp.), holly (*Ilex* sp.), a possible holly seed (*Ilex* sp. cf.), a possible knotweed seed (*Polygonum* sp. cf.), wax myrtle (*Myrica* sp.), and a few seeds from the grass family (Poaceae). People may have

consumed the seeds of bearsfoot, chenopod¹, and knotweed. Chenopod and knotweed may also have been eaten green or as potherbs (Hedrick 1972; Medsger 1966, Ulmer and Beck 1951). While some of these seed species may have been eaten as food or may represent weedy inclusions, the majority of them have documented medicinal uses as well. Bearsfoot was used by native Indians in poultices and salves, and as a laxative and stimulant (Chevallier 1970; Grieve 1984; Usher 1974). The root can be rendered and taken orally for the treatment of indigestion and liver malfunction (Chevallier 1970). Bearsfoot root can also be made into a salve for treating burns, cuts, and skin inflammations (Moerman 1998). Although bedstraw is widely known for its use as bedding (e.g., stuffing in pillows and mattresses), it also boasts several medicinal purposes, including use as a diuretic, astringent, and antispasmodic, in addition to treatment of kidney problems (Coffey 1993). Bedstraw may also have been consumed as a tea and the weedy legume may have been used as food (Coffey 1993; Hedrick 1972; Peterson 1977). In addition to its use as food, chenopod is also known as a treatment for worms in children (Coffey 1993) and as an antispasmodic (Coon 1979), and can therefore also be considered a medicinal plant. The holly seed (and possible holly seed) is notable in that it may represent yaupon holly (*Ilex vomitoria*), a natural emetic and primary ritual ingredient in the native Black Drink (Coon 1979; Porcher 1970). “The Indians drank it very strong, and in copious draughts, at a certain period of the year, in order to purify themselves” (Porcher 1970:394; see also Coon 1979). The root of the knotweed has astringent properties and is also a natural emetic/purgative; it can be used to treat diarrhea, constipation, dysentery, and uterine bleeding (Porcher 1970). The leaves of the knotweed can be made into an infusion to stop bleeding in the mouth (Coffey 1993). Finally, wax myrtle represents one of the most widely documented medicinal plants discussed thus far (Coon 1979; Porcher 1970). Also known by the common name bayberry, wax myrtle has astringent properties useful in the treatment of ulcers, diarrhea, dysentery, jaundice, and uterine bleeding; in large doses it can also be used as an emetic (Coon 1979; Porcher 1970). When dried and ground, wax myrtle can be inhaled as snuff for nasal congestion (Coon 1979; Porcher 1970).

An assessment of seasonality for these plants indicates the harvesting and collection of resources from April through December (Table 2). Corn begins to ripen in the mid-summer and continue to be harvested throughout the early fall. Hickories and walnuts begin to ripen in October. The remaining taxa (classified as “other seeds”) ripen and are available in the late spring and summer. Collectively, the seasonality information gleaned from the plant remains points to an occupation sometime during late spring–early fall at 44RN220.

Table 2. Seasonality of 44RN220 plant taxa in ascending order by bloom.

	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
Holly				X	X							
Wax Myrtle				X	X	X	X	X	X	X		
Bedstraw					X	X	X	X				
Corn							X	X	X			
Bearsfoot							X	X	X			
Chenopod							X	X	X	X	X	

¹ It is unlikely that the chenopod seeds identified here represent domesticates as seed coat thickness for these specimens is more consistent with wild chenopod. Domesticated and wild chenopod can be distinguished based on thickness of the inner seed coat; domesticated chenopod has a much thinner seed coat than its wild counterpart (Smith 1985).

Knotweed	X	X	X	X	X
Hawthorn			X	X	
Sumpweed			X	X	X
Hickory				X	
Walnut				X	

Table 3. Identified plant remains from 44RN220 macrobotanical samples

Provenience	Wood (g)	Hickory <i>Carya</i> sp.		Walnut <i>Juglans</i> sp.		Walnut Family Juglandaceae		Unidentified	
		(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)
<u>Piece Plots</u>									
17	0.15								
19	2.98								
23	0.04	2	0.01						
24	0.13								
78	0.65								
85	0.01								
172	0.02								
204	0.05								
247	0.01								
620	0.34								
661				3	0.02	28	0.06		
667		40	0.33						
848	0.08								
958	0.14								
1132				5	0.12				
1133		2	0.07	2	0.35				
1198	0.01								
1263	0.03								
1272		5	0.02						
1342				18	1.40				
1346	0.03								
1360	0.02								
1399	0.02								
<u>Test Units</u>									
17	0.35								
20	1.42	3	0.72					1	0.05
23	0.37								
31	0.28								
33	0.30								
34	0.25								
39	11.51	5	0.12						
40	0.61								
<u>Features</u>									
1	0.79								
6	0.12								

7	0.29								
9	1.74								
12	0.22								
Miscellaneous									
Area B/ Backhoe	0.77								
TOTALS	23.73	57	1.27	28	1.89	28	0.06	1	0.05

Taxa identified from the macrobotanical remains were limited to large specimens greater than 2.0 mm in size (Table 3). Not surprisingly, no carbonized seeds were identified among the macrobotanical specimens. Rather, the macrobotanical assemblage consists of large wood specimens and nutshell from hickories and walnuts.

Data Analysis

Analysis of the plants identified in the assemblage is restricted to data from flotation samples. Plant specimens identified in the macrobotanical samples are too few and biased in terms of size. The primary goal of the analysis is to determine the overall importance of different plants in the assemblage in order to assess site function.

To determine the importance of different plants in the assemblage, I use ubiquity analysis and relative percentages. Ubiquity analysis essentially measures the relative presence of different taxa at the site. I use individual samples as the level of aggregation for determining ubiquity values. For example, 34 flotation samples were collected; wood was identified in all 34 samples, resulting in a ubiquity value of 100%. Ubiquity values for taxa identified at 44RN220 are presented in descending order in Table 4. After wood, bearsfoot yields the highest ubiquity value (65%), followed by corn (41%), hickory (35%), and bedstraw (12%). All other taxa have ubiquity values less than ten percent.

Table 4. Ubiquity Values in descending order for plants identified at 44RN220.

Common Name	Samples Present	Total Samples	Ubiquity Value
Wood	34	34	100%
Bearsfoot	22	34	65%
Corn	14	34	41%
Hickory	12	34	35%
Bedstraw	4	34	12%
Chenopod	3	34	9%
Walnut	2	34	6%
Holly	2	34	6%
Hawthorn cf.	1	34	3%
Knotweed	1	34	3%
Sumpweed	1	34	3%
Wax myrtle	1	34	3%

For the purposes of calculating relative percentages, I use taxa counts and group plant taxa into the following categories: medicinal seeds, nuts, cultigens, grass seeds, and fruits. Medicinal seeds include bearsfoot, bedstraw, chenopod, holly, holly cf., knotweed, and wax myrtle; nuts include hickory and walnut; cultigens include corn and sumpweed cf.; grass seeds are represented by specimens identified to the family Poaceae; and fruits consist entirely of one possible hawthorn seed. Relative percentages are listed in descending order in Table 5. Medicinal seeds make up the bulk of the assemblage, representing 43.3% of the plants identified. Eighty-seven percent of the medicinal seed category (or 37.5% of the total assemblage) is represented by bearsfoot. Thus, in addition to being the most ubiquitous plant at 44RN220, bearsfoot is also the most abundant. Medicinal plants are followed in importance by nuts (34.6%), cultigens (18.8%), grass seeds (2.9%), and fruits (0.5%).

Table 5. Relative Percentages in descending order for plants identified at 44RN220.

	Count	Percentage
Medicinal seeds	90	43.3%
Nuts	72	34.6 %
Cultigens	39	18.8 %
Grass seeds	6	2.9 %
Fruits	1	0.5 %
<u>TOTALS</u>	208	100.0 %

The Zooarchaeological Assemblage

Recovery and Preservation Bias

The interpretation of zooarchaeological data depends upon the careful consideration of preservational biases affecting bone assemblages. As with any archaeological assemblage, what is recovered and studied by archaeologists does not directly represent what was originally discarded and deposited by humans. As with carbonized plant remains, whether or not a bone survives deposition to be recovered archaeologically depends in part on its structural density (Binford and Bertram 1977; Brain 1969; Voohries 1969; Lyman 1993, 1994). Denser, compact bones with more cortical tissue are more likely to survive than are fragile bones with more cancellous tissue. Thus, long bone diaphyses will be more resilient than epiphyses, skull fragments more than vertebral fragments, large mammal bones more than small mammal bones, and mammal bones more than bird bones, etc. Thus, generally speaking, we can expect a bias towards the preservation of larger mammalian remains relative to that of smaller, non-mammalian remains. In addition to preservation bias, we also must consider the affects of size bias in recovery techniques. Most field projects use standard ¼-inch mesh screens for recovering animal bones²—while this mesh size recovers a significant amount of bone from the surrounding dirt matrix, skeletal elements from smaller animals (e.g., fish vertebrae and ribs) will often fall through ¼ inch mesh.

² The screened faunal assemblage from 44RN220 was recovered using ¼-inch mesh screens.

Methods of Quantification

Most zooarchaeologists calculate a standard set of summary measures that form the basis for further analysis. The most basic statistic is the Number of Identified Specimens (NISP). NISP is the count of identified specimens per animal taxon (Grayson 1984). While NISP is relatively easy to calculate, there are disadvantages to using it as an estimate for the relative abundance of different animal taxa in an assemblage. Different taxa vary in the number of elements that compose their skeletons, and NISP is unable to control for this (Grayson 1979, 1984; Reitz and Wing 1999). Another problem with NISP is that it does not account for differential preservation or bone fragmentation (Grayson 1984; Klein and Cruz-Uribe 1984; Reitz and Wing 1999). Clearly the bones of a white-tailed deer have more surface area than those of a cottontail and are thus likely to fragment into more pieces, significantly inflating the NISP of deer relative to cottontail. Thus, NISP may overestimate the contribution of larger animals relative to smaller animals.

MNI (Minimum Number of Individuals) is a secondary measure based in part on NISP. MNI is estimated for each species by calculating the occurrence of the most abundant element of the animal, while accounting for the side of the element (if applicable), portion represented, and relevant age information (Grayson 1984; Reitz and Wing 1999). For example, if the most abundant element of a white-tailed deer is the proximal end of a femur ($n=12$), and eight come from the right side of the animal and four from the left site, the minimum number of white-tailed deer would be eight. MNI has several advantages over NISP, the primary one being that it provides units that are independent of each other (Grayson 1973, 1984). While NISP does not account for the fact that different taxa are composed of varying numbers of skeletal elements, MNI is totally unaffected by this problem. Moreover, MNI is much less affected by the problems of fragmentation and preservation than NISP.

As with NISP, however, there are also disadvantages to using MNI, including the inflation of rarer species in the assemblage and the problem of aggregation (Grayson 1984; Reitz and Wing 1999). NISP and MNI can best be understood as separate ends of a spectrum in which NISP represents the maximum number of individuals identified in an assemblage. NISP overestimates the importance of larger, more common taxa. At the other end of the spectrum, MNI (through setting a minimum) has the opposite effect and overestimates rarer taxa. Moreover, MNI calculations can vary based on how the analyst aggregates the data. There are many ways that the data can be grouped and MNI values calculated—by site, feature, feature type, stratigraphic level, etc. For example, calculating MNI on a feature by feature basis would yield a larger total MNI for each taxon than simply calculating MNI for the site as a whole. In my analysis below, I tabulate NISP and MNI for the site as a whole. NISP and bone weight are presented for individual contexts in Appendix B, C, and D.

Laboratory Procedures

Screened bone specimens were sorted to the lowest possible taxonomic category. Specimens were identified with reference to the author's zooarchaeological comparative collection. Identification of screened materials included the recording of provenience, animal class, genus and species, element, percentage and portion of the element represented, number of specimens, side of element (when applicable), basic observations regarding the age of the animal and extent of bone modification (whether natural or cultural), and weight (grams). Each specimen was first assigned to the appropriate animal class whenever possible (e.g., mammal,

bird, etc.). The anatomical element was recorded when identified. When the element could not be identified, it was placed in an unidentified category.

Basic Results

The data are summarized by NISP, MNI, and weight for the site as a whole (Table 6) and by NISP and weight for each piece plot, test unit, and feature (see Appendix B, C, D). Counts and percentages are provided for each animal class designation (e.g., mammals, birds; see Table 7). The screened faunal assemblage yielded a total of 5,578 bone specimens weighing 1,673 grams. Three animal taxa were identified, in addition to unidentified snake, turtle, bird, and mammal specimens. A single molar from a human (*Homo sapiens*) was also identified. Reptiles identified in the assemblage consist of unidentified turtle and unidentified snake specimens. No amphibians were identified in the assemblage. Only one bird specimen was encountered, but was not identifiable beyond class.

Over 90% of the animal bones that could be identified were classified as mammals. One opossum (*Didelphis virginianus*) specimen was identified. The opossum prefers disturbed habitats, including areas along forest edges, secondary growth, and weedy areas (Reid 1997:43–44, 192). Raccoon (*Procyon lotor*) was also identified in the assemblage. Raccoons are highly adapted to disturbed habitats and can be considered crop pests (Reid 1997:258). White-tailed deer (*Odocoileus virginianus*) compose the bulk of the identified assemblage. It is important to note that over 3,000 specimens were also identified to a “large mammal” category. While some of these “large mammal” specimens could be bear (*Ursus americanus*), the majority are probably white-tailed deer. Deer inhabit a variety of different ecozones, including forests, forest edges, grasslands, disturbed areas, and occasionally agricultural fields (Benyus 1989; Sutton and Sutton 1985).

Bones identified in flotation samples are presented in Tables 8 and 9. Like the screened assemblage, mammals are the most prevalent class identified, followed by unidentified specimens. Only one bird specimen and no reptile remains were identified. If we compare the animal class percentages from the screened assemblage with that from the flotation assemblage, it appears at first glance that mammals are less represented in the flotation assemblage. Such a comparison, however, is misleading. The relatively lower percentage of mammals in the flotation assemblage is a product of the higher percentage of unidentified specimens; this pattern is to be expected from a flotation assemblage as smaller specimens have less diagnostic features which results in a lower level of identifiability.

Overall, large mammals dominate both screened and floated assemblages in terms of both NISP and bone weight. Other classes of animals were less represented in the assemblages. Given the similarities between screened and floated contexts, the under-representation of non-mammalian fauna does not appear to be a product of recovery/size bias. Other taphonomic factors, however, cannot be ruled out at this time. In the following section, I consider the effects of density-mediated attrition on the white-tailed deer specimens from the screened assemblage.

Table 6. Summary of animals from screened samples

Common Name	Taxonomic Name	NISP	MNI	Weight
<u>REPTILES</u>				
UID snake		18		0.11
UID turtle		4		0.74
<u>BIRDS</u>				
UID Bird		1		0.05
<u>MAMMALS</u>				
Opossum	<i>Didelphis virginianus</i>	1	1	0.16
Human	<i>Homo sapiens</i>	1	1	2.28
UID Rodent	Rodentia	5		0.04
Raccoon	<i>Procyon lotor</i>	4	1	0.99
White-tailed deer	<i>Odocoileus virginianus</i>	1238	5	1163.68
Large Mammal		3164		474.35
UID Mammal		619		18.85
<u>UNIDENTIFIED</u>		<u>523</u>		<u>11.71</u>
TOTALS		5578	8	1672.96

Table 7. Summary of animal class statistics from screened samples

	NISP	% NISP	Weight	% Weight
Reptiles	22	0.4%	0.85	0.1%
Birds	1	0.0%	0.05	0.0%
Mammals	5032	90.2%	1660.35	99.2%
Unidentified	523	9.4%	11.71	0.7%

Table 8. Summary of animals from flotation samples

Common Name	Taxonomic Name	NISP	MNI	Weight
<u>BIRDS</u>				
UID Bird		1		0.01
<u>MAMMALS</u>				
White-tailed deer	<i>Odocoileus virginianus</i>	1	1	0.87
Large Mammal		91		17.09
UID Mammal		15		1.63
<u>UNIDENTIFIED</u>		48		5.55
TOTALS		156		25.15

Table 9. Summary of animal class statistics from flotation samples

	NISP	% NISP	Weight	% Weight
Birds	1	0.6%	0.01	0.0%
Mammals	107	68.6%	19.59	77.9%
Unidentified	48	30.8%	5.55	22.1%

Data Analysis:

Because the faunal data consist primarily of large mammal elements, I necessarily restrict my analysis to the white-tailed deer identified in the assemblage. Upon initial inspection, it might seem that the assemblage is biased towards larger mammals because of poor bone preservation or taphonomic bias. However, comparison to the flotation assemblage reveals that size bias (at least in terms of recovery methods) is not an issue. To consider whether other taphonomic issues have biased the faunal assemblage, I consider the effects of density-mediated attrition on the white-tailed deer specimens from the screened assemblage. If density-mediated attrition has affected the white-tailed deer assemblage, then we can expect the assemblage to be composed of more elements with higher density values relative to elements with low density values. This follows the logic that denser bones are going to preserve better than fragile, porous bones in the face of taphonomic processes (e.g., weathering, wetting/drying, freezing, soil acidity, etc.).

To examine this issue, I consider the relationship between element survivorship and known volume density values for white-tailed deer elements (Table 10; see also Lyman 1994; Reitz and Wing 1999). Survivorship is calculated for each skeletal element by dividing observed MNE (Minimum Number of Elements) values by expected MNE values. MNE is relatively easy to calculate; for example, 12 distal humerii specimens (NISP=12) were identified in the white-tailed deer assemblage, and these 12 specimens represent a minimum of 7 different distal humerii (thus an observed MNE of 7). Of these 7 distal humerii, 4 side right and 3 side left, yielding an MNI (Minimum Number of Individuals) of 4 white-tailed deer based on the distal humerus. Given an MNI of 4, we would expect there to be an MNE of 8 distal humerii (MNI of 4 X 2 sides). Thus, if we divide observed MNE (7) by expected MNE (8), we get an 88% survivorship rate.

Survivorship and volume density values are plotted against each other in Figure 1. Volume density values for white-tailed deer are taken from Lyman (1994) and Reitz and Wing (1999). Based on the scatterplot and the corresponding Pearson's R correlation value (0.05), there appears to be almost no relationship between element survivorship and volume density. In other words, density-mediated attrition does not appear to have significantly affected the white-tailed deer assemblage. Thus, if differential bone density has not affected the deer assemblage, it is possible that differential bone density is not responsible for the over-representation of mammals with respect to other classes of animals. In other words, deer (and large mammals as a whole) may be over-represented because people purposefully targeted large mammals over other types of animal prey.

It appears that people may have placed more importance on hunting deer than on other types of animal exploitation at the site. If people were indeed targeting deer, then the next question we must ask is what type of field processing/butchering strategy they used? If 44RN220 was a special seasonal encampment established for the purpose of deer hunting (and perhaps the collection of medicinal plants), then we might expect the deer assemblage to be

dominated by low meat-yielding bones, or low-utility elements. Low-utility elements include the skull and mandible, and lower limb bones (metapodia, carpals/tarsals, and phalanges). We would expect fewer mid-utility parts (axial elements) and high-utility parts (forelimbs and hindlimbs) as these parts would presumably be transported back to a permanent settlement. To examine deer body part distributions at 44RN220, I consider the assemblage in terms of transport decisions. Following Binford (1978) and Metcalfe and Jones (1988), I plot the Food Utility Index (FUI) against percent MAU (Minimum Anatomical Unit) (see also Lyman 1994; Reitz and Wing 1999). MAU is calculated as observed MNE divided by the number of that element that occurs in a normal deer skeleton; MAU values are then scaled as percentages against the largest MAU value for the assemblage (Reitz and Wing 1999). The resulting plot shown in Figure 2 most closely resembles a reverse utility strategy (see Reitz and Wing 1999:24). As defined by Reitz and Wing (1999:24), “the reverse utility strategy graph reflects the types of elements that would be found at a kill/butchery site at which elements with low utility would be abundant; elements with high utility would be underrepresented because they are removed to consumption sites”.

Table 10. 44RN220 white-tailed deer parts: meat utility and bone mineral densities (ranked by descending %MAU).

	NISP	Observed MNE ^a	Expected MNE	%Survivorship (ObMNE/ExMNE)	MAU ^b	%MAU	FUI ^c	VD ^d
calcaneous	9	9	10	90%	4.5	100.0%	1424	0.49
humerus, distal	12	7	8	88%	3.5	77.8%	1891	0.51
scapula	368	6	6	100%	3	66.7%	2295	0.35
mandible	223	4	4	100%	2	44.4%	590	0.51
radius, distal	3	3	4	75%	1.5	33.3%	1039	0.4
cervical vertebra	59	6	10	60%	1.2	26.7%	1905	0.17
metapodial, distal	14	4	4	100%	1	22.2%	578	0.5
metacarpal, prox.	9	2	4	50%	1	22.2%	461	0.66
astragulas	6	2	4	50%	1	22.2%	1424	0.56
tibia, distal	2	2	4	50%	1	22.2%	2267	0.5
1st phalanx	11	7	8	88%	0.875	19.4%	443	0.45
radius, proximal	5	1	2	50%	0.5	11.1%	1323	0.52
femur, distal	1	1	2	50%	0.5	11.1%	5139	0.32
femur, proximal	1	1	2	50%	0.5	11.1%	5139	0.37
humerus, shaft	1	1	2	50%	0.5	11.1%	--	0.53
innominate	1	1	2	50%	0.5	11.1%	2531	0.33
ulna, proximal	1	1	2	50%	0.5	11.1%	1323	0.37

^a Minimum Number of Elements

^b Minimum Anatomical Unit

^c Food Utility Index (Metcalf and Jones 1988)

^d Volume Density (Lyman 1994; Reitz and Wing 1997)

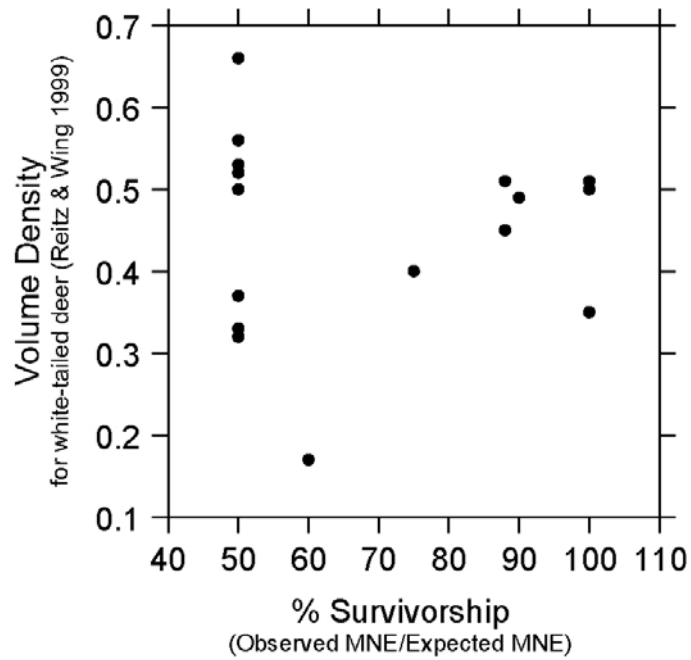


Figure 1. Known volume density values for white-tailed deer elements plotted against bone survivorship (Pearson's $R = 0.05$)

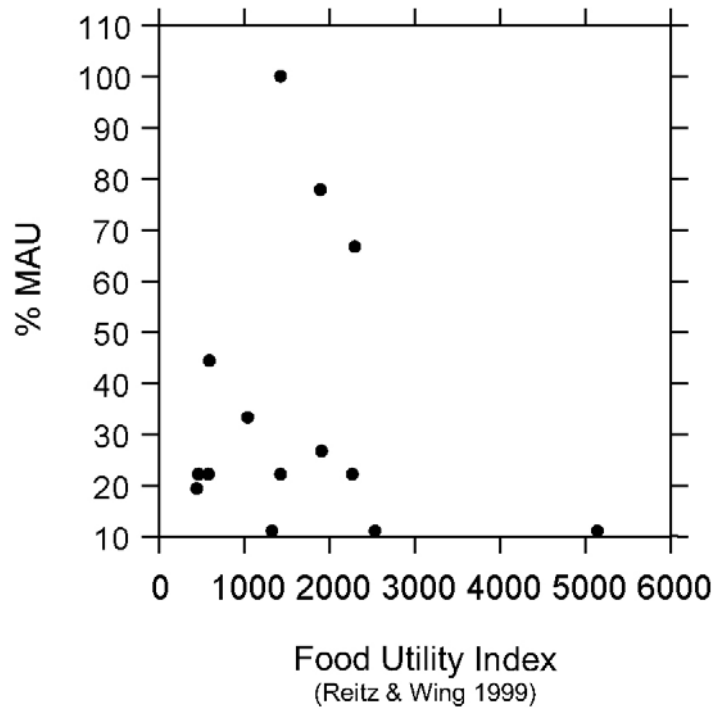


Figure 2. Food Utility Index (FUI) for white-tailed deer elements plotted against % MAU (Pearson's $R = -0.197$)

SUMMARY OF SUBSISTENCE DATA FOR 44RN220

The taxonomic composition of flora and fauna in the organic assemblage from 44RN220 is not what one would expect from a year-round habitation site. The plant assemblage is dominated by medicinal plants with relatively fewer remains of corn and hickory. If 44RN220 were a typical domestic assemblage, one would expect corn and hickory (as staple foodstuffs) to be more ubiquitous and abundant than they are. Instead, bearsfoot, a wildflower with an array of medicinal properties, is more abundant and was identified in more samples than any other plant taxon at the site. In addition to bearsfoot, a suite of other medicinal plants were also identified, including bedstraw, holly, knotweed, chenopod, and wax myrtle. The animal assemblage is dominated by a single taxon, white-tailed deer. If 44RN220 were a typical domestic assemblage, one would expect deer to be an important resource, but one would also expect a richer array of animal taxa in addition to deer. The 44RN220 faunal assemblage, however, is so heavily skewed towards white-tailed deer that virtually no other taxa were even present in the assemblage. An examination of the deer assemblage ruled out density-mediated attrition as a taphonomic factor. In other words, poor preservation is not the reason that bones of other animals were not recovered or identified. Rather, it appears that people at 44RN220 were intentionally targeting deer. In addition, analysis of deer body part distributions produced a reverse utility curve, an outcome that strongly suggests that 44RN220 represents a short-term butchery/kill site. People at 44RN220 killed and butchered a minimum of 5 deer, removed high-utility (fore- and hindlimbs) and mid-utility (ribs and vertebra) cuts of venison, and transported these cuts somewhere else, possibly to a separate year-round habitation site. A consideration of seasonality with respect to hunting deer and collecting bearsfoot suggests an occupation in the August-October range. Peak hunting time for white-tailed deer is during the fall, especially during September and October. Bearsfoot begins to bloom in July and can be collected through September (see Table 2). Seasonality for the other medicinal species varies, but all are ripe and available for collection during August and September (except for bedstraw, which is usually only available through August (see Table 2). In summary, analysis of the plant and animal data suggest that 44RN220 represents a short-term seasonal encampment geared towards the collection of medicinal plants and the hunting of deer.

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Appendix A. 44RN220 plant taxa from flotation samples listed for test units and features.

Provenience	TU 20		TU 23		TU 26		TU 27		TU 29		TU 31		TU 34		TU 37	
N of Samples	1		1		1		1		1		1		1		1	
Total Volume (liters)	5		13		11		10		5		5		5		7	
Plant Weight (grams)	5.93		0.40		0.53		0.43		0.39		3.62		0.27		0.25	
Wood Weight (grams)	5.93		0.40		0.53		0.43		0.39		3.62		0.25		0.25	
Count/Weight	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)
<u>CROPS</u>																
Corn cupule										1	0.00					
Corn kernel																
Corn kernel cf.			1	0.00												
Nuts																
Hickory													2	0.00		
Walnut													1	0.02		
<u>FRUITS</u>																
Hawthorn cf.															1	0.00
<u>OTHER SEEDS</u>																
Bearsfoot			3		2		2		4		2				2	
Bedstraw																
Chenopod			1													
Grass family																
Holly																
Holly cf.																
Knotweed cf.																
Sumpweed cf.																
Wax myrtle																
<u>UNIDENTIFIED</u>			1													
<u>UNIDENTIFIED SEED</u>			1													

Appendix A cont'd. 44RN220 plant taxa from flotation samples listed for test units and features.

Provenience	TU 38		TU 39		Feat. 1		Feat. 1 (below)		Feat. 6		Feat. 7		Feat. 8		Feat. 9	
N of Samples	1		1		2		1		2		3		1		7	
Total Volume (liters)	12		6		20		10		25		31		14		75	
Plant Weight (grams)	2.87		0.09		4.96		0.45		1.21		108.17		0.44		23.39	
Wood Weight (grams)	2.55		0.09		4.96		0.40		1.14		108.15		0.43		23.05	
Count/Weight	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)
<u>CROPS</u>																
Corn cupule			1	0.00											3	0.00
Corn kernel	1	0.00					1	0.00			1	0.02			23	0.14
Corn kernel cf.																
<u>NUTS</u>																
Hickory	15	0.32	1	0.00			4	0.05	12	0.07			1	0.00	1	0.00
Walnut															1	0.05
<u>FRUITS</u>																
Hawthorn cf.																
<u>OTHER SEEDS</u>																
Bearsfoot					1		5				1		4		41	
Bedstraw							1								3	
Chenopod																
Grass family															4	
Holly																
Holly cf.							1									
Knotweed cf.															1	
Sumpweed cf.																
Wax myrtle																
<u>UNIDENTIFIED</u>																
<u>UNIDENTIFIED SEED</u>									1						1	

Appendix A cont'd. 44RN220 plant taxa from flotation samples listed for test units and features.

Provenience	Feat. 10		Feat. 11		Feat. 12		Feat. 13		?	
N of Samples	1		2		1		2		1	
Total Volume (liters)	4		25		13		27		9	
Plant Weight (grams)	0.43		0.94		0.67		1.10		18.32	
Wood Weight (grams)	0.19		0.94		0.66		0.69		18.32	
Count/Weight	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)	(n)	(g)
<u>CROPS</u>										
Corn cupule										
Corn kernel	2	0.00			1	0.00	2	0.00		
Corn kernel cf.										
<u>NUTS</u>										
Hickory	15	0.25			2	0.01	17	0.41		
Walnut										
<u>FRUITS</u>										
Hawthorn cf.										
<u>OTHER SEEDS</u>										
Bearsfoot	1		1		1		8			
Bedstraw					1					
Chenopod							2			
Grass family			1				1			
Holly							1			
Holly cf.										
Knotweed cf.										
Sumpweed cf.					1					
Wax myrtle							1			
<u>UNIDENTIFIED</u>										
<u>UNIDENTIFIED SEED</u>										

Appendix B. 44RN220 animal taxa from piece plots.

Piece Plot #	Bag #	Common Name	Element	NISP	Wt (g)
1	1	large mammal	long bone fragment	1	2.47
2	2	white-tailed deer	scapula	1	20.81
2	2	white-tailed deer	scapula fragments	77	10.37
6	5	large mammal	UID	6	0.16
7	6	large mammal	long bone fragment	3	1.42
14	7	large mammal	UID	--	0.72
15	8	large mammal	long bone fragment	--	2.53
16	9	large mammal	long bone fragment	25	5.07
17	10	large mammal	long bone fragment	--	11.30
18	11	large mammal	long bone fragment	4	1.79
22	13	white-tailed deer	calcaneum	1	7.74
24	15	UID	UID	7	0.07
25	16	white-tailed deer	teeth	4	3.85
25	16	white-tailed deer	maxilla fragments	18	0.77
26	17	large mammal	long bone fragment	1	0.90
26	17	large mammal	UID	51	1.79
26	17	white-tailed deer	cervical vertebra	1	9.09
27	18	large mammal	UID	4	0.62
28	19	white-tailed deer	mandible	1	14.70
29	20	large mammal	long bone fragment	3	0.23
30	21	large mammal	long bone fragment	4	4.32
31	22	white-tailed deer	calcaneum	1	18.29
33	23	large mammal	UID	20	0.27
34	24	large mammal	UID	19	0.96
38	25	large mammal	UID	118	3.36
39	26	white-tailed deer	skull fragments	1	25.98
40	27	large mammal	UID	1	0.49
44	28	large mammal	long bone fragment	27	1.51
46	29	large mammal	UID	5	1.07
57	31	large mammal	long bone fragment	29	3.20
58	32	large mammal	UID	24	7.15
59	33	large mammal	UID	1	0.50
61	34	large mammal	UID	7	0.18
62	35	white-tailed deer	calcaneum	1	19.26
63	36	large mammal	long bone fragment	1	0.12
64	37	UID	UID	--	0.04
65	38	white-tailed deer	scapula	1	24.34

65	38	white-tailed deer	scapula fragments	16	0.70
66	39	white-tailed deer	scapula	1	17.79
66	39	white-tailed deer	scapula fragments	72	4.63
67	40	large mammal	long bone fragment	2	1.86
69	41	UID	UID	3	0.02
70	42	large mammal	UID	6	0.97
71	43	large mammal	UID	1	0.12
72	44	large mammal	UID	18	0.63
72	44	white-tailed deer	scapula	1	11.33
75	45	large mammal	long bone fragment	1	0.04
76	743	large mammal	long bone fragment	1	0.23
78	46	white-tailed deer	lumbar vertebral fragments	6	13.95
82	47	large mammal	long bone fragment	14	0.27
85	48	UID mammal	UID	15	0.09
91	49	large mammal	long bone fragment	5	0.14
92	50	large mammal	long bone fragment	1	0.22
93	51	large mammal	UID	1	0.15
94	52	UID	UID	2	0.02
96	756	large mammal	long bone fragment	1	0.63
102	53	large mammal	long bone fragment	32	6.27
105	56	large mammal	long bone fragment	3	0.22
106	57	UID	UID	1	0.01
107	58	large mammal	long bone fragment	40	1.48
110	60	large mammal	long bone fragment	26	4.10
114	63	large mammal	long bone fragment	26	0.68
117	64	large mammal	long bone fragment	1	1.11
120	67	large mammal	long bone fragment	2	0.30
122	68	large mammal	long bone fragment	2	0.81
124	69	large mammal	long bone fragment	16	0.30
125	70	large mammal	long bone fragment	2	0.19
127	71	UID mammal	UID	49	0.54
133	72	UID mammal	UID	2	0.02
134	73	large mammal	long bone fragment	1	0.11
136	74	large mammal	long bone fragment	6	0.18
137	75	large mammal	long bone fragment	14	0.32
138	76	large mammal	UID	1	0.73
145	77	large mammal	UID	2	0.17
149	79	large mammal	long bone fragment	1	0.15
150	80	large mammal	long bone fragment	2	0.47
152	785	large mammal	long bone fragment	2	0.19

154	81	large mammal	patella fragment?	1	2.01
156	82	large mammal	UID	34	4.26
157	83	UID	UID	1	0.07
163	84	large mammal	long bone fragment	5	0.58
164	85	UID	UID	2	0.04
165	86	large mammal	long bone fragment	3	0.08
168	87	large mammal	long bone fragment	3	0.18
170	88	large mammal	long bone fragment	1	0.48
171	796	white-tailed deer	carpal	1	1.85
172	89	large mammal	long bone fragment	1	0.83
177	90	large mammal	long bone fragment	5	0.13
178	801	large mammal	long bone fragment	1	0.07
179	91	large mammal	long bone fragment	12	1.30
180	92	white-tailed deer	molar	1	2.64
187	94	large mammal	long bone fragment	2	0.35
188	95	medium mammal	canine	1	0.56
188	95	UID mammal	UID	25	1.56
188	95	white-tailed deer	mandible	1	2.09
188	95	white-tailed deer	premolars	3	0.61
196	96	white-tailed deer	metapodial fragments	25	11.08
197	97	UID	UID	3	0.02
199	98	large mammal	long bone fragment	1	1.80
200	99	large mammal	long bone fragment	2	0.41
202	100	white-tailed deer	antler fragment	74	60.57
203	101	large mammal	long bone fragment	14	0.19
204	102	large mammal	long bone fragment	4	1.12
205	103	large mammal	long bone fragment	31	6.95
206	104	large mammal	long bone fragment	10	0.86
208	106	large mammal	long bone fragment	7	0.78
213	108	large mammal	long bone fragment	11	2.27
217	821	large mammal	long bone fragment	1	0.22
218	110	large mammal	long bone fragment	1	0.09
223	112	large mammal	UID	1	0.79
224	113	white-tailed deer	calcaneum	1	14.56
235	115	large mammal	long bone fragment	38	1.13
236	116	large mammal	long bone fragment	1	0.19
237	117	large mammal	metapodial	1	2.49
239	119	large mammal	long bone fragment	4	1.22
240	120	large mammal	long bone fragment	1	0.70
241	121	UID	UID	6	0.15

242	122	large mammal	long bone fragment	3	0.31
243	123	UID	UID	3	0.04
244	124	white-tailed deer	tibia	1	49.07
245	125	large mammal	UID	2	0.25
246	126	large mammal	long bone fragment	1	0.07
247	127	large mammal	long bone fragment	1	0.36
248	128	UID	UID	7	0.14
251	129	large mammal	UID	29	0.78
255	131	large mammal	long bone fragment	10	0.59
258	132	large mammal	long bone fragment	1	0.41
259	133	large mammal	long bone fragment	8	0.29
265	135	large mammal	long bone fragment	1	0.31
266	136	UID	UID	1	0.10
267	137	white-tailed deer	antler fragment	181	32.32
267	137	white-tailed deer	lateral malleolus	1	0.56
268	138	large mammal	long bone fragment	4	2.21
269	139	large mammal	long bone fragment	2	0.43
273	140	UID	UID	1	0.05
274	141	UID	UID	5	0.17
277	142	large mammal	long bone fragment	7	0.98
278	143	UID mammal	long bone fragment	14	0.34
279	144	large mammal	long bone fragment	21	2.87
282	145	large mammal	long bone fragment	1	1.74
283	146	large mammal	long bone fragment	7	6.73
284	147	white-tailed deer	tibia	1	53.73
285	148	white-tailed deer	scapula	1	4.98
285	148	white-tailed deer	scapula fragments	196	24.55
286	149	UID	UID	3	0.01
287	150	white-tailed deer	femur	1	2.24
288	151	white-tailed deer	metacarpal	1	7.94
289	152	large mammal	long bone fragment	2	1.77
290	153	large mammal	long bone fragment	7	0.39
290	153	white-tailed deer	tibia	1	7.03
294	154	UID	UID	8	0.07
306	155	large mammal	long bone fragment	7	0.84
307	156	large mammal	UID	11	0.32
308	157	large mammal	UID	2	0.31
310	158	UID mammal	UID	1	0.01
311	159	large mammal	UID	11	0.54
312	160	large mammal	long bone fragment	9	0.84

313	161	UID	UID	2	0.03
315	162	large mammal	long bone fragment	1	0.49
316	163	UID	UID	4	0.08
318	164	large mammal	UID	1	0.21
321	165	UID	UID	2	0.01
323	167	large mammal	long bone fragment	1	3.22
326	168	UID	UID	4	0.07
327	169	white-tailed deer	axis	1	7.95
328	170	large mammal	canine	1	0.31
328	170	UID mammal	UID	3	0.02
331	171	UID	UID	1	0.01
338	172	large mammal	long bone fragment	14	0.91
338	172	white-tailed deer	humerus	1	5.84
340	173	large mammal	long bone fragment	1	0.80
340	173	white-tailed deer	carpal/tarsal	1	0.41
342	174	large mammal	UID	1	14.65
343	175	large mammal	long bone fragment	4	0.96
358	176	large mammal	long bone fragment	7	0.27
362	177	UID	UID	12	0.16
363	178	large mammal	long bone fragment	1	0.43
364	179	large mammal	long bone fragment	3	0.36
366	180	large mammal	UID	17	2.12
367	181	large mammal	long bone fragment	1	0.30
368	182	UID	UID	2	0.17
375	184	large mammal	long bone fragment	2	2.72
382	186	large mammal	long bone fragment	2	0.66
386	187	large mammal	long bone fragment	23	0.69
395	189	large mammal	long bone fragment	2	0.14
397	190	large mammal	long bone fragment	2	1.37
399	191	white-tailed deer	antler fragment	1	0.52
403	193	large mammal	long bone fragment	3	0.32
410	194	large mammal	UID	3	0.28
415	196	UID	UID	3	0.07
421	197	UID	UID	1	0.01
422	198	white-tailed deer	premolar	1	0.72
423	199	large mammal	long bone fragment	48	0.73
424	200	white-tailed deer	vertebral fragments	5	1.86
427	201	large mammal	long bone fragment	4	0.23
432	202	large mammal	UID	1	0.23
437	203	large mammal	long bone fragment	1	0.26

438	204	large mammal	long bone fragment	2	0.35
447	206	large mammal	UID	25	0.44
449	207	UID mammal	UID	4	0.14
451	208	UID	UID	1	0.03
453	209	UID	UID	1	0.01
457	210	UID	UID	4	0.06
459	211	white-tailed deer	metapodial	1	2.69
460	212	large mammal	UID	1	0.31
461	213	UID	UID	1	0.06
462	214	UID	UID	1	0.04
463	215	large mammal	UID	16	0.34
464	216	UID mammal	UID	4	0.03
464	216	white-tailed deer	vertebral fragments	2	1.73
468	218	large mammal	long bone fragment	1	0.30
478	219	large mammal	long bone fragment	2	0.27
481	220	UID	UID	2	0.01
485	221	UID	UID	1	0.03
488	222	large mammal	long bone fragment	34	0.67
489	223	UID	UID	8	0.14
495	224	UID	UID	1	0.01
496	225	large mammal	long bone fragment	1	0.65
498	226	large mammal	long bone fragment	1	0.10
500	227	white-tailed deer	tooth fragment	1	0.15
501	228	UID	UID	2	0.05
506	229	UID	UID	3	0.01
507	230	large mammal	long bone fragment	1	1.26
508	231	large mammal	long bone fragment	5	1.19
509	232	white-tailed deer	molar	1	1.34
510	233	UID	UID	9	0.09
513	234	large mammal	long bone fragment	4	0.38
516	235	large mammal	long bone fragment	2	0.38
518	236	large mammal	UID	4	0.18
518	236	white-tailed deer	ulna	1	0.54
519	237	UID	UID	1	0.08
520	238	white-tailed deer	skull fragments	8	6.37
523	239	large mammal	UID	10	2.16
524	240	large mammal	long bone fragment	3	0.17
525	241	large mammal	long bone fragment	4	0.73
526	242	large mammal	UID	4	0.15
528	243	white-tailed deer	cervical vertebral fragments	14	14.33

530	245	white-tailed deer	cervical vertebra	1	28.60
531	246	UID	UID	--	0.19
532	247	white-tailed deer	cervical vertebral fragments	1	2.53
533	248	large mammal	UID	--	2.93
533	248	white-tailed deer	cervical vertebral fragments	18	22.92
544	249	white-tailed deer	tooth fragment	11	0.88
546	217	large mammal	long bone fragment	3	0.45
549	250	UID	UID	2	0.08
553	215	white-tailed deer	mandiublar fragment	1	0.51
555	252	large mammal	long bone fragment	1	0.65
557	253	large mammal	long bone fragment	2	0.09
559	254	large mammal	long bone fragment	16	1.04
560	255	white-tailed deer	thoracic vertebra	1	14.55
561	256	white-tailed deer	skull fragments	37	9.37
562	257	UID	UID	7	0.03
563	258	large mammal	long bone fragment	28	1.47
564	259	white-tailed deer	mandibular teeth	4	4.18
564	259	white-tailed deer	mandibular fragments	52	6.15
565	260	large mammal	UID	13	1.45
566	261	UID	UID	1	0.20
567	262	large mammal	UID	38	0.50
570	263	UID	UID	9	0.01
571	264	UID	UID	3	0.02
574	266	large mammal	long bone fragment	13	8.40
576	267	large mammal	long bone fragment	60	2.44
582	268	UID	UID	2	0.04
584	269	white-tailed deer	antler	1	47.94
585	270	white-tailed deer	mandible	1	0.85
586	271	white-tailed deer	1st phalanx	1	1.49
587	272	large mammal	UID	31	1.28
588	273	white-tailed deer	calcaneum	1	9.75
595	276	large mammal	long bone fragment	3	2.36
597	277	large mammal	UID	33	1.25
598	278	white-tailed deer	tooth	1	0.83
599	279	large mammal	long bone fragment	18	1.14
599	279	white-tailed deer	radius	1	10.28
600	280	UID	UID	3	0.01
602	281	large mammal	long bone fragment	102	5.92
603	282	UID	UID	3	0.04
604	283	UID	UID	9	0.03

605	284	large mammal	long bone fragment	8	2.26
606	285	UID mammal	UID	11	0.12
607	286	UID	UID	1	0.07
608	287	opossum	molar	1	0.16
608	287	white-tailed deer	cervical vertebra	1	27.12
609	288	large mammal	UID	18	2.10
610	289	large mammal	long bone fragment	4	0.22
611	290	large mammal	UID	11	0.44
612	291	white-tailed deer	metapodial	1	2.70
613	292	large mammal	long bone fragment	48	3.91
613	292	white-tailed deer	metapodial	1	2.48
615	293	large mammal	long bone fragment	5	0.21
616	294	white-tailed deer	humerus	1	13.08
617	295	UID mammal	UID	3	0.05
618	296	large mammal	long bone fragment	1	0.24
621	297	large mammal	long bone fragment	3	0.36
622	297	large mammal	long bone fragment	4	0.72
623	299	large mammal	long bone fragment	1	0.12
624	300	large mammal	long bone fragment	1	0.07
625	301	UID	UID	1	0.14
630	302	large mammal	long bone fragment	2	0.37
632	303	white-tailed deer	rib fragments	10	0.66
634	305	large mammal	long bone fragment	3	2.05
635	306	UID mammal	UID	13	0.41
636	307	large mammal	long bone fragment	3	0.77
637	308	white-tailed deer	humerus	1	30.33
639	309	large mammal	UID	23	2.31
639	309	white-tailed deer	humerus	1	5.61
640	310	UID mammal	UID	32	1.08
641	311	large mammal	long bone fragment	18	8.35
641	311	raccoon	teeth	3	0.76
641	311	UID mammal	UID	3	0.43
642	312	large mammal	long bone fragment	2	0.52
643	313	large mammal	long bone fragment	1	0.39
644	314	large mammal	long bone fragment	1	0.32
644	314	UID turtle	carapace/plastron fragment	2	0.28
645	315	UID mammal	UID	31	1.04
648	316	UID	UID	1	0.07
649	317	large mammal	long bone fragment	2	0.88
652	1046	large mammal	UID	4	1.92

654	318	white-tailed deer	calcaneum	1	15.33
656	319	white-tailed deer	1st phalanx	1	2.90
657	320	UID mammal	UID	16	0.30
657	320	white-tailed deer	metacarpal	1	1.62
658	321	UID mammal	UID	40	0.97
659	322	white-tailed deer	teeth	4	2.63
659	322	white-tailed deer	mandibular fragments	53	2.37
660	323	large mammal	UID	8	0.69
660	323	white-tailed deer	naviculocuboid	1	2.49
662	325	large mammal	UID	8	1.72
663	304	UID	UID	12	0.05
665	326	UID	UID	7	0.05
666	1051	UID	UID	1	0.01
667	327	UID	UID	4	0.01
669	328	UID	UID	1	0.01
672	329	large mammal	long bone fragment	6	0.30
673	330	white-tailed deer	radius	1	4.68
674	331	large mammal	long bone fragment	7	0.27
676	332	white-tailed deer	humerus	1	1.40
677	333	large mammal	long bone fragment	5	1.44
678	334	UID mammal	UID	4	0.13
679	335	UID mammal	UID	63	1.25
680	1056	large mammal	UID	17	0.36
681	336	large mammal	long bone fragment	16	0.65
682	337	large mammal	UID	2	1.18
683	338	white-tailed deer	1st phalanx	1	3.41
693	340	large mammal	long bone fragment	2	0.29
694	341	large mammal	long bone fragment	5	0.51
696	342	UID	UID	1	0.10
697	343	white-tailed deer	sesamoid	1	0.18
721	345	UID	UID	2	0.02
722	1087	white-tailed deer	metapodial	1	1.02
724	346	large mammal	long bone fragment	1	0.13
725	1089	large mammal	UID	1	0.12
728	347	UID mammal	UID	6	0.39
728	347	white-tailed deer	metapodial	2	1.36
730	348	UID	UID	1	0.01
733	349	large mammal	long bone fragment	1	0.18
737	350	white-tailed deer	phalanx	1	0.34
747	352	white-tailed deer	humerus	1	23.38

748	353	large mammal	UID	1	0.17
752	354	UID	UID	1	0.09
759	355	large mammal	long bone fragment	2	1.10
760	356	large mammal	long bone fragment	15	0.89
774	358	UID	UID	2	0.14
777	360	large mammal	long bone fragment	1	0.58
778	361	large mammal	long bone fragment	1	0.31
782	362	UID	UID	1	0.03
798	364	UID mammal	UID	28	0.82
804	365	large mammal	long bone fragment	44	1.43
814	367	large mammal	long bone fragment	1	0.55
814	367	white-tailed deer	metapodial	1	4.83
818	368	UID	UID	3	0.15
819	369	large mammal	long bone fragment	10	0.94
819	369	large mammal	mandibular fragments	1	0.20
823	370	large mammal	long bone fragment	1	0.22
825	371	large mammal	long bone fragment	5	0.17
827	372	UID	UID	1	0.01
828	373	UID	UID	2	0.20
829	1167	UID	UID	1	0.10
837	374	UID	UID	1	0.13
843	375	UID	UID	2	0.20
845	1181	large mammal	UID	1	0.23
854	1190	large mammal	long bone fragment	4	0.26
855	376	large mammal	long bone fragment	16	0.13
866	377	white-tailed deer	scapula	1	28.56
874	378	white-tailed deer	radius	1	19.35
876	379	UID	UID	1	0.27
878	380	UID	UID	2	0.07
881	381	large mammal	long bone fragment	1	0.14
897	382	large mammal	long bone fragment	7	2.33
901	383	UID	UID	8	0.08
905	384	UID mammal	UID	1	0.35
909	386	large mammal	UID	1	0.15
923	387	large mammal	long bone fragment	11	2.25
928	388	large mammal	long bone fragment	5	3.49
932	390	UID	UID	17	0.18
938	391	large mammal	long bone fragment	2	0.11
941	392	large mammal	long bone fragment	1	0.22
943	393	large mammal	long bone fragment	1	1.88

944	394	large mammal	long bone fragment	1	0.16
945	395	large mammal	long bone fragment	3	0.73
948	396	large mammal	long bone fragment	4	0.38
963	399	large mammal	long bone fragment	5	0.28
964	400	white-tailed deer	carpal	1	1.27
965	401	rodent	maxillary fragments	3	0.02
965	401	rodent	incisors	2	0.02
971	402	UID	UID	1	0.18
973	403	large mammal	long bone fragment	12	1.17
988	1292	large mammal	long bone fragment	1	2.41
991	406	large mammal	long bone fragment	1	0.27
995	407	large mammal	long bone fragment	1	0.30
998	409	UID	UID	5	0.05
999	410	large mammal	long bone fragment	1	0.27
1002	411	white-tailed deer	1st phalanx	1	2.55
1003	412	UID	UID	2	0.16
1010	413	large mammal	long bone fragment	1	0.65
1014	414	white-tailed deer	metacarpal	1	3.76
1017	415	large mammal	long bone fragment	1	2.81
1018	416	large mammal	long bone fragment	1	0.63
1022	417	large mammal	long bone fragment	1	0.12
1027	418	large mammal	long bone fragment	1	0.01
1029	419	large mammal	UID	14	4.75
1036	420	large mammal	long bone fragment	13	1.09
1040	421	large mammal	long bone fragment	2	0.32
1041	422	UID	UID	2	0.07
1042	1327	UID	UID	1	0.01
1044	1329	large mammal	UID	1	0.26
1048	1332	large mammal	long bone fragment	1	0.10
1056	423	UID	UID	1	0.01
1058	424	large mammal	UID	6	0.15
1059	425	large mammal	long bone fragment	6	0.57
1062	426	large mammal	long bone fragment	1	0.24
1063	1343	white-tailed deer	1st phalanx	1	1.56
1064	427	large mammal	long bone fragment	2	0.40
1072	428	large mammal	long bone fragment	11	1.02
1080	429	large mammal	long bone fragment	4	0.36
1084	430	large mammal	long bone fragment	1	0.02
1084	430	large mammal	long bone fragment	1	0.11
1085	431	white-tailed deer	1st phalanx	1	1.13

1087	432	UID	UID	6	0.15
1088	433	large mammal	long bone fragment	10	3.89
1089	434	large mammal	UID	2	0.16
1090	435	large mammal	long bone fragment	9	0.65
1091	436	large mammal	long bone fragment	20	0.84
1098	437	white-tailed deer	1st phalanx	1	2.67
1104	438	large mammal	UID	12	1.03
1116	439	large mammal	long bone fragment	1	1.07
1118	1387	UID	UID	7	0.16
1121	440	large mammal	long bone fragment	3	0.47
1122	441	large mammal	long bone fragment	1	0.11
1123	442	large mammal	long bone fragment	2	0.66
1124	443	large mammal	long bone fragment	3	0.42
1127	444	UID mammal	UID	8	0.13
1128	445	large mammal	long bone fragment	7	0.57
1128	445	UID bird	UID	1	0.05
1129	446	large mammal	UID	3	1.15
1130	447	large mammal	long bone fragment	1	0.67
1130	447	UID mammal	UID	2	0.09
1131	448	large mammal	long bone fragment	1	0.15
1134	1394	large mammal	long bone fragment	1	0.33
1135	450	large mammal	long bone fragment	20	9.13
1136	451	large mammal	long bone fragment	1	0.19
1137	452	large mammal	long bone fragment	1	0.76
1138	453	UID	UID	37	0.62
1139	454	large mammal	long bone fragment	2	0.31
1140	455	large mammal	long bone fragment	2	0.18
1141	456	UID mammal	UID	17	0.17
1142	457	large mammal	long bone fragment	1	0.11
1143	458	large mammal	long bone fragment	10	0.40
1144	459	large mammal	long bone fragment	1	0.36
1145	460	large mammal	long bone fragment	3	0.82
1146	461	large mammal	UID	54	2.11
1147	462	white-tailed deer	metapodial	3	3.11
1148	463	large mammal	long bone fragment	1	0.83
1149	464	large mammal	long bone fragment	11	0.58
1151	465	white-tailed deer	pelvis	1	8.28
1152	466	large mammal	long bone fragment	1	1.73
1153	467	large mammal	UID	3	0.17
1154	468	UID	UID	4	0.06

1155	469	large mammal	long bone fragment	3	0.38
1156	470	UID mammal	UID	13	1.19
1159	471	large mammal	long bone fragment	16	12.86
1160	472	white-tailed deer	tooth fragments	1	0.06
1160	472	UID	UID	8	0.12
1165	473	UID mammal	UID	60	0.43
1166	474	large mammal	long bone fragment	2	0.24
1169	475	white-tailed deer	tooth fragments	9	0.57
1170	--	UID	UID	1	0.01
1178	--	large mammal	UID	7	1.27
1183	478	large mammal	UID	1	0.08
1185	479	large mammal	long bone fragment	3	0.44
1191	480	UID	UID	3	0.19
1192	481	UID	UID	9	0.12
1206	483	large mammal	UID	1	0.09
1208	484	large mammal	long bone fragment	3	0.23
1211	485	UID snake	vertebral fragments	18	0.11
1218	488	large mammal	long bone fragment	1	0.66
1235	489	UID	UID	2	0.02
1236	490	UID	UID	1	0.01
1252	492	large mammal	long bone fragment	2	0.14
1259	494	UID	UID	10	0.28
1294	496	large mammal	UID	4	0.10
1295	497	large mammal	UID	1	0.08
1296	498	white-tailed deer	antler	1	60.22
1298	499	UID	UID	18	0.12
1299	500	large mammal	long bone fragment	1	0.13
1301	502	white-tailed deer	calcaneum	1	10.33
1303	503	large mammal	UID	9	0.12
1305	504	UID	UID	1	0.01
1324	505	white-tailed deer	sesamoid	1	0.15
1355	508	large mammal	UID	1	0.43
1356	509	large mammal	long bone fragment	2	0.26
1358	510	large mammal	metapodial	1	1.81
1359	511	UID	UID	5	0.03
1360	512	large mammal	long bone fragment	1	0.15
1365	513	large mammal	long bone fragment	3	0.13
1378	1574	large mammal	UID	2	0.30
1379	514	large mammal	UID	2	0.81
1391	515	large mammal	UID	7	0.48

1392	516	large mammal	long bone fragment	12	0.62
1393	517	white-tailed deer	cervical vertebral fragments	9	7.83
1396	518	large mammal	long bone fragment	5	0.17
1397	519	white-tailed deer	cervical vertebral fragments	14	9.44
1399	520	UID	UID	15	0.05
1403	521	UID	UID	5	0.04
1404	522	white-tailed deer	metapodial	1	6.63
1406	524	large mammal	long bone fragment	1	0.26
1407	525	UID	UID	2	0.01
1410	526	UID	UID	2	0.01
1411	527	large mammal	long bone fragment	1	0.17
1413	529	large mammal	long bone fragment	8	2.68
1415	531	raccoon	tooth	1	0.23
1415	531	UID mammal	UID	2	0.04
1419	532	white-tailed deer	scapula	1	5.60
1421	533	white-tailed deer	axis	1	36.57
1430	534	large mammal	UID	5	0.28
1430	534	UID	UID	1	0.01
1431	535	white-tailed deer	teeth	6	6.13
1431	535	white-tailed deer	maxilla fragments	68	1.16
1433	536	large mammal	UID	44	1.15
1436	538	UID	UID	1	0.04
1437	539	UID	UID	2	0.11
1438	540	UID	UID	15	0.67
1449	541	large mammal	long bone fragment	28	3.46
1452	542	white-tailed deer	tooth fragments	3	0.80
1452	542	white-tailed deer	mandibular fragments	75	3.04
1453	543	UID	UID	1	0.01
1456	544	large mammal	UID	10	2.04
1131b	449	large mammal	long bone fragment	7	5.58

Appendix C. 44RN220 animal taxa listed by unit and feature.

Bag #	TU/Feature	Level	Common Name	Element	NISP	Wt (g)
555	TU17	1.39-1.48	large mammal	long bone fragment	3	1.01
555	TU17	1.39-1.48	large mammal	UID	10	0.44
555	TU17	1.39-1.48	white-tailed deer	humerus fragments	6	3.76
555	TU17	1.39-1.48	white-tailed deer	tooth fragments	1	0.10
556	TU17	5	large mammal	long bone fragment	2	0.67
556	TU17	5	large mammal	UID	3	0.27
556	TU17	5	white-tailed deer	astragulas	1	6.14
556	TU17	5	white-tailed deer	astragulas fragments	4	1.81
557	TU17	6	large mammal	long bone fragment	3	0.38
557	TU17	6	large mammal	long bone fragment	2	0.18
558	TU17	7	large mammal	long bone fragment	4	0.36
558	TU17	7	large mammal	UID	1	0.95
558	TU17	7	white-tailed deer	tooth fragments	1	0.20
560	TU17	10	large mammal	long bone fragment	2	2.07
560	TU17	10	white-tailed deer	metapodial	1	13.62
564	TU17	14	large mammal	long bone fragment	1	0.12
564	TU17	14	large mammal	long bone fragment	1	0.61
579	TU20	19	UID	UID	1	0.01
582	TU23	3	UID	UID	1	0.01
583	TU23	4	UID mammal	UID	103	2.66
584	TU23	5	UID	UID	1	0.05
589	TU26	3	UID mammal	long bone fragment	7	0.42
590	TU26	4	UID	UID	15	0.28
591	TU26	5	UID	UID	6	0.10
592	TU26	6	large mammal	UID	18	0.27
592	TU26	6	large mammal	long bone fragment	82	2.59
592	TU26	6	white-tailed deer	molars	2	3.77
593	TU26	7	white-tailed deer	tooth	2	2.33
593	TU26	7	UID	UID	16	0.23
596	TU26	10	UID	UID	2	0.07
598	TU27	5	UID mammal	UID	2	0.08
599	TU27	6	white-tailed deer	mandible fragments	2	0.76
600	TU27	7	white-tailed deer	tooth fragments	3	1.11
600	TU27	7	white-tailed deer	mandible fragments	32	5.53

604	TU29	4	UID mammal	UID	6	0.31
605	TU29	5	large mammal	long bone fragment	3	0.51
605	TU29	5	white-tailed deer	tooth fragments	1	0.20
607	TU29	7	large mammal	long bone fragment	1	0.30
608	TU29	10	white-tailed deer	astragulas	1	6.01
609	TU31	4	large mammal	long bone fragment	44	4.32
609	TU31	4	large mammal	UID	1	0.90
610	TU31	15	large mammal	long bone fragment	20	2.46
610	TU31	15	large mammal	UID	1	0.52
610	TU31	15	white-tailed deer	humerus	1	4.29
615	TU32	5	UID mammal	UID	1	0.21
620	TU33	4	large mammal	long bone fragment	2	1.79
621	TU33	5	UID	UID	5	0.18
622	TU33	6	white-tailed deer	1st phalanx	2	0.56
623	TU33	7	white-tailed deer cf.	tooth fragments	6	0.42
625	TU33	19	large mammal	long bone fragment	2	0.33
625	TU33	19	large mammal	long bone fragment	2	0.26
627	TU34/F.2	4	white-tailed deer	vertebral fragments	2	1.05
628	TU34	6	large mammal	UID	4	0.62
628	TU34	6	large mammal	UID	65	2.65
628	TU34	6	white-tailed deer	mandible	1	1.55
629	TU34	7	large mammal	long bone fragment	12	1.61
629	TU34	7	white-tailed deer	premolar	1	0.58
632	TU34	12	UID	UID	2	0.29
634	TU35	3	UID	UID	46	0.48
635	TU35	4	white-tailed deer cf.	humerus cf.	1	1.27
636	TU35	6	UID	UID	3	0.67
640	TU36	1	large mammal	long bone fragment	5	2.60
640	TU36	1	large mammal	UID	2	0.66
640	TU36	1	large mammal	UID	73	2.08
647	TU37	4	UID mammal	long bone fragment	23	1.70
648	TU37	5	large mammal	long bone fragment	3	0.42
651	TU38	4	UID	UID	19	0.69
652	TU38	5	large mammal	long bone fragment	10	3.36
653	TU38	6	large mammal	long bone fragment	3	0.48
656	TU38	9	UID	UID	1	0.14
656	TU38	9	UID	UID	3	0.08
657	TU38	10	UID	UID	2	0.01
658	TU38	11	large mammal	long bone fragment	1	0.09
659	TU38	12	UID mammal	UID	4	0.16

660	TU39	1	large mammal	long bone fragment	6	4.26
660	TU39	1	large mammal	long bone fragment	9	2.85
661	TU39	2	large mammal	long bone fragment	2	2.80
661	TU39	2	large mammal	UID	28	5.81
661	TU39	2	large mammal	UID	17	2.74
661	TU39	2	UID turtle	carapace/plastron frag.	2	0.46
661	TU39	2	white-tailed deer	carpal	1	0.57
662	TU39	13	large mammal	long bone fragment	5	1.19
669	TU40	5	large mammal	long bone fragment	3	0.99
673	TU41	1	large mammal	long bone fragment	13	2.67
673	TU41	1	white-tailed deer	metapodial	1	1.01
676	F.1		large mammal	UID	1	0.37
677	F.6		large mammal	long bone fragment	2	0.55
677	F.6		large mammal	long bone fragment	18	2.45
677	F.6		medium mammal	femur	2	0.61
680	F.9		large mammal	skull fragment	2	1.06
680	F.9		large mammal	long bone fragment	19	2.41
680	F.9		large mammal	long bone fragment	41	18.86
680	F.9		white-tailed deer	metapodial	1	2.16
680	F.9		white-tailed deer	femur	1	2.39
680	F.9		white-tailed deer	femur	1	2.51
680	F.9		white-tailed deer	radius	1	10.65
681	F.11		large mammal	long bone fragment	2	0.91
682	F.13		large mammal	long bone fragment	33	4.32
683	Area B		large mammal	UID	1	0.56
683	Area B		large mammal	long bone fragment	158	32.04
683	Area B		white-tailed deer	calcaneous	1	13.55
683	Area B		white-tailed deer	calcaneous	1	9.12
683	Area B		white-tailed deer	1st phalanx	1	2.15
683	Area B		white-tailed deer	1st phalanx	1	1.33
683	Area B		white-tailed deer	teeth	3	4.58
683	Area B		white-tailed deer	metapodial	1	3.21
684	Backdirt A		human	molar	1	2.28
684	Backdirt A		large mammal	UID	1	2.24
1621	F.12		large mammal	long bone fragment	13	4.19

Appendix D. 44RN220 animal taxa from flotation samples.

Bag #	TU/Feature	Level/Half	Common Name	Element	NISP	Wt (g)
693	TU37/F.5	5	UID	UID	1	0.12
699	F.6	West	large mammal	long bone fragment	10	0.71
700	F.6	West	UID	UID	14	1.20
706	F.9		large mammal	long bone fragment	36	8.78
706	F.9		large mammal	long bone fragment	8	1.12
707	F.9		white-tailed deer	lateral malleolus	1	0.87
707	F.9		UID	UID	25	3.65
708	F.9		large mammal	UID	4	1.28
709	F.9		large mammal	long bone fragment	2	0.22
709	F.9		large mammal	long bone fragment	2	0.04
709	F.9		medium/large bird	long bone fragment	1	0.01
710	F.9		UID mammal	UID	4	0.33
711	F.9		large mammal	UID	5	0.34
711	F.9		large mammal	UID	1	0.14
712	F.9		large mammal	UID	7	1.01
713	F.10		large mammal	long bone fragment	1	0.09
713	F.10		large mammal	long bone fragment	3	0.82
714	F.11		UID	UID	7	0.52
715	F.11		UID mammal	long bone fragment	4	0.83
716	F.12		large mammal	long bone fragment	1	0.91
716	F.12		large mammal	long bone fragment	11	1.63
717	F.13		UID mammal	long bone fragment	7	0.47
718	F.13		UID	UID	1	0.06