How Much is Enough? An Approach to Sampling Ichthyofaunas

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This paper focuses on the issue of characterizing richness and diversity of a faunal assemblage. This issue is presupposed by Grayson's (1984) seminal volume and it is of pragmatic interest to academic and contract researchers. The question, then, is how much of an excavated assemblage must be examined in order for that assemblage's richness and diversity to be accurately identified? The skeletal characteristics of different taxa, and taphonomic variability among sites or assemblages suggest that no single method may work reliably in every case. The completely identified Ma'acoah (DfSi-5) assemblage is used to examine several approaches to characterizing assemblage richness and diversity in order to identify the methods that may be appropriate under certain conditions. This exercise is intended to help analysts to evaluate an assemblage in terms of their research aim and choose the method(s) most likely to help achieve that aim.

Introduction

A panel discussion at the eighth International Council for ArchaeoZoology meeting revealed that there was little agreement among participants and members of the audience on effective sampling procedures for the analysis of fish assemblages. One issue that was not clear in the discussion was the purpose for which the analysis was being done. Characterization of an assemblage for subsistence analysis or chronological analysis might easily require procedures that differed from each other and from those aimed at simply characterizing richness and diversity of the total assemblage. It is the latter issue on which this paper focuses. The reason for this choice is twofold. First, this is the most coarse level of analysis and, therefore, the one that is likely to be undertaken first, and second, the issue is presupposed in Grayson's (1984) seminal volume on quantification in zooarchaeology and it is of pragmatic interest to academic and contract researchers. The question, then, is how much of an excavated assemblage must be examined in order for that assemblage's richness and diversity to be accurately identified? Others have posed this same question (e.g., Betz 1991:57) and dealt with it in a variety of ways (e.g., Jones et al. 1983:69; Jones and Leonard 1989). The reason for continuing to pursue this issue here is that the differences in assemblage richness and diversity, skeletal characteristics of different taxa, and taphonomic variability among sites or assemblages suggests that no single method may work reliably in every case. What I believe is needed is a recognized *set* of methods that can be shown through case studies to have produced reliable results. An analyst can then evaluate an assemblage in terms of his or her research aim and choose the method(s) most likely to help achieve that aim.

Ichthyofaunal assemblages present unique analytic problems compared to mammalian or avian assemblages. Since few bones of fish fuse together, the number of skeletal elements produced by an individual fish is much higher than that produced by a mammal or a bird, and fusion schedules cannot be used to age individuals. In addition, the bones of fish are usually small in comparison to mammal and bird bones, so they are often more difficult to recover, recognize and identify. Since fish grow continuously, but at varying rates throughout their lives – unlike mammals and birds that reach and maintain a modal size – the size criterion cannot be used to assist in identifying fish. Skeletal elements of fish are usually smaller and more delicate than mammal or bird elements, so they are often more easily fragmented by comparison, and this renders element and taxonomic identification more difficult.

In addition, porous matrices, such as shell middens, in which fish remains are often found, raise the possibility of percolation of small elements into underlying deposits, creating further taphonomic issues to be resolved. The variability in element morphology, even between closely related taxa, often renders the identification of taxon and element difficult without a prodigious memory and an excellent comparative collection, especially when a wide variety of fish was being exploited. Finally, many fish elements, such as rays, fin spines, and pterygiophores, are not particularly diagnostic, so along with element fragments that are broken beyond recognition, an assemblage often consists of a large proportion of unidentifiable bone.

This paper will focus on sampling the fish assemblage from the Ma'acoah site (DfSi-5). This assemblage has already been identified *in toto* and may therefore serve as a "standard" against which to measure the results of the different approaches. Few studies have been able to evaluate their results against a known standard; instead, they typically adopt one of three approaches. One approach is to offer statistical probabilities about the characteristics of the excavated assemblage in relation to the site assemblage (Grayson 1984; Bobrowsky 1985; Bobrowsky and Ball 1989). Grayson's (1984:147-151) approach compares observed and predicted taxonomic richness across a series of assemblages in order to detect unexpectedly high or low richness values in assemblages. This information is valuable, but the adequacy of the sample sizes is not addressed. Bobrowsky's (1985:394-395) approach, like that of Bobrowsky and Ball (1989:23), provides a means of predicting how many taxa should be expected if the whole site was excavated, but provides no empirical test of the predictions. In a second approach, selected elements are chosen as proxies for the richness and diversity of taxa (Leach 1986, 1997). This approach often has the advantage of speed, but three problems with it have been experienced. One problem is that differential preservation and/or bone transport can remove selectively the very bones of interest. A second problem is that such element selection approaches do not demonstrate that the elements are accurate proxies of the richness or diversity of the assemblages from which they are taken. A third problem is that such a large number of different elements must be used as proxies to obtain an accurate picture of the assemblage richness and diversity that the time spent sorting and selecting the elements could have been devoted to identifying the entire assemblage (Greenspan and Wigen 1994). The third approach is simply to identify the assemblage *in toto*. While a small assemblage of fish bone may be easy to identify completely, a huge investment of time and money is required to identify an assemblage of considerable size.

The Ma'caoah Site

The Ma'caoah site is located in a sheltered "inside" location in northern Barkley Sound (Figure 1) where it is well protected from the strong southwesterly winds that bring heavy rain and create rough seas along the outer coast of Vancouver Island in the winter. The site abuts the base of a small, rocky headland from which the site draws its name in the Nuu-chah-nulth (Nootka) language (Ma'acoah=the nose). From this headland, the site extends for over 100 m along the shore and extends inland about 25 m from the beach. Oral history of the Toquaht people tells that the site was a winter village where their ancestors came after taking salmon in the late fall from the nearby Toquart River. Today the site is a Toquaht reserve and home to several families who generously allowed us to camp in their back yards and dig up their front yards. Five arbitrarily located excavation units, each measuring two square metres, were chosen for examination. These units revealed that the deepest part of the midden lay about 2.4 m below the surface near the rocky headland. The other units averaged about 1.6 m in depth and lay above an old beach composed of large, rounded pebbles. The only date for the site is 580±60 B.P. (Beta-47310) uncalibrated radiocarbon years (McMillan and St. Claire 1991: 79-80).

The Ma'acoah site assemblage is the smallest of the main faunal assemblages from the Toquaht Archaeological Project (McMillan and St. Claire

1991, 1992, 1994, 1996) (Figure 1). As such, an examination of sampling in this assemblage can serve as a guide for sampling in the two much larger assemblages from Ch'uumat'a (DfSi-4) and T'ukw'aa (DfSj-23). The issue to be focussed upon here is finding the sample size that will accurately mirror the richness and diversity of the entire assemblage. The approach will be an empirical one, as if an analyst were working through a new assemblage and gauging, as progress continued, whether the characteristics of the entire assemblage were likely to be accurately reflected by the sample that had been analyzed so far.

The Ma'caoah Data

The Ma'acoah fish assemblage is presented in Table 1. All identifications less specific than the family level have been omitted, which reduced the total NISP of 7,533 and MNI of 365 for the assemblage to the NISP of 5,552.5 and the MNI of 342 presented here (NISP values of 0.5 are shown in cases where fragments were counted during taxonomic identification). A Spearman's rank order test of NISP against MNI showed a strong positive correlation (+0.864) that was significant well beyond the 0.01 probability level, so either measure can be used with confidence as an ordinal estimate of taxonomic abundance. Nevertheless, the following analyses will use only NISP in order to reduce the numbers of tied ranks, since there is greater variability in the NISP values than in the MNI estimates, and to reduce the interpretive difficulties associated with MNI estimates. Table 1, then, forms the known standard against which the sampling procedures investigated below can be tested.

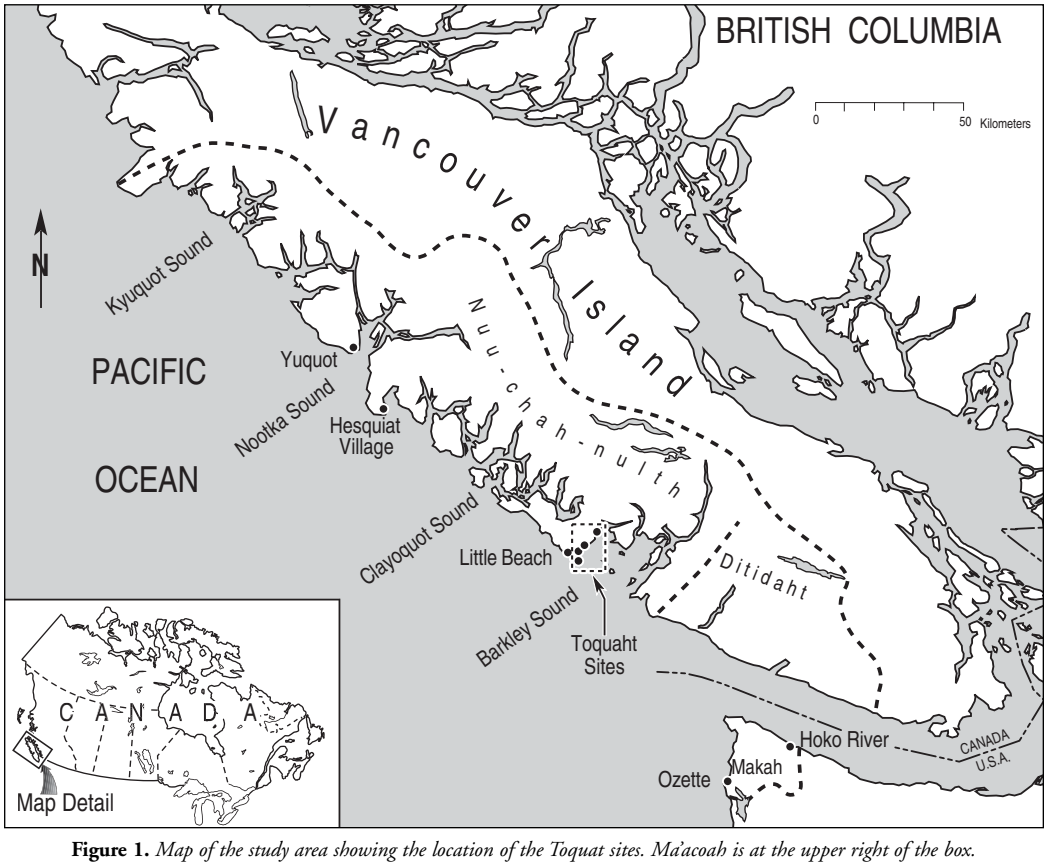

Figure 1. *Map of the study area showing the location of the Toquat sites. Ma'acoah is at the upper right of the box.*

Table 1. *Taxonomic Identification, NISP and MNI values for the Ma'acoah site fish assemblage.*

Order	Taxon	NISP	MNI
Clupeiformes (herrings)	*Clupea harengus* (Pacific herring)	2437.5	139
	Engraulididae (sardines, unidentified)	342	7
Salmoniformes (salmon)	*Oncorhynchus* sp. (salmon species)	945	12
Gadiformes (cods)	Gadidae (cod, unidentified)	5	1
	Gadus macrocephalus (Pacific cod)	34	2
	Theragra chalcogramma (whiting)	2	1
	Merluccius productus (hake)	1	1
Perciformes (perches)	Percidae (perch, unidentified)	4	4
	Embiotocidae (sea perches)	24	2
	Rachochilus vacca (pile perch)	168	46
	Thunnus thynnus (bluefin tuna)	19	1
Scorpaeniformes (rockfishes)	Scorpionidae (rockfish, unidentified)	9	4
	Sebastes sp. (rockfish species)	235	9
	Anoplopoma fimbria (sablefish)	1	1
	Hexagrammidae (greenling, unidentified)	3	2
	Hexagrammos sp. (greenling species)	34	5
	Ophiodon elongatus (ling cod)	82	10
	Cottidae (sculpins, unidentified)	29	3
	Enophrys bison (buffalo sculpin)	9	1
	Hemilepidotus sp. (Irish Lord, red or brown)	7	1
	Leptocottus armatus (staghorn sculpin)	1	1
	Myoxocephalus polyacanthocephalus (great sculpin)	50	3
Pleuronectiformes (flatfishes)	Pleuronectidae (flatfish, unidentified)	430	9
	Atheresthes stomias (arrowtooth flounder)	22	5
	Hippoglossus stenolepis (halibut)	11	3
	Lepidopsetta bilineata (rock sole)	2	1
	Microstomus pacificus (Dover sole)	1	1
	Parophrys vetulus (lemon sole)	2	1
	Platichthys stellatus (starry flounder)	50	12
Batrachoidiformes (toadfishes)	*Porichthys notatus* (midshipman)	66	4
Chimaeriformes (chimeras)	*Hydrolagus colliei* (ratfish)	20	8
Squaliformes (sharks)	*Squalus acanthius* (dogfish)	496	40
Rajiformes (skates)	Rajidae (skates, unidentified)	2	1
	Total	**5552.5**	**342**

Figure 2 and Table 2 present the taxonomic richness of the assemblage. Thirty-four taxa are represented, and it can be seen that the richness profile is typical of most assemblages (cf. Grayson 1984:Figure 5.4), with a few taxa being represented by large NISP values and most other taxa represented by much smaller values. Herring and salmon are by far the most abundant, followed by dogfish, flatfish (flounders and soles), anchovy, rockfish, and pile perch. Diversity of the assemblage was evaluated by applying the reciprocal of Simpson's index $1/\hat{A}r_i^2$ (Grayson 1984:160) which provided a value of 4.118.

The Ma'acoah data are unlike the examples cited in Grayson (1984:116-130) in which a series of phases or well-defined strata are available for the site. Neither are there other assemblages with which comparisons based on correlation of sample size and relative abundance can be made (Grayson 1984:126-127). Lacking external comparative standards, the evaluation of the Ma'acoah fish assemblage will consider internal criteria for the evaluation of sample size sufficiency.

The question thus becomes a practical one. If a faunal assemblage is necessarily an incomplete picture of the skeletal elements originally deposited at the site, and if the deposited assemblage bears an undefined relationship to the death assemblage and to the living population of animals from which individuals were culled, and if continued excavation and identification will continue to yield additional taxa, albeit at an ever decreasing rate, until the entire site is excavated and identified (cf. Grayson 1984:116), then what quantity of remains must be examined in order to adequately characterize the assemblage? In other words, how much is enough? The answer to this question will depend, of course, on the analyst's purpose, but there may be some

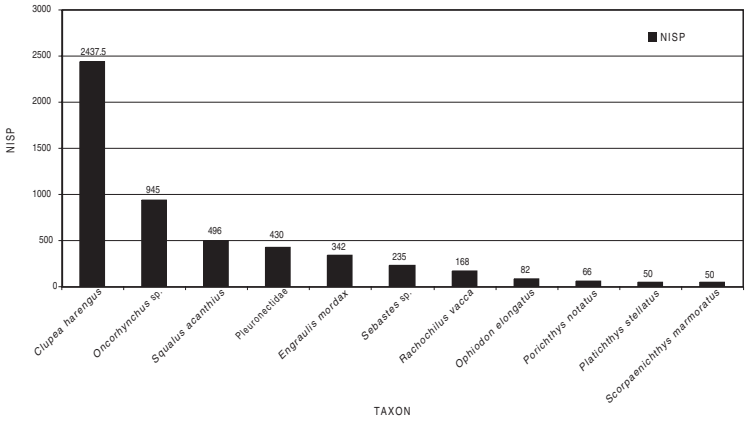

Figure 2. *Taxonomic richness as represented by the 11 most abundant taxa in the Ma'acoah assemblage.*

Table 2. *Taxonomic richness profile (NISP) for the Ma'coah assemblage.*

Taxon	NISP
Clupea harengus	2437.5
Oncorhynchus sp.	945
Squalus acanthius	496
Pleuronectidae	430
Engraulis mordax	342
Sebastes sp.	235
Rachochilus vacca	168
Ophiodon elongatus	82
Porichthys notatus	66
Scorpaenichthys marmoratus	50
Platichthys stellatus	50
Gadus macrocephalus	34
Hexagrammos	34
Cottidae	29
Embiotocidae	24
Atheresthes stomias	22
Hydrolagus colliei	20
Thunnus thynnus	19
Hippoglossus stenolepis	11
Scorpionidae	9
Enophrys bison	9
Myoxocephalus polyacanthocephalus	9
Hemilepidotus sp.	7
Gadidae	5
Percidae	4
Hexagrammidae	3
Theragra chalcogramma	2
Lepidopsetta bilineata	2
Parophrys vetulus	2
Rajidae	2
Merluccius productus	1
Anoplopoma fimbria	1
Leptocottus armatus	1
Microstomus pacificus	1

ways to measure the extent to which an assemblage has been sampled so that other observers can evaluate where, on a curve of diminishing returns, the examination terminated. This at least would be of value to the analyst in evaluating how much additional time/effort was required to adequately characterize an assemblage.

The greater the taxonomic richness and diversity embodied in an assemblage, the larger the identified sample size must be in order to characterize these dimensions. In the Ma'acoah assemblage, there are 34 taxa identified to the family level or better. If one were to follow Grayson (1984) and only use taxa identified to the genus level or better, this number would drop to 24. Even if this were done, there would still be some unacceptable consequences; for example, there would still be a number of species represented by NISP values of one or two, and some important taxa, such as Pleuronectidae (NISP=430), would be eliminated simply because many smaller flatfish species are not distinguishable from each other on the basis of their vertebrae. In this analysis, therefore, the larger, more generally identified list of taxa will be used. The decision to proceed this way rests on the argument that, if the present aim is to characterize an entire assemblage in terms of richness and diversity, then it is preferable to work with these more coarse parameters to encompass the maximum numbers in the sample, rather than restrict them by insisting on species-level taxonomic identification.

In recording the Ma'acoah identifications, all the same elements of the same taxa from the

same bag/recovery unit were assigned to a single record line which contained an "NISP" field that recorded the number of elements. Thus, in the following discussion, the number of samples that were successively drawn represent record lines, and the corresponding NISP values are larger. Simple random sampling without replacement was used to select record lines in groups of 100, and each successive group was added to the previously selected record lines thus creating a cumulative sample of identified elements. The results are presented in Table 3. All calculations have been performed on actual NISP values rather than on sample sizes of multiples of 100.

It is quickly apparent that the sample size of N=100 record lines (NISP=275.5) captured only 58.8 percent of the taxonomic richness of the entire assemblage; the reciprocal of Simpson's index for this sample is 5.456. Since the analyst is proceeding empirically here, and since one would not expect a sample of this size to accurately reflect the richness and diversity of an assemblage the size of that from Ma'acoah, a second group of 100 record lines was added, raising the cumulated sample size to NISP=787.5. The results show that the taxonomic richness of the identified sample has risen to N=27 (79.4 percent) and that the corresponding diversity index is 4.014. Adding a third group of 100 record lines produces an increase of only one new taxon (82.4 percent), although the cumulated sample size has risen to NISP=1296.5. The diversity

Table 3. *NISP values for cumulative samples compared with the entire Ma'acoah assemblage.*

Taxon	**NISP**$_{(1026)}$	**NISP**$_{(100)}$	**NISP**$_{(200)}$	**NISP**$_{(300)}$	**NISP**$_{(400)}$
Clupea harengus	2437.5	93	338	597	691
Oncorhynchus sp.	945	48.5	171.5	273.5	373.5
Squalus acanthius	496	32	76	129	148.5
Pleuronectidae	430	11	21	28	49
Engraulis mordax	342		1	1	29.5
Sebastes sp.	235	36	52	75	91
Rachochilus vacca	168	9	19	23	31
Ophiodon elongatus	82	14	22	28	40
Porichthys notatus	66	11	27	35	41
Platichthys stellatus	50	4	10	25	28
Scorpaenichthys marmoratus	50	2	3	9	14
Hexagrammos	34	2	5	7	13
Gadus macrocephalus	34		1	6	8
Cottidae	29	1	11	12	15
Embiotocidae	24	1	2	3	6
Atheresthes stomias	22		5	10	13
Hydrolagus colliei	20	3	4	8	9
Thunnus thynnus	19	2	2	8	10
Hippoglossus stenolepis	11				2
M. polyacanthocephalus	9	2	3	3	4
Enophrys bison	9	1	1	1	2
Scorpionidae	9	1	1	1	1
unknown cottid	7	1	2	2	4
Gadidae	5		3	3	4
Percidae	4		4	4	4
Hexagrammidae	3		1	1	1
Parophrys vetulus	2			2	2
Lepidopsetta bilineata	2		1	1	1
Theragra chalcogramma	2				
Rajidae	2				
Microstomus pacificus	1	1	1	1	1
Merluccius productus	1				
Anoplopoma fimbria	1				
Leptocottus armatus	1				
N	**5552.5**	**275.5**	**787.5**	**1296.5**	**1636.5**
# Taxa	**34**	**20**	**27**	**28**	**29**

index of this sample is 3.670. A fourth group of 100 record lines raises the list of taxa to 29 (85.3 percent), raises the sample size to NISP=1636.5, and produces a diversity index of 4.078. These data are summarized in Table 4 and depicted in Figures 3 and 4.

Richness indicators reveal that, after almost 800 identifiable specimens (200 record lines) have been processed, a quantum jump in richness has been achieved and over 80 percent of all taxa have been discovered. The diversity index has dropped dramatically as well and is near the "unknown" index for the entire assemblage. After almost 1300 elements (300 record lines) have been identified, only one more taxon has been added to the sample richness, and the diversity index has dropped only slightly and is now just below the "unknown" assemblage value. Finally, addition of a further 100 record lines raises the NISP to just over 1600 specimens (31 percent of the total NISP) but adds only one more taxon to the sample richness and results in a slight rise in the diversity index. One test that seemed revealing was calculating the mean and standard deviation of the diversity indices for samples of 200, 300 and 400 record lines. The results showed that the mean was 3.921 and the standard deviation was 0.179. This indicates that the diversity index for N=100 record lines falls outside the +3 standard deviation units whereas the index value of the total assemblage falls just outside +1 standard deviation unit. These data suggest that the point may have been passed where further increases in sample size will add much to the picture of richness and diversity in the sample in return for the time and effort involved. These data indicate that by N=300 record lines (NISP=1296.5, or just under 25 percent of the total identifiable assemblage) the richness and diversity of the assemblage had been reasonably characterized, and that by N=400 record lines (NISP=1636.5) this characterization had been confirmed.

Table 4. *Taxonomic richness and diversity by sample sizes for the Ma'acoah assemblage.*

#Records	NISP	#Taxa	1/Simpson's
100	275.5	20	5.465
200	787.5	27	4.014
300	1296.5	28	3.670
400	1636.5	29	4.078
1026	5552.5	34	4.118

There are, nevertheless, conditions in the data that require discussion. One obvious point is the lack of representation in the final sample (400 record lines) for five taxa that are contained in the total assemblage. At first, this situation may seem to introduce unacceptable shortcomings in the sample; however, the very nature of sampling makes it likely that infrequently occurring items in a population will not be represented in any sample (Flannery 1976:132-135). The recognition that the entire assemblage is itself a sample of

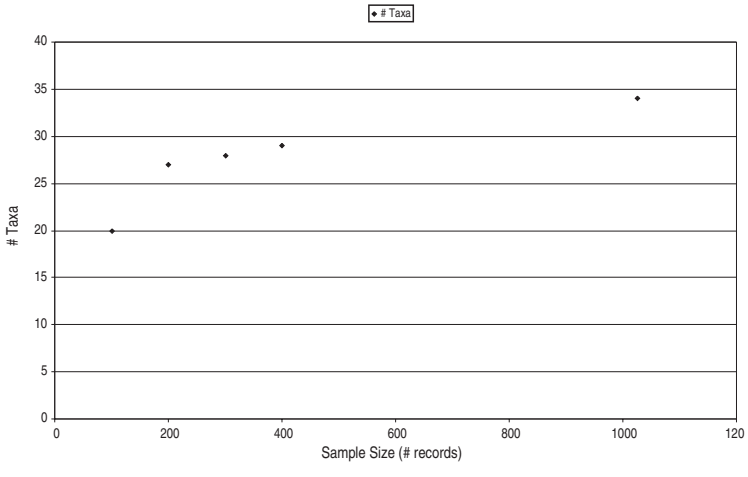

Figure 3. *Taxonomic richness by sample size in the Ma'acoah assemblage.*

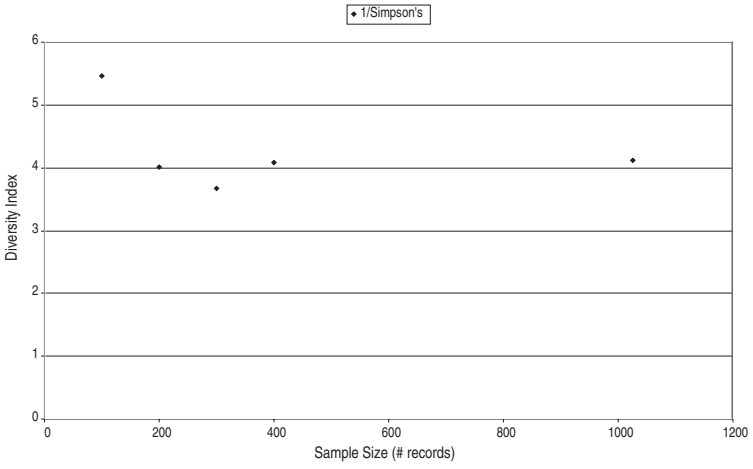

Figure 4. *Taxonomic diversity by sample size in the Ma'acoah assemblage.*

what was killed, transported to the site, disposed of, preserved and excavated renders most possible objections minor. The one objection to this situation is that raised by Grayson (1984:134) who notes the potential difficulties of comparisons of taxonomic richness between assemblages or samples of different sizes. In the present exercise, however, there are no other assemblages or samples for comparison. Instead, the issue is the time and effort required to reach one's research aims that must be balanced against the possible discovery of progressively smaller amounts of information if progressively larger proportions of the assemblage are identified. For the purposes stated at the beginning of this paper, such time and effort is not justified.

Another obvious situation that requires discussion is the consistent absence or under-representation of *Engraulis mordax* (anchovy). There are many remains of these fish, and they contribute greatly to the total NISP of the assemblage. Unfortunately, they are found in only 11 record lines, one of which has an NISP=204, and are therefore unlikely to be selected randomly. In the draw for the present sample, only the record lines with the two smallest NISP values were selected. In the unlikely event that the single large record line had been selected instead, the proper rank ordering of this taxon would have occurred, but it would have made little difference to the overall accuracy of the sample.

A final method of evaluating the sufficiency of the sample size involves an examination of Spearman's rank order correlation of paired assemblages (Table 5). These data present pairings of cumulative samples with each other and pairings of cumulative samples with the entire sample. All are significant at the 0.01 probability level. The data show high levels of predictability for the N=200-300 and the N=300-400 pairings. The coefficient values indicate that the sample size of 400 record lines (300-400 and 400-1026) provide a close reflection of the total assemblage. The accurate prediction of the assemblage richness and diversity through the knowledge of the richness and diversity of the sample is possible at this point.

Replication of the sampling procedure used here might produce slightly different results as sampling distributions become clear, and this aspect of the research is currently underway. Still, the data presented here seem robust since they fall within the overall sampling distributions that would be produced by performing such repetitions, and the data are also consistent with the

Table 5. *Spearman's Coefficient values for paired samples in the Ma'acoah assemblage.*

Pair	Pair Type	Coefficient
100-200	sample:sample	0.811
200-300	sample:sample	0.940
300-400	sample:sample	0.894
100-1026	sample:total	0.767
200-1026	sample:total	0.824
300-1026	sample:total	0.851
400-1026	sample:total	0.957

known standard/total assemblage. The method used here to identify the point at which close reflection of the total assemblage is achieved is analogous to that presented by Grayson (1984:126-7). He ascertained which samples were too small to provide an accurate indication of taxonomic richness and diversity by testing the rank order of sample size against the rank order of the NISP values for the taxon in which he was interested. Samples of insufficient size would reduce the coefficient value because the NISP for the taxon in question would be affected by the size of the sample, not by the true frequency of that taxon within it. These small samples were eliminated one by one until high coefficient values were obtained, indicating that the frequency of the taxon was independent of sample size. In the present case, the sample size is increased in a stepwise fashion until consistently high coefficient values are obtained. While the sample:total results would be unknown to the analyst as work proceeded, the results of sample:sample pairings, in the present case the second and third pairs, indicate that coefficients and the reciprocals of Simpson's index begin to vary around a mean when the sample size has passed the threshold of diminishing returns. The known sample:total results simply confirm this observation.

Discussion

This discussion has proceeded in a manner that mirrors the real logical steps that are, or could be, taken in the performance of an ichthyofaunal analysis. It has been assumed that all fish bones have been cleaned and separated from other bone, that all fish bones are stored in bags according to the stratum or level within the excavation unit of their recovery, and that the bags are numbered 1-N. A simple random sample of 50 percent of the bags can be selected as the maximum size of the sample to be examined because any more than 50 percent does not require random sampling in order to characterize the assemblage probabilistically. It should be remembered that, unless the excavation units (cluster samples) were chosen randomly before excavation began, the only universe that can be characterized by the sample is the assemblage itself. Taking each bag in the order in which it was drawn, the analyst then proceeds to identify the elements. In recording the identifications, the analyst may choose to assign each element its own record line in a spreadsheet, or all the same elements of the same taxa from the same bag/recovery unit can be assigned a single record line, which is what was done in the Ma'acoah analysis.

After the first 100 record lines have been completed, the number of identified taxa and the NISP by taxon should be recorded, and the diversity index should be calculated. The identification and quantification should proceed until a second 100 record lines are completed, and these results should be cumulated with those of the first 100 lines. Again, the number of identified taxa and the NISP by taxon should be recorded, and the diversity index should be calculated. In addition, a rank order correlation between the two samples should be calculated. This procedure should continue until it is clear that all three of the following richness and diversity criteria have been met. First, the addition of successive groups of 100 record lines adds no more than one taxon to the sample richness. Second, the rank order of taxonomic frequency stabilizes, as judged by rank order correlation coefficient values of successive samples that vary around a central value. Third, the diversity of the sample, as measured by the reciprocal of Simpson's Index, begins to vary around a central value. Once these criteria have been met, the analyst can argue that the characteristics of the total assemblage have been accurately described. Clearly, there is no assurance that all taxa in the excavated assemblage have been identified. On the other hand, neither is there any assurance that all taxa in this assemblage represent all taxa that were deposited at the site or that were brought to the site or that were killed, or that lived in the surrounding environment. All that can be said is that, in terms of the time and effort involved, the cumulated sample can be shown to represent what was excavated with statistically defensible accuracy.

Conclusion

The method proposed here permits the ichthyofaunal analyst to sample a total assemblage in a time and cost effective manner. The richness and diversity of the assemblage can be characterized by a sample that, in this case, represented 25-30 percent of the total assemblage. This represents a considerable saving in time and money to the analyst and the project with little loss of information. What loss of information does occur lies in the richness of the assemblage, yet full exploration of this dimension of the analysis would involve identification of all bone with little additional information being produced. Archaeologists will find the method proposed here to be of value in several situations. Research in its early stages can be fine-tuned according to the implications of taxonomic richness and diversity in relation to a previously established research design. The method will also be of value to contract archaeologists whose task it is to provide a quick and accurate picture of faunal assemblages. The problems of large and diverse samples are certainly apparent in the case of fish, but the method is not necessarily limited to this class. Abundant remains of any and all classes, separately and together, can be addressed with this method.

There are, nevertheless, instances where complete identification and quantification of the excavated assemblage may be required. Environmental reconstruction may rely on rare key indicator taxa that could only be found by processing most, or all, of the excavated sample. Information on exchange systems or exotic introduced taxa may also require full processing. Likewise, analyses of variability in faunal material over time and space, butchering studies, and seasonality studies would necessarily involve different sample sizes to suit each purpose. It is argued here, however, that the procedure outlined above could be used to evaluate the adequacy of the sample sizes in each of these cases and, at the same time, cut down on the amount of time and money expended on basic identification and quantification.

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