

Differential Recovery of Pacific Island Fish Remains: Evidence from the Moturakau Rockshelter, Aitutaki, Cook Islands



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DIFFERENTIAL RECOVERY refers to the introduction of bias into archaeological data through different recovery techniques; such bias can dramatically affect relative abundance estimates. As a recovery technique, screening samples archaeological material according to size. Recovery bias across different screen mesh sizes is well documented for archaeological mammalian assemblages (Casteel 1972; Payne 1972; Shaffer 1992; Thomas 1969). These studies show that the use of large-mesh screens (i.e., $\frac{1}{2}$ in. [12.70 mm] and $\frac{1}{4}$ in. [6.35 mm]) biases assemblages toward large taxa. Understanding the effects of this kind of bias is critical because interpretations of human subsistence and palaeoecology demand accurate taxonomic abundance estimates.

Although a number of studies have documented screen size bias with mammalian faunas, can these results be generalized to all archaeological faunas? Archaeological fish remains may be more susceptible to the biases created when large-mesh screens are used because of the variability in the size of diagnostic elements across taxa. Indeed, differential recovery has been documented for ichthyofaunal assemblages, particularly from Europe and North America (e.g., Bullock 1990; Butler 1987; Wheeler and Jones 1989). As with mammalian faunas, these analyses show that small taxa are consistently underrepresented in assemblages recovered from large-mesh screens.

In the case of Pacific Island fish assemblages, however, recovery bias may not parallel that shown for terrestrial faunal and other fish assemblages for several reasons. The higher diversity of taxa naturally occurring in the Pacific makes it difficult to compile a comprehensive reference collection. Without such reference material, only a few elements are used in identifications, which are limited to the family level. In comparison, fish analyses for other regions consist of identification of a range of elements to the genus or species level. With the smaller range of elements used in the Pacific, there is a greater likelihood of introducing bias toward fish with those particular elements that are large or robust, potentially

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increasing the effects of recovery bias. On the other hand, the use of family-level, instead of genus- or species-level, identifications reduces the possible number of taxa identified for an assemblage. With fewer classes, the effects of recovery bias may be dampened.

Given these differences, it is important to understand the particular effects of differential recovery for Pacific Island fish assemblages. The effects of screen size on ichthyofaunal recovery have previously received little attention for Pacific Island fish assemblages (see Butler 1988, in prep.; Gordon 1991, 1993; Nagao-ka 1993). As an exceptionally large dataset, the fish assemblage from the Moturakau site in the Cook Islands provides an excellent opportunity to examine recovery bias for a Pacific Island case. The fish remains recovered from $\frac{1}{4}$ in. (6.36 mm) and $\frac{1}{8}$ in. (3.18 mm) mesh screens are compared to determine how the relative abundance and number and kind of taxa represented are affected by recovery bias. The implications of these findings for Pacific Island subsistence interpretations are discussed and some suggestions are made toward controlling this problem.

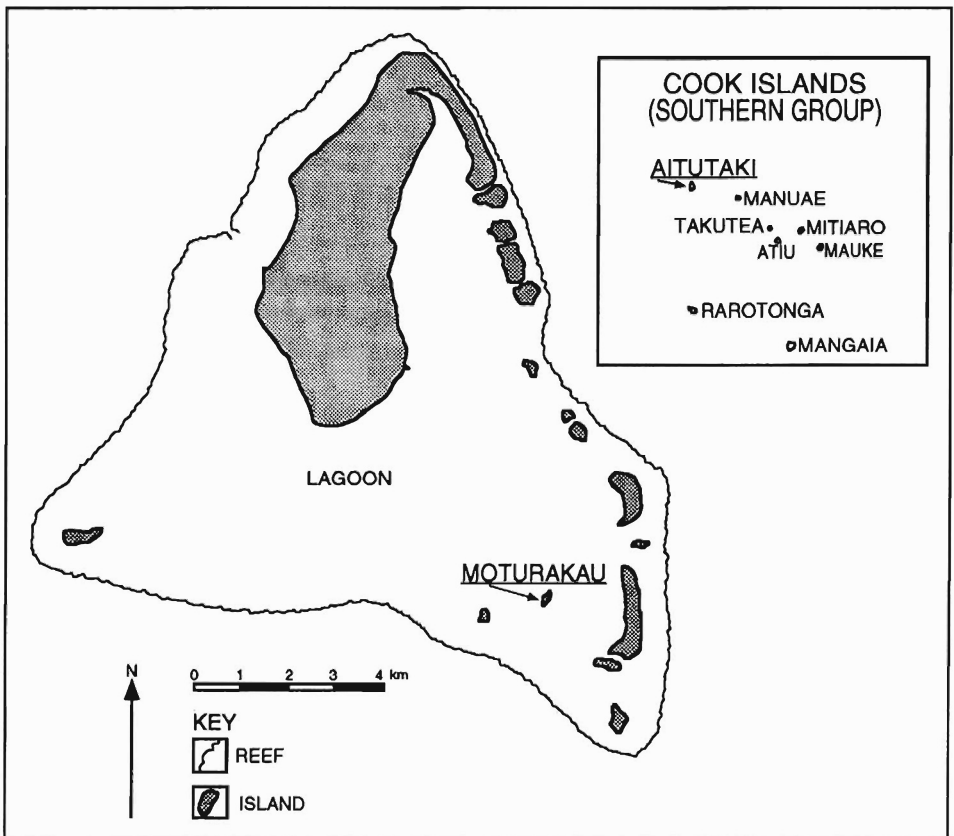


Fig. 1. Map of Aitutaki showing Moturakau, with inset of the Southern Cook Islands (after Allen 1992a, b).

SITE DESCRIPTION

The fish assemblage used in this analysis was recovered from the Moturakau site (MR-1), Aitutaki, Cook Islands. Moturakau is a small offshore volcanic islet near the southern edge of the lagoon of Aitutaki (Fig. 1). Site MR-1 consists of two adjacent rockshelters that may have formed a single shelter before being filled by sediments. Test excavations were conducted at the site in 1987 as part of an interdisciplinary research project to study the biogeographic changes of avifauna in the Cook Islands from both cultural and palaeontological contexts (Allen and Schubel 1990; Steadman 1991). Allen and Schubel excavated a 1-m² test unit in the northern rockshelter. Although the test unit contained very few bird remains, it yielded cultural deposits with a large sample of fish bones, shell, fishhooks, and lithic debris. Allen and Schubel (1990) suggested that the rockshelter was occupied during fishing expeditions to the outer reef and in conjunction with basalt procurement and the preliminary stages of adze manufacture.

In 1989, Allen excavated 15 additional units at the Moturakau site to study temporal variation in subsistence practices on Aitutaki (Allen 1992*a*, 1992*b*). The excavated sediments were dry-screened through nested $\frac{1}{4}$ in. and $\frac{1}{8}$ in. mesh screens. The fish remains used in the present analysis were recovered from Units 7 and 8, excavated during the 1989 field season. Unit 7 is located outside, and Unit 8 inside, the drip-line of the southern shelter. These two units were selected for analysis because they contained a large fish and invertebrate sample and several fishhooks. The sequence of occupation was securely dated from A.D. 1200 through the historic period (Allen 1992*a*, 1992*b*). The fish remains from Units 7 and 8 of the Moturakau site constitute one of the largest assemblages known from the Pacific. Over 11,000 specimens, representing 30 taxa and more than 2000 individuals, were identified (Allen 1992*a*; Nagaoka 1992). The density of identified bone from each unit is quite high when compared with that of fish assemblages from other Pacific Island sites. Table 1 compares the Moturakau assemblages from Units 7 and 8 with four of the largest samples of fish from recent excavations in the Pacific. The Moturakau site produced several thousand bones per cubic meter; in contrast, the other four sites have a density of less than 50

TABLE 1. COMPARISON OF THE DENSITY OF IDENTIFIED FISH REMAINS FROM MOTURAKAU (MR-1) AND OTHER PACIFIC ISLAND SITES

| SITE | m ³ | NISP ^a /m ³ | MNI ^b /m ³ |
|--|----------------|-----------------------------------|----------------------------------|
| Moturakau, Unit 7, $\frac{1}{4}$ in. and $\frac{1}{8}$ in. | 1.55 | 5676.8 | 949.7 |
| Moturakau, Unit 8, $\frac{1}{4}$ in. and $\frac{1}{8}$ in. | 1.25 | 1836.0 | 423.2 |
| Moturakau, Unit 7, $\frac{1}{4}$ in. | 1.55 | 2781.3 | 549.7 |
| Moturakau, Unit 8, $\frac{1}{4}$ in. | 1.25 | 1151.2 | 277.6 |
| Belau, Micronesia, $\frac{1}{4}$ in. (Masse 1989) | 123.20 | — | 16.2 |
| Hanamiiai, Marquesas, $\frac{1}{8}$ in. (Rolett 1989) | 34.00 | 14.6 | — |
| To'aga, American Samoa, $\frac{1}{4}$ in. (Nagaoka 1993) | 60.00 | 36.6 | — |
| Tikopia, $\frac{1}{4}$ in. (Kirch and Yen 1982) | 208.65 | 27.7 | — |

^a Number of identified specimens.

^b Minimum number of individuals.

NISP (number of identified specimens) or MNI (minimum number of individuals) per cubic meter.

METHODS

Identification

Identifying fish remains to the genus or species level requires modern reference material that covers the natural diversity of fish in the region. In temperate areas, the diversity of fish species is generally low. Northern Europe, for example, has about 350 fish species (Colley 1990; Wheeler and Jones 1989), but areas of North America may contain a few hundred to less than 20 species (Moyle and Cech 1988). In contrast, the Pacific marine fish fauna is extremely rich, with over 100 families and 1300 species (Springer 1982). The best reference collections of Pacific Island fish are those of the Australian National University and Foss Leach's collection at the National Museum of New Zealand, containing 300 to 400 specimens. A collection of 50 specimens comprising Bishop Museum specimens and the personal collections of Melinda Allen and the author were used in this analysis (see Nagaoka 1992). In general, Pacific Island fish collections may include a wide range of families, but lack detailed coverage at the species level. As a result, fishes from Pacific sites are routinely identified only to the family level.

Because of the limited reference material for the Pacific, temperate and Pacific Island fish analyses also differ in the number of elements used in identification. In temperate areas, 15 or more elements typically are used to identify fish remains, although most analysts identify all elements to some taxonomic level (Butler 1988; Colley 1990; Wheeler and Jones 1989). In contrast, only five jaw bones (premaxilla, dentary, maxilla, articular, quadrate) and a set of "special bones," elements distinctive for a particular taxon, are used to identify Pacific Island fish remains (Leach 1986). Even then, for many Pacific Island assemblages, only the premaxilla, dentary, and special bones are identified (e.g., Best 1984; Goto 1986; Kirch 1989; Kirch and Yen 1982; Rolett 1989). The use of a smaller number of elements, particularly jaw parts, may bias the analysis toward those fish with jaw parts that preserve well and that are large enough to be recovered in the screen employed (Butler 1988). Although some researchers are beginning to expand the number of elements used in identification (Butler in prep.), most still use the five jaw elements and special bones. This study is therefore limited to understanding the effects of recovery bias on this traditional set of elements.

Counting Units

Although NISP and MNI have their strengths, they also have problems that affect their usefulness as counting units (Grayson 1979, 1984; Ringrose 1993). MNI values vary depending on how the data are aggregated (e.g., by arbitrary level, layer, or site). The sum of level MNIs for an excavation unit does not necessarily equal MNI values calculated for the unit as a whole. In addition, because there are several ways to calculate MNI, the comparability of data is not assured (e.g., Allen and Guy 1984; Bökönyi 1970; White 1953). NISP values are problematic because they may violate the statistical assumption of independence. Each individual animal can be represented in a faunal assemblage by several elements,

and each element can fragment into several identifiable pieces. Regression analyses show that NISP often contains information on relative abundances similar to that of MNI. Given this predictable relationship between the two counting units and the negative effects of aggregation inherent in MNI, NISP is often the better measure (Grayson 1984).

To determine if the relationship between NISP and MNI for the Moturakau assemblage is predictable, both measures were used to quantify the fish remains. MNI was calculated using White's (1953) method of siding and quantifying the most abundant element. The aggregation unit was the level; the total MNI for each unit is the sum of the MNI from each level. MNI was calculated as one for cases in which only such bones as scutes, spines, or scales were identified for a taxon, because the presence of multiple individuals could not be determined with these elements.

Regression analysis was performed on the level totals of NISP and MNI data from Units 7 and 8 to determine the relationship between the two counting units. Because the relationship was curvilinear, the data were transformed logarithmically to produce a linear relationship between MNI and NISP (Fig. 2). The standardized residuals show a random scatter around zero, suggesting that the regression equation appropriately describes the relationship. This analysis of the relationship between MNI and NISP shows that for this assemblage, the two measures vary in a predictable fashion and carry similar information on rela-

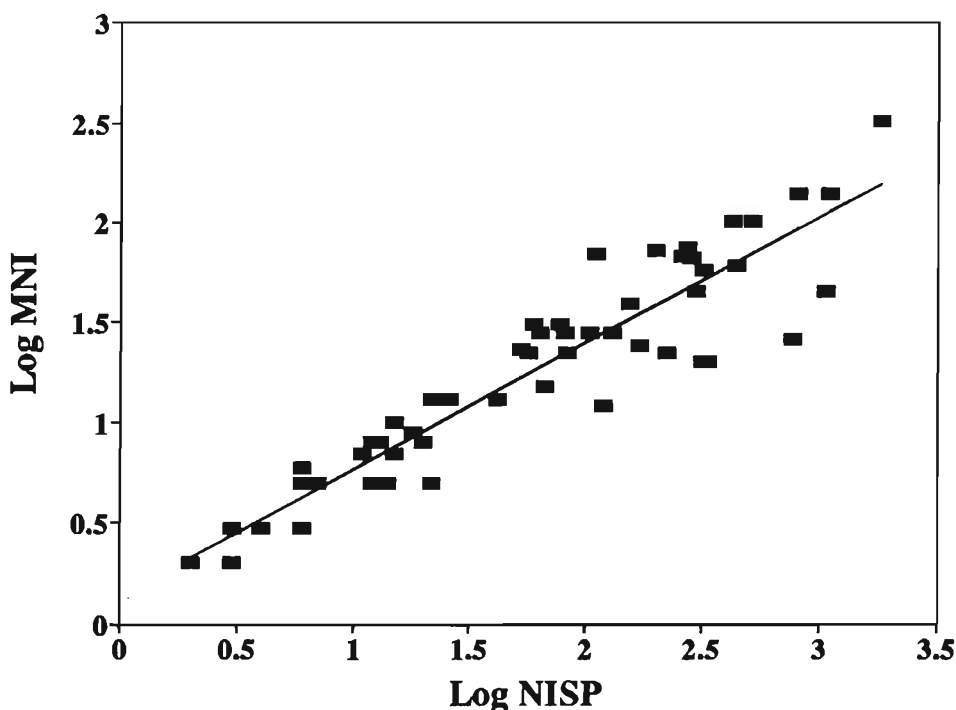


Fig. 2. Regression plot of MNI and NISP ($MNI = 1.38NISP^{0.63}$; $r = 0.93$, $P < 0.001$) calculated for each taxon of each level in Units 7 and 8.

tive abundances. Given the aggregation problem associated with MNI and the focus of this analysis on the number of bones recovered, NISP values are used here.

ANALYSIS OF DIFFERENTIAL RECOVERY

The effects of differential recovery on faunal assemblages have been studied using two approaches. In one approach, osteological reference specimens of known weight or size are passed through different-sized mesh screens (e.g., Shaffer 1992; Thomas 1969). These screening experiments inform on the kinds of taxa expected to be recovered or lost archaeologically using mesh of a certain size. This information can then be used to gain an understanding of the presence or absence of taxa and develop expectations about particular faunal datasets. In the second approach, the effects of differential recovery for a particular archaeological faunal assemblage are studied by comparing the relative abundances of taxa retrieved using various recovery techniques (e.g., Casteel 1972; Payne 1972). This approach also can be used on control or bulk samples to gain an understanding of recovery rates of different screen sizes for a site, which can then be used to develop sampling strategies for subsequent work. Although the two approaches address different aspects of the problem of recovery bias, the information gained by both is important for understanding the problem as a whole.

Initial investigations in the Pacific concerning the effects of recovery bias on fish remains have used only archaeological data (Butler 1988, in prep.; Gordon 1991, 1993), though screening experiments using fish reference collections are in progress (Nagaoka in prep.). A detailed analysis of the Moturakau data will provide information on the effects of recovery bias for this particular assemblage, but may also contribute to our understanding of this problem for Pacific Island sites in general.

Taxonomic Abundances

To determine if taxonomic abundances in the Moturakau fish assemblage are affected by recovery bias, the rank order abundance of taxa from $\frac{1}{4}$ in. and $\frac{1}{8}$ in. fractions was compared for every level of Units 7 and 8. Spearman's rho (r_s), a nonparametric correlation coefficient, was used because the problems associated with NISP may render the counting unit reliable only to the ordinal level (Grayson 1984). The correlation between the two fractions was significant ($P < 0.05$) for most levels (Table 2), indicating that the materials from the two screen sizes provide similar information about the rank order abundances of taxa. The levels that were not significantly correlated had relatively smaller-sized samples.

The similarity between the $\frac{1}{4}$ in. and $\frac{1}{8}$ in. data is unusual compared with previous analyses of recovery bias in faunal assemblages. Although the correlation between the samples for the Moturakau assemblage suggests that the effects of recovery bias may be minimal, this result may be contingent upon the level of identification. Using family-, instead of genus- or species-, level identifications lessens the effects of recovery bias by reducing the number of taxa possible, as well as by masking the variation in size within a family. With fewer taxa, statistical redundancy between the samples can be attained at lower sample sizes than

TABLE 2. RESULTS OF THE SPEARMAN'S RANK ORDER CORRELATION ANALYSIS BETWEEN $\frac{1}{4}$ IN. AND $\frac{1}{8}$ IN. SAMPLES WITH THE SAMPLE SIZES (NISP) OF THE TWO SCREEN SIZE FRACTIONS

| UNIT 7 | | | | | UNIT 8 | | | | |
|--------|-------|---------------------|-------------------|-------------------|--------|-------|-------------------|-------------------|-------------------|
| LEVEL | r_s | P | $\frac{1}{4}$ in. | $\frac{1}{8}$ in. | LEVEL | r_s | P | $\frac{1}{4}$ in. | $\frac{1}{8}$ in. |
| 2 | 0.63 | 0.005 > P > 0.001 | 176 | 229 | 2 | 0.54 | 0.05 > P > 0.01 | 39 | 27 |
| 3 | 0.67 | P < 0.001 | 313 | 385 | 3 | 0.61 | 0.05 > P > 0.01 | 55 | 25 |
| 4 | 0.70 | P < 0.001 | 373 | 455 | 4 | 0.36 | 0.50 > P > 0.10 | 70 | 47 |
| 5 | 0.66 | P < 0.001 | 397 | 305 | 5 | 0.33 | 0.50 > P > 0.10 | 122 | 52 |
| 6 | 0.62 | 0.005 > P > 0.001 | 191 | 190 | 6 | 0.36 | 0.50 > P > 0.10 | 95 | 38 |
| 7 | 0.74 | P < 0.001 | 570 | 364 | 7 | 0.32 | 0.50 > P > 0.10 | 22 | 13 |
| 8 | 0.84 | P < 0.001 | 501 | 548 | 8 | 0.06 | 1.00 > P > 0.50 | 19 | 28 |
| 9 | 0.77 | P < 0.001 | 514 | 548 | 9 | 0.74 | P < 0.001 | 203 | 137 |
| 10 | 0.78 | P < 0.001 | 838 | 609 | 10 | 0.82 | P < 0.001 | 814 | 489 |
| 11 | 0.73 | P < 0.001 | 438 | 854 | | | | | |

if the data were identified to genus or species level. Therefore, the significant correlations between the $\frac{1}{4}$ in. and $\frac{1}{8}$ in. fractions of the Moturakau assemblage may result from apportioning large samples across a relatively small number of families, producing statistical redundancy between the two samples.

With family-level identifications, size variability of species within families is not expressed. Instead, the range of sizes between families becomes far more important. Families that contain larger species are more likely to be represented in assemblages collected using large-mesh screens than families comprising only small species. For example, Lutjanidae (snappers) is diverse in terms of size, ranging in length from 30 to 100 cm (Randall et al. 1990). Thus, snappers as a family are likely to be represented in the sample even if large-mesh screens are used. In contrast, families like Pomacentridae (damselfishes) are uniformly small in size; all pomacentrids measure under 35 cm in total length. These families are less likely to be retrieved in large screens.

If fish remains were identified to species, not only would the number of possible classes increase, but fish of varying size within families could be distinguished. This, in effect, would increase the differences between the data from $\frac{1}{4}$ in. and $\frac{1}{8}$ in. screens. Thus, as the fish reference collections for the Pacific improve and genus- and species-level identifications become possible, the effects of screen size bias are likely to increase.

Variation across Sample Size

Although the data from $\frac{1}{4}$ in. and $\frac{1}{8}$ in. screens are significantly correlated for many of the Moturakau excavation levels, the strength of the correlations varies considerably. This variability appears to be related to differences in sample size. The relationship between Spearman's rho and sample size per level is curvilinear (Fig. 3). The inflection in the curve is seen at about 200 NISP; below 200 NISP, the correlation coefficient varies considerably. For all samples over 200 NISP, the correlation between the $\frac{1}{4}$ in. and $\frac{1}{8}$ in. samples is significant ($r_s > 0.60$,

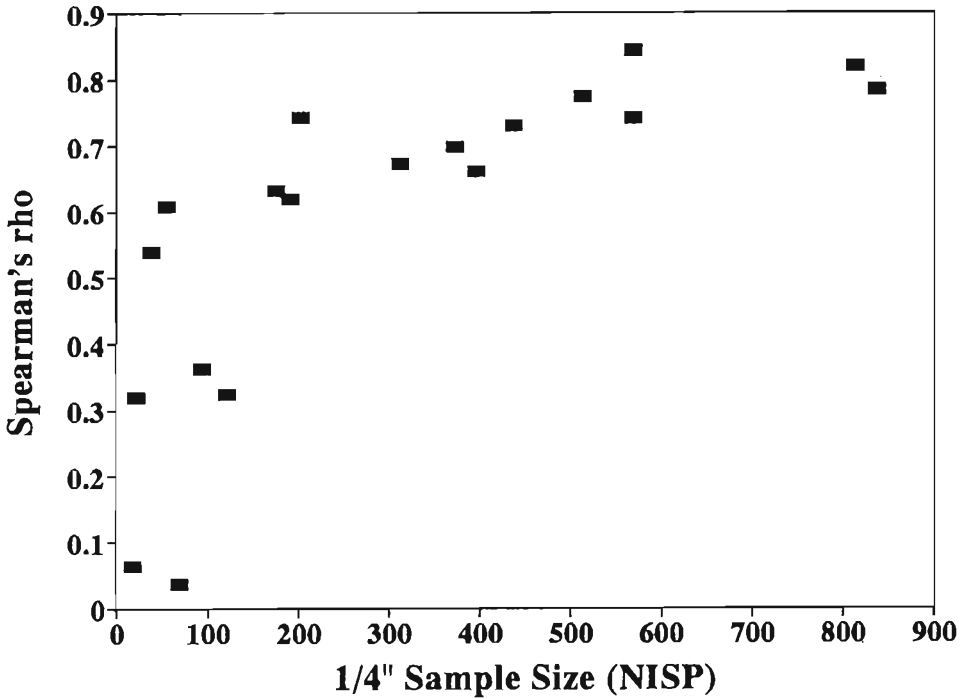


Fig. 3. Scatterplot of Spearman's rho across sample size.

$P < 0.001$). For these larger samples, regression analysis shows that the relationship between sample size and correlation strength as described by the regression line is positive, linear, and significant ($r_s = 0.00018$ (NISP) + 0.65, $r = 0.65$, $0.05 < P < 0.01$). As sample size increases, the data from the $\frac{1}{8}$ in. screen become increasingly similar to those from the $\frac{1}{4}$ in. screen.

The relationship between correlation strength and sample size is expected given probabilistic sampling theory. In general, larger samples are more representative of a population than smaller samples. As sample size increases, additional information does not significantly change the distribution of the data and redundancy is reached (cf. Avery 1982; Kintigh 1989; Leonard 1987)¹. For the Moturakau assemblage, a sample size of about 200 NISP is the inflection point at which the information on relative abundance provided by the $\frac{1}{8}$ in. sample becomes redundant of the $\frac{1}{4}$ in. sample. The redundancy of information at 200 NISP is an empirical observation of this particular dataset. It should not be taken and applied to other situations as "the" sample size above which $\frac{1}{8}$ in. screens are not necessary. The relationship between the data collected using different-sized mesh screens will vary depending on factors such as breakage patterns, preservation, and the number and kinds of taxa represented in the assemblage.

Increased Sample Size and Number of Taxa

Although the Moturakau fish assemblage is not severely affected by recovery bias in terms of relative abundances of taxa, the $\frac{1}{8}$ in. screen significantly increases the

TABLE 3. NUMBER OF TAXA ADDED BY THE $\frac{1}{8}$ IN. SAMPLE, THE TOTAL NUMBER OF TAXA PRESENT, AND THE SAMPLE SIZE (NISP) OF THE LAYER

| UNIT 7 LEVEL | NO. OF TAXA ADDED | TOTAL NO. OF TAXA | TOTAL SAMPLE SIZE | UNIT 8 LEVEL | NO. OF TAXA ADDED | TOTAL NO. OF TAXA | TOTAL SAMPLE SIZE |
|-----------------|-------------------------|-------------------------|-------------------------|-----------------|-------------------------|-------------------------|-------------------------|
| 2 | 4 | 22 | 405 | 2 | 2 | 14 | 66 |
| 3 | 5 | 23 | 698 | 3 | 1 | 13 | 80 |
| 4 | 1 | 22 | 828 | 4 | 4 | 17 | 117 |
| 5 | 2 | 21 | 702 | 5 | 3 | 19 | 174 |
| 6 | 2 | 22 | 381 | 6 | 3 | 18 | 133 |
| 7 | 3 | 26 | 934 | 7 | 5 | 14 | 35 |
| 8 | 2 | 22 | 1049 | 8 | 4 | 14 | 47 |
| 9 | 4 | 23 | 1062 | 9 | 3 | 22 | 340 |
| 10 | 4 | 27 | 1447 | 10 | 0 | 23 | 1303 |
| 11 | 2 | 25 | 1292 | | | | |

sample size and the number of taxa recovered. The increase in NISP for a level with the addition of the data from the $\frac{1}{8}$ in. screen ranges from 40 percent to nearly 200 percent, with a significant average increase of 89 percent ($t=9.5$, $P < 0.001$). As noted above, the increase in sample size is important because larger samples tend to produce more representative distributions of relative abundance than smaller samples.

The addition of the data from the $\frac{1}{8}$ in. screen also increases the number of taxa (richness) found in each level (Table 3). The average increase of 15 percent per level is significant ($t=6.9$, $P < 0.001$). An increase in richness is expected with an increase in sample size because larger samples generally have more taxa represented than smaller ones (Grayson 1984). This relationship between richness and sample size also holds true for the Moturakau dataset, with sample size and the number of taxa being highly correlated ($r_s = 0.93$, $P < 0.001$).

TABLE 4. NUMBER OF LEVELS TO WHICH EACH TAXON HAS BEEN ADDED BY THE $\frac{1}{8}$ IN. SAMPLE AND THE TOTAL NUMBER OF LEVELS IN WHICH THE TAXA ARE PRESENT

| UNIT 7 | $\frac{1}{8}$ in. | TOTAL | UNIT 8 | $\frac{1}{8}$ in. | TOTAL |
|----------------|-------------------|-------|----------------|-------------------|-------|
| Belonidae | 8 | 10 | Ostraciidae | 6 | 9 |
| Siganidae | 4 | 4 | Pomacentridae | 2 | 3 |
| Elasmobranchii | 3 | 7 | Balistidae | 2 | 4 |
| Pomacentridae | 3 | 8 | Belonidae | 2 | 4 |
| Mugilidae | 2 | 4 | Elasmobranchii | 2 | 6 |
| Scombridae | 2 | 4 | Aulostomidae | 2 | 7 |
| Cirrhitidae | 2 | 10 | Mullidae | 2 | 9 |
| Polynemidae | 1 | 1 | Congridae | 1 | 1 |
| Apogonidae | 1 | 3 | Polynemidae | 1 | 1 |
| Kyphosidae | 1 | 5 | Holocentridae | 1 | 8 |
| Bothidae | 1 | 10 | Bothidae | 1 | 8 |
| Aulostomidae | 1 | 10 | Tetraodontidae | 1 | 8 |
| | | | Carangidae | 1 | 9 |

As previous research on recovery bias has shown, small taxa are often lost through larger screens. Table 4 lists the taxa missed by the $\frac{1}{4}$ in. mesh but recovered in the $\frac{1}{8}$ in. mesh screen. Not only does the smaller mesh increase the occurrence of several taxa across levels, but it also recovers taxa that otherwise would not have been recorded. Congridae, Polynemidae, and Siganidae are taxa recovered only in the $\frac{1}{8}$ in. fractions.

Although body size has been identified as an important variable in screen size bias, a critical factor, in this case, is the minimum size of the diagnostic elements. Figure 4 presents a comparison of the recovery rates across taxa for the five jaw elements. The y axis shows the percentage of data from the $\frac{1}{8}$ in. screen relative to the total sample ($\frac{1}{4}$ in. and $\frac{1}{8}$ in.) minus 50 percent. Fifty percent is subtracted from the data from the $\frac{1}{8}$ in. screen to better illustrate which elements were recovered most often by either screen size. The zero value of the graph represents an equal recovery rate for both $\frac{1}{4}$ in. and $\frac{1}{8}$ in. meshes; half of the sample was recovered by the $\frac{1}{8}$ in. mesh; the remaining half by $\frac{1}{4}$ in. For those elements with positive values, relatively more specimens were recovered by the $\frac{1}{8}$ in. mesh. Those elements with negative values were recovered less often by $\frac{1}{8}$ in. mesh. For some taxa, the recovery rate is correlated with body size. The elements of larger taxa like Carangidae (tunas), Lethrinidae (emperors), and Scaridae (parrotfishes)

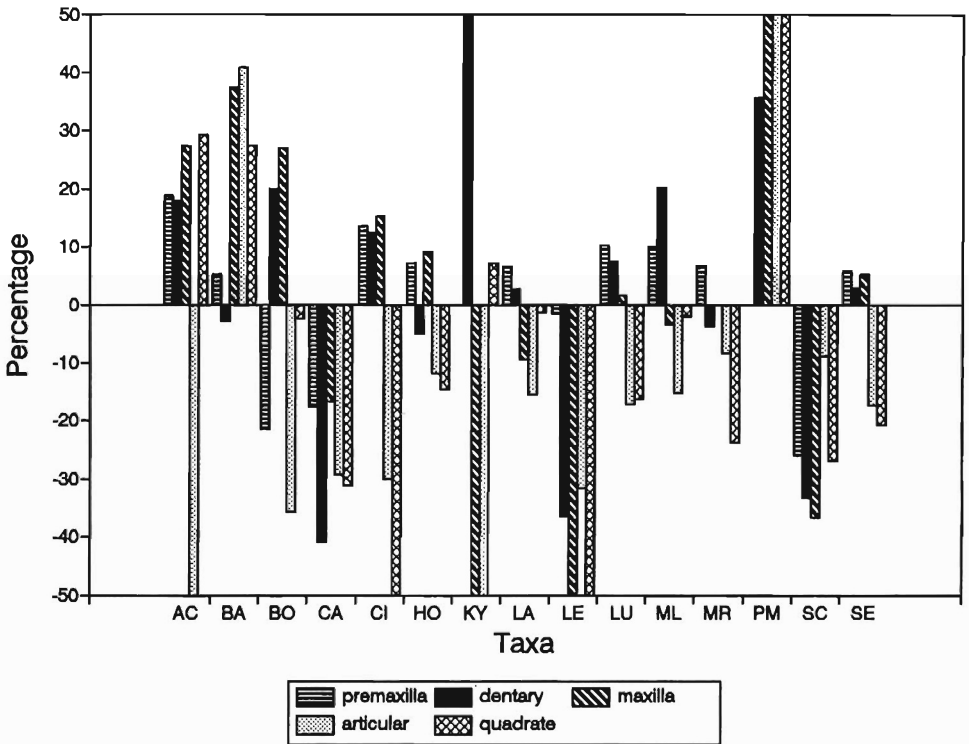


Fig. 4. Comparison of the recovery rate of the $\frac{1}{8}$ in. mesh for the five jaw elements across elements and taxa in relation to the total sample. AC, Acanthuridae; BA, Balistidae; BO, Bothidae; CA, Carangidae; CI, Cirrhitidae; HO, Holocentridae; KY, Kyphosidae; LA, Labridae; LE, Lethrinidae; LU, Lutjanidae; ML, Mullidae; MR, Muraenidae; PM, Pomacentridae; SC, Scaridae; SE, Serranidae.

were sufficiently recovered by the $\frac{1}{4}$ in. screens, but elements of small taxa like Pomacentridae (damselfishes) were recovered almost solely by the $\frac{1}{8}$ in. mesh. For most taxa, however, the pattern of recovery varies across elements. In general, quadrates and articulars were found more often in the $\frac{1}{4}$ in. screens; the $\frac{1}{8}$ in. screen tended to recover more premaxillae, dentaries, and maxillae. The shape of the elements may play an important role in their recovery. The identifiable portions of the quadrates and articulars are wedge-shaped or triangular, shapes relatively difficult to get through the mesh. The identifiable fragments for premaxillae and dentaries can be L-shaped or straight, and the maxilla is a relatively straight bone. Because recovery bias varies across elements, this effect can be compounded by the elements used in identification. For example, if the premaxilla and dentary were used to identify only the material from the $\frac{1}{4}$ in. screen, the analysis would be biased against acanthurids, lutjanids, and mullids and favor carangids and scarids. Screening experiments on reference material will be useful for identifying and describing the size variation of elements for particular taxa. Although these studies will not account for differences in recovery caused by breakage and preservation, they may lead to a better general understanding of why particular taxa and elements are differentially recovered or lost.

As the above comparisons of correlation strength and sample size have shown, the effects of differential recovery on relative abundances tend to decrease as sample size increases. Simply increasing the size of the samples from the $\frac{1}{4}$ in. screen, however, will not remove the effects of screen size bias. If this were true, then the number of taxa added by the sample from the $\frac{1}{8}$ in. screen would decrease as

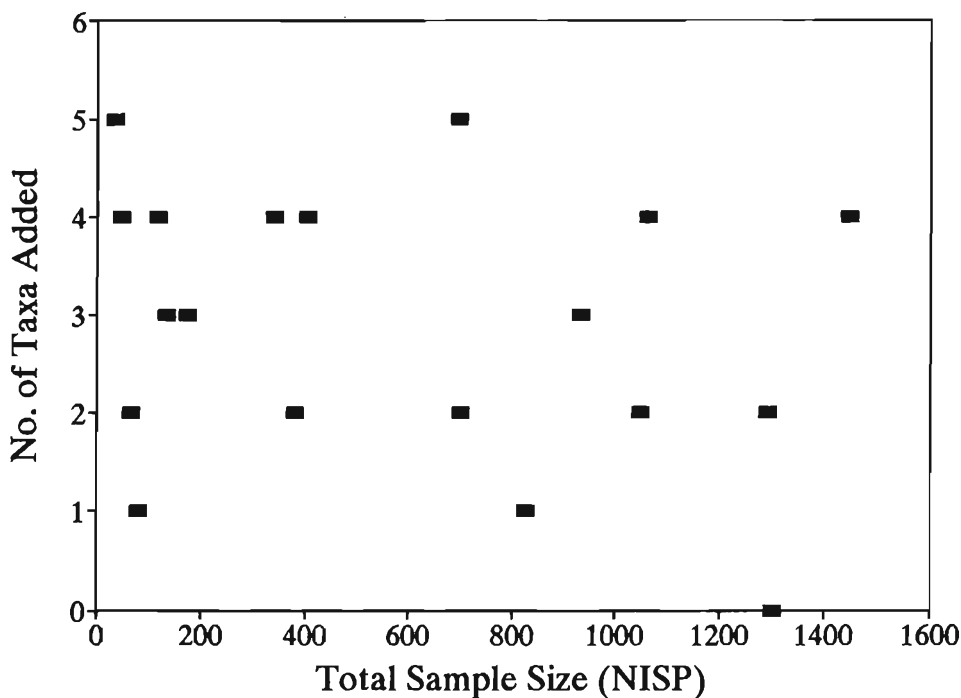


Fig. 5. Scatterplot of the number of taxa recovered only in the $\frac{1}{8}$ in. sample across sample size.

sample size increases. Instead, the number of taxa present in the sample from the $\frac{1}{8}$ in. screen, but absent in the corresponding sample from the $\frac{1}{4}$ in. screen, is random across sample size (Fig. 5). The randomness of this relationship is probably due to the presence of taxa with small diagnostic elements in particular levels. The $\frac{1}{4}$ in. screens will miss most of these taxa whether the sample taken is large or small. Thus, interpretations based on the number and kinds of taxa represented, such as richness and diversity measures, will be affected by this aspect of recovery bias.

Interpretations of the Moturakau fish assemblage can be used as an example of how recovery bias affects data and interpretations. Using fish remains and artifactual data, Allen (1992*b*) argued for less reliance on angling and decreased use of the outer reef and deep-water environments over time. A temporal increase in Balistidae (triggerfishes), an inner-reef taxon often caught by netting, was used as one line of evidence to support this interpretation. The use of only the data from the $\frac{1}{4}$ in. screen, however, would have altered this evidence. Although there is differential recovery across elements (see Fig. 4), Balistidae, in general, was less likely to be recovered in $\frac{1}{4}$ in. screens. Only one-fourth of the Moturakau balistid sample was recovered by the $\frac{1}{4}$ in. mesh, dropping in rank from sixth in the total sample to thirteenth. More importantly, this ranking does not change over time. Thus, if only the $\frac{1}{4}$ in. fraction had been used in Allen's analysis, Balistidae could not be used to support the interpretations about fishing strategies and utilization of the marine environment. Even this large $\frac{1}{4}$ in. sample of nearly 6000 specimens is affected by screen size bias.

DISCUSSION

The analysis of the Moturakau data provides insights into how recovery bias may affect other Pacific Island fish assemblages and the interpretations drawn from them. However, the use of smaller screen sizes has drawbacks. They increase the amount of material recovered, thus increasing the time required for processing and analyzing the material (e.g., Davidson 1964; Meighan 1969; Nichol and Williams 1980). Coupled with this increase in time cost is a decrease in the identifiability of the material. For the Moturakau assemblage, the identifiability of the material from the $\frac{1}{8}$ in. screen was 10–20 percent less than that of the sample from the $\frac{1}{4}$ in. screen. Despite these costs, this analysis has shown that the benefits of using smaller-mesh screens are substantial. Although the use of small-sized mesh may not affect the relative abundance of fish for larger samples (in this case samples over 200 NISP), it is important for increasing the sample size and the number of taxa for both large and small samples, thereby producing a more representative sample.

The data from the $\frac{1}{8}$ in. screen constitute about half of the total assemblage for the Moturakau site. In his Belau research, Masse (1989) estimated that as much as 88 percent of the potentially identifiable fish remains were lost by using only $\frac{1}{4}$ in. mesh (see also Butler 1987, 1988; Casteel 1972). The density of fish bone for Pacific Island sites is often quite low, with sample sizes typically well under 200 NISP. Sample sizes are even lower for single excavation units and layers. For this study, sample sizes larger than 200 NISP were required before moderate correla-

tions between the data for the $\frac{1}{4}$ in. and $\frac{1}{8}$ in. screens were reached. Although this observation is particular to this dataset, if the recovery rates and taxonomic richness of fish remains for other Pacific Island sites are reasonably similar to that of the Moturakau assemblage, then most fish assemblages will be seriously affected by differential recovery. The sample size of fish remains for Pacific sites could be increased if smaller mesh screens were used, thus providing more precise and accurate estimates of the relative abundance of taxa.

The use of smaller-mesh screens not only increases the number of taxa represented, but adds different kinds of taxa. The addition of taxa was found to be largely independent of sample size in the $\frac{1}{4}$ in. setting. As a result, increasing the size of the sample from the $\frac{1}{4}$ in. screen will not solve the problem of recovery bias. Unlike the situation with mammalian fauna, element size, not body size, is a determinant factor in the kind of taxa added. Because of the differential recovery across elements, the kind of taxa represented in an assemblage will depend on both the mesh size and the diagnostic elements used. By adding taxa that would otherwise be lost, smaller-mesh screens provide a more representative sample of the population than large-mesh screens alone.

The widespread use of large-mesh screens, coupled with small sample sizes typical of Pacific Island sites, suggests that many of these fish assemblages are severely affected by screen size bias. The effects of screen size bias may render data robust only to the nominal or ordinal level². The implications for Pacific Island subsistence interpretations are important. In the Pacific, fish were an integral part of the prehistoric diet. Archaeological fish data, therefore, are essential for understanding prehistoric subsistence patterns, such as changing resource exploitation (Kirch and Yen 1982; Rolett 1989) and fishing technologies (Dye 1983; Green 1986; Kirch and Dye 1979; Leach and Anderson 1979; Masse 1989). These research questions require data that are robust and accurately reflect the population of fish exploited, requirements not met when screen size bias compromises the dataset. Frequency, richness, and diversity measures are used in these studies to inform on prehistoric subsistence. However, because screen size bias can affect the relative abundance, the number, and the kinds of taxa, these measures may be an artifact of the bias rather than any prehistoric subsistence pattern. The uncertainty as to what the data actually represent can only lead to questionable interpretations.

There are ways to minimize the effects of differential recovery on archaeological assemblages and interpretations. Ideally, the effects of recovery bias should be examined before extensive excavation to determine which mesh size(s) to use (Rootenberg 1964). The recovery rates of different mesh sizes can be determined during test excavations. Screening experiments using comparative collections are also invaluable sources of information for understanding recovery bias because they help develop expectations about what should be recovered. The information gained from both pre-excavation analysis and screening experiments can be incorporated into the sampling design for the site. However, if pre-excavation analysis is not possible, bulk and control samples can be used to assess the effects of screen size bias on the collected data. Like other sampling techniques, the choice of screen size(s) should be based on the amount and kind of information needed to address the research questions. The cost of using smaller

screen sizes should be weighed against the benefit of producing a more representative sample. However, because archaeological material often varies in size, no one screen size is ideal for all situations or material types.

CONCLUSIONS

Fish remains are critical to understanding marine resource exploitation and Pacific Island subsistence. The analysis of the Moturakau fish data has shown that the use of large-mesh screens may severely compromise our ability to investigate this aspect of prehistoric subsistence. Smaller-mesh screens can be costly in terms of time and effort, but their use will produce the quality of data required to confidently address important subsistence issues in Pacific Island archaeology.

The last five years has seen significant improvement in the analytic and quantitative rigor of Pacific fish analyses. Efforts are being made to expand our reference collections, improve subfamilial identifications, and gain a better understanding of the methodological problems involved with fish analyses. As these advancements come to fruition, we will increase the reliability and accuracy of the data used to derive explanations about prehistoric subsistence strategies.

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NOTES

1. Redundancy can also be used as a means for determining when a sufficient sample size has been reached. Populations are sampled incrementally until the difference between the previous sample and that with the additional data is not significant. This technique has been used for determining sample size in point counting in geology (Galehouse 1971; Stein and Teltser 1989) and pollen counting (Birks and Birks 1980).
2. Levels of measurement and power are important to understanding issues of data quality. See Blalock (1972) and Thomas (1986) for detailed discussions on these concepts.

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ABSTRACT

Effects of differential recovery on faunal remains from archaeological sites have been documented by numerous researchers in Europe and North America. However, similar research is lacking for Pacific Island fish assemblages. Here, the fish assemblage from the Moturakau rockshelter in the Cook Islands is analyzed to determine effects of recovery bias on relative abundance, number, and kinds of taxa represented. Smaller-mesh screens are shown to have significant effects on relative abundance estimates for smaller samples and for increasing sample size and number of taxa across all samples. Kinds of taxa recovered are shown to be dependent on both body size and element size of the taxa. Implications of these findings for Pacific Island subsistence interpretations are discussed and suggestions are made for curbing the effects of differential recovery. KEYWORDS: faunal analysis, screen size, Pacific Islands, fish remains.