# ANALYSIS OF SAMPLING PROCEDURES FOR BENTHIC INFAUNAL COMMUNITIES AT AN OCEAN DREDGED MATERIAL DISPOSAL SITE

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## I. INTRODUCTION

Several environmental studies have been completed within the last five years offshore of the greater Tampa Bay, Florida area in the Gulf of Mexico. Some of these studies have been strictly qualitative with regard to benthic animal communities (Rice, et al., 1981; EPA, 1981; CCI, 1982), while others have included quantitative measurements (IEC, 1980; Taylor, 1979, 1982; JRB Associates, 1982; Mahadevan, 1982). Most of the quantitative faunal surveys conducted in the Gulf of Mexico have employed a box corer as a sampling device: fewer studies utilized a diver-operated hand coring device. In no case (except Mahadevan, 1982) have the species saturation characteristics of the sampling methodologies been reported for the studies listed above.

In most all contemporary benthic faunal surveys, it is desirable to assess the adequacy of sampling design and number of replicate samples by construction of a standard species saturation curve for each stat ion sampled (Gleason, 1922; Holme, 1953; Gaufin et al., 1956; Dauer et al., 1979). This process consists of plotting the cumulative number of species encountered with the addition of each replicate sample selected at random. The result is a curve depicting the relationship between number of replicate samples obtained and total number of species identified. Typically, this curve rises sharply with the first several replicates analyzed, and then begins to flatten as more and more replicates are added. An example of this process is presented by Dauer et al., 1979. When the plotted curve becomes asymptotic, any additional replicates beyond that point will add few new species to the cumulative species list. It is essential to understand the relationship between number of replicates collected and descriptive community parameters, including species

saturation characteristics for each station sampled, since all subsequent faunal comparisons are based upon the assumption that each station has been adequately sampled.

Surveys of benthic communities in the Gulf of Mexico at water depths beyond the reach of SCUBA divers can best be accomplished by use of a box corer. However, for purposes of impact assessment where specific stations must be sampled and resampled through time, a box corer is not the preferred instrument, if water depths allow for diver operations. Small scale variations in benthic habitat characteristics can have a large impact upon the type of organisms present. Diver collected samples can avoid many problems which cannot be controlled when using remote sampling devices.

Benthic communities in the Gulf of Mexico can provide sensitive indications of physical and biological perturbations in the habitat. These communities have been repeatedly used to gauge the impact of dredged material disposal (Hirsch, DiSalvo and Peddicord, 1978; Taylor, 1979, 1982). Changes in the density of species, the composition of benthic communities, and the diversity of species assemblages can reveal significant information concerning spatial and temporal effects of dredged material disposal.

The success of a benthic sampling program aimed at impact assessment depends upon use of a well-documented procedure for obtaining samples, and a method for determining that the community has been sampled in a representative manner with regard to diversity and density. The present studies were undertaken to provide basic information on the relationship between the number of replicate samples collected by divers, and the standard ecological parameters used when comparing spatial or temporal differences among benthic infaunal communities. Fifteen replicate samples of benthic infauna were

collected by divers at each of two locations within Ocean Dredged Material Disposal Site 4, which has been designated by the U.S. Environmental Protection Agency as the disposal area for material removed from the Tampa Harbor Project. These samples were progressively analyzed in order to identify the lowest number of replicates that would need to be collected and analyzed to provide sufficient community characterization for spatial and temporal comparisons.

## II. METHODS

### A. Field Sampling

Benthic samples were collected on May 11, 1984 from two stations within Site 4 (Figure 1). The two stations sampled roughly corresponded to Stations 28 and 30 from the EPA survey of May 1982, reported in JRB Associates (1982). The coordinates of these stations were 27°31.5' N, 83°04.9'W, and 27°30.5'N, 83°03.8' W.

Two sampling stations were visited in order to assess the degree of natural variability which might be expected in benthic infaunal communities. Station 28 and 30 were selected based upon an indication in the JRB Associates (1982) report that sediment characteristics at these two stations were most divergent, compared to all the stations sampled within Site 4.

Samples for infaunal analysis were collected with stainless steel plug corers (dimensions: 12.5cm x 12.5cm x 23cm, with a surface area of 0.016$m^3$) that were fitted with handles and a screen mesh (0.5mm) top to prevent loss of organisms. This coring device was used by SCUBA divers to collect samples and is pictured in Figure 2. Taylor (1982) used a similar coring device to sample benthic infauna at two ocean dredged material disposal sites in the Gulf of Mexico.

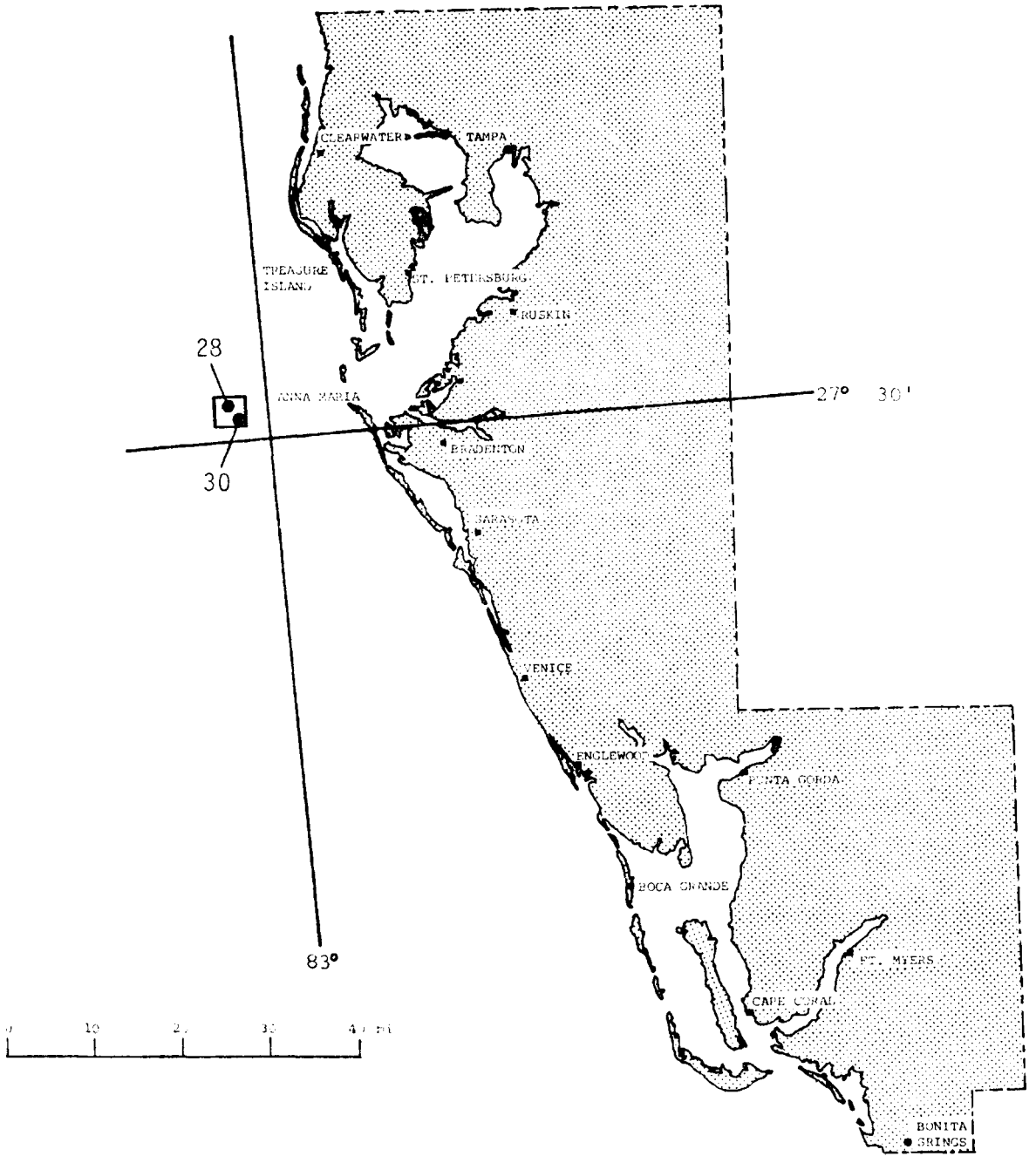


Figure 1. Location of Dump Site and the two benthic stations sampled for this study.

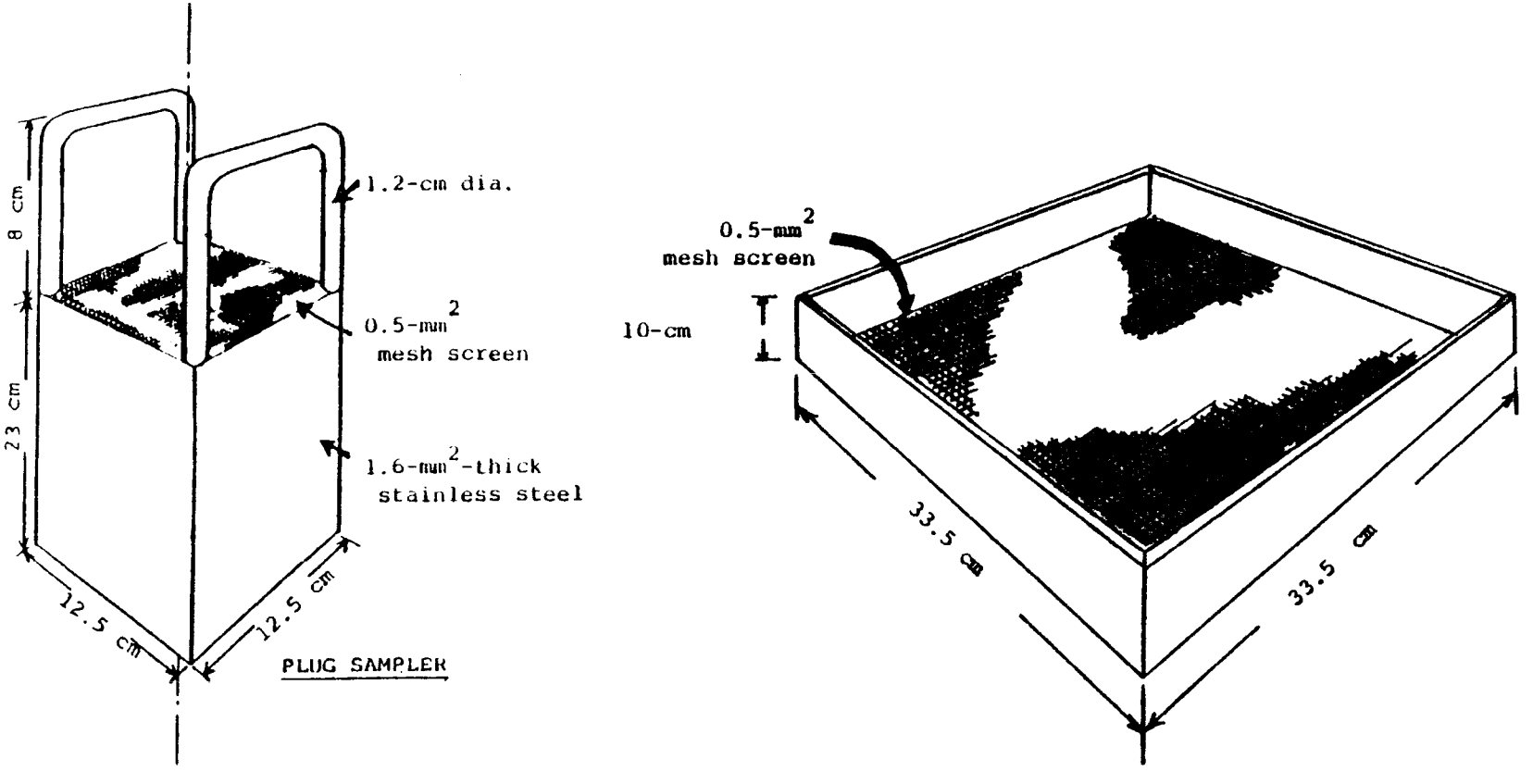


**Figure 2** Sieve and Plug Sampler used for Quantitative Benthic Studies.

Fifteen core samples were collected from each of the two stations. The sampling device was pushed into the substratum to a depth of approximately 15cm, and removed so that the diver's hand covered the bottom of the device. The core was then placed into a labeled cloth bag and returned to the ship. On board, the samples were emptied and rinsed into the cloth bags, tied securely, and placed into a container of 10%, $MgCl_2$ solution for narcotization of enclosed animals. Following one hour in the $MgCl_2$ solution, samples were washed through a 0.5mm sieve (Figure 2), and fixed with 10% formalin in seawater with rose bengal stain added. The material remaining on the sieve was washed into label led jars for storage.

In the laboratory, faunal samples were decanted into light and heavy fractions and preserved in 70% isopropyl alcohol. The light fraction contained the majority of the fauna, which were sorted into major taxa using a Unitron ZSB Stereozoom dissection microscope. The heavy fraction, containing primarily molluscs and larger animals, was sorted by hand in white enamel pans.

Taxonomic identification of species were accomplished through use of descriptive literature, invertebrate archive collections, and consultation with taxonomic experts outside the laboratory.

B. Data Analysis

Of the 15 replicate samples collected at the two sites (30 samples total), seven replicates from each site (14 samples total) were initially sorted, enumerated, identified, and numerically analyzed. These first seven replicates (chosen at random) were used to calculate faunal density, species diversity, species richness, equitability, and degree of species saturation.

These data indicated that seven replicate samples were not adequate to describe the faunal community. The next three replicates from each site (6 samples) were then analyzed and reevaluated in combination with the initial seven replicates. The same parameters as above were recalculated and evaluated for adequacy.

Evaluation of the cited parameters in this staged approach involved quantitative estimates of species saturation, (as outlined above) coupled with qualitative analysis of changes in species diversity, richness, and equitability with each analyzed replicate. This approach provides the best estimate possible for designing an optimal sampling strategy for the disposal site.

1. Species Saturation Curves

Because of the random method of obtaining and labeling bottom core samples (i.e., divers cannot recognize faunally depauperate or abundant areas), there is no real need for additional randomization of replicates for determination of species saturation curves. However, certain combinations of replicate order will change the configuration of the species saturation curves. Therefore, each plotted curve represents the mean of two replicate combination orders as follows: 1) replicates 1-10; 2) replicates 10-1. The ideal species saturation curve would be the average or mean curve of all possible replicate orders, which would be "x factorial" combinations, where x equals the number of replicates. The total number of possible combinations or curves for 10 replicates is $3.6 \times 10^6$. We have found that a mean curve using two replicate combinations significantly reduces the bias of a single curve, yet is not nearly as time-consuming to construct as the "ideal" curve.

There are no universally accepted standards of sampling adequacy for the marine benthos. The species area criterion has been discussed by various authors (Gleason, 1922; Holme, 1953; Ursin, 1960; Williams, 1964; and Holme and McIntyre, 1971) but a universal standard of "saturation" has not been established. This is partially due to the fact that the number of samples required to "adequately" sample an area depends on the variability of the individual observations, which in turn is dependent on the size or scale of the individual "station". A "large" station would require a greater number of samples than a "small" station, presumably because the "large" station would encompass a greater number of micro-habitats, and therefore a greater number of species. The stations sampled for this study appeared to have relatively homogeneous surface sediments, although the question of habitat size was not directly addressed. Habitat patch sizes are known to be quite variable for the west Florida continental shelf (Gould and Stewart, 1955; Doyle and Sparks, 1980; Culter and Mahadevan, 1984, in prep.).

Recent developments in community ecology have provided powerful analytical tools for evaluation of differences between biotic assemblages and changes within a community over time. Through careful review and application, we have chosen the following parameters as the most reliable and realistically interpretable for benthic community ecology in the Gulf of Mexico.

2. Species Diversity

Menzies, George, and Rowe (1973) define diversity as a concept in community ecology which refers to the heterogeneity (or lack of it) in a community or assemblage of organisms. Thus, diversity is dependent upon the number of species present (Species richness, S) and the distribution of individuals among species (Equitability or Evenness). A second definition of

diversity is simply the number of species found in a unit area (Whittaker, 1972). However, indices to measure diversity, species richness, and equitability are so numerous that confusion is rampant (Reviews in Hairston, 1964; Sanders, 1968; Hurlbert, 1971; Whittaker, 1972; Fager, 1972; Peet, 1974; Pielou, 1975; Smith et al., 1979). This proliferation of indices has prompted Hurlbert (1971) and Peet (1975) to recommend discarding diversity as a measure in ecological studies. However, placed in the proper perspective, diversity indices have been shown to be useful in 'bio-environmental" studies (Boesch, 1972; Borowitzka, 1972; Swartz, 1972; Pearson, 1975; Swartz, 1978). In this study the final data analysis was restricted to the most commonly used diversity measure: the Shannon-Weaver index.

The Shannon-Weaver index of diversity (Shannon and Weaver, 1963) is based upon 'information' techniques, where diversity is equated to the amount of uncertainty which exists in the species identity of an individual selected at random from a community. The more species and the more even their representation, the greater the uncertainty of each individual's identity and hence, the greater the diversity. The computational formula for Shannon's index is:

$$H' = C/N \left(N \log_{10} N - \Sigma^{S} n_{ii=1} \log_{10} n_i\right)$$

where C = 2.3026 (for units of "nats"), N = total number of individuals, and $n_1$ = number of individuals in the i th species. Lloyd et al. (1968) have presented the functions $n\log_{10}n$ for all integers from n = 1 to n = 1050 to simplify the use of Shannon's index.

3. Species Richness

Species richness was estimated as the Margalef's index and as the total number of species (S) collected per station.

a) Margalef's Index (Margalef, 1958)

Margalef's index of species richness was computed as follows:

$D = S - 1 / \log_e N$

where S is the number of species in the sample, and N the total number of organisms.

b) Number of Species/Station

The total number of species found at each station for each replicate and ultimately, for all replicates combined.

4. Equitability

Equitability was computed by Pielou's (Pielou, 1966) conventional method. The computational formula is:

J' (Pielou's index) = $H'/\log_e S$

Equitability is a measure of the evenness of distribution of the total fauna found over the enumerated taxa. Values can theoretically range from 0.0 to 1.00, where a high value indicates an even distribution, and a low value indicates an uneven distribution or dominance by a few taxa.

5. Faunal Density

Faunal density is an estimate of organism abundance and is conventionally expressed as numbers of organisms per unit surface area. For this study, faunal density was calculated as follows: FD = N/A, where N equals the number of organisms from one replicate or a combination of replicates, and A equals the surface area of one sample or a combination of samples. The surface area of the core used for computation was $0.0156 m^2$.

## III. RESULTS

### A) Species Saturation Curves

Results of the species saturation analysis are graphically presented in Figure 3. Both stations exhibited similar trends for species saturation. Each station appears to be nearing the asymptote of the curve with relatively few new species being added between replicates 9 and 10 (3.1% for Station 28 and 4.5% for Station 30). Although there are no generally accepted points of acceptability for saturation, the authors have found from past studies that values not exceeding 10% (increase in species numbers between last two replicates) are adequate for benthic surveys. Species added beyond this limit are generally considered "rare" and seldom offer additional critical information. In marginal cases, it may be necessary to take other information into account in order to determine the total number of replicates needed. For example, the percentage increases between replicates 6 and 7 were 7.8 and 9.4%, levels of increase which might be considered only marginally acceptable and graphically not appearing to have reached the asymptote. Such "marginal" replication could become inadequate during another season as species numbers and concentrations change. In contrast, the ten replicate sampling leaves a wide margin of acceptability not likely to be significantly changed by seasonality.

### B) Species Richness

A total of 244 taxa were identified from 5881 organisms collected for this study. For Station 28, 180 taxa were identified, with 164 for Station 30. The number of taxa identified for each replicate are presented in Tables 1 and 2. Values ranged from 49 to 71 taxa for Station 28, and from 35 to 68

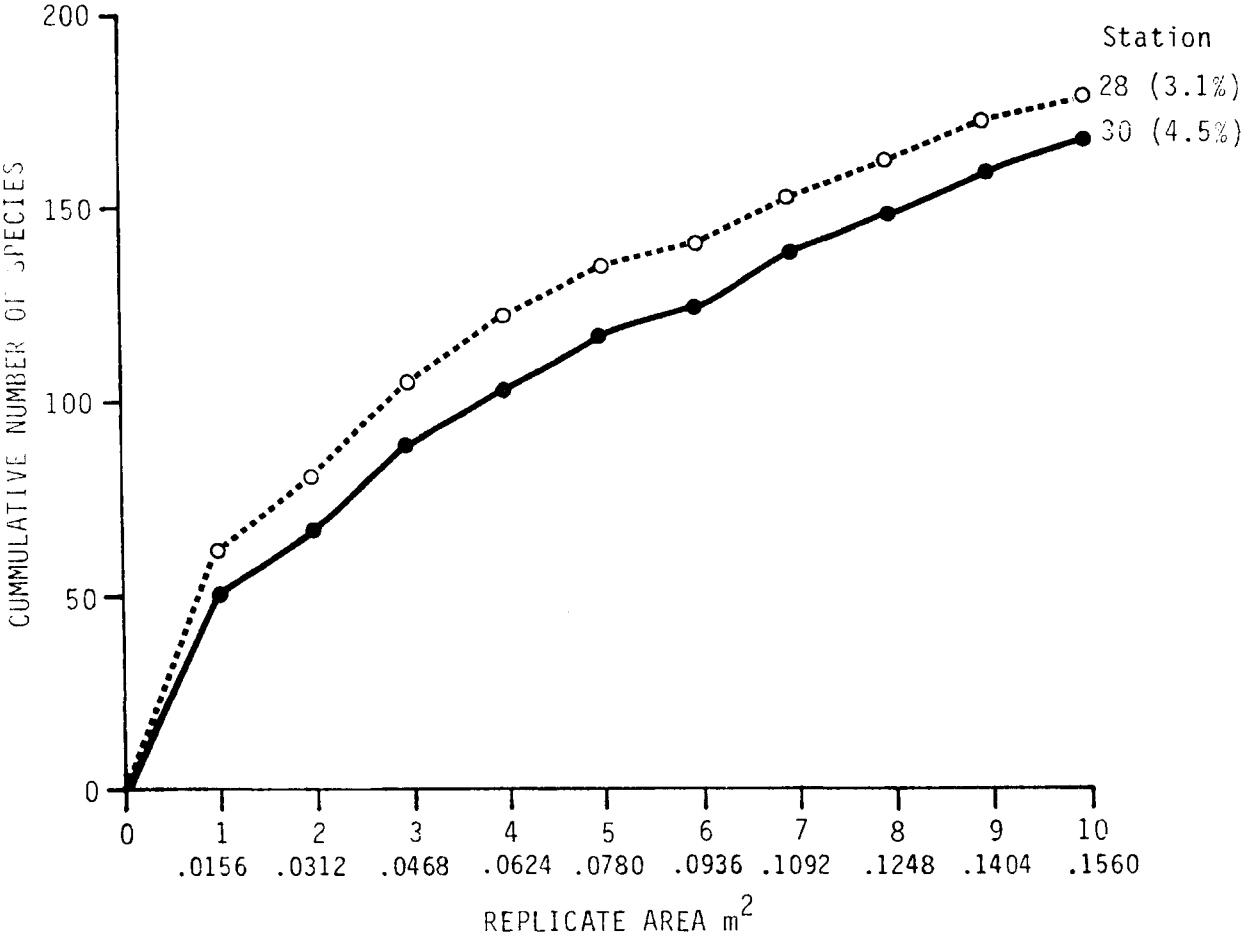


Figure 3. Species saturation curves for two benthic stations of the nearshore Gulf of Mexico. Percentages in brackets indicate the relative increase between replicates nine and ten.

**Table 1. Values for species richness and faunal density for Station 28 on a per replicate basis.**

| Replicate | Species Richness #Taxa | Margalef's w/Nematoda | Margalef's w/oNematoda | Faunal Density #/$m^2$ w/Nematoda | w/o Nematoda |
|---|---|---|---|---|---|
| 1 | 68 | 10.55 | 11.39 | 36603 | 23013 |
| 2 | 52 | 9.33 | 9.99 | 15192 | 10577 |
| 3 | 52 | 9.30 | 10.34 | 15449 | 8910 |
| 4 | 62 | 10.39 | 11.42 | 22692 | 13397 |
| 5 | 71 | 11.13 | 12.17 | 37756 | 20192 |
| 6 | 55 | 9.60 | 10.32 | 17756 | 11987 |
| 7 | 56 | 9.02 | 10.47 | 28526 | 12244 |
| 8 | 49 | 8.58 | 9.21 | 17244 | 11731 |
| 9 | 67 | 11.45 | 12.35 | 20449 | 13397 |
| 10 | 53 | 9.15 | 9.69 | 18782 | 13718 |
| **Mean x** | 58.5 | 9.85 | 10.74 | 23045 | 13917 |
| **Standard Deviation S** | 7.8 | 0.96 | 1.05 | 8408 | 4349 |

**Table 2. Values for species richness and faunal density for Station 30 on a per replicate basis.**

| Replicate | Species Richness #Taxa | Margalef's w/Nematoda | Margalef's w/oNematoda | Faunal Density #/$m^2$ w/Nematoda | w/o Nematoda |
|---|---|---|---|---|---|
| 1 | 68 | 10.85 | 11.56 | 30769 | 21090 |
| 2 | 37 | 7.47 | 8.04 | 7949 | 5641 |
| 3 | 43 | 8.07 | 9.18 | 11667 | 6218 |
| 4 | 37 | 8.36 | 8.62 | 4744 | 4167 |
| 5 | 61 | 9.86 | 10.41 | 28077 | 20449 |
| 6 | 38 | 7.36 | 8.28 | 9477 | 5577 |
| 7 | 35 | 6.42 | 7.14 | 12821 | 7500 |
| 8 | 37 | 6.74 | 7.98 | 13333 | 5833 |
| 9 | 43 | 8.11 | 9.58 | 11410 | 5128 |
| 10 | 51 | 8.99 | 9.86 | 16667 | 10192 |
| Mean x | 45.0 | 8.22 | 9.07 | 14718 | 9180 |
| Standard Deviation S | 11.4 | 1.37 | 1.32 | 8404 | 6322 |

taxa for Station 30. Station 28 exhibited a greater mean value of taxa per replicate, along with a lower standard deviation. Cumulative species richness is presented in the species saturation curves (Figure 3) and will not be discussed further here.

Margalef's index of species richness was also calculated, and the values for each replicate are presented in Tables 1 and 2. For Station 28, values ranged from 9.02 to 11.45; Station 30 values ranged from 6.42 to 10.85. Because this index takes into consideration the number of organisms (N) found, as well as the number of species, the values were recalculated after deleting the nematode contribution. As seen in Tables 1 and 2, this serves to increase the value of the index. The standard deviation between replicates was relatively low for both stations. Margalef's index generally reflects trends in species numbers, and therefore it was not deemed necessary to calculate values cumulatively as was done for species saturation.

C) Diversity

The effect of increased replication on diversity values is demonstrated in Figure 4. If too few replicates (1-4) are taken, it will seriously underestimate the community diversity for both stations, because the number of new species collected by each additional replicate is increasing rapidly at this point. Beyond the fifth replicate, species diversity exhibits only a slow increase and there is almost no difference between Replicates Six and Seven. The problems in estimating "true" community diversity have been discussed by Pielou (1966; 1975).

The effects of deleting the Nematoda spp. group were also examined. Nematodes are typically considered merofaunal by many investigators, even though they are often many millimeters in length and retained on a 0.5mm

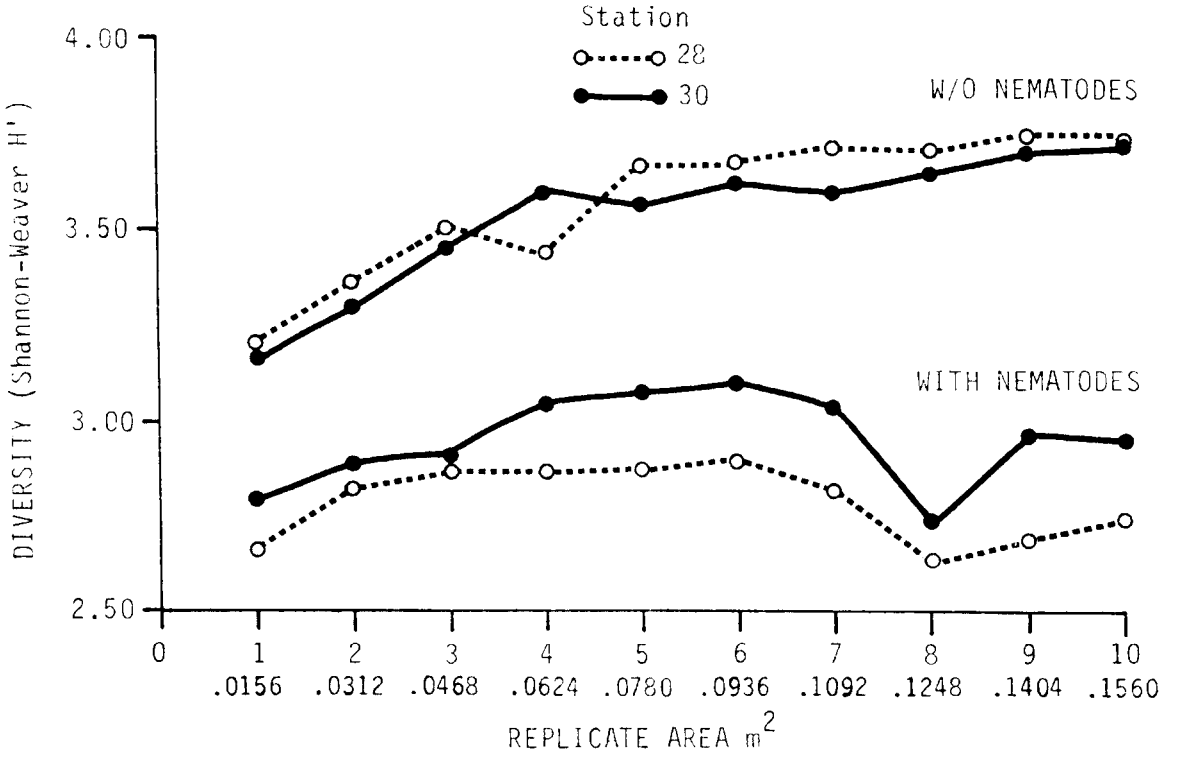


Figure 4. Diversity values based upon the Shannon-Weaver index for two nearshore benthic stations in the Gulf of Mexico. Values were calculated with nematodes included (lower curve) and with nemotodes deleted (upper curves).

sieve. However, the effect of a composite taxon (i.e., one not identified to generic or specific level) can be dramatic if present in large numbers. The net effect was to depress the overall diversity values and make the curve more erratic.

For Station 28, diversity appears to reach an acceptable asymptote after five replicate analyses. Station 30, although leveling off considerably after five replicates, does not appear to reach a stable asymptote until after Replicate Eight.

D) Equitability

The equitability measure is dependent on diversity and therefore behaves in a similar although inverse manner, requiring a greater number of replicates for stabilization (Figure 5). A small number of replicates tends to overestimate evenness. Equitability values do not appear to stabilize for either station until Replicates 8 through 10. The effects of Nematoda spp. on equitability values are also shown in Figure 5. The nematodes dramatically depress equitability values in a nearly continuous manner. This effect is more pronounced for Station 28, which had a relatively greater proportion of nematodes than did Station 30.

E) Faunal Density

Faunal density values are presented in Tables 1 and 2. Values ranged from 15192 to 37756 organisms per square meter at Station 28; for Station 30 densities ranged from 4744 to 30769 organisms per square meter. Average faunal densities were greater for Station 28 than Station 30, although the standard deviation between replicates was nearly identical for both stations. The deletion of nematodes significantly reduces the faunal densities for both stations. Figure 6 graphically presents the results of the cumulative faunal

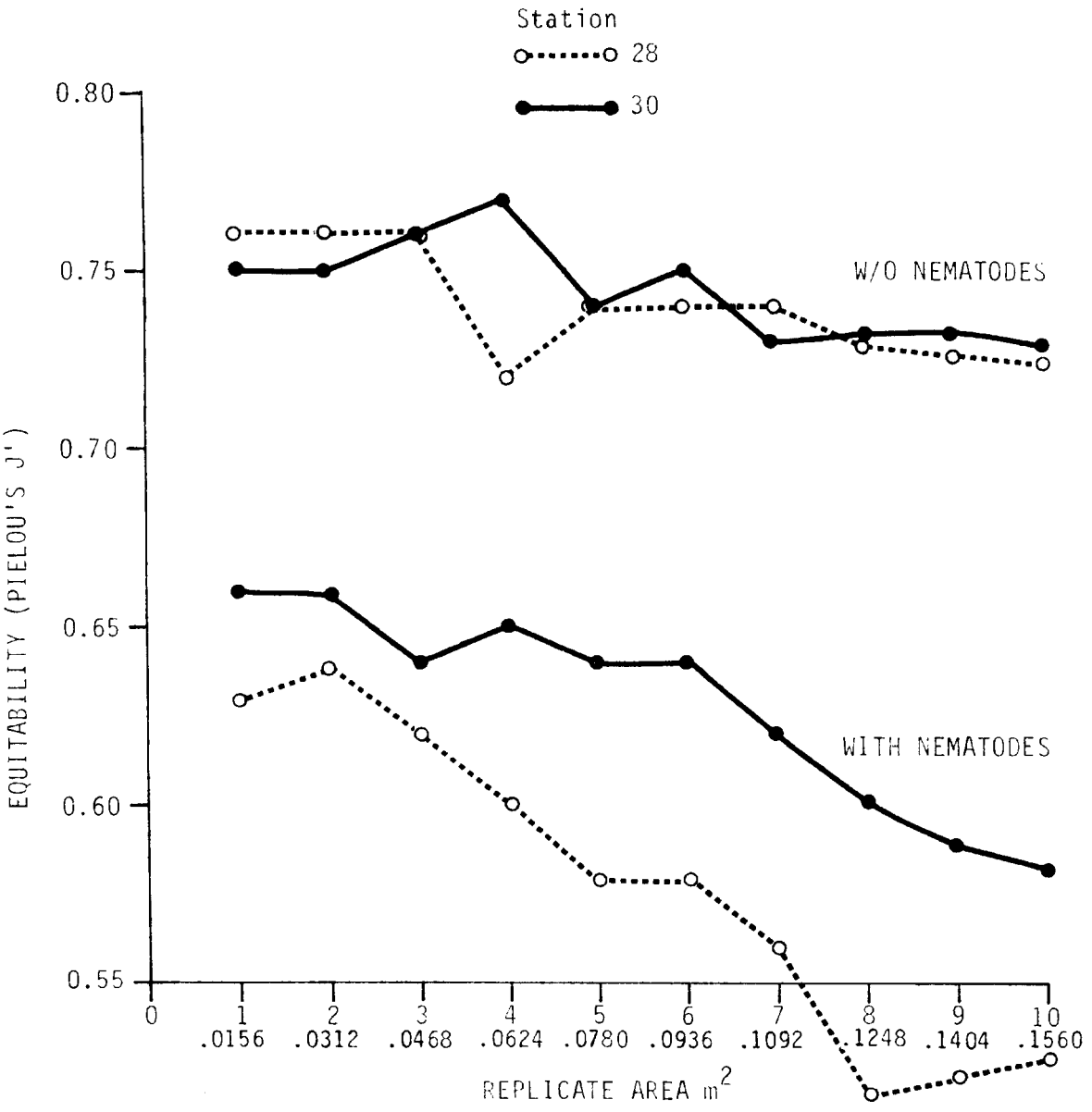


**Figure 5. Equitability (Evenness) values based on Pielou's 1966 index for two nearshore benthic stations in the Gulf of Mexico. Values were calculated with nematodes included (lower curves) and with nematodes deleted (upper curves).**

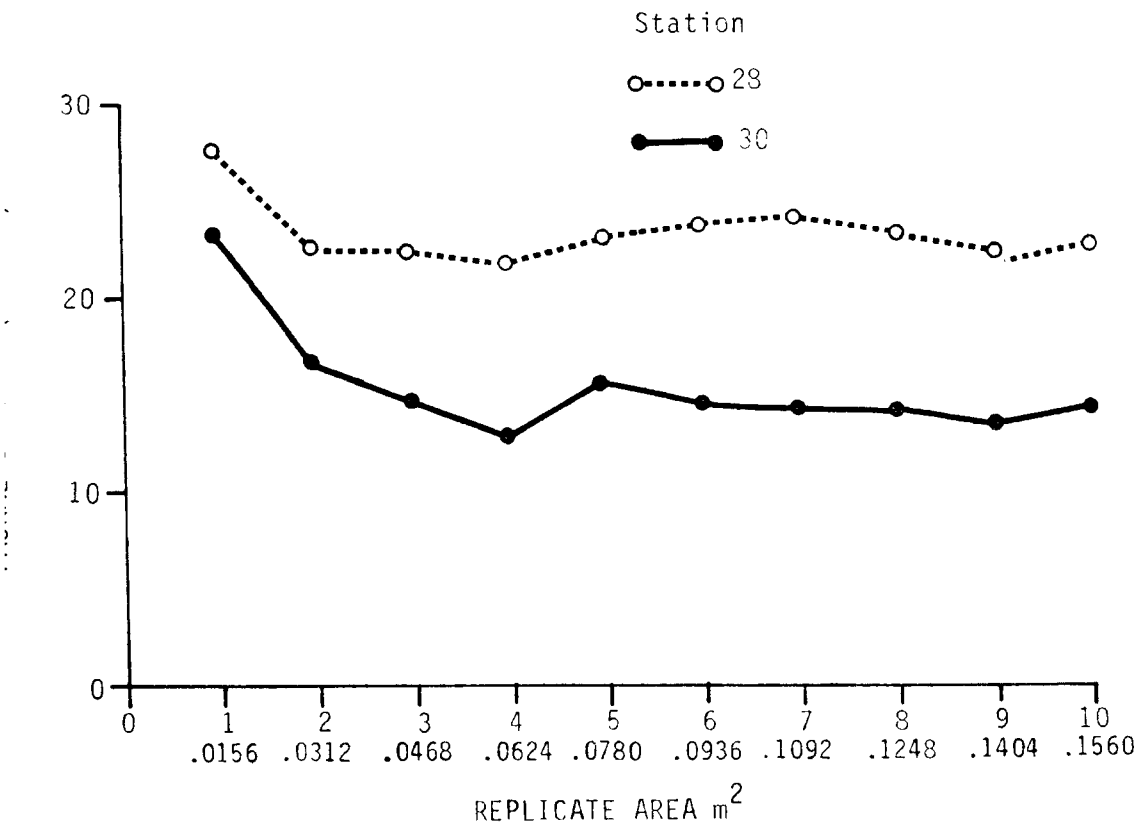


**Figure 6. Faunal density values (#/m$^2$) based upon cumulative sample replication for two nearshore stations in the Gulf of Mexico.**

density calculations. This graph was constructed by successively adding the organisms for each new replicate and calculating the faunal density based upon the cumulative area. There seems to be little effect upon faunal density estimates beyond the first four replicate samples for either Station 28 or 30.

F) Faunal Composition

Composite taxonomic listings for Stations 28 and 30 are presented in Table 3. This table lists the number of specimens collected at each station and the relative percentage composition. Polychaetes dominated the fauna with 127 total taxa for the combined stations; 101 taxa at Station 28 and 86 taxa at Station 30. There were very few dominant taxa at either station. Three polychaetes Armandia maculata (6.7%), Cirrophorus lyra (7.2%), and Pionosyllis aesae (8.2%) comprised amounts which were greater than or equal to 5% of the total fauna at Station 28. For Station 30, only the bryozoan Selenaria sp. (14.3%) occurred in large numbers. All percentages for dominants were calculated after deleting the nematodes. Overall, crustaceans contributed 55 taxa, molluscs 45, and echinoderms 6 taxa.

Tables 4 and 5 present the percentage composition of fauna by major taxonomic groupings, with and without nematodes. Polychaetes were the dominant fauna for both stations. Oligochaetes were also abundant at both stations. However, oligochaetes were not identified to generic or specific levels because the taxonomic status of marine oligochaetes is currently confused. There are virtually no current taxonomic keys to genera or species of marine oligochaetes (Brinkhurst, pers. comm.). Crustaceans also represented a relatively large portion of the fauna at both stations (number of species). Molluscs, although represented by relatively large numbers of species, were not present in large numbers.

**Table 3. Composite species list exhibiting the number of organisms found and the relative percentage composition for each taxon.**

| | STATION | | | |
|---|---|---|---|---|
| | 4-28 | | 4-30 | |
| TAXON | No. | % Composition | No. | % Composition |
| CNIDARIA | | | | |
| Anthozoa | | | | |
| Actiniaria (unid. sp.) | 2 | 0.1 | -- | -- |
| PLATYHELMINTHES | | | | |
| *Stylochus* sp. | 3 | 0.1 | -- | -- |
| RHYNCHOCOELA | | | | |
| Nemertina spp. | 46 | 1.3 | 15 | 0.7 |
| ASCHELMINTHES | | | | |
| Priapulida | | | | |
| *Tubiluchus corallicola* | 1 | <0.1 | -- | -- |
| Nematoda | | | | |
| Nematoda spp. | 1424 | 39.6 | 864 | 37.6 |
| BRYOZOA | | | | |
| *Selenaria* sp. | 55 | 1.5 | 205 | 8.9 |
| PHORONIDA | | | | |
| *Phoronis architecta* | -- | -- | 3 | 0.1 |
| BRACHIOPODA | | | | |
| *Glottidia pyramidata* | 3 | 0.1 | 6 | 0.3 |
| MOLLUSCA | | | | |
| Polyplacophora | | | | |
| Unidentified species | 2 | 0.1 | 3 | 0.1 |
| Gastropoda | | | | |
| *Arene tricarinata* | -- | -- | 2 | 0.1 |
| *Caecum pulchellum* | -- | -- | 3 | 0.1 |
| *Corbula contracta* | -- | -- | 2 | 0.1 |
| *Cylichna* sp. | 1 | <0.1 | -- | -- |
| *Episcynia multicarinata* | 1 | <0.1 | 1 | <0.1 |
| *Marginella apicinum* | -- | -- | 1 | <0.1 |
| *Marginella hartleyanum* | -- | -- | 1 | <0.1 |
| *Melanella* sp. | 1 | <0.1 | 2 | 0.1 |
| *Mitrella* cf. *lunata* | 1 | <0.1 | -- | -- |
| *Natica canrena* | 2 | 0.1 | 1 | <0.1 |
| *Olivella moorei* | 1 | <0.1 | -- | -- |
| *Olivella* sp. | 1 | <0.1 | -- | -- |
| *Solariella* sp. | 2 | 0.1 | 3 | 0.1 |
| *Strombiformis* sp. (juv.) | -- | -- | 1 | <0.1 |
| *Teinostoma* sp. | 1 | <0.1 | -- | -- |
| *Terebra dislocata* | 1 | <0.1 | -- | -- |
| *Turbonilla conradi* | 1 | <0.1 | -- | -- |
| *Turbonilla* sp. A (juv.) | -- | -- | 1 | <0.1 |

**Table 3. continued.**

| TAXON | STATION 4-28 No. | % Composition | 4-30 No. | % Composition |
|---|---|---|---|---|
| Turbonilla sp. B (juv.) | -- | -- | 1 | < 0.1 |
| Unidentified sp. (juv.) | 3 | 0.1 | 2 | 0.1 |
| Vitrinellidae sp. | 2 | 0.1 | -- | -- |
| Scaphopoda | | | | |
| Dentalium sp. | 4 | 0.1 | 2 | 0.1 |
| Scaphopoda sp. | -- | -- | 1 | < 0.1 |
| Bivalvia | | | | |
| Asthenothaerus hemphilli | 3 | 0.1 | -- | -- |
| Cardiidae sp. (juv.) | 1 | < 0.1 | -- | -- |
| Crassinella lunulata | 3 | 0.1 | 1 | < 0.1 |
| Laevicardium mortoni | 1 | < 0.1 | 2 | 0.1 |
| Lasaeidae sp. | 1 | < 0.1 | -- | -- |
| Limopsis cristata | -- | -- | 1 | < 0.1 |
| Lucina sp. | -- | -- | 1 | < 0.1 |
| Lucinidae sp. | 1 | < 0.1 | -- | -- |
| Musculus sp. (juv.) | 1 | < 0.1 | -- | -- |
| Mysella planulata | 5 | 0.1 | 2 | 0.1 |
| Neaeromya floridana | -- | -- | 1 | < 0.1 |
| Nucula proxima | 1 | < 0.1 | -- | -- |
| Nucula sp. (juv.) | 2 | 0.1 | -- | -- |
| Pteromeris perplana | -- | -- | 1 | < 0.1 |
| Semele muculoides | -- | -- | 1 | < 0.1 |
| Tellina listeri | 1 | < 0.1 | 2 | 0.1 |
| Tellina sp. (juv.) | -- | -- | 3 | 0.1 |
| Tellinidae sp. (spat) | 11 | 0.3 | -- | -- |
| Unidentified spp. (spat) | 13 | 0.4 | 11 | 0.5 |
| Vericorbula operculata | -- | -- | 2 | 0.1 |
| Verticordia ornata | 1 | < 0.1 | -- | -- |
| ANNELIDA | | | | |
| Polychaeta | | | | |
| Acrocirrus frontifilis | -- | -- | 1 | < 0.1 |
| Amaeana trilobata | 3 | 0.1 | 1 | < 0.1 |
| Ampharete sp. (juv.) | 1 | < 0.1 | -- | -- |
| Ampharetidae (juv.) | -- | -- | 1 | < 0.1 |
| Ancistrosyllis hartmanae | 39 | 1.1 | 29 | 1.3 |
| Aonides mayaguezensis | 2 | 0.1 | -- | -- |
| Arabella mutans | 1 | < 0.1 | 1 | < 0.1 |
| Aricidea cerrutii | 3 | 0.1 | 1 | < 0.1 |
| Aricidea fragilis | 1 | < 0.1 | 1 | < 0.1 |
| Aricidea suecica | 1 | < 0.1 | 1 | < 0.1 |
| Aricidea sp. A | 3 | 0.1 | -- | -- |
| Aricidea sp. (damaged) | 1 | < 0.1 | -- | -- |
| Aricidea taylori | 15 | 0.4 | 3 | 0.1 |
| Armandia maculata | 145 | 4.0 | 71 | 3.1 |
| Asychis elongata | 1 | < 0.1 | -- | -- |
| Axiothella mucosa | 6 | 0.2 | 4 | 0.2 |
| Boguea enigmatica | 6 | 0.2 | 4 | 0.2 |
| Brania wellfleetensis | 1 | < 0.1 | 2 | 0.1 |

**Table 3. continued.**

| TAXON | STATION 4-28 No. | % Composition | 4-30 No. | % Composition |
|---|---|---|---|---|
| Caraziella hobsonae | 1 | < 0.1 | -- | -- |
| Caulleriella sp. | 2 | 0.1 | -- | -- |
| Ceratocephale oculata | 3 | 0.1 | 1 | < 0.1 |
| Ceratonereis mirabilis | 2 | 0.1 | 1 | < 0.1 |
| Chone americana | 6 | 0.2 | 4 | 0.2 |
| Cirrophorus branchiatus | 36 | 1.0 | 14 | 0.6 |
| Cirrophorus lyra | 156 | 4.3 | 64 | 2.8 |
| Cirrophorus sp. A | 3 | 0.1 | -- | -- |
| Clymenella torquata | 1 | < 0.1 | -- | -- |
| Dentatisyllis carolinae | 21 | 0.6 | 18 | 0.8 |
| Ehlersia cornuta | 41 | 1.1 | 25 | 1.1 |
| Ehlersia ferrugina | 1 | < 0.1 | -- | -- |
| Eteone sp. | 1 | < 0.1 | -- | -- |
| Eulalia sanguinea | 3 | 0.1 | 3 | 0.1 |
| Eunice vittata | 24 | 0.7 | 16 | 0.7 |
| Eunice websteri | 1 | < 0.1 | 1 | < 0.1 |
| Eusyllinae sp. A | -- | -- | 1 | < 0.1 |
| Exogone dispar | -- | -- | 4 | 0.2 |
| Exogone lourei | 22 | 0.6 | 17 | 0.7 |
| Exogone sp. B | 1 | < 0.1 | -- | -- |
| Exogone sp. C | -- | -- | 5 | 0.2 |
| Fabricia sabella | 8 | 0.2 | 2 | 0.1 |
| Glycera oxycephala | 1 | < 0.1 | 1 | < 0.1 |
| Goniadides carolinae | 84 | 2.3 | 53 | 2.3 |
| Gyptis brevipalpa | 8 | 0.2 | 3 | 0.1 |
| Hesionura elongata | 12 | 0.3 | 21 | 0.9 |
| Heteropodarke cf. heteromorpha | 6 | 0.2 | -- | -- |
| Heteropodarke sp. A | 29 | 0.8 | 19 | 0.8 |
| Hydroides crucigera | 8 | 0.2 | 3 | 0.1 |
| Isolda pulchella | 4 | 0.1 | -- | -- |
| Leiocapitella sp. A | 3 | 0.1 | -- | -- |
| Lumbrinerides dayi | 6 | 0.2 | -- | -- |
| Lumbrineris candida | -- | -- | 1 | < 0.1 |
| Lumbrineris latreilli | 1 | < 0.1 | 3 | 0.1 |
| Lumbrineris verrilli | 55 | 1.5 | 11 | 0.5 |
| Lysidice minetta | 4 | 0.1 | -- | -- |
| Magelona cf. cincta | -- | -- | 1 | < 0.1 |
| Magelona pettiboneae | 19 | 0.5 | 6 | 0.3 |
| Malacoceros vanderhorsti | 1 | < 0.1 | -- | -- |
| Mediomastus spp. | 63 | 1.8 | 15 | 0.7 |
| Megalomma bioculatum | -- | -- | 3 | 0.1 |
| Megalomma vesiculosum | -- | -- | 1 | < 0.1 |
| Minuspio cirrifera | 2 | 0.1 | -- | -- |
| Mooreonuphis nebulosa | -- | -- | 5 | 0.2 |
| Myriochele oculata | 2 | 0.1 | -- | -- |
| Neanthes micromma | 1 | < 0.1 | -- | -- |
| Nematonereis hebes | 1 | < 0.1 | -- | -- |
| Neoleprea sp. A | -- | -- | 1 | < 0.1 |

**Table 3. continued.**

| TAXON | STATION 4-28 No. | % Composition | 4-30 No. | % Composition |
|---|---|---|---|---|
| Nephtys simoni | 11 | 0.3 | 9 | 0.4 |
| Nephtys squamosa | 4 | 0.1 | 4 | 0.2 |
| Nereis sp. | 21 | 0.6 | 15 | 0.7 |
| Notomastus americanus | -- | -- | 1 | < 0.1 |
| Odontosyllis enopla | 1 | < 0.1 | -- | -- |
| Onuphidae (juv.) | 1 | < 0.1 | -- | -- |
| Opisthodonta sp. A | -- | -- | 1 | < 0.1 |
| Opisthodonta sp. B | -- | -- | 2 | 0.1 |
| Owenia fusiformis | 10 | 0.3 | 21 | 0.9 |
| Palaenotus heteroseta | 23 | 0.6 | 23 | 1.0 |
| Paramphinome sp. B | 2 | 0.1 | 5 | 0.2 |
| Paraonidae (unid.) | -- | -- | 1 | < 0.1 |
| Parapionosyllis longicirrata | 19 | 0.5 | 8 | 0.3 |
| Paraprionospio pinnata | 5 | 0.1 | 4 | 0.2 |
| Pettiboneia sp. A | 1 | < 0.1 | -- | -- |
| Pholoe sp. | 2 | 0.1 | 4 | 0.2 |
| Phyllodoce arenae | 2 | 0.1 | 2 | 0.1 |
| Phyllodoce castanea | 2 | 0.1 | 2 | 0.1 |
| Phyllodocidae unid. | 3 | 0.1 | -- | -- |
| Pilargidae unid. | 1 | < 0.1 | -- | -- |
| Pilargis sp. | -- | -- | 1 | < 0.1 |
| Pionosyllis gesae | 177 | 4.9 | 28 | 1.2 |
| Pisione remota | 19 | 0.5 | 20 | 0.9 |
| Pista cristata | 2 | 0.1 | 1 | < 0.1 |
| Pista sp. | 1 | < 0.1 | -- | -- |
| Plakosyllis quadrioculata | 2 | 0.1 | 2 | 0.1 |
| Podarke obscura | 3 | 0.1 | 4 | 0.2 |
| Poecilochaetus johnsoni | -- | -- | 1 | < 0.1 |
| Polycirrus sp. | 7 | 0.2 | -- | -- |
| Polydora sp. | 1 | < 0.1 | -- | -- |
| Polynoid Genus B | -- | -- | 1 | < 0.1 |
| Polynoidae spp. unid. | -- | -- | 1 | < 0.1 |
| Prionospio cristata | 4 | 0.1 | -- | -- |
| Protodorvillea kefersteini | 55 | 1.5 | 32 | 1.4 |
| Sabellidae spp. | 1 | < 0.1 | -- | -- |
| Schistomeringos rudolphi | 36 | 1.0 | 19 | 0.8 |
| Schlerobregma stenocerum | 1 | < 0.1 | -- | -- |
| Scolelepis squamata | 1 | < 0.1 | -- | -- |
| Scoloplos rubra | 1 | < 0.1 | -- | -- |
| Serpulidae damaged | 1 | < 0.1 | 7 | 0.3 |
| Sigambra sp. | 2 | 0.1 | -- | -- |
| Sphaerosyllis glandulata | -- | -- | 2 | 0.1 |
| Sphaerosyllis piriferopsis | 1 | < 0.1 | 3 | 0.1 |
| Sphaerosyllis riseri | 1 | < 0.1 | -- | -- |
| Sphaerosyllis taylori | 1 | < 0.1 | -- | -- |
| Spiochaetopterus c. oculatus | -- | -- | 2 | 0.1 |
| Spionidae (juv.) | 12 | 0.3 | 3 | 0.1 |
| Spiophanes bombyx | 5 | 0.1 | 2 | 0.1 |

**Table 3. continued.**

| TAXON | STATION 4-28 No. | % Composition | 4-30 No. | % Composition |
|---|---|---|---|---|
| *Streblosoma hartmanae* | 1 | < 0.1 | 1 | < 0.1 |
| Syllidae unid. | -- | -- | 2 | 0.1 |
| *Syllides floridanus* | 1 | < 0.1 | -- | -- |
| *Synelmis albini* | 3 | 0.1 | 5 | 0.2 |
| *Tharyx* cf. *dorsobranchialis* | -- | -- | 2 | 0.1 |
| *Tharyx* cf. *marioni* | -- | -- | 1 | < 0.1 |
| *Tharyx* sp. | -- | -- | 1 | < 0.1 |
| *Trichobranchus glacialis* | 2 | 0.1 | 1 | < 0.1 |
| *Trypanosyllis* sp. | 1 | < 0.1 | -- | -- |
| *Typosyllis* cf. *lutea* | 9 | 0.3 | 2 | 0.1 |
| *Typosyllis prolifera* | 1 | < 0.1 | -- | -- |
| *Typosyllis* sp. A | -- | -- | 2 | 0.1 |
| *Vermiliopsis* sp. | 14 | 0.4 | 5 | 0.2 |
| Oligochaeta | | | | |
| Oligocheata spp. unid. | 381 | 10.6 | 263 | 11.5 |
| SIPUNCULIDA | | | | |
| Unidentified spp. | 17 | 0.5 | 12 | 0.5 |
| ARTHROPODA | | | | |
| Ostracoda | | | | |
| Mydocopa spp. | 22 | 0.6 | 10 | 0.4 |
| *Parasterope pollex* | 1 | < 0.1 | -- | -- |
| Podocopa spp. | 1 | < 0.1 | 1 | < 0.1 |
| Copepoda | | | | |
| Calanoid spp. | 3 | 0.1 | 6 | 0.3 |
| Cyclopoid spp. | 3 | 0.1 | 3 | 0.1 |
| Harpacticoid spp. | 80 | 2.2 | 42 | 1.8 |
| Cumacea | | | | |
| *Campylaspis* sp. E | 13 | 0.4 | 1 | < 0.1 |
| *Cyclaspis bacescui* | 2 | 0.1 | -- | -- |
| *Cyclaspis* cf. *unicornis* | -- | -- | 6 | 0.3 |
| *Cyclaspis* sp. A | 2 | 0.1 | 11 | 0.5 |
| *Cyclaspis* sp. B | -- | -- | 5 | 0.2 |
| *Cyclaspis* sp. D | 1 | < 0.1 | -- | -- |
| *Cyclaspis* spp. (juv.) | 3 | 0.1 | 3 | 0.1 |
| *Cumella* sp. A | 1 | < 0.1 | 1 | < 0.1 |
| *Cumella* sp. B | -- | -- | 1 | < 0.1 |
| *Oxyurostylis smithi* | 4 | 0.1 | 7 | 0.3 |
| Tanaidacea | | | | |
| *Apseudes propinquus* | -- | -- | 1 | < 0.1 |
| *Calozodion wadei* | 2 | 0.1 | -- | -- |
| *Hargeria rapax* | 2 | 0.1 | -- | -- |
| *Kalliapseudes* sp. A | 8 | 0.2 | 2 | 0.1 |
| *Leptochelia* sp. A | 4 | 0.1 | 1 | < 0.1 |
| Isopoda | | | | |
| *Apanthura* cf. *signata* | 1 | < 0.1 | -- | -- |
| *Edotea triloba* | 1 | < 0.1 | -- | -- |
| *Eurydice littoralis* | -- | -- | 1 | < 0.1 |
| *Munna* sp. | -- | -- | 2 | 0.1 |

**Table 3. continued.**

| TAXON | STATION 4-28 No. | % Composition | 4-30 No. | % Composition |
|---|---|---|---|---|
| Pananthura formosa | -- | -- | 1 | < 0.1 |
| Amphipoda | | | | |
| Acuminodeutopus naglei | 2 | 0.1 | -- | -- |
| Ampelisca abdita | 1 | 0.1 | 1 | < 0.1 |
| Ampelisca bicarinata | 6 | 0.2 | 3 | 0.1 |
| Ampelisca sp. A | -- | -- | 2 | 0.1 |
| Ampelisca sp. B | -- | -- | 2 | 0.1 |
| Amphilocus sp. | 1 | 0.1 | 1 | < 0.1 |
| Batea sp. | -- | -- | 1 | < 0.1 |
| Corophium sp. A | 3 | 0.1 | -- | -- |
| Ericthonius brasiliensis | -- | -- | 3 | 0.1 |
| Gammaropsis sp. | 2 | 0.1 | 6 | 0.3 |
| Listriella cf. barnardi | -- | -- | 3 | 0.1 |
| Maera sp. | -- | -- | 1 | < 0.1 |
| Microdeutopus myersi | -- | -- | 1 | < 0.1 |
| Photis macrocoxa | 7 | 0.2 | -- | -- |
| Podocerus sp. | -- | -- | 2 | 0.1 |
| Rildordanus laminosa | 1 | 0.1 | -- | -- |
| Synchelidium americanum | 9 | 0.3 | 3 | 0.1 |
| Tiron triocellatus | 1 | 0.1 | -- | -- |
| Tiron tropakis | 2 | 0.1 | -- | -- |
| Mysidacea | | | | |
| Bowmaniella portoricensis | 12 | 0.3 | 4 | 0.2 |
| Mysidopsis bigelowi | -- | -- | 1 | < 0.1 |
| Decapoda | | | | |
| Automate sp. | -- | -- | 1 | < 0.1 |
| Callianassa batei | 2 | 0.1 | -- | -- |
| Leptochela serratorbita | 2 | 0.1 | 1 | < 0.1 |
| Paguristes hummi | 1 | 0.1 | -- | -- |
| Panopeus sp. | -- | -- | 1 | < 0.1 |
| Sicyonia typica | 1 | 0.1 | -- | -- |
| Xanthidae sp. (juv.) | 1 | 0.1 | -- | -- |
| Caprellidea | | | | |
| Hemiaegina minuta | -- | -- | 3 | 0.1 |
| ECHINODERMATA | | | | |
| Ophiuroidea | | | | |
| Amphiodia planispina | 1 | 0.1 | -- | -- |
| Amphiodia pulchella | 4 | 0.1 | 6 | 0.3 |
| Amphiura fibulata | -- | -- | 1 | < 0.1 |
| Amphiuridae sp. (juv.) | 17 | 0.5 | 18 | 0.8 |
| Amphiolepis sp. | -- | -- | 1 | < 0.1 |
| Unidentified sp. | 1 | 0.1 | -- | -- |
| CHORDATA | | | | |
| Cephalochordata | | | | |
| Branchiostoma sp. | 7 | 0.2 | 6 | 0.3 |
| TOTALS: | 3585 | | 2296 | |
| | TOTAL TAXA: 180 | | TOTAL TAXA: 164 | |

TOTAL CUMULATIVE TAXA FOR BOTH STATIONS: 244

**Table 3. continued.**

| TAXON | STATION 4-28 No. | % Composition | 4-30 No. | % Composition |
|---|---|---|---|---|
| *Pananthura formosa* | -- | -- | 1 | < 0.1 |
| Amphipoda | | | | |
| *Acuminodeutopus naglei* | 2 | 0.1 | -- | -- |
| *Ampelisca abdita* | 1 | 0.1 | 1 | < 0.1 |
| *Ampelisca bicarinata* | 6 | 0.2 | 3 | 0.1 |
| *Ampelisca* sp. A | -- | -- | 2 | 0.1 |
| *Ampelisca* sp. B | -- | -- | 2 | 0.1 |
| *Amphilocus* sp. | 1 | 0.1 | 1 | < 0.1 |
| *Batea* sp. | -- | -- | 1 | < 0.1 |
| *Corophium* sp. A | 3 | 0.1 | -- | -- |
| *Ericthonius brasiliensis* | -- | -- | 3 | 0.1 |
| *Gammaropsis* sp. | 2 | 0.1 | 6 | 0.3 |
| *Listriella* cf. *barnardi* | -- | -- | 3 | 0.1 |
| *Maera* sp. | -- | -- | 1 | < 0.1 |
| *Microdeutopus myersi* | -- | -- | 1 | < 0.1 |
| *Photis macrocoxa* | 7 | 0.2 | -- | -- |
| *Podocerus* sp. | -- | -- | 2 | 0.1 |
| *Rildordanus laminosa* | 1 | 0.1 | -- | -- |
| *Synchelidium americanum* | 9 | 0.3 | 3 | 0.1 |
| *Tiron triocellatus* | 1 | 0.1 | -- | -- |
| *Tiron tropakis* | 2 | 0.1 | -- | -- |
| Mysidacea | | | | |
| *Bowmaniella portoricensis* | 12 | 0.3 | 4 | 0.2 |
| *Mysidopsis bigelowi* | -- | -- | 1 | < 0.1 |
| Decapoda | | | | |
| *Automate* sp. | -- | -- | 1 | < 0.1 |
| *Callianassa batei* | 2 | 0.1 | -- | -- |
| *Leptochela serratorbita* | 2 | 0.1 | 1 | < 0.1 |
| *Paguristes hummi* | 1 | 0.1 | -- | -- |
| *Panopeus* sp. | -- | -- | 1 | < 0.1 |
| *Sicyonia typica* | 1 | 0.1 | -- | -- |
| Xanthidae sp. (juv.) | 1 | 0.1 | -- | -- |
| Caprellidea | | | | |
| *Hemiaegina minuta* | -- | -- | 3 | 0.1 |
| ECHINODERMATA | | | | |
| Ophiuroidea | | | | |
| *Amphiodia planispina* | 1 | 0.1 | -- | -- |
| *Amphiodia pulchella* | 4 | 0.1 | 6 | 0.3 |
| *Amphiura fibulata* | -- | -- | 1 | < 0.1 |
| Amphiuridae sp. (juv.) | 17 | 0.5 | 18 | 0.8 |
| *Amphiolepis* sp. | -- | -- | 1 | < 0.1 |
| Unidentified sp. | 1 | 0.1 | -- | -- |
| CHORDATA | | | | |
| Cephalochordata | | | | |
| *Branchiostoma* sp. | 7 | 0.2 | 6 | 0.3 |
| TOTALS: | 3585 | | 2296 | |
| | TOTAL TAXA: 180 | | TOTAL TAXA: 164 | |

TOTAL CUMULATIVE TAXA FOR BOTH STATIONS: 244

Table 4. Percentage composition by major taxonomic groupings of benthic macroinfauna for Station 28. Percentages are presented for total organisms and with contribution of nematodes deleted.

| Taxon | Percentage With Nematodes | Percentage Without Nematodes |
|---|---|---|
| Nematoda | 39.7 | - - |
| Polychaeta | 37.6 | 62.3 |
| Oligochaeta | 10.6 | 17.6 |
| Gastropoda* | 0.7 | 1.1 |
| Bivalvia | 1.3 | 2.1 |
| Crustacea | 5.8 | 9.6 |
| Echinodermata | 0.6 | 1.1 |
| Miscellaneous | 3.7 | 6.2 |
| TOTAL : | 100.0 | 100.0 |

*Includes Polyplacophora and Scaphapoda.

Table 5. Percentage composition by major taxonomic groupings of benthic macroinfauna for Station 30. Percentages are presented for total organisms and with contribution of nematodes deleted.

| Taxon | Percentage With Nematodes | Percentage Without Nematodes |
|---|---|---|
| Nematoda | 37.6 | - - |
| Polychaeta | 30.3 | 48.6 |
| Oligochaeta | 11.5 | 18.4 |
| Gastropoda* | 1.2 | 1.9 |
| Bivalvia | 1.2 | 2.0 |
| Crustacea | 6.3 | 10.1 |
| Echinodermata | 1.1 | 1.8 |
| Miscellaneous | 10.8 | 17.2 |
| TOTALS : | 100.0 | 100.0 |

*Includes Polyplacophora and Scaphopoda.

## IV. DISCUSSION AND CONCLUSIONS

Little quantitative data are available from previous studies in the Gulf of Mexico for comparison with the present study. Variations in sampling techniques and methods of data analysis make direct comparisons difficult. For example, JRB Associates (1982) sampled 20 stations in the Gulf using a box corer a 1.0mm sieve for separating fauna from sediments. The annelids were the only group enumerated and identified from benthic samples. At JRB (1982) Station 4-28 (our Station 28), they found 44 species of polychaetes and a total density of 418/$m^2$. Our samples revealed 180 total taxa with a mean density of 13,917 individuals/$m^2$ (excluding nematodes). At JRB (1982) Station 4-30 (our Station 30), 85 polychaete taxa were identified with a total density of 612/$m^2$. Our Station 30 contained 164 total taxa with a mean density of 9,180/$m^2$ (without nematodes). Samples collected in both studies were obtained in the month of May. The lesson to be learned from such discrepant results is that consistent techniques for sampling and analysis must be used if spatial and temporal comparisons of benthic fauna are to be meaningful. In addition, the methods selected, whatever they may be, need to be fully documented and justified.

For maximum reproducibility and reliability, it is recommended that the procedures outlined in this report for sample collection and data analysis be employed in any subsequent studies intended to document temporal or spatial variation in benthic infaunal communities. It is further recommended that 10 replicate samples be collected and analyzed using diver-operated core samplers. The species saturation curves presented in Figure 3 indicate that 10 replicate samples will capture the vast majority of the species present,

and will provide an adequate sampling of the community composition for purposes of comparison. Ten replicate samples may seem excessive, since the 10th replicate only accounted for 3.1 or 4.5% of the total number of species (Figure 3). However, considering of natural variation between stations, and seasonal variations in species abundances, 10 replicate samples appeared to be justified. Furthermore, because the importance of the regulatory decisions which may be based in part upon those benthic community analyses, a definitive sampling design is warranted. In addition, species diversity (Figure 4), equitability (Figure 5), and faunal density (Figure 6) all indicate that 10 replicate samples will provide fully adequate characterization of the benthic community at Site 4.

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