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PROJECT REPORT PR-2003-04

BENTHIC FAUNAL SAMPLING ADJACENT TO SAND ISLAND OCEAN OUTFALL, O'AHU, HAWAI'I, AUGUST 2002

Richard C. Swartz
Julie H. Bailey–Brock
William J. Cooke
E. Alison Kay

March 2003

WATER RESOURCES RESEARCH CENTER
UNIVERSITY OF HAWAI'I AT MĀNOA
Honolulu, Hawai'i 96822

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[12] ABSTRACT (PURPOSE, METHOD, RESULTS, CONCLUSIONS)

In August 2002, benthic fauna in the vicinity of the Sand Island Ocean Outfall was sampled at fifteen stations established in 1999. Five stations were located on each of three transects along isobaths of approximately 20 m (Transect C), 50 m (Transect D), and 100 m (Transect E). Each transect included two stations near the diffuser at or inshore of the boundary of the zone of mixing (ZOM) and three stations beyond the diffuser at distances of approximately 2.4 to 2.7 km west, 4.4 to 4.9 km east, and 5.9 to 6.5 km east of the center of the diffuser. The 2002 survey followed the design initiated in 1999. The eleven surveys at this site prior to 1999 were based on seven stations located on one transect (herein called Transect B) at 58 to 77 m, the approximate depth of the outfall diffuser. Measurements of total organic carbon, total Kjeldahl nitrogen, and oxidation-reduction potential showed no indication of significant organic buildup in sediments at any station. The biological data indicate that there are few, if any, negative effects of the Sand Island outfall on the macrobenthic community. Most statistically significant differences in nonmollusk abundance and taxa richness among the fifteen stations were associated with differences among the three transects and reflect the influence of depth-related factors. The abundance and number of taxa of polychaetes, crustaceans, and all nonmollusks were usually significantly greater at several Transect D stations than at many stations on Transects C and E. When stations were pooled by proximity to the outfall, there were no significant differences between the near-diffuser station group and the beyond-diffuser station group in the abundance or taxa richness of polychaetes, crustaceans, and all nonmollusks. Taxa composition, diversity, and evenness of nonmollusks were also more closely associated with water depth than proximity to the outfall. Cluster analysis of nonmollusk taxa composition and abundance resulted in station groups that were associated primarily with the three transects. Most of the statistically significant differences in mollusk abundance and taxa richness among the fifteen stations were associated with high values at two near-diffuser stations (C3A and E3) and one beyond-diffuser station (E5), as well as low values at three beyond-diffuser stations (E1, E6, and C1A) and one near-diffuser station (C2A). There were no significant differences in mollusk abundance or taxa richness among transects or between the near-diffuser station group and the beyond-diffuser station group. Depth-related differences in mollusk taxa composition resulted in station clusters generally associated with transects. Four Transect D stations were grouped in an individual cluster. Another cluster included three stations on Transect C. Stations E3 and E5 were also linked together. There was no between-transect grouping of stations that might reflect a common influence of the outfall on either the mollusks or nonmollusks. There were no significant pairwise contrasts in the abundance and taxa richness of mollusks at Transect C, D, or E in 1999, 2000, and 2002, nor at Transect B in any previous sampling year. The abundance and taxa richness of nonmollusks and crustaceans were often significantly greater at Transect D in 1999, 2000, and 2002 than at Transect B in several previous years, and often significantly less at Transect C in 1999, 2000, and 2002 and at Transect E in 1999 and 2000 than at Transect B in many previous years. The abundance and taxa richness of nonmollusks and crustaceans were greater at Transect E in 2002 than in 1999 and 2000. The temporal differences in nonmollusks among Transects B, C, D, and E are probably associated with water depth. There is no indication of a negative temporal trend over the fourteen study years of the diffuser effluent on the macrobenthos. In summary, the response patterns of benthic fauna near the Sand Island Ocean Outfall in 2002 showed little or no indication of a significant influence by the diffuser effluent.

2540 Dole Street • Honolulu, Hawai'i 96822 • U.S.A. • (808) 956-7847

AUTHORS:

Dr. Richard C. Swartz
Environmental Consultant
P.O. Box 397
Placida, Florida 33946-0397
Tel.: 941/697-3612
Email: swartz@ewol.com

Dr. Julie H. Bailey–Brock
Professor (Invertebrate Zoology)
Department of Zoology
University of Hawai'i at Mānoa
2538 The Mall, Edmondson Hall 357
Honolulu, Hawai'i 96822
Tel.: 808/956-6149
FAX: 808/956-9812
Email: jbrock@hawaii.edu

Dr. William J. Cooke
Ecological Consultant
Marine Environmental Research
705 Nunu St.
Kailua, Hawai'i 96734
Tel.: 808/254-0203
Email: w.j.cooke@worldnet.att.net

Dr. E. Alison Kay
Professor (Malacology)
Department of Zoology
University of Hawai'i at Mānoa
2538 The Mall, Edmondson Hall 351
Honolulu, Hawai'i 96822
Tel.: 808/956-8620
FAX: 808/956-9812
Email: ekay@hawaii.edu

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Richard C. Swartz
Julie H. Bailey–Brock
William J. Cooke
E. Alison Kay

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Honolulu, Hawai'i 96822

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ABSTRACT

In August 2002, benthic fauna in the vicinity of the Sand Island Ocean Outfall was sampled at fifteen stations established in 1999. Five stations were located on each of three transects along isobaths of approximately 20 m (Transect C), 50 m (Transect D), and 100 m (Transect E). Each transect included two stations near the diffuser at or inshore of the boundary of the zone of mixing (ZOM) and three stations beyond the diffuser at distances of approximately 2.4 to 2.7 km west, 4.4 to 4.9 km east, and 5.9 to 6.5 km east of the center of the diffuser. The 2002 survey followed the design initiated in 1999. The eleven surveys at this site prior to 1999 were based on seven stations located on one transect (herein called Transect B) at 58 to 77 m, the approximate depth of the outfall diffuser. Measurements of total organic carbon, total Kjeldahl nitrogen, and oxidation-reduction potential showed no indication of significant organic buildup in sediments at any station. The biological data indicate that there are few, if any, negative effects of the Sand Island outfall on the macrobenthic community. Most statistically significant differences in nonmollusk abundance and taxa richness among the fifteen stations were associated with differences among the three transects and reflect the influence of depth-related factors. The abundance and number of taxa of polychaetes, crustaceans, and all nonmollusks were usually significantly greater at several Transect D stations than at many stations on Transects C and E. When stations were pooled by proximity to the outfall, there were no significant differences between the near-diffuser station group and the beyond-diffuser station group in the abundance or taxa richness of polychaetes, crustaceans, and all nonmollusks. Taxa composition, diversity, and evenness of nonmollusks were also more closely associated with water depth than proximity to the outfall. Cluster analysis of nonmollusk taxa composition and abundance resulted in station groups that were associated primarily with the three transects. Most of the statistically significant differences in mollusk abundance and taxa richness among the fifteen stations were associated with high values at two near-diffuser stations (C3A and E3) and one beyond-diffuser station (E5), as well as low values at three beyond-diffuser stations (E1, E6, and C1A) and one near-diffuser station (C2A). There were no significant differences in mollusk abundance or taxa richness among transects or between the near-diffuser station group and the beyond-diffuser station group. Depth-related differences in mollusk taxa composition resulted in station clusters generally associated with transects. Four Transect D stations were grouped in an individual cluster. Another cluster included three stations on Transect C. Stations E3 and E5 were also linked together. There was no between-transect grouping of stations that might reflect a common influence of the outfall on either the mollusks or nonmollusks. There were no significant pairwise contrasts in the abundance and taxa richness of mollusks at Transect C, D, or E in 1999, 2000, and 2002, nor at

Transect B in any previous sampling year. The abundance and taxa richness of nonmollusks and crustaceans were often significantly greater at Transect D in 1999, 2000, and 2002 than at Transect B in several previous years, and often significantly less at Transect C in 1999, 2000, and 2002 and at Transect E in 1999 and 2000 than at Transect B in many previous years. The abundance and taxa richness of nonmollusks and crustaceans were greater at Transect E in 2002 than in 1999 and 2000. The temporal differences in nonmollusks among Transects B, C, D, and E are probably associated with water depth. There is no indication of a negative temporal trend over the fourteen study years of the diffuser effluent on the macrobenthos. In summary, the response patterns of benthic fauna near the Sand Island Ocean Outfall in 2002 showed little or no indication of a significant influence by the diffuser effluent.

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INTRODUCTION

The Sand Island Wastewater Treatment Plant (WWTP) is a primary treatment system. Wastewaters of mainly domestic origin are treated at the WWTP prior to discharge through an 84-in. (2.13-m) diameter outfall located off the southern coast of O'ahu, Hawai'i.

The renewal of a waiver of secondary treatment for sewage discharge through the Sand Island Ocean Outfall was granted to the City and County of Honolulu (CCH) in September 1998 by the Region IX office of the U.S. Environmental Protection Agency (EPA). This report provides the results of the fourteenth in an ongoing series of studies of the macrobenthic, soft-bottom community in the vicinity of the discharge; it also provides an overview of trends in biological communities adjacent to the outfall over the seventeen-year period from 1986 to 2002. The number and location of stations sampled in 2002 are different from those sampled in most previous years. From 1986 through 1998, there was a single transect of seven stations along the approximate diffuser isobath. In 1999, 2000, and 2002 there were three transects of five stations each. These transects are located along three depth contours, two shallower and one deeper than that of the diffuser. The samples on which the fourteenth study is based were collected during August 2002.

PROJECT ORGANIZATION

General coordination for this project is provided by James E.T. Moncur, director of the Water Resources Research Center (WRRC) of the University of Hawai'i at Mānoa and project principal investigator. The principal members of the project team (in alphabetical order) and their contributions to the 2002 Sand Island study are as follows:

Julie H. Bailey–Brock	Invertebrate analysis and report, excluding crustaceans and mollusks
William J. Cooke	Crustacean analysis and report
E. Alison Kay	Mollusk analysis and report
Richard C. Swartz	Statistical analysis and final report preparation
Ross S. Tanimoto	City and County of Honolulu project representative and coordinator for sediment grain size, total Kjeldahl nitrogen, total organic carbon, and oxidation-reduction potential analyses

MATERIALS AND METHODS

General locations of the sampling stations are shown in Figure 1, and a general vicinity map of the area serviced by the Sand Island WWTP is shown in Figure 2. The stations are located along three depth contours: Transect C at approximately 20 m, Transect D at approximately 50 m, and Transect E at approximately 100 m. Sediment samples could not be collected at some stations in 1999 because of the presence of a hard substrate. In such cases, nearby soft-substrate positions along the same depth contour were chosen to replace originally designated positions. The replacement stations are designated with an "A" to indicate an alternative position, e.g., Station C1A. Soft substrate could not be found near Stations C4, D4, and E4, so a new set of stations—C6, D6, and E6—was substituted for the original set (Figure 1). The outfall diffuser is located between Transects D and E at a water depth of approximately 75 m. The stations on the three transects are located at five distances from the diffuser. Survey stations and their locations, as established in 1999, are as follows:

Stations C1A, D1, E1	Approximately 2.7 km (Station C1A), 2.5 km (Station D1), and 2.4 km (Station E1) west of the center of the outfall diffuser to evaluate beyond-diffuser effects
Stations C2A, D2, E2	At or near the west boundary of the zone of mixing (ZOM) approximately 1.3 km (Station C2A), 0.7 km (Station D2), and 0.7 km (Station E2) from the center of the outfall diffuser to evaluate near-diffuser effects
Stations C3A, D3A, E3	At or near the east boundary of the ZOM approximately 1.5 km (Station C3A), 0.8 km (Station D3A), and 0.7 km (Station E3) from the center of the outfall diffuser to evaluate near-diffuser effects
Stations C5A, D5, E5	Approximately 4.9 km (Station C5A), 4.7 km (Station D5), and 4.4 km (Station E5) east of the center of the outfall diffuser to evaluate beyond-diffuser effects
Stations C6, D6, E6	Approximately 6.5 km (Station C6), 6.1 km (Station D6), and 5.9 km (Station E6) east of the center of the outfall diffuser to evaluate beyond-diffuser effects

The fifteen stations were divided into two groups to facilitate comparisons of sediment and biological conditions with respect to proximity to the diffuser. The "near-diffuser" station group includes six stations (C2A, C3A, D2, D3A, E2, and E3) whose locations range from 0.7 to 1.5 km from the center of the diffuser. The "beyond-diffuser" station group includes nine stations (C1A, C5A, C6, D1, D5, D6, E1, E5, and E6) whose locations range from 2.4 to 6.5 km from the center of the diffuser.

Prior to 1999, the Sand Island benthic faunal survey was based on seven stations (B1, B2, B3, B4, HZ, B5, and B6) located along the diffuser isobath, within a water depth range of approximately 58 to 77 m (Russo et al. 1988; Bailey–Brock et al. 1991; Nelson et al. 1992a, 1992b, 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999). In this report the historic transect is referred to as Transect B.

Station Positioning

The positioning of each station was established using the Garmin differential global positioning system. General station locations are shown in Figure 1. Positions for each replicate grab sample at each station are given in Appendix Table A.1. The depth range for Transect C stations was 18.6 to 21.0 m; for Transect D stations, 49.1 to 53.3 m; and for Transect E stations, 83.8 to 101.8 m.

Sampling Methods

The sampling methodology used in this study generally followed the recommendations of Swartz (1978) and U.S. EPA guidelines (U.S. EPA 1987a, 1987b), hereafter referred to as EPA procedures.

A 0.16-m^2 modified van Veen grab sampler deployed from a stern-mounted A-frame on the research vessel *Noi I Kai* was used to obtain bottom samples at all fifteen stations. Sampling dates were 29–30 August 2002. Penetration of the sampler was adequate for all replicates. The minimum penetration depth for all grabs was 6.0 cm and the maximum was 14.5 cm (Appendix Table A.2).

Three van Veen grab samples were taken at each station. A subsample 7.6 cm in diameter by 5 cm deep was taken from each grab sample for nonmollusk analysis and a subsample 4.8 cm in diameter by 5 cm deep for mollusk analysis. Subsampling was necessary because the epifauna and infauna in the area are known to be both small and abundant (Nelson 1986; Russo et al. 1988) and processing of the entire sample would be impractical. Replicated grab samples taken at each station, rather than replicated subsamples from one grab sample, were used to provide information on intrastation variability. All three nonmollusk subcores were processed on a 0.5-mm screen.

Samples for geochemical analyses (total organic carbon [TOC], oxidation-reduction potential [ORP], total Kjeldahl nitrogen [TKN], and grain size) were obtained from the grabs from which the biological subcores were taken. Each replicate van Veen grab contained more than enough sediment for both purposes (methods established in National Pollutant Discharge Elimination System [NPDES] permit no. HI 0020117). Three subsamples 7.6 cm in diameter

by 5 cm deep (one from each of three different grab samples) were taken for the analyses for each station. The top 2 cm of the grab were used for geochemical analysis. Samples for TOC analysis were put in screw-cap jars, placed on ice, and taken to the laboratory for analysis. Sediment ORP was done immediately after the samples were brought aboard the ship. Laboratory analyses of sediment grain size, ORP, and TKN followed EPA procedures. Analysis of TOC followed ASTM method D4129-82M.

Sample Processing

Handling, processing, and preservation of biological samples followed EPA procedures. Nonmollusk samples were fixed in 15% buffered formalin for a minimum of 24 hours. The fixed samples were elutriated using the technique of Sanders et al. (1965). This method successfully removes from the sediment all organisms that are not heavily calcified. The samples were washed several times, and the water from each was poured through 0.5-mm mesh sieves. Polychaetes and other invertebrates retained on the sieve were transferred to alcohol, stained with rose bengal solution, and stored in 70% ethanol. Mollusk samples were fixed in 75% isopropyl alcohol for 48 hours and then air dried. Aliquot portions (15 cm^3) were then sorted following the methods of Kay (1980) and Kay and Kawamoto (1983). The picked shells were identified and counted using Kay (1979a) as the primary taxonomic reference.

When large carbonate rubble fragments were collected in the samples, the rubble fragments were carefully washed and visually examined to ensure that any organisms on the external surfaces were removed. The fragments were then placed in a nitric acid bath for 24 hours to dissolve the carbonate and to recover organisms living in burrows. The acid dissolution techniques used were modified from the methods of Brock and Brock (1977), as described in Nelson (1986). In the 2002 samples, the following replicates had acid dissolution applied to rubble fragments: replicate 3 at Station C5A and replicate 2 at Station D3.

Because the biological subcores had to be processed using two different procedures, one for mollusks and the other for all other organisms, the two components of the fauna were not directly comparable and thus were analyzed separately. Because the mollusks were not separated into living and dead shell fractions, they represent time-averaged samples. Mollusks have been extensively analyzed by Kay (1975, 1978, 1979b, 1982), Kay and Kawamoto (1980, 1983), Nelson (1986), and Russo et al. (1988).

All specimens were identified to the lowest taxonomic level possible. Voucher specimens were submitted to taxonomic specialists for verification when necessary. All specimens were archived and will be maintained for six years at the University of Hawai'i.

Data Analysis

All data were tested for assumptions of normality (Kolmogorov–Smirnov test; Sokal and Rohlf 1995) and homogeneity of variances (F_{max} test) prior to statistical analysis. Where data sets failed tests of assumptions, either square root or $\log_{10}$ transformation was applied. Comparisons of mean values among stations were made with one-way analysis of variance (ANOVA). Following significant ANOVA results, a posteriori Student–Newman–Keuls tests were used to determine which differences among stations were significant. If transformation failed to correct violations of assumptions of ANOVA, nonparametric Kruskal–Wallis ANOVA on ranks was carried out. All statistical analyses were carried out using Prophet and Microsoft Excel software. Detailed statistical results are provided in Appendixes B and C.

An overall comparison of taxa composition among stations was carried out separately for the nonmollusks and mollusks using cluster analysis (Pielou 1984). The Bray–Curtis similarity index (Bloom 1981) on double square root transformed data was performed using the group-average sorting strategy. To make the analysis more manageable, only those taxa that contributed at least 0.05% of the total abundance were included. This reduced the data sets for analysis from 198 to 108 nonmollusk taxa and from 251 to 105 mollusk taxa. The similarity matrices were computed with BioDiversity Pro software.

The Shannon–Wiener diversity index (H') (ln) and evenness index (J) were calculated for all stations (all replicates pooled), as recommended in the EPA procedures. Calculations of these parameters were carried out with Microsoft Excel software.

To examine trends from 1986 to the present, mean station values were used as data and comparisons were made for all sampling dates for the B transect (1986 through 1998) and for the C, D, and E transects (1999, 2000, and 2002) using one-way ANOVA and Student–Newman–Keuls tests. Mean station values for 1999, 2000, and 2002 were also used as data to compare all sampling stations on the C, D, and E transects using one-way ANOVA and Student–Newman–Keuls tests.

In contrast to some previous reports in this series on the macrobenthic, soft-bottom community in the vicinity of the outfall discharge (Russo et al. 1988; Bailey–Brock et al. 1991), no statistical analysis is made of polychaete trophic or motility categories as separate entities. Similarly, mollusk subgroupings (e.g., bivalves, gastropods, and various trophic categories) are not analyzed separately. Previous statistical analyses of these categories showed few differences between the response patterns of the taxonomic subcategories and the major taxon of which they are a part (Russo et al. 1988; Bailey–Brock et al. 1991). Therefore, such analyses are considered largely redundant and are omitted here.

RESULTS

Sediment Parameters

Results of sediment grain-size analysis are given in Appendix Table A.3. The mean sediment compositions of replicate samples from the fifteen stations, based on four grain-size categories, are compared in Figure 3. The grain-size categories (Folk 1968) are as follows: coarse sediment, retained on a +1-phi sieve; medium sand, passed through a +1-phi sieve but retained on a +2-phi sieve; fine sand, passed through a +2-phi sieve but retained on a +4-phi sieve; and silt and clay, passed through a +4-phi sieve.

Sediment grain-size distribution differed among stations (Appendix Table A.3). Sediments at all stations contained a mean silt-and-clay fraction of less than 15% (Figure 3). Sediments at Transect C stations were characterized by a very low mean silt-and-clay fraction (<2.3%) and, with one exception, a dominance of medium sand and coarse sediment (>64%). The exception was Station C1A, where the mean percent of the combined medium-sand and coarse-sediment fractions was only 34.8% and most of the sediment dry weight (61.5%) was in the fine-sand fraction. Sediments at Transect D stations were predominantly fine sand (39.5% to 71.5%), although the mean percent of the combined medium-sand and coarse-sediment fractions was 56.0% at Station D3A. Grain-size distribution was most variable on Transect E, where fine sand dominated strongly at Stations E1 and E6 (>71%) and to a lesser extent at Station E5 (53.6%). Sediments at Stations E2 and E3 were composed primarily of medium sand and coarse sediment (>61%). Statistical comparison of the percentage of the combined medium-sand and coarse-sediment fractions among stations did not meet the assumption of homogeneity of variance. The nonparametric Kruskal–Wallis test showed that the mean percent of the combined medium-sand and coarse-sediment fractions was significantly greater at Station C2A (87.9%) than at Station E6 (3.3%). There were significant differences in mean percent of the combined medium-sand and coarse-sediment fractions among Transects C, D, and E ($F = 7.871, p = 0.002$). Student–Newman–Keuls comparisons showed that the mean percent of the combined medium-sand and coarse-sediment fractions was significantly greater on Transect C (70.0%) than on Transect D (37.0%) or Transect E (35.9%). The mean percent of the combined medium-sand and coarse-sediment fractions was significantly less among all samples collected at beyond-diffuser stations (35.0%) than at near-diffuser stations (66.5%) ($t = 3.880$, $p = 0.0006$). Recent surveys (1996 through 1998) showed that sediments on Transect B were also characterized by a low proportion of silt and clay, whereas the fine sand and the combined medium-sand and coarse-sediment fractions were more evenly distributed than at many stations in the present survey (Nelson et al. 1997; Swartz et al. 1998, 1999). Analysis of duplicate samples for Stations C3A, D6, and E6 indicated consistency of analytical techniques.

Direct electrode measurements of ORP were positive in the range from 25 to 210 mV (Appendix Table A.2). These readings show no evidence of strongly reducing conditions in the surface sediments at any station. ORP ranged from 25 to 210 mV at beyond-diffuser stations and from 145 to 205 mV at near-diffuser stations. There were significant differences in ORP values among stations (ANOVA, $F = 4.800$, $p = 0.00016$). Mean ORP was significantly higher at Stations D2, C3A, D5, C5A, C6, C2A, D3A, E3, and D6 than at Stations E1 and E6. The two stations with the lowest mean ORP values (63.3 and 68.3 at Stations E1 and E6, respectively) were also the two stations with the finest sediment grain-size distributions. There were significant differences in mean ORP among transects (ANOVA, $F = 6.476$, $p = 0.0035$). Mean ORP was significantly higher at Transect C (173 mV) and D (173 mV) stations than at Transect E stations (119 mV). Mean ORP was significantly greater at near-diffuser stations (178 mV) than at beyond-diffuser stations (139 mV) ($t = 2.600$, $p = 0.013$). Values of ORP measured in 2002 on the C, D, and E transects were similar to those measured in 1997 and 1998 on the B transect and to those measured in 1999 and 2000 on the C, D, and E transects. The significantly greater ORP measurements at near-diffuser stations compared to beyond-diffuser stations indicates the effluent is not causing an increase in reducing conditions in the vicinity of the outfall, since higher ORP values indicate a lower probability of anaerobic conditions.

Values of TKN ranged from 133 to 336 mg/dry kg (Appendix Table A.2). TKN values ranged from 133 to 336 mg/kg at beyond-diffuser stations and from 141 to 300 mg/kg at near-diffuser stations. Statistical comparisons are limited because of the lack of replicate samples at stations on Transect E. However, there were no significant differences in mean TKN among Transect C (254.5 mg/kg), Transect D (232.8 mg/kg), and Transect E (246.4 mg/kg) (ANOVA, $F = 0.467$, $p = 0.633$) or between beyond-diffuser stations (252.2 mg/kg) and near-diffuser stations (232.3 mg/kg) ($t = 0.982$, $p = 0.336$). There is no evidence of nitrogen enrichment in sediments at stations near the outfall.

Sediment TOC values ranged from 0.23% to 0.59% (Appendix Table A.2). TOC ranged from 0.23% to 0.56% at beyond-diffuser stations and from 0.24 to 0.59% at near-diffuser stations. Statistical comparisons are limited because of the lack of replicate samples at stations on Transect E. However, there were no significant differences in mean TOC among Transect C (0.41%), Transect D (0.33%), and Transect E (0.36%) (ANOVA, $F = 2.222$, $p = 0.132$). There were no significant differences in TOC between beyond-diffuser stations (0.38%) and near-diffuser stations (0.36%) ($t = 0.552$, $p = 0.586$). There is no evidence of organic carbon enrichment in sediments at stations near the outfall.

Biological Parameters

Nonmollusks

The nonmollusk fraction of the benthic fauna included polychaetes, oligochaetes, nematodes, platyhelminths, chaetognaths, a phoronid species, sipunculans, nemerteans, echinoderms, anthozoans, hydrozoans, priapulids, bryozoans, a kinorhynch species, urochordates, a chordate species, insect larvae, mites, pycnogonids, amphipods, copepods, cumaceans, decapods, isopods, ostracods, tanaids, and mysids. The insect larvae, possibly originating in the sewage treatment facility or nearby environment, but definitely not marine in origin, were found at Stations D2, D3A, D5, and D6.

The 10,937 nonmollusk specimens counted and identified for all stations and replicates represent 198 taxa. Nematodes, which were not identified to species, were the dominant nonmollusk taxon in terms of abundance (3,413 individuals, 31.2%). Polychaetes, the second dominant taxon (3,102 individuals, 28.4%), had the highest taxa richness (127 taxa, 64.1%) of groups identified to the species level. Crustaceans (2,649 individuals) contributed 24.2% of the nonmollusk abundance. The 50 crustacean taxa, 16 of which were amphipods, represented 25.3% of the total number of nonmollusk taxa. Discussion of crustaceans in this report includes all crustacean taxa, as well as mites, pycnogonids, and mysids. Oligochaetes (704 individuals) constituted 6.4% of total nonmollusk abundance. A complete list of abundances for each taxon from each replicate is provided for each station in Appendix D.

Basic statistics for the nonmollusk data, including 95% confidence limits and a Kolmogorov–Smirnov test for normality of distribution, are provided in Appendix Tables B.1 (number of individuals) and B.2 (number of taxa). Data for number of nonmollusk individuals were normally distributed at all stations (Appendix Table B.1) and met the assumption of homogeneity of variances in ANOVA (Appendix Table B.3). Data for number of nonmollusk taxa were also normally distributed at all stations (Appendix Table B.2) and met the assumption of homogeneity of variances in ANOVA (Appendix Table B.4).

Mean total nonmollusk abundance ranged from 31.7 individuals per sample (6,988 individuals/m^2, at Station C2A) to 825.7 individuals per sample (182,014.2 individuals/m^2, at Station D5) (Figure 4). Mean abundance of nonmollusks differed significantly among stations (ANOVA, Appendix Table B.3). The mean number of nonmollusks was significantly greater at Station D5 than at Stations C2A, C6, C3A, C1A, E2, C5A, E5, and E1.

The mean number of nonmollusk taxa per sample ranged from 11.7 (at Station C2A) to 61.3 (at Station E3) (Figure 5, Appendix Table B.4). Mean number of taxa differed significantly among stations (ANOVA, Appendix Table B.4). Stations E3, D5, D2, D3A, E5, D6, E1, and E6 had a significantly larger number of taxa than Stations C2A, C6, C1A, and C3A.

The number of nonmollusk taxa was also significantly larger (1) at Stations E3, D5, D2, and D3A than at Stations E2, D1, and C5A and (2) at Station E3 than at Stations E6, E1, D6, and E5.

Composite station diversity (H') and evenness (J) for nonmollusks at all stations are shown in Figure 6. Values for H' ranged from 2.00 (at beyond-diffuser station C1A) to 3.19 (at near-diffuser station E2). Lower diversity was observed at some stations in 1999, 2000, and 2002 compared with stations on Transect B in previous sampling years (Russo et al. 1988; Bailey–Brock et al. 1991; Nelson et al. 1992a, 1992b, 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999, 2000, 2001). The highest H' value in 2002 was due to the absence of a strong dominant (only 15.6% of all individuals was represented by the most abundant taxon) at Station E2, which had the lowest mean abundance and taxa richness of any station on the D and E transects. The lowest H' value was due to relatively low taxa richness (13.7 taxa/sample), low abundance (55.0 individuals/sample), and high dominance by a single taxon (50.3% of all individuals) at Station C1A. H' was relatively low at most Transect C stations and relatively high at most Transect E stations, but each transect had at least one station with an H' value of less than 2.40. Low diversity at Transect C stations (excluding Station C5A) is associated with low abundance and taxa richness (Appendix Tables B.1 and B.2). High diversity at Stations D2, D3A, E1, E3, and E5 is related to relatively high abundance (168.3 to 490.7 individuals/sample), high taxa richness (35.0 to 61.3 taxa/sample), and the absence of strong dominants (15.7% to 31.4% of all individuals represented by the most abundant taxon). Values for evenness ranged from 0.55 (at beyond-diffuser station D5) to 0.85 (at near-diffuser station E2). Maximum and minimum evenness values were higher in 2002 than in 1999 and similar to values in 2000 and in most previous years at Transect B (Russo et al. 1988; Bailey–Brock et al. 1991; Nelson et al. 1992a, 1992b, 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999, 2000, 2001). As in the case of H', the highest J value was recorded at Station E2 where there were no strong dominants. The highest H' and J values were also recorded at Station E2 in 2000. Evenness was relatively high at Transect C stations (except for Station C1A) and at Stations D2, D3A, E1, E2, and E5 because of the absence of strong dominants. A few numerically dominant taxa caused lower evenness at Stations C1A, D1, D5, and E6 where 36.6% to 50.3% of the individuals were represented by the most abundant taxon. As in 1999 and 2000, diversity and evenness in 2002 were more closely associated with water depth than proximity to the outfall.

Results of the cluster analysis indicating the relative similarity of stations based on the 108 most abundant nonmollusk taxa are shown in Figure 7. The 2002 cluster analysis indicated a low similarity among all combined stations (51.1%). In most previous years, the similarity among all combined stations on Transect B exceeded 60% (Russo et al. 1988; Bailey–Brock et al. 1991; Nelson et al. 1992a, 1992b, 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999). The

low overall similarity in 1999, 2000, and 2002 reflects the new survey design, i.e., sampling of stations along three different depth contours represented by Transects C, D, and E. With a few exceptions, the dendrogram shows clusters of stations that correspond to the three transects. Stations C2A, C3A, C5A, and C6 linked together at a similarity of 55.6%. Most of the Transect D and Transect E stations combined to form a large cluster with an overall similarity of 59.8%. Within that large cluster, stations on the same transect were usually more similar than stations on different transects. Stations E2 and C1A were the last two stations added to the dendrogram (52.0% and 51.1% similarity, respectively), indicating that their faunal composition was somewhat different from that of all other stations. The mean within-transect similarity was 51.4% for Transect C, 63.1% for Transect D, and 57.3% for Transect E. There was no between-transect grouping of stations that might reflect a common influence of the outfall. The cluster pattern in 2002 is associated primarily with the direct and indirect influences of water depth on the macrobenthos.

Among the three transects, there were distinct differences in dominant nonmollusk taxa composition (Table 1). No species was collected at all fifteen stations in 2002. *Pionosyllis heterocirrata* was widely distributed and ranked as a dominant at least at two stations on each transect. It was the only species collected at all five Transect C stations and was the most abundant species at all of them except Station C1A. No other species was particularly abundant at any Transect C station. *P. heterocirrata* was also a dominant at Stations D2, D3A, E2, E3, and E5. *Prionospio cirrifera* was widely distributed and a dominant at least at one station on each transect (it qualified as a dominant at two Transect C stations with fewer than 10 specimens each). *Leptochelia dubia* was the most abundant species collected in 2002 (699 individuals). It was a dominant at Stations D2, D3A, D5, D6, E3, and E5. In 2000, *L. dubia* was a strong dominant at Station C5A, where only two specimens were collected in 2002. *Ophiodromus angustifrons* (previously listed as *Podarke angustifrons*) and *Sphaerosyllis* sp. G were widely distributed on all three transects, but they ranked among the five most abundant taxa only on Transect C. *Myriochele oculata* was a dominant at all stations on Transect D but rare or absent at stations on the other transects. *Synelmis acuminata* was also abundant and usually a dominant on Transect D stations. *Aspidosiphon muelleri* was a dominant at four stations each on Transect D and Transect E. *Dipolydora normalis*, an opportunistic species, was very abundant (161 individuals) at Station D3A but absent at all other stations except Station D1 (5 individuals). *Prionospio cirrobranchiata* and *Tanaissus* sp. A ranked among the five dominants at least at two Transect E stations but were not a dominant at any station on the other transects. Spionidae sp. D is characteristic of Transect E. It was found at all Transect E stations in 2000 and 2002 and was a dominant at three of them in 2002. It has never been collected on Transects C and D. The abundance of *Euchone* sp. B decreased by an order of

magnitude from 1999 (1,443 individuals collected in all samples) to 2000 (143 individuals), but it increased in 2002 to 376 individuals. This taxon was a dominant at Stations D1, D2, D5, and D6 in 1999, at Station D1 in 2000, and at Stations D1 and D5 in 2002. The opportunistic species *Ophryotrocha adherens* was a dominant only at Station D2 in 2002.

The analyses of diversity, faunal similarity, and dominant taxa all indicate distinct faunal differences among the three transects. Statistical comparisons among the three transects in the number of individuals and taxa of nonmollusks, crustaceans, and mollusks are summarized in Table 2. There were consistent significant differences in abundance and taxa richness for the nonmollusks and crustaceans. Transects D and E had significantly higher mean number of individuals and taxa than Transect C for nonmollusks and crustaceans. The abundance of nonmollusks and the abundance of crustaceans were significantly greater at Transect D than at Transect E.

There were no significant differences between beyond-diffuser stations and near-diffuser stations in the abundance of nonmollusks (beyond-diffuser mean = 243.6 individuals/sample, near-diffuser mean = 242.1 individuals/sample, $t = 0.017$, $p = 0.986$) and crustaceans (beyond-diffuser mean = 54.7 individuals/sample, near-diffuser mean = 65.1 individuals/sample, $t = 0.327$, $p = 0.745$) or in the number of taxa of nonmollusks (beyond-diffuser mean = 30.4 taxa/sample, near diffuser mean = 34.4 taxa/sample, $t = 0.809$, $p = 0.423$) and crustaceans (beyond-diffuser mean = 6.2 taxa/sample, near-diffuser mean = 6.7 taxa/sample, $t = 0.318$, $p = 0.752$).

Polychaetes

The polychaete communities were taxa rich at all stations on Transects D and E (27 to 66 taxa/station) and in this respect are comparable to the 1991 through 1998 samples collected on Transect B (Nelson et al. 1992a, 1992b, 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999) and the 1999 and 2000 samples collected on Transects D and E (Swartz et al. 2000, 2001). Fewer polychaete taxa were collected at all Transect C stations (13 to 18 taxa/station) except Station C5A, where 28 taxa were collected. There were 3,102 polychaete individuals representing 127 taxa from 36 families identified from the 45 samples collected in the entire survey (Appendix Tables D.1 through D.9).

Station D5 had the highest mean number of polychaetes (201.7 individuals/sample, 44,462 individuals/m^2) and Station C1A the lowest (8.3 individuals/sample, 1,830 individuals/m^2) (Figure 8). In decreasing order of polychaete abundance Station D5 was followed by Stations D3A, D2, E3, D1, E6, D6, E5, E1, C5A, E2, C3A, C6, C2A, and C1A. The highest mean number of polychaete taxa per sample was observed at Station E3 (38.7 taxa/sample, 66 taxa/station) and the lowest at Station C6 (6.0 taxa/sample,

14 taxa/station) (Figure 9). In decreasing order of mean number of polychaete taxa per sample, Station E3 was followed by Stations D5, D2, D3A, E5, E6, E1, D6, E2, C5A, D1, C3A, C2A, C1A, and C6.

When the polychaetes and other miscellaneous invertebrates (excluding mollusks and crustaceans) are considered together, Station D5 had the highest mean number of individuals (624.0 individuals/sample, 137,552 individuals/m^2), followed in decreasing order by Stations D3A, D2, E3, D6, E6, D1, E5, E1, C5A, E2, C1A, C3A, C6, and C2A. Station E3 had the highest mean number of invertebrate taxa (47.7 taxa/sample, excluding mollusks and crustaceans; 79 taxa/station), followed in decreasing order by Stations D2, D5, D3A, E5, E6, D6, E1, C5A, D1, E2, C3A, C1A, C2A, and C6.

Polychaetes are such a diverse group of invertebrates in tropical ecosystems that analysis of their role in benthic communities warrants some interpretation (Russo et al. 1988; Bailey–Brock et al. 1991; Nelson et al. 1992a, 1992b, 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999, 2000, 2001). Aspects of their biology that are relevant to community analysis are how polychaetes feed and what they eat; how they move around, stabilize, and redistribute sediments; and what is known about their reproduction and life history. Most of the information about the feeding biology and locomotion of polychaetes is at the family or species level. Therefore, trophic and motility analyses were applied to our community studies. We looked for evidence of reproduction in all taxa. We noted whether there were maturing gametes in the coelom of polychaetes and sipunculans, if developing larvae or attached epitokes were present (which indicate that individuals are reproducing), or if specialized setae were present (which indicate swarming and spawning behavior). Evidence of reproduction was found in the families Hesionidae, Spionidae, Nereididae, Serpulidae, Questidae, and Syllidae. The syllids *Grubeosyllis mediodentata*, *Sphaerosyllis* sp. G, *Exogone longicornis*, and *Exogone* sp. E had embryos or juveniles attached to the external body wall. A number of syllids—*Sphaerosyllis riseri*, *Odontosyllis* sp. B, *Pionosyllis heterocirrata*, and *Nereis* sp. B—showed characteristics of a swimming stage. These characteristics include enlarged eyes and elongated capillary setae that are used during a spawning behavior in the water column (Schroeder and Hermans 1975). The serpulid *Salmacina dysteri* showed signs of schizoparity, and a *Capitella capitata* individual had copulatory hooks.

Interstitial polychaetes are included in our analysis. These worms, which occupy the spaces among sand grains, are extremely small and frequently highly specialized. They may lack eyes and head structures and may have appendages modified to anchor themselves around sediment particles. Many are hermaphroditic, and specific segments may be modified for gamete production and transfer. Because these worms were retained on a 0.5-mm screen, they do not fit the strict definition of meiofauna (less than 0.5 mm), even though some were very

close to this size limit. A number of taxa belonging to the families Hesionidae, Pilargidae, Questidae, and Syllidae are interstitial/meiofaunal polychaetes. Of these, *Pionosyllis heterocirrata*, *Ophiodromus angustifrons*, and *Synelmis acuminata* were abundant at many stations (Table 1).

Trophic categories. Trophic categories are based on Fauchald and Jumars (1979) and are summarized in Figures 10 and 11.

1. Detritivores. The most abundant trophic group at the study site was the detritivores (42.5% of all polychaete individuals), followed by the omnivores (26.9%), suspension feeders (18.5%), and carnivores (12.1%). By station, detritivores were highest in abundance at Stations C1A (48.0% of all polychaete individuals), D2 (47.2%), D3A (51.7%), D6 (36.3%), E1 (65.6%), E2 (47.8%), E3 (40.2%), E5 (57.2%), and E6 (71.3%) (Figure 10). Also, they comprised the most taxa-rich group at fourteen stations: C1A (46.2% of all polychaete taxa), C2A (50.0%), C3A (61.1%), C5A(42.9%), D1 (51.9%), D2 (37.8%), D3A (46.5%), D5 (40.9%), D6 (34.4%), E1 (47.1%), E2 (53.6%), E3 (39.4%), E5 (54.8%), and E6 (57.5%) (Figure 11). They were never the least abundant group or the least taxa-rich group at any station. Detritivore abundance was highest at Station D3A (265 individuals) and lowest at Station C6 (7 individuals). Taxa richness was highest at Station E3 (26 taxa) and lowest at Station C6 (5 taxa). *Myriochele oculata* was the dominant detritivore species at Stations D1 (14.5% of all polychaete individuals), D2 (22.9%), D5 (9.4%), and D6 (17.5%) and ranked second (4.1%) to *Dipolydora normalis* (31.4%) at Station D3A. *Prionospio cirrifera* was the dominant detritivore species at Stations C3A (7.7%, tied with *Saccocirrus waianaensis*), C5A (9.7%), and C6 (4.5%, tied with *Pisione remota*) and ranked second at five other stations. The spionid *Prionospio cirrobranchiata* was the dominant species at Station E3 (10.4%). Spionidae sp. D was an abundant species at Stations E1 (19.2%), E5 (8.8%), and E6 (9.2%). *Spio blakei*, another spionid, dominated at Station C1A (16%). *Pisione* sp. A was dominant at Station C2A (13.9%). *Protodorvillea biarticulata* dominated at Station E2 (16.3%).

2. Suspension feeders. Suspension feeders were the most abundant trophic group at Stations D1 (50.2% of all polychaete individuals) and D5 (45.3%) and the least abundant group at Stations C1A (4.0%), C2A (2.8%), C3A (1.5%), C5A (2.2%), C6 (0%), D3A (1.0%), D6 (16.4%), E2 (2.2%), E3 (11.6%), E5 (5.0%), and E6 (7.2%) (Figure 10). Abundance of suspension feeders was highest at Station D5 (274 individuals) and lowest at Station C6 (0 individuals). The highest percentage of polychaete individuals represented by suspension feeders occurred at Station D1 (50.2%) and the lowest at Station C6 (0%). Suspension feeders, which never had the most taxa of any trophic category at any station, accounted for the fewest taxa at fourteen stations: C1A (7.7%), C2A (7.1%), C3A (5.6%), C5A (7.1%), C6 (0%), D2 (17.8%), D3 (11.6%), D5 (15.9%), D6 (15.6%), E1 (8.8%), E2 (7.1%), E3 (12.1%), E5 (4.8%),

and E6 (10.0%) (Figure 11). Taxa richness was highest at Stations D2 and E3 (8 taxa each) and lowest at Station C6 (0 taxa). The highest percentage of polychaete taxa represented by suspension feeders occurred at Station D1 (25.9%) and the lowest at Station C6 (0%). *Aonides* sp. A was the most abundant suspension feeder at Stations C1A (4.0% of all polychaete individuals), C2A (2.8%), C3A (1.5%), C5A (1.1%, tied with *Amphicorina* sp. B), E2 (1.1%, tied with *Euchone* cf. *rosea*), and E6 (3.1%, tied with *Euchone* sp. B). *Euchone* sp. B was the most abundant suspension feeder at Stations D1 (46.7%), D2 (5.5%), D5 (35.7%), E1 (7.3%), E5 (3.1%), and E6 (3.1%) and the most abundant polychaete species at Stations D1 and D5. The serpulid *Salmacina dysteri* was the dominant suspension-feeding species at Station E3 (3.7%).

3. Carnivores. Carnivores did not dominate any station with respect to number of individuals. They were the least abundant trophic group at four stations: D1 (4.4% of all polychaete individuals), D2 (10.8%), D5 (12.4%), and E1 (7.3%) (Figure 10). The highest number of carnivore individuals was collected at Station D5 (75 individuals) and the lowest at Station C3A (5 individuals). The greatest percentage of polychaete individuals represented by carnivores occurred at Station C1A (28.0%) and the lowest at Station D1 (4.4%). Taxa richness was highest at Station E3 (16 taxa) and lowest at Station C3A (2 taxa) (Figure 11). At many stations the most abundant carnivores were hesionids. For example, *Micropodarke* sp. A was dominant at Stations C1A (12.05%, tied with *Ophiodromus angustifrons*), C2A (16.7%), C5A (7.5%), and D1 (1.8%, shared with *Lumbrineris latreilli*). In addition to being tied for dominance at Station C1A, the hesionid *O. angustifrons* was the dominant species at Stations C3A (6.2%), C6 (11.4%), D2 (6.3%), D3A (2.1%), D6 (9.4%), and E3 (6.7%). Another hesionid, *Ophiodromus* sp. B, dominated at Station E2 (9.8%). *Lumbrineris tetraura* dominated at Stations D5 (5.3%), E1 (2.6%), and E5 (5.0%). The lumbrinid *Lumbrineris latreilli*, which shared dominance with *Micropodarke* sp. A at Station D1 (1.8% each), was also dominant at Station E6 (3.6%).

4. Omnivores. Omnivores were the most abundant trophic group at Stations C2A (38.9% of all polychaete individuals), C3A (53.8%), C5A (48.4%), and C6 (65.9%) (Figure 10). Abundance of omnivores was highest at Station D3A (219 individuals) and lowest at Station C1A (5 individuals). The highest percentage of polychaete individuals represented by omnivores occurred at Station C6 (65.9%) and the lowest at Station E6 (8.2%). Omnivores were the least taxa-rich trophic group at Station D1 (7.4% of all polychaete taxa) and the most taxa-rich group at Station C6 (42.9%) (Figure 11). The number of polychaete taxa represented by omnivores ranged from 2 (at both Stations C2A and D1) to 16 (at Station E3). *Pionosyllis heterocirrata* was the dominant omnivore at Stations C1A (12.0%), C2A (30.6%), C3A (46.2%), C5A (17.2%), C6 (52.3%), D2 (12.3%), E2 (13.0%), E3 (9.1%), and E5 (8.8%) and

the most abundant polychaete species at Stations C2A, C3A, C5A, and C6. The pilargid *Synelmis acuminata* was the dominant omnivore at Stations D1 (13.7%), D3A (28.3%), D6 (16.4%), E1 (6.6%), and E6 (3.6%). *Nereis* sp. B was dominant at Station D5 (6.8%).

Motility categories. Motility categories are based on Fauchald and Jumars (1979) and are summarized in Figures 12 and 13.

1. Tubicolous polychaetes. Tubicolous polychaetes were the dominant motility group with respect to abundance at Stations D1 (64.8% of all polychaete individuals) and D5 (55.2%), and second in abundance to motile polychaetes at Stations D2 (42.2%) and D6 (35.7%). They were the least abundant motility group at the remaining eleven stations: C1A (0%), C2A (0%), C3A (1.5%), C5A (1.1%), C6 (0%), D3A (6.6%), E1 (9.3%), E2 (1.1%), E3 (12.5%), E5 (6.3%), and E6 (7.7%) (Figure 12). Abundance of tubicolous worms was highest at Station D5 (334 individuals) and lowest at Stations C1A, C2A, and C6 (all with no individuals). Tubicolous polychaetes were represented by fewer taxa than any other motility group at fourteen stations: C1A (0%), C2A (0%), C3A (5.6%), C5A (3.6%), C6 (0%), D1 (29.6%, tied with discretely motile polychaetes), D3A (16.3%), D5 (22.7%), D6 (21.9%, tied with discretely motile polychaetes), E1 (8.8%), E2 (3.6%), E3 (15.2%), E5 (9.5%), and E6 (15.0%) (Figure 13). They were never dominant at any station with respect to number of taxa. The highest number of tubicolous taxa was collected at Stations D2, D5, and E3 (10 taxa each) and the lowest at Stations C1A, C2A, and C6 (all with no taxa). The highest percentage of polychaete taxa represented by tubicolous polychaetes was at Station D1 (29.6%) and the lowest at Stations C1A, C2A, and C6 (0% each). *Euchone* sp. B was the dominant polychaete at Stations D1 (46.7%) and D5 (35.7%) and the most abundant tubicolous taxon at Stations E1 (7.3%), E5 (3.1%), and E6 (3.1%). *Myriochele oculata* was the dominant polychaete at Stations D2 (22.9%) and D6 (17.5%) and the most abundant tubicolous species at Stations C3A (1.5%) and D3A (4.1%). *Amphicorina* sp. B dominated the tubicolous taxa abundance at Station C5A with 1.1%. The serpulid *Salmacina dysteri* was the dominant tubicolous species at Station E3 (3.7%). *Euchone* cf. *rosea* was dominant at Station E2 (1.1%).

2. Motile polychaetes. The most abundant motility group at the study site was the motile polychaetes (47.0% of all polychaete individuals), followed by tubicolous polychaetes (26.7%) and discretely motile polychaetes (26.4%). By station, motile individuals were highest in abundance at Stations C1A (76.0%), C2A (86.1%), C3A (78.5%), C5A (81.7%), C6 (93.2%), D2 (46.5%), D3A (54.0%), D6 (48.0%), E2 (69.6%), E3 (54.3%), E5 (54.7%), and E6 (51.3%); they were never lowest in abundance (Figure 12). Abundance of motile worms was highest at Station D3A (277 individuals) and lowest at Station C1A (19 individuals). The highest percentage of all polychaetes represented by motile individuals occurred at Station C6 (93.2%) and the lowest at Station D1 (21.6%). Among all three motility categories, the motile

group had the most taxa at all stations. The highest number of motile taxa was collected at Station E3 (39 taxa) and the lowest at Stations C1A, C2A, and C3A (10 taxa each). The highest percentage of polychaete taxa represented by motile worms occurred at Station C6 (85.7%) and the lowest at Station D1 (40.7%) (Figure 13). Four motile species—*Micropodarke* sp. A, *Ophiodromus angustifrons*, *Notomastus tenuis*, and *Pionosyllis heterocirrata*—shared dominance at Station C1A (12.0% each). This year, *P. heterocirrata* replaced *Capitella* sp. A at Station C2A (30.6%) and *Synelmis acuminata* at Station E5 (8.8%) as the most abundant motile species. *P. heterocirrata* remained the most abundant motile polychaete species at Stations C3A (46.2%), C5A (17.2%), C6 (52.3%), D2 (12.3%), and E3 (9.1%), and it again ranked second in abundance at Station D3A (7.0%). *Synelmis acuminata* remained most abundant at Stations D1 (13.7%), D3A (28.3%), D5 (6.4%), and D6 (16.4%); moreover, it replaced the cirratulid *Aphelochaeta marioni* (previously listed as *Tharyx marioni*) as the dominant species at Station E1 (6.6%). *Protodorvillea biarticulata* remained dominant at Station E2 (16.3%), as did *Acrocirrus* sp. A at Station E6 (18.5%). Among the polychaetes, three motile taxa were highest in abundance at seven of fifteen stations: *Pionosyllis heterocirrata* at Stations C2A, C3A, C5A, C6, and E5 (tied with the discretely motile taxon Spionidae sp. D); *Protodorvillea biarticulata* at Station E2; and *Acrocirrus* sp. A at Station E6.

3. Discretely motile polychaetes. Discretely motile polychaetes were the most abundant motility group at Station E1 (53.6% of all polychaete individuals) and the least abundant group at Stations D1 (13.7%), D2 (11.3%), D5 (18.2%), and D6 (16.4%) (Figure 12). Abundance was highest at Station D3A (202 individuals) and lowest at Station C6 (3 individuals). The highest percentage of all polychaetes represented by discretely motile worms occurred at Station E1 (53.6%) and the lowest at Station D2 (11.3%). Discretely motile polychaetes were most abundant on Transect D and least abundant on Transect C. They were not the most taxa-rich motility group at any station. The highest number of discretely motile taxa occurred at Station E3 (17 taxa) and the lowest at Station C6 (2). The highest percentage of polychaete taxa represented by discretely motile worms occurred at Station C3A (38.9%) and the lowest at Station C6 (14.3%) (Figure 13). *Prionospio cirrifera* remained the dominant discretely motile species at Stations C5 (9.7%), C6 (4.5%), D1 (4.4%), and D6 (7.0%); moreover, it replaced *Aonides* sp. A as the dominant species at Stations C2A (5.6%) and C3A (7.7%) and *Nereis* sp. B as the dominant species at Station D2 (6.0%). *Prionospio cirrobranchiata* remained dominant at Station E3 (10.4%) and replaced Spionidae sp. D as the dominant species at Station E2 (9.8%). Spionidae sp. D was again dominant at Station E1 (19.2%); in addition, it became the dominant discretely motile worm at Stations E5 (8.8%) and E6 (9.2%). *Nereis* sp. B dominated at Station D5 (6.8%), *Dipolydora normalis* at Station D3A (31.4%), and *Spio blakei*

at Station C1A (16.0%). Discretely motile worms were the most abundant polychaete taxa at Stations CIA (*Spio blakei*), D3A (*Dipolydora normalis*), E1 (Spionidae sp. D), E3 (*Prionospio cirrobranchiata*), and E5 (Spionidae sp. D, tied with the motile *Pionosyllis heterocirrata*).

Crustaceans

A total of 2,649 crustaceans, representing 50 taxa and accounting for 24.2% of the nonmollusk abundance, were collected (Appendix Tables D.10 through D.18). Basic statistics for the crustacean data, including 95% confidence limits and a Kolmogorov–Smirnov test for normality of distribution, are provided in Appendix Tables B.5 (number of individuals) and B.6 (number of taxa). The abundance of crustacean individuals was found to be normally distributed (Appendix Table B.5). Data sets for crustacean individuals were square root transformed to meet the assumption of homogeneity of variances in ANOVA (Appendix Table B.7). Data for number of crustacean taxa were normally distributed at all stations (Appendix Table B.6) and met the assumption of homogeneity of variances in ANOVA (Appendix Table B.8).

Mean crustacean abundance (no./sample) ranged from 3.7 (816/m^2, at Station C2A) to 204.0 (44,969/m^2, at Station E3) (Figure 14). There were significant differences in mean abundance among stations (ANOVA, square root transformed data, Appendix Table B.7). Mean crustacean abundance was significantly higher at Station D5 than at Station C2A. This result requires explanation since the untransformed mean crustacean abundance was slightly higher at Station E3 (204.0) than at Station D5 (201.7). Most of the crustaceans at Station E3 (88.9%, 544 of 612 individuals) were collected in only one of the three replicates. The square root transformed mean crustacean abundance (the basis of ANOVA to meet the assumption of homogeneity of variance) was higher at Station D5 (13.7) than at Station E3 (11.6). Thus, the only statistically significant difference in crustacean abundance involved Station D5 rather than Station E3.

A total of 50 crustacean taxa (copepods and cumaceans were not identified to the species level), of which 16 taxa were amphipods, were collected. Crustacean taxa were more numerous at most stations on Transect D and Transect E than at most stations on Transect C. Mean number of taxa ranged from 1.3 (at Station C2A) to 13.7 (at Station E3) (Figure 15). There were significant differences in mean number of crustacean taxa among stations (ANOVA, untransformed data, Appendix Table B.8). Student–Newman–Keuls multiple comparisons showed that the number of crustacean taxa was significantly higher (1) at Stations E3, D5, and D3A than at Stations C2A, C1A, C3A, C6, and E2; (2) at Stations E3 and D5 than at Station D1; and (3) at Station E3 than at Station E6.

Five crustacean taxa ranked among the five most abundant nonmollusk taxa at least at one station (Table 1). The tanaid *Leptochelia dubia* was the most abundant nonmollusk in the entire survey (699 individuals, 6.4% of the nonmollusk total, 26.4% of the crustacean total) and ranked among the top five dominants at Stations D2, D3A, D5, D6, E3, and E5. *Leptochelia dubia* was also the most abundant nonmollusk in the 2000 survey (Swartz et al. 2001). The amphipod *Eriopisella sechellensis* was one of the dominant species at Stations C5A and D6, the tanaid *Tanaissus* sp. A at Stations E1 and E3, the amphipod *Konatopus paao* at Station E1, and the decapod *Processa aequimana* at Station C2A. Copepods accounted for 46.5% of the crustacean individuals. A complete list of crustacean abundance for each taxa from each replicate is provided for each station in Appendix D (Tables D.10 through D.18).

Mollusks

A total of 14,566 mollusk specimens representing 251 taxa were collected. Mean abundance of mollusks per sample (no./15 cm^3) ranged from 49.3 (at Station E6) to 718.3 (at Station E5) (Figure 16). Mean number of mollusk taxa per sample (taxa/15 cm^3) ranged from 16.0 (at Station E6) to 59.3 (at Station C3A) (Figure 17). A complete list of mollusk abundance for all taxa is provided for all stations in Appendix E (Tables E.1 through E.9).

Basic statistics for the mollusk data, including 95% confidence limits and a Kolmogorov–Smirnov test for normality of distribution, are provided in Appendix Tables C.1 (number of individuals) and C.2 (number of taxa). The abundance of mollusk individuals was normally distributed at all stations (Appendix Table C.1). Data sets for mollusk individuals were square root transformed to meet the assumption of homogeneity of variances in ANOVA (Appendix Table C.3). Data for number of mollusk taxa were normally distributed at all stations (Appendix Table C.2) and met the assumption of homogeneity of variances in ANOVA (Appendix Table C.4).

There were significant differences in mean mollusk abundance among stations (ANOVA, square root transformed data, Appendix Table C.3). Student–Newman–Keuls multiple comparisons showed that the mean number of mollusk individuals was significantly higher (1) at Stations E5 and E3 than at all other stations except each other; (2) at Station E2 than at Station D6; (3) at Stations E2, C3, C5, D2, D1, and D6 than at Station D3; (4) at Stations E2, C3, C5, D2, D5, C6, D1, and D6 than at Stations E6, C1, C2, and E1; (5) at Station D3 than at Station C1; and (6) at Stations D3, E1, and C2 than at Station E6 (Appendix Table C.3).

Significant differences in mean number of mollusk taxa among stations were indicated by ANOVA (untransformed, Appendix Table C.4). There were significantly more mollusk taxa (1) at Stations C3A and E3 than at Stations D6 and C5A; (2) at Stations C3A, E3, C6, D5, and E5 than at Stations E6, E1, C1A, C2A, D2, D3A, D1, and E2; (3) at Stations C5A and D6 than at

Stations E6, E1, and C1A; and (4) at Station E2 than at Stations E6 and E1 (Student–Newman–Keuls tests, Appendix Table C.4).

H' diversity of mollusks ranged from 1.76 (at Station E1) to 3.27 (at Station C3A) (Figure 18). Evenness ranged from 0.49 (at Station E5) to 0.82 (at Station D3A). Diversity and evenness were generally higher and less variable on Transect C and Transect D than on Transect E (Figure 18). The lower diversity and evenness on Transect E are due to the presence of strong numerically dominant species like *Diala scopulorum* at Station E5 or low taxa richness at Stations E1 and E6 (Table 3). The low diversity and evenness values obtained for some Transect E stations in 1999, 2000, and 2002 are lower than the minimum values obtained for Transect B stations in surveys from 1996 through 1998 (Nelson et al. 1997; Swartz et al. 1998, 1999, 2000, 2001).

Sixteen mollusk taxa ranked among the five most abundant taxa at least at one of the fifteen stations (Table 3). Although most of these taxa were widely distributed, only three (*Cerithidium perparvulum*, *Pusillina marmorata*, and *Diala semistriata*) were a top-five dominant at least at one station on each of the three transects. One of these three, *C. perparvulum* was a top-five dominant at all fifteen stations. *Balcis* spp. was abundant at all stations on Transects D and E except Station E3. Similarly, *Diala scopulorum* was abundant at all stations on Transects D and E except Station D2. Five taxa were more abundant on Transect C than on the other transects: *Parashiela beetsi*, *Lophocochlias minutissimus*, *Tricolia variabilis*, *Triphora* spp., and *Orbitestella regina*. *Finella pupoides*, *Acteocina* sp., and *Ervilia bisculpta* were substantially more abundant on Transect D than on the other transects. There were no unique dominants on Transect E; however, *Diala scopulorum*, which was very abundant, was the most dominant species at all stations on that transect. *D. scopulorum* was less abundant, but qualified as a top-five dominant, at three stations on Transect D. The five most abundant taxa were *D. scopulorum*, *Cerithidium perparvulum*, *Pusillina marmorata*, *Finella pupoides*, and *Scaliola* spp. Together, these five taxa accounted for 52.3% of the total mollusk abundance. *Diala semistriata* and *Balcis* spp. were the sixth and seventh most abundant mollusk taxa in 2002. The same seven taxa were the numerically dominant mollusks collected on Transects C, D, and E in 1999 and 2000 and on Transect B from 1994 through 1998 (Nelson et al. 1995, 1996, 1997; Swartz et al. 1998, 1999, 2000, 2001).

The most abundant mollusks were detritivores except for the parasite *Balcis*, which feeds on holothurians and sea cucumbers. The presence of so many *Balcis* shells on Transects D and E may be interpreted as an indication of numerous sea cucumbers and/or sea urchins in the area.

Results of the cluster analysis indicating the relative similarity of stations based on the 105 most abundant mollusk taxa are shown by a dendrogram (Figure 19). The analysis

indicated a relatively low similarity among all combined stations (45.7%). The low overall similarity reflects the new survey design initiated in 1999, i.e., sampling of stations along three different depth contours represented by Transects C, D, and E. There is a correspondence between station clusters and transects in 2002, but it is not as strong as it was in 2000. Stations D1, D2, D5, and D6 linked together at a similarity of 61.7%. Two additional clusters were represented by Stations C3A, C5A, and C6 (69.4% similarity) and by Stations E3 and E5 (65.6% similarity). A mixed transect cluster included beyond-diffuser station C1 and near-diffuser stations C2A and D3A (61.6% similarity). Stations E1 and E6 were the last two stations added to the dendrogram (58.8% and 45.7% similarity, respectively), indicating that their faunal composition was somewhat different from all other stations. The molluscan fauna at Stations E1 and E6 was relatively diminished, with low numbers of taxa and individuals. Separation of stations along Transect E, a pattern also seen in 1999 and 2000 (Swartz et al. 2000, 2001), is probably related to natural faunal variations. There was no well-defined, between-transect grouping of stations that might reflect a common influence of the outfall. The cluster pattern in 2002 is associated primarily with the direct and indirect influences of water depth on the mollusks.

There were no significant differences in the number of mollusk individuals or taxa among Transects C, D, and E (Table 2). There were no significant differences in the abundance of mollusks ($t = 1.46$, $p = 0.153$) or the number of mollusk taxa ($t = 0.787$, $p = 0.435$) between beyond-diffuser stations and near-diffuser stations.

DISCUSSION

The renewal of a modified National Pollutant Discharge Elimination System permit for the Sand Island WWTP specified that a new monitoring program be established. Hence, completely new sampling stations were introduced for the Sand Island Ocean Outfall survey in 1999. In earlier years, seven stations located along the approximate diffuser isobath (referred to as Transect B) were sampled. At each station six replicate samples were taken, for a total of 42 samples. Four of the previous sampling stations were located in or at the boundary of the zone of mixing (ZOM), and three stations were located beyond the influence of the ZOM. In 1999, 2000, and 2002, fifteen stations located along three different isobaths (referred to as Transects C, D, and E) were sampled. Five stations each were positioned on the transects. Three replicate samples were taken at each station, for a total of 45 samples. Two of the sets of new beyond-diffuser stations, the "5" series and the "6" series, are respectively located approximately 4.7 and 6.2 km east of the diffuser center. They are much farther east of the ZOM than the previous

eastern beyond-diffuser station (B6). The "5" series is located off Ala Moana Beach Park, while the "6" series is located off Waikīkī Beach. Another difference is the location of Transect C stations at considerably shallower depths (approximately 20 m) than previous stations in this ongoing study. On tropical reef slopes, the benthic community is influenced by depth, primarily through water motion and sediment characteristics. As well as being much farther east of the previous study area, the new eastern beyond-diffuser stations also differed in being located on a southwesterly oriented deep reef slope. The deep reef slope across the previous study area was generally oriented to the south. Slope orientation may influence benthic communities through differences in current regimes and susceptibility to large ocean swells. The increase in number of sampling stations and the extension of the sampling into different habitats would be expected to increase the range of benthic structural parameters, e.g., taxa composition, abundance, taxa richness, and diversity. The reduction in the number of replicates per station would be expected to decrease taxa richness and increase the variance of structural parameters at individual stations.

Cluster analysis using the quantitative Bray–Curtis similarity index suggested that nonmollusk abundance and taxa composition varied substantially among the fifteen stations. The final cluster of all stations was formed at a relatively low similarity value of 51.1% (Figure 7). The cluster pattern showed two primary station groups that, with a few exceptions, reflected high faunal similarity within specific transects. The first station group included four of the five stations on Transect C (Stations C2A, C3A, C5A, and C6). Station C1A was the last station added to the dendrogram. The benthos at Station C1A was poorly defined; e.g., no taxon identified to the species level was represented by more than four individuals. Station C1A was distinctly different from other Transect C stations in the relatively low abundance of *Pionosyllis heterocirrata*, a top-five dominant at all of the other Transect C stations (Table 1). The second group included stations from Transects D and E that usually combined in subgroups according to transect. Neither of the primary clusters was composed exclusively of beyond-diffuser stations or near-diffuser stations, a pattern that would indicate the importance of proximity to the outfall. Beyond-diffuser stations E1, E5, and E6 combined to form a station subgroup, but near-diffuser station E3 was most closely related to beyond-diffuser stations D5 and D6. Station E2, the second to last station added to the dendrogram, had the lowest abundance and taxa richness of all stations on Transects D and E (Figures 4 and 5). Three of the top-five dominants at Station E2 were rare or absent at the other Transect D and E stations (Table 1). The association of the clusters with specific transects indicates that the taxa composition and abundance of the macrobenthos in the study area were determined primarily by factors related to water depth rather than to outfall effects. Thus, there was no clear segregation of stations near the diffuser from those beyond the diffuser.

For comparative purposes, a recalculation was made of the Swartz et al. (1986) cluster analysis of macrobenthic samples collected in 1980 from the Palos Verdes Shelf, California, near the Los Angeles County sewage outfalls along the 60-m depth contour, using the same similarity index and sorting strategy used in the 2002 Sand Island cluster analysis. In contrast to the Sand Island nonmollusk overall faunal similarity index value of 51.1%, the similarity index value of the macrobenthos at the Palos Verdes stations was just 26.8%. Clearly, the higher faunal similarity observed at the Sand Island stations does not indicate substantial biological perturbations, as does the lower faunal similarity at the Palos Verdes stations.

Nonmollusk faunal similarity on Transect B from 1996 through 1998 (63.7% to 66.8%) (Nelson et al. 1997; Swartz et al. 1998, 1999) exceeded the range recorded for Transects C, D, and E in 2002 (51.4% to 63.1%). The higher faunal similarity on Transect B is probably related to the fact that there were more stations (seven) positioned along a shorter transect. Faunal similarity generally increases with spatial proximity of stations along depth contours (Swartz et al. 2000).

Molluscan faunal similarity in 2002 was similar to that of the nonmollusks. Clusters formed primarily within transects, reflecting the influence of water depth. Stations D1, D2, D5, and D6 clustered together, as did Stations C3A, C5A, and C6. Stations E3 and E5 linked together, but in general the Transect E stations were more fragmented than stations on the other transects. Stations E1 and E6 were the last two stations added to the dendrogram. A diminished molluscan fauna was evident at beyond-diffuser stations E1 and E6 in 2000 and 2002. There was no well-defined, between-transect grouping of stations that might reflect a common influence of the outfall discharge.

The substantial differences among stations in grain-size distribution may have influenced the structure of the macrobenthic community. These differences are associated primarily with water depth rather than with proximity to the outfall. The sediments on Transect C had a significantly higher mean percentage of coarse sand and medium sediment and a lower mean percentage of silt and clay than the sediments on Transects D and E. The abundance and taxa richness of the nonmollusks and crustaceans were significantly less on Transect C than on Transect D or E. However, grain-size characteristics were similar for most stations on Transects D and E and, thus, differences in grain size cannot explain the significantly higher nonmollusk and crustacean abundances on Transect D compared to Transect E. Faunal differences among stations were sometimes associated with differences in grain-size characteristics on Transect B. Stations B1 and B2 had a high proportion of fine-grained sediments in 1997 and together formed a well-defined faunal cluster in the similarity dendrogram (Swartz et al. 1998). However, the relationship between grain size and community structure was not always evident on

Transect B (Swartz et al. 1999). These comparisons indicate that neither grain size nor any other single environmental factor can consistently control faunal abundance and richness.

All ORP measurements were positive, indicating the presence of aerobic surficial sediments throughout the study area. Mean ORP was significantly higher at stations on Transects C and D than at stations on Transect E, but mean ORP on each transect exceeded 110 mV, which is well above values that would be associated with reducing conditions. Mean ORP values were significantly higher at near-diffuser stations than at beyond-diffuser stations, indicating that the effluent is not promoting anaerobic conditions near the outfall. There were no significant differences in sediment TKN among transects or between beyond-diffuser stations and near-diffuser stations. The range of values for nitrogen observed (133 to 336 mg/kg) is within that for low organic content marine sediments and does not indicate a buildup of organic material near the ZOM. Sediments (e.g., marsh) with high organic content (TOC of 4% to 6%) (Bowden 1984) would be an order of magnitude greater in nitrogen content than those observed.

Sediment TOC values for all samples ranged from 0.23% to 0.58%. Maximum TOC values were higher in 1999 (1.34%) and 2000 (2.08%) than in 2002. There were no significant differences in mean TOC among transects or between beyond-diffuser stations and near-diffuser stations in 2002. Thus, the effluent from the Sand Island discharge has not caused sediment organic enrichment near the outfall.

Mean nonmollusk abundance is compared among sampling dates for data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 (Figure 20). ANOVA results for log-transformed data showed significant differences among sampling dates ($p = 0.0001$). Student–Newman–Keuls tests comparing 1999, 2000, and 2002 means among themselves and with those of earlier years showed that mean nonmollusk abundance was (1) significantly greater at Transect B in 1998 and at Transect D in 1999 and 2002 than at Transect B in 1986 and 1987, at Transect C in 1999, 2000, and 2002 and at Transect E in 1999 and 2000; (2) significantly greater at Transect B in 1995 and 1996 than at Transect C in 1999, 2000, and 2002 and at Transect E in 1999 and 2000; (3) significantly greater at Transect B in 1990, 1993, and 1997 and at Transect D in 2000 than at Transect C in 1999, 2000, and 2002 and at Transect E in 1999; (4) significantly greater at Transect B in 1991, 1992, and 1994 and at Transect E in 2002 than at Transect C in 1999 and 2002; and (5) significantly greater at Transect B in 1986 and 1987 than at Transect C in 2002. The changes in nonmollusk abundance at Transect D from 1999 to 2000 to 2002 are not statistically significant and are within the temporal range of variability recorded at Transect B. Transects B and D lie between the shallower Transect C and the deeper Transect E. The differences among Transects B, C, D, and E in these temporal comparisons of mean nonmollusk abundance are

probably associated with water depth and do not reflect a long-term temporal trend related to the outfall discharge.

Mean nonmollusk abundance is compared among sampling stations for data collected in 1999, 2000, and 2002 (Figure 21). ANOVA results for square root transformed data showed significant differences among sampling stations ($p < 0.0001$). Student–Newman–Keuls tests showed that mean nonmollusk abundance was significantly greater (1) at Stations D2 and D5 than at Stations C2A, C6, C1A, E2, C3A, E1, E5, and E6; (2) at Station D3A than at Stations C2A, C6, C1A, E2, C3A, E1, and E5; and (3) at Station D6 than at Station C2A. Nonmollusk abundance was quantitatively greater at all Transect D stations than at any station on Transect C or Transect E (except Station E3). These differences are probably associated with water depth and do not reflect a spatial pattern related to the outfall discharge.

Mean number of nonmollusk taxa is compared among sampling dates for data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000 and 2002 (Figure 22). The temporal pattern of changes in mean nonmollusk taxa and its interpretation are similar to that for mean nonmollusk abundance discussed above. ANOVA results for untransformed data showed significant differences among sampling dates ($p < 0.0001$). Student–Newman–Keuls tests comparing 1999, 2000, and 2002 means among themselves and with those of earlier years showed that the mean number of nonmollusk taxa was (1) significantly greater at Transect D in 1999 and 2002 and at Transect B in 1995 and 1998 than at Transect C in 1999, 2000, and 2002 and at Transect B in 1986; (2) significantly greater at Transect B in 1993, 1994, and 1996 and at Transect E in 2002 than at Transect C in 1999, 2000, and 2002; and (3) significantly greater at Transect B in 1990 and at Transect D in 2000 than at Transect C in 1999 and 2002. The changes in the number of nonmollusk taxa at Transect D from 1999 to 2000 to 2002 are not statistically significant and are within the temporal range of variability recorded at Transect B. The differences among Transects B, C, D, and E in these temporal comparisons of mean number of nonmollusk taxa are probably associated with water depth and do not reflect a long-term temporal trend related to the outfall discharge.

Mean number of nonmollusk taxa is compared among sampling stations for data collected in 1999, 2000, and 2002 (Figure 23). ANOVA results for untransformed data showed significant differences among sampling stations ($p < 0.0001$). Student–Newman–Keuls tests showed that mean number of nonmollusk taxa was significantly greater (1) at Station D2 than at Stations C2A, C6, C1A, C3A, E2, D1, and C5A; (2) at Stations E3, D5, and D3A than at Stations C2A, C6, C1A, C3A, E2, and D1; (3) at Station D6 than at Stations C2A, C6, C1A, and C3A; (4) at Station E5 than at Stations C2A, C6, and C1A; and (5) at Stations E1 and E6 than at Station C2A. The higher numbers of nonmollusk taxa at stations on Transects D and E

compared to that at most stations on Transect C are probably associated with water depth and do not reflect a spatial pattern related to the outfall discharge.

Nonmollusks

Twenty-four taxa were found for the first time at the Sand Island Ocean Outfall site: the polychaetes *Aricidea (Aedicira)* sp. A, *Brania* sp. B, *Caulleriella* sp. A, *Caulleriella* sp. B, *Cirratulus africanus*, *Eumida* sp. B, Hesionidae sp. G, Hesionidae sp. H, *Lygdamis nesiotes*, *Lysidice* sp. A, *Micropodarke* sp. B, *Monticellina* sp. A, *Monticellina* sp. B, *Palmyra* sp. A, *Paramphinome* sp. A, *Progoniada* sp. C, *Sabella* sp. A, *Syllides bansei*, and *Travisia* sp. A; the sipunculid Sipuncula sp.; the podocope ostracod *Bythoceratina* cf. *monstruosa*; the isopod *Janira algicola*; the caprellid amphipod tentatively identified as *Caprella inequilibra*; and the crab *Portunus macrophthalamus*. Twelve of the newly found taxa—the polychaetes *Aricidea (Aedicira)* sp. A, *Brania* sp. B, *Caulleriella* sp. B, *Eumida* sp. B, Hesionidae sp. G, *Lysidice* sp. A, *Micropodarke* sp. B, *Progoniada* sp. C, *Sabella* sp. A, and *Travisia* sp. A; the sipunculid Sipuncula sp.; and the ostracod *Bythoceratina* cf. *monstruosa*—had not been found before at any of the four outfall sites sampled (Sand Island, Barbers Point, Wai'anae, and Mōkapu).

Polychaetes

The polychaete community, comprised of the most abundant and speciose soft-bodied invertebrates at this site, is comparable to that reported annually from 1991 through 2000 (Nelson et al. 1992a, 1992b, 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999, 2000, 2001). Polychaetes are such a diverse group of invertebrates in tropical ecosystems that analysis of their role in benthic communities is essential to understand ecological conditions at this ocean outfall site. How polychaetes feed and what they eat, how they move around, how they stabilize and redistribute sediments, and what is known about their reproduction and life history are aspects of their biology that are relevant to this community analysis.

The polychaete communities were most abundant and diverse at Stations D5 and E3, respectively. Mean polychaete abundance ranged from 8.3 individuals per sample (1,830/m^2, at Station C1A) to 201.7 individuals per sample (44,462/m^2, at Station D5). There were significant differences in abundance of polychaetes among stations (one-way ANOVA, square root transformed data, $F = 10.256$, $p < 0.0001$). Mean polychaete abundance was significantly greater (1) at Stations D5 and D3A than at Stations C1A, C2A, C6, C3A, C5A, E2, E1, E5, D6, E6, and D1; (2) at Station D2 than at Stations C1A, C2A, C6, C3A, C5A, and E2; (3) at Station E3 than at Stations C1A, C2A, C6, and C3A; and (4) at Station D1 than at Station C1A. There were significant differences in polychaete abundance among transects (one-way ANOVA, log transformed data, $F = 38.457$, $p < 0.0001$). Mean polychaete abundance was significantly greater on Transect D (127.6 individuals/sample) than on Transect C (17.5 individuals/sample)

or Transect E (61.7 individuals/sample). There was no significant difference in mean polychaete abundance between beyond-diffuser stations (61.9 individuals/sample) and near-diffuser stations (79.6 individuals/sample) ($t = 0.879$, $p = 0.384$). Differences in polychaete abundance are associated primarily with water depth rather than proximity to the outfall.

The mean number of polychaete taxa per sample ranged from 6.0 (at Station C6) to 38.7 (at Station E3). There were significant differences in the number of polychaete taxa among stations (one-way ANOVA, untransformed data, $F = 11.522$, $p < 0.0001$). Mean number of polychaete taxa was significantly greater (1) at Station E3 than at all other stations; (2) at Stations D5 and D2 than at Stations C6, C1A, C2A, C3A, D1, C5A, and E2; (3) at Stations D3A, E5, and E6 than at Stations C6, C1A, C2A, and C3A; and (4) at Stations E1 and D6 than at Stations C6, C1A, and C2A. There were significant differences in the number of polychaete taxa among transects (one-way ANOVA, square root transformed data, $F = 27.236$, $p < 0.0001$). Mean number of polychaete taxa was significantly greater on Transects E (24.0 taxa/sample) and D (22.9 taxa/sample) than on Transect C (8.4 taxa/sample). There was no significant difference in the mean number of polychaete taxa between beyond-diffuser stations (17.3 taxa/sample) and near-diffuser stations (20.2 taxa/sample) ($t = 0.953$, $p = 0.346$). Differences in polychaete taxa richness are associated primarily with water depth rather than proximity to the outfall.

Abundance of polychaetes in terms of trophic and motility categories also differed among transects and among stations. Tubicolous polychaetes were more abundant at Transect D than at Transect C or Transect E. Suspension feeders were also more abundant at Transect D. Discretely motile detritivores were more abundant at Transects D and E than at Transect C. Transect D was more similar to Transect E than to Transect C in terms of the relative abundance and taxa richness of trophic and motility categories. Each station on Transect C was dominated by motile polychaetes. Suspension feeders and tubicolous polychaetes were most abundant at Station D5, where all trophic and motility categories were well represented. Motile omnivores and discretely motile detritivores shared dominance at Station D3A. All trophic and motility categories were moderately abundant at Station D6. Dominance at Transect E was shared between motile and discretely motile detritivores.

The abundance of the sabellid *Euchone* sp. B declined by an order of magnitude from 1999 (1,443 individuals, Swartz et al. 2000) to 2000 (143 individuals, Swartz et al. 2001), but it increased this year (376 individuals, Table 1). In 2002, *Euchone* sp. B was the most abundant nonmollusk at Stations D1 and D5; however, it did not qualify as a top-five dominant at any other station. In 2000, *Euchone* sp. B ranked among the five most abundant nonmollusk taxa only at Station D1. It was the most abundant polychaete found in 1999, as it had been on Transect B from 1994 to 1998 (Nelson et al. 1995, 1996, 1997; Swartz et al. 1998, 1999).

However, *Euchone* sp. B has a very patchy distribution; it is not characteristically found in the entire survey area (Table 1). In 1999, this taxon was very abundant only at Stations D1, D2, and D5. Data from previous surveys show that *Euchone* sp. B was very abundant only at three of the seven stations on Transect B. This sabellid forms sand-grain tubes that apparently develop into dense populations (tube lawns) at these stations. A much more ubiquitous species that was present and often one of the top-five dominants at most stations on Transects C, D, and E in 1999, 2000, and 2002 and on Transect B in recent years is the syllid *Pionosyllis heterocirrata.*

Ophryotrocha adherens (previously called *Ophryotrocha* sp. A) is regarded as an indicator species (Bailey–Brock 1996). It was abundant at all near-diffuser stations on Transect B from 1993 through 1998 (Nelson et al. 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999) but was absent at beyond-diffuser stations B1, B2, and B6 in 1997 and 1998. Mean abundance of *O. adherens* at the near-diffuser stations in 1998 was 61.5 individuals per sample (13,566/m^2). In 1999 *O. adherens*, which was not collected at eleven of the fifteen stations, was common (11.0 individuals/sample, 2,425/m^2) only at Station E3 (Swartz et al. 2000). This species did not rank among the five most abundant nonmollusk taxa at any station in 2000 (Swartz et al. 2001). That year it was collected at three stations (D2, E2, and E5), and its maximum mean abundance at Station D2 was 3.7 individuals per sample (816/m^2). In 2002, although it was the fifth most-abundant species at Station D2 (8.7 individuals/sample, 1,918/m^2; Table 1), only 34 specimens of *O. adherens* were collected in the entire survey.

There have been major temporal changes in the abundance of the omnivorous nereidid *Neanthes arenaceodentata.* This species, which was dominant at Stations B3 and Z on Transect B prior to 1993, was virtually absent from 1993 to 1995 but was dominant again in 1996, 1997, and 1998, especially at Station Z. Only two specimens of *N. arenaceodentata*, one each at Stations E2 and E3, were collected in 1999 (Swartz et al. 2000). No specimens were collected at any of the Sand Island stations in 2000 (Swartz et al. 2001). Only one specimen of *N. arenaceodentata* was collected in 2002; it was found at Station E1.

There were 47.1% fewer polychaete individuals collected in 2000 (2,262 individuals) than in 1999 (4,278 individuals). Polychaete abundance increased by 37.1% from 2000 to 2002 (3,102 individuals). Despite these fluctuations there was a consistency among years along transects, i.e., the samples from similar depths were similar from year to year, and the distinctiveness of each transect was similar in 1999, 2000, and 2002. Polychaete taxa composition varied more between years at Transect C (the shallowest transect) than at Transect D or Transect E.

A review of specimens led to several name changes this year. *Capitella* sp. A, Capitellidae sp. B, and Capitellidae sp. C were all combined as Capitellidae sp.; and *Microphthalmus sczelkowii* and *Microphthalmus aberrans* were combined as *Microphthalmus* sp. In addition,

Phyllodocidae sp. D was further identified as *Phyllodoce* sp. F; *Ophryotrocha* sp. A as *Ophryotrocha adherens* (Paavo et al. 2000); *Saccocirrus* sp. A and *Saccocirrus* sp. B as *Saccocirrus oahuensis* and *Saccocirrus waianaensis*, respectively (Bailey–Brock and Dreyer, in press); *Eunice* sp. A as *Eunice havaica* (K. Fauchald pers. obs.); and *Prionospio* sp. A as *Prionospio steenstrupi*. Other changes include *Pisione africana* as *Pisione* sp. A; and *Sphaerodoropsis* sp. A as *Sphaerodoropsis* sp. C. *Parapionosyllis* sp. A and *Scolelepis* sp. A were found to be invalid taxa and thus were removed from the list of taxa.

The taxonomic literature was used to arrive at the following name changes: *Brania mediodentata* to *Grubeosyllis mediodentata* (Diaz–Castaneda and San Martin 2001); *Langerhansia* sp. A to *Typosyllis* sp. G (Licher 1999); *Polydora normalis*, *P. pilikia*, and *Polydora* sp. B to *Dipolydora normalis*, *D. pilikia*, and *Dipolydora* sp. B, respectively (Blake 1996a); *Sabellastarte sanctijosephi* to *Sabellastarte spectabilis* (P. Knight–Jones pers. comm.); and *Tharyx marioni* to *Aphelochaeta marioni* (Blake 1996b). In addition, *Podarke* was found to be a junior synonym of *Ophiodromus* (Pleijel 1998) and *Oriopsis* a junior synonym of *Amphicorina* (Rouse 1994). Also, *Arabella* was referred to the family Oenonidae (Pleijel 2001).

A change in the name of the sipunculan *Apionsoma misakiana* (e.g., Cutler and Cutler 1980, Popkov 1993) to *A. misakianum* recently took place in the literature (Staton and Rice 1999, Pechenik and Rice 2001). We are following this revised declension. There are several species of Sipuncula that are not easily identifiable as separate taxa. To avoid any misidentification, they will be referred to as Sipuncula spp. until differences among taxa are clear.

Crustaceans

The crustacean community across the expanded study area can still be characterized as relatively abundant and moderately diverse, dominated by small forms (copepods, ostracods, tanaids, isopods, and amphipods) with scattered, occasionally abundant collections of small decapods. Collections in 2002 yielded 50 discrete crustacean taxa, more than the 41 taxa collected in both 1999 and 2000. An average of about 39 crustacean taxa were collected annually at Transect B from 1990 through 1998. In 2002, four taxa were newly collected and one found in 1998 (*Pasiphaea hawaiiensis*) was included within *Leptochela hawaiiensis*, bringing the total number of discretely identified/reported taxa in twelve years to 98. Copepods are enumerated as a single taxon, although several different species are present. Cumaceans also have not been identified to the species level, even though several species may be present.

A rather comprehensive picture of the crustacean community in the study area has been developed for specimens smaller than 1 cm over the survey years, despite the rather small areal

coverage (45.4 cm^2) of the sediment samples. The four new taxa found in 2002 do not indicate any significant change in the crustacean community. Although the ostracod had not been previously collected alive off O'ahu, the isopod, caprellid, and crab had previously been collected on O'ahu reef slopes in other studies. Their presence in this expanded study area is not unexpected. Larger (>2 cm) shrimps and crabs, while certainly present in the sampling area, have little chance of being collected by the van Veen grab. In general, the crustacean fauna in the Sand Island study area is somewhat less diverse than that in comparable study areas near the Honouliuli and Wai'anae WWTP outfalls.

Mean crustacean abundance is compared among sampling dates for data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 (Figure 24). Crustacean abundance was much higher at Transect D in 1999, 2000, and 2002 and at Transect E in 2002 than at Transect B in all of the eleven survey years between 1986 and 1998. In contrast, crustacean abundance was lower at Transect C in 1999, 2000, and 2002, and Transect E in 1999 and 2000 than at Transect B in most of the eleven survey years between 1986 and 1998. All data transformations failed to meet the assumption of homogeneity of variance. Kruskal–Wallis test results for untransformed data showed significant differences among sampling dates ($p < 0.05$). Multiple comparisons of 1999, 2000, and 2002 means among themselves and with those of earlier years showed that mean crustacean abundance was significantly greater (1) at Transect D in 1999 and 2002 than at Transect B in 1986, Transect C in 2002, and Transect E in 1999 and (2) at Transect D in 2000 and Transect E in 2002 than at Transect B in 1986. Transects B and D lie between the shallower Transect C and the deeper Transect E. The differences in these temporal comparisons among Transects B, C, D, and E are probably associated with water depth and do not reflect a long-term trend related to a negative effect of the diffuser effluent on crustacean abundance.

Mean crustacean abundance is compared among sampling stations for data collected in 1999, 2000, and 2002 (Figure 25). Crustacean abundance was generally higher on Transect D stations than on Transect C and Transect E stations (except Station E3). ANOVA results for untransformed data showed significant differences among sampling stations ($p = 0.0004$). Student–Newman–Keuls tests showed that mean crustacean abundance was significantly greater (1) at Station D5 than at Stations C2A, E2, C6, C1A, C3A, E5, E6, and E1 and (2) at Station D3A than at Stations C2A, E2, and C6. The greater abundance on Transect D is probably associated with water depth and does not reflect a spatial pattern related to the outfall discharge.

Taxonomic richness expressed as number of taxa may be a better measure of the condition of the crustacean community since abundance (number of individuals) can be strongly influenced by brooded juveniles from such groups as isopods, amphipods, and tanaids.

Abundance data for other taxa (e.g., mollusks, most polychaetes, and many decapods) indicate a settlement from the plankton of a larval form which has found the site suitable. Even though high crustacean abundance data (particularly if juveniles are being produced) clearly indicate that the site is suitable, low abundance data are not necessarily indicative of unsuitability.

Mean number of crustacean taxa is compared among sampling dates for data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 (Figure 26). The temporal pattern of changes in crustacean taxa and its interpretation are similar to the pattern and interpretation for crustacean abundance discussed above. Mean number of crustacean taxa was higher at Transect D in 1999, 2000, and 2002 than at Transect B in all of the eleven survey years between 1986 and 1998. In contrast, mean crustacean taxa richness was lower at Transect C in 1999, 2000, and 2002 and at Transect E in 1999 than at Transect B in all but one (1986) of the eleven survey years between 1986 and 1998. Mean crustacean taxa richness at Transect E in 2000 was near the historic average at Transect B. In 2002, mean crustacean taxa richness at Transect E exceeded that of all Transect B annual surveys except the one in 1998. ANOVA results for untransformed data showed significant differences among sampling dates ($p < 0.0001$). Student–Newman–Keuls tests comparing 1999, 2000, and 2002 means among themselves and with those of earlier years showed that mean number of crustacean taxa was significantly greater (1) at Transect D in 1999 than at Transect B in 1986, 1987, 1991, and 1992, Transect C in 1999, 2000, and 2002, and Transect E in 1999; (2) at Transect D in 2002 than at Transect B in 1986 and Transect C in 2000 and 2002; (3) at Transect D in 2000 than at Transect B in 1986; and (4) at Transect E in 2002 than at Transect B in 1986. The increases in mean number of crustacean taxa per sample from 3.7 in 1999 to 5.5 in 2000 to 7.1 in 2002 are not statistically significant and are within the range of temporal variability at Transect B from 1986 to 1998. Transects B and D lie between the shallower Transect C and the deeper Transect E. The differences in these temporal comparisons among Transects B, C, D, and E are probably associated with water depth and do not reflect a long-term trend related to a negative effect of the diffuser effluent on crustacean taxa richness.

Mean number of crustacean taxa is compared among sampling stations for data collected in 1999, 2000, and 2002 (Figure 27). ANOVA results for untransformed data showed significant differences among sampling stations ($p < 0.0001$). Student–Newman–Keuls tests showed that mean number of crustacean taxa was significantly greater (1) at Station D5 than at Stations C2A, C1A, C6, E2, C3A, E6, D1, E5, E1, and C5A; (2) at Stations D3A, D6, and D2 than at Stations C2A, C1A, C6, E2, and C3A; and (3) at Station E3 than at Stations C2A, C1A, and C6. The greater crustacean richness on Transect D is probably associated with water depth and does not reflect a spatial pattern related to the outfall discharge.

The influence of environmental factors associated with water depth on crustacean abundance and taxa richness is evident in the differences among transects in 2002. Crustacean abundance and taxa richness were higher at most stations on Transect D than at most stations on Transect C or Transect E. These differences were not usually statistically significant because of the low number of replicate samples (three) per station and the inherent variability in the diminished crustacean assemblages at most stations on Transects C and E. Comparisons of pooled samples on each transect showed that both crustacean abundance and taxa richness were significantly greater at Transect D than at Transects C and E. They also showed that crustacean taxa richness was significantly greater at Transect E than at Transect C.

Shallower depth, greater wave-induced sediment perturbations, and coarser sediment grain size may have contributed to the diminished crustacean fauna on Transect C, but these factors do not explain the reduced abundance and diversity of crustaceans on Transect E. Comparison of mean crustacean abundance per sample between beyond-diffuser stations (54.7 individuals) and near-diffuser stations (65.1 individuals) revealed no significant difference ($t = 0.327$, $p = 0.745$). Similarly, there was no significant difference in mean number of crustacean taxa per sample between beyond-diffuser stations (6.2 taxa) and near-diffuser stations (6.7 taxa) ($t = 0.318$, $p = 0.752$). Proximity to the outfall does not appear to be related to the reduced crustacean fauna on Transects C and E.

Amphipod crustaceans are considered good biological indicators for the absence of effects of wastewaters discharged from ocean outfalls. Amphipods were collected at all stations in 2002 except at beyond-diffuser station C1A, where amphipods were also absent in 1999 and 2000. Amphipods were relatively rare (0 to 15 individuals/station, 0 to 3 taxa/station) at all Transect C stations. Amphipods were relatively abundant (34 to 96 individuals/station) and diverse (5 to 8 taxa/station) at beyond-diffuser stations D5 and D6 and at near-diffuser stations D2, D3A, and E3. The presence of phoxocephalid amphipods at near-diffuser stations has been used as an indicator of the absence of significant sediment contamination (Swartz et al. 1998, 1999). In 1997 and 1998, collections on Transect B included individuals of *Paraphoxus* sp. A. Phoxocephalids were rarely found throughout the study area in 1999 and 2000, when a single specimen of *Paraphoxus* sp. A was collected at beyond-diffuser station E1 in each year. In 2002 a total of three *Paraphoxus* sp. A specimens were collected at near-diffuser stations D2 and E3 and two *Paraphoxus* sp. B specimens at near-diffuser station C3A.

In summary, there is no evidence in 2002 that crustaceans, including stress-sensitive amphipods, are negatively affected by proximity to the Sand Island Ocean Outfall. The rarity of crustaceans on Transect C is probably related to factors associated with shallow water depth. There were no significant differences in crustacean abundance or taxa richness between near-diffuser and beyond-diffuser stations. Mean abundance and taxa richness were highest at

beyond-diffuser stations D5 and D6 and at near-diffuser stations D3A and E3 (81.0 to 204.0 individuals/sample; 9.3 to 13.7 taxa/sample). Stress-sensitive phoxocephalid amphipods were rare, but all specimens collected were from near-diffuser stations. More crustacean taxa were collected in 2002 than in 1999 or 2000.

Mollusks

This year fifty-five mollusk taxa found in the Sand Island Ocean Outfall survey for the first time were added to the mollusk taxon list. The new bivalve taxa include *Acar* cf. *plicata*, *Adipicola* cf. *crypta*, *Amygdalum* sp., *Anguipecten* cf. *lamberti*, *Anisodonta lutea*, *Anomia nobilis*, *Ctena* sp., *Cuspidaria pailoloana*, *Epicodakia* sp., *Kellia hawaiensis*, *Lioconcha hieroglyphica*, *Malleus* sp., *Modiolus* sp., *Nemocardium* sp., Pectinidae sp. A, *Scintilla hiloa*, Bivalvia sp. A, Bivalvia sp. B, and Bivalvia sp. C. The new gastropod taxa include Aplysiidae, Architectonicidae sp., *Brookula* sp., *Caecum* cf. *glabriformis*, *Clavus pusilla*, *Cyclostremiscus striatus*, Cypraeidae spp., *Eatoniella janetaylorae*, *Erato sandwicensis*, *Etrema acricula*, *Eulima peasei*, *Glyphostoma kihikihi*, *Granulina* sp., *Heliacus implexus*, Juliidae sp., *Koloonella* sp., *Metaxia albicephala*, *Metaxia* sp., *Mitra earlei*, *Nerita* spp., *Neritopsis radula*, *Omalogyra* spp., *Pseudodaphnella pulchella*, *Pyramidelloides suta*, Rissoidae spp., *Rissoina* sp., *Scaphander* sp., *Sinezona insignis*, *Trivia* spp., *Tugali* sp., *Turbonilla thaanumi*, Vermetidae spp., *Vexillum rufofilosum*, *Vexillum tusum*, *Xenuroturris* sp., and Gastropoda sp. A.

Mean mollusk abundance is compared among sampling dates for data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 (Figure 28). Mean mollusk abundance at Transect E in 1999, 2000, and 2002 was higher than at Transect B in any of the eleven previous survey years. Also, it was lower at Transects C and D in 1999, 2000, and 2002 than at Transect B in 1996, 1997, and 1998. However, ANOVA results for $\log_{10}$-transformed data showed no significant differences among sampling dates ($p = 0.0845$). Because the mollusks were not separated into living and dead shell material, they represent time-averaged collections that integrate conditions at a site over a longer period of time than that of an annual base. As a consequence, temporal variability levels within stations are generally somewhat less than is the case for the total nonmollusk and crustacean fractions. The lack of significant differences among sampling dates indicates the diffuser effluent is not having any long-term negative effect on mollusk abundance.

Mean mollusk abundance is compared among sampling stations for data collected in 1999, 2000, and 2002 (Figure 29). Mollusk abundance was quantitatively greater at Stations E2, E3, E5, and E6 than at most other stations. ANOVA results for untransformed data showed significant differences among sampling stations ($p = 0.0020$). Mean mollusk abundance was

significantly greater at Station E3 that at all other stations. The greater mollusk abundance on Transect E is probably associated with water depth and does not reflect a spatial pattern related to the outfall discharge.

Mean number of mollusk taxa is compared among sampling dates for data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 (Figure 30). The number of mollusk taxa collected at Transects C, D, and E in 1999, 2000, and 2002 is similar to that collected at Transect B since 1993. ANOVA results for untransformed data showed significant differences among sampling dates (p = 0.0070). However, Student–Newman–Keuls tests showed no significant pairwise multiple contrasts. The number of mollusk taxa in the study area has been greater since 1993. There is no indication over the fourteen study years of a negative impact of the diffuser effluent on mollusk taxa richness.

Mean number of mollusk taxa is compared among sampling stations for data collected in 1999, 2000, and 2002 (Figure 31). ANOVA results for untransformed data showed significant differences among sampling stations (p = 0.0059). Mean number of mollusk taxa was significantly greater at Station E3 than at Stations E1, E6, D1, C1A, and C2A. The greater mollusk taxa richness at Station E3 is probably associated with water depth and does not reflect a spatial pattern related to the outfall discharge.

SUMMARY AND CONCLUSIONS

There continues to be no evidence of a buildup of organic matter in the vicinity of the Sand Island outfall diffuser. This conclusion is confirmed by measurements of ORP, TOC, and TKN. Sediment organic content was below 0.60% in all samples from both beyond-diffuser and near-diffuser stations. Organic carbon concentrations near the outfall are consistent with results of past years for all stations on Transect B. As a general comparison, organic content ranged from 1.2% to 10.9% for sediments of the Kattegat (Pearson et al. 1985) and from 0.6% to 8.9% for sediments off the coast of Maine (Bader 1954). Total organic content ranged from 1.4% to 4.1% for stations near the Los Angeles County ocean sewage outfalls (Swartz et al. 1986). In Kingston Harbour, Jamaica, total organic carbon of sediments ranged from 4% to 10.7% in a semi-enclosed bay subject to organic pollution (Wade 1972; Wade et al. 1972).

The biological data indicate that there are few, if any, negative effects of the Sand Island outfall on the macrobenthic community. Most statistically significant differences in nonmollusk abundance and taxa richness among the fifteen stations were associated with differences between the three transects and reflect the influence of depth-related factors. Parametric

statistical comparisons showed that the abundance and number of taxa of polychaetes, crustaceans, and all nonmollusks were often significantly greater at several Transect D stations (especially Stations D5 and D3A) than at many stations on Transects C and E. Station E3 was an exception. Polychaete, crustacean, and nonmollusk abundances were much greater at Station E3 than at any other Transect E station. More polychaete, crustacean, and nonmollusk taxa were collected at Station E3 than at any other station in the survey. The nonmollusk fauna at Station C5A, the deepest station on Transect C, was usually more abundant and diverse than that at the other Transect C stations. When stations were pooled by transect, the abundances of polychaetes, crustaceans, and all nonmollusks were significantly greater on Transect D than on Transect C or Transect E. The taxa richness of polychaetes, crustaceans, and all nonmollusks were significantly greater on Transect D and on Transect E than on Transect C. When stations were pooled by proximity to the outfall, there were no significant differences between beyond-diffuser stations and near-diffuser stations in the abundance or taxa richness of polychaetes, crustaceans, and all nonmollusks.

Diversity (H') of nonmollusks was relatively low at most Transect C stations and relatively high at most Transect E stations, but each transect had at least one low-diversity station. Low diversity on Transect C was associated with low abundance and taxa richness. Higher diversity at some stations on Transects D and E was related to the absence of strong dominants. Evenness (J) was also relatively high on Transect E because of the absence of strong dominants. Diversity and evenness of nonmollusks in 2002 were more closely associated with water depth than proximity to the outfall.

Nonmollusk taxa composition was also related to water depth. *Pionosyllis heterocirrata* and *Prionospio cirrifera* were widely distributed among the fifteen stations and ranked among the five most abundant taxa at least at one station on each transect. *Podarke angustifrons* and *Sphaerosyllis* sp. G were widely distributed on all three transects, but they ranked among the five most abundant taxa only on Transect C. All of the remaining dominant taxa were abundant at only one or two of the transects. No taxon was characteristic of Transect C. *Prionospio cirrifera* was the only species collected at all Transect C stations. *Leptochelia dubia* was the most abundant species collected in 2002 (699 individuals). It was a dominant at Stations D2, D3A, D5, D6, E3, and E5. *Myriochele oculata* was a dominant at all stations on Transect D but was rare or absent at stations on the other transects. *Synelmis acuminata* was also abundant and usually a dominant on Transect D stations. *Aspidosiphon muelleri* was a dominant at four stations each on Transect D and Transect E. *Dipolydora normalis*, an opportunistic species, was very abundant at Station D3A but was rare or absent at all other stations. *Prionospio cirrobranchiata* and *Tanaissus* sp. A ranked among the five dominants at least at two Transect E stations, but they were not a dominant at any station on the other transects. The

abundance of *Euchone* sp. B has fluctuated greatly, but this taxon has been a dominant at least at one Transect D station in 1999 (Stations D1, D2, D5, D6), 2000 (Station D1), and 2002 (Stations D1, D5). The opportunistic species *Ophryotrocha adherens* was a dominant only at Station D2 in 2002.

Quantitative assessment of nonmollusk faunal similarity resulted in station clusters that are generally associated with the three transects. There was no between-transect grouping of stations that might indicate a common influence of the outfall. The relatively low overall similarity resulted from the new survey design (begun in 1999), i.e., sampling of stations along three different depth contours represented by Transects C, D, and E. The similarity analysis reflects the many significant differences among the three transects in abundance, number of taxa, diversity, and taxa composition of the nonmollusks.

Changes in abundance and taxa richness for the mollusks were not as clearly related to water depth as was the case for the nonmollusks. Most of the significant differences among the fifteen stations in the structure of the mollusk assemblage were associated with high values at Stations C3A, C6, D5, E2, E3, and E5 and low values at Stations C1, C2A, D3A, E1, and E6 for both number of individuals and number of taxa. Transect comparisons showed no significant differences among Transects C, D, and E in mollusk abundance and taxa richness. There was no significant difference in mollusk abundance or number of mollusk taxa between beyond-diffuser stations and near-diffuser stations. The results of these comparisons do not indicate a negative impact related to the discharge of effluent from the outfall diffuser.

Although most of the 16 dominant mollusk taxa were widely distributed, only 3—*Cerithium perparvulum*, *Pusillina marmorata*, and *Diala semistriata*—were dominant at least at one station on each of the three transects. *C. perparvulum* was a top-five dominant at all fifteen stations. Transects D and E were more similar to each other with respect to taxa composition than to Transect C. *Balcis* spp. and *Diala scopulorum* were abundant at most stations on Transects D and E. Five taxa were more abundant on Transect C than on the other transects: *Parashiela beetsi*, *Lophocochlias minutissimus*, *Tricolia variabilis*, *Triphora* spp., and *Orbitestella regina*. *Finella pupoides*, *Acteocina* sp., and *Ervilia bisculpta* were substantially more abundant on Transect D than on the other transects. There were no unique dominants on Transect E; however, *Diala scopulorum* was very abundant and the most dominant species at all stations on that transect. The seven most abundant mollusk taxa in the 2002 survey (*Diala scopulorum*, *Cerithium perparvulum*, *Pusillina marmorata*, *Finella pupoides*, *Scaliola* spp., *Diala semistriata*, and *Balcis* spp.) were the same seven taxa that dominated in the 1999 and 2000 surveys and that dominated Transect B in the 1994 through 1998 surveys (Nelson et al. 1995, 1996, 1997; Swartz et al. 1998, 1999, 2000, 2001). Diversity (H') and evenness (J) of mollusks were generally higher and less variable on Transect C and

Transect D than on Transect E. The lower diversity and evenness on Transect E are due to the presence of strong numerically dominant species like *Diala scopulorum* at Station E5 or low taxa richness at Stations E1 and E6. The low diversity and evenness values obtained for some Transect E stations in 1999, 2000, and 2002 are lower than the minimum values obtained for Transect B stations in surveys from 1996 through 1998 (Nelson et al. 1997; Swartz et al. 1998, 1999, 2000, 2001).

Although the quantitative structure of the mollusks was similar among transects, qualitative differences in taxa composition resulted in a pattern of faunal similarity that reflected the depth gradient. Four stations on Transect D linked together (Stations D1, D2, D5, and D6). Two additional clusters were represented by Stations C3A, C5A, and C6 and by Stations E3 and E5. A mixed transect cluster included beyond-diffuser station C1 and near-diffuser stations C2A and D3A. Stations E1 and E6 were the last two stations added to the dendrogram, indicating that their faunal composition was somewhat different from all others. The molluscan fauna at Stations E1 and E6 was relatively diminished, with low numbers of taxa and individuals. Separation of the stations on Transect E—also seen in 1999 and 2000—is probably related to natural faunal variations. There was no well-defined, between-transect grouping of stations that might reflect a common influence of the outfall. The cluster pattern was associated with the influences of water depth, as in the case of the nonmollusks. Also as in the case of the nonmollusks, the low overall similarity reflected the new survey design.

Faunal conditions at Transects C, D, and E in 2002 were compared with historic conditions observed at Transects C, D, and E in 1999 and 2000 and at Transect B during eleven annual surveys between 1986 and 1998. There were no significant pairwise contrasts in the abundance and taxa richness of mollusks at Transects C, D, and E in 1999, 2000, and 2002 and at Transect B in any previous survey year. The abundance and taxa richness of nonmollusks and crustaceans were significantly greater at Transect D in 1999, 2000, and 2002 than at Transect B in several previous years and significantly lower at Transects C and E in 1999 and 2000 than at Transect B in many previous years. There were no significant changes in nonmollusk and crustacean abundance or taxa richness within Transect C, D, or E among survey years 1999, 2000, and 2002. The differences among Transects B, C, D, and E in the temporal comparisons of nonmollusk abundance and taxa richness are probably associated with water depth. There is no indication over the fourteen study years of a negative impact of the diffuser effluent on the mollusk and nonmollusk assemblages.

Data for 1999, 2000, and 2002 were pooled to compare faunal conditions among the fifteen stations. The abundance and taxa richness of both nonmollusks and crustaceans were typically significantly greater at Stations D2, D3A, and D5 than at most stations on Transect C and Transect E, except Station E3. The abundance and taxa richness of mollusks were

significantly greater at Station E3 than at most other stations. These differences are associated with water depth rather than a negative influence of the outfall.

The model of benthic organic enrichment proposed by Pearson and Rosenberg (1978) suggests that, in the transition zone on an enrichment gradient, a few species increase and are extremely dominant, while overall diversity and evenness are low. There was no evidence in 2002 of the high density and dominance by a few opportunistic species at stations near the outfall. In fact, there were no significant differences in the density of nonmollusks or mollusks between beyond-diffuser stations and near-diffuser stations. The 2002 survey results suggest that there is no evidence of a community response, such as that predicted by the Pearson and Rosenberg model, for the benthic fauna in the vicinity of the Sand Island Ocean Outfall. Similar conclusions were reached for previous surveys (Nelson 1986; Russo et al. 1988; Bailey–Brock et al. 1991; Nelson et al. 1992a, 1992b, 1994, 1995, 1996, 1997; Swartz et al. 1998, 1999, 2000, 2001).

Maurer et al. (1993) proposed that the Pearson and Rosenberg model might be inappropriate for erosional continental shelf environments. In their study of an outfall on the continental shelf of California, Maurer et al. found that even with some organic enrichment near the diffuser, there was no evidence of elimination of rare species, although three species did achieve numerical dominance. The response of the benthic community near the Sand Island Ocean Outfall does not show the alternate response pattern described by Maurer et al. (1993), presumably because sediment organics do not show even the moderate enrichment found near the Orange County outfall.

In conclusion, there is very little evidence of adverse effects from sewage effluent discharged through the Sand Island Ocean Outfall on the macrobenthic community in 2002. Sediments near the outfall have not been enriched by organic material. Significant differences in the abundance and taxa richness of polychaetes, crustaceans, and all nonmollusks among stations were related to difference among transects and reflected the influence of ecological factors associated with water depth. There were no significant differences between near-diffuser and beyond-diffuser stations in the abundance and taxa richness of polychaetes, crustaceans, all nonmollusks, and mollusks. Changes in the macrobenthos since 1986 do not reflect any long-term temporal trends related to the outfall. A diverse and abundant macrobenthos was present at stations near the diffuser of the Sand Island Ocean Outfall in 2002.

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TEXT FIGURES

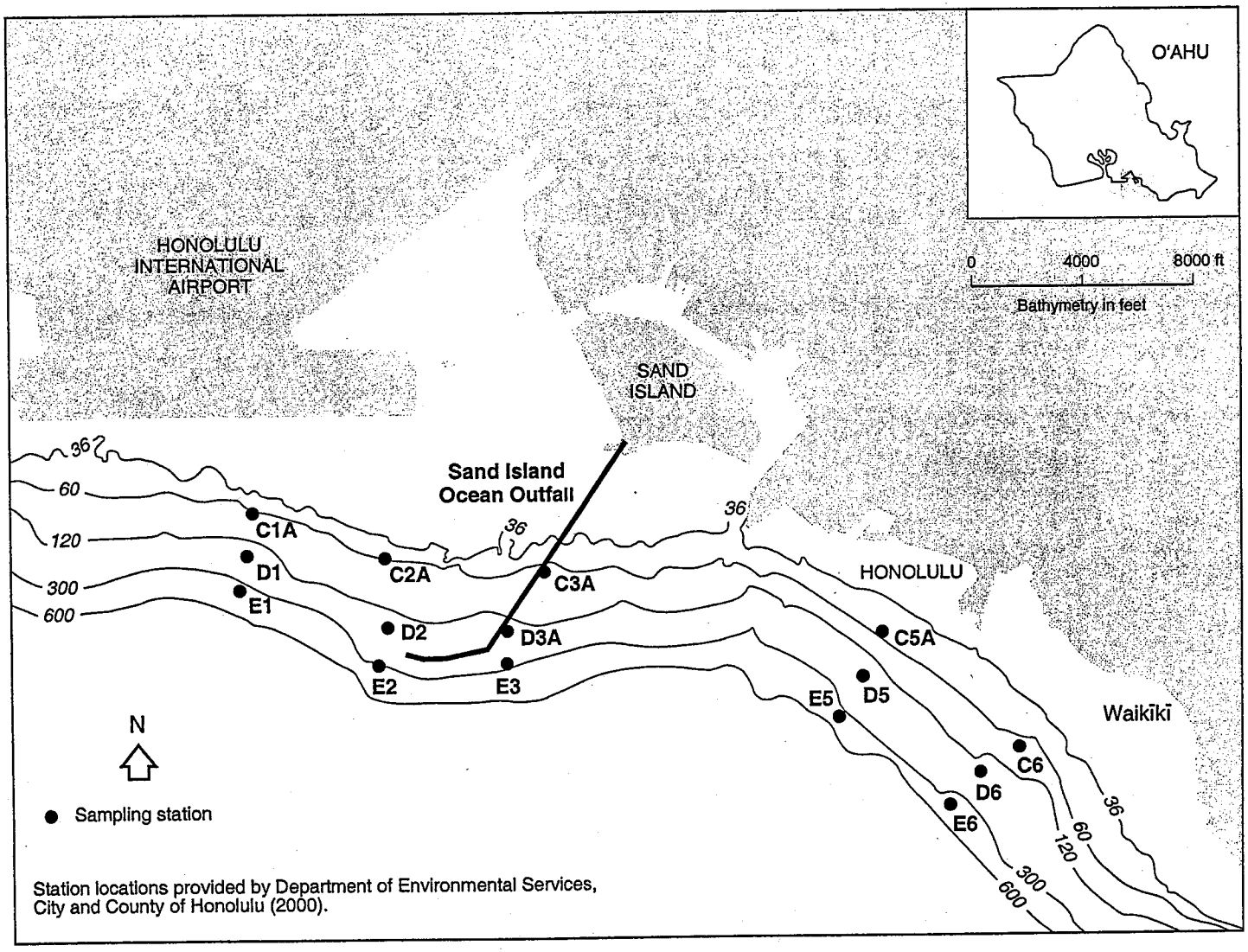
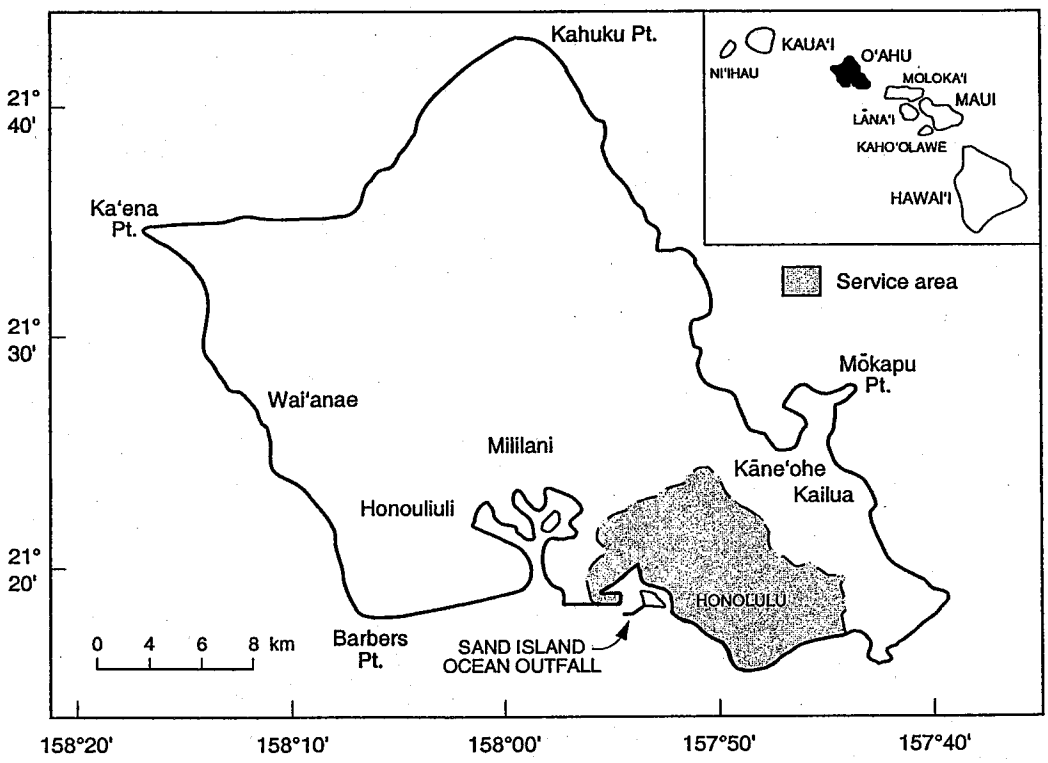


FIGURE 1. General locations of Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i



From Russo et al. (1988).

FIGURE 2. Sand Island Ocean Outfall site and wastewater treatment plant service area, O'ahu, Hawai'i

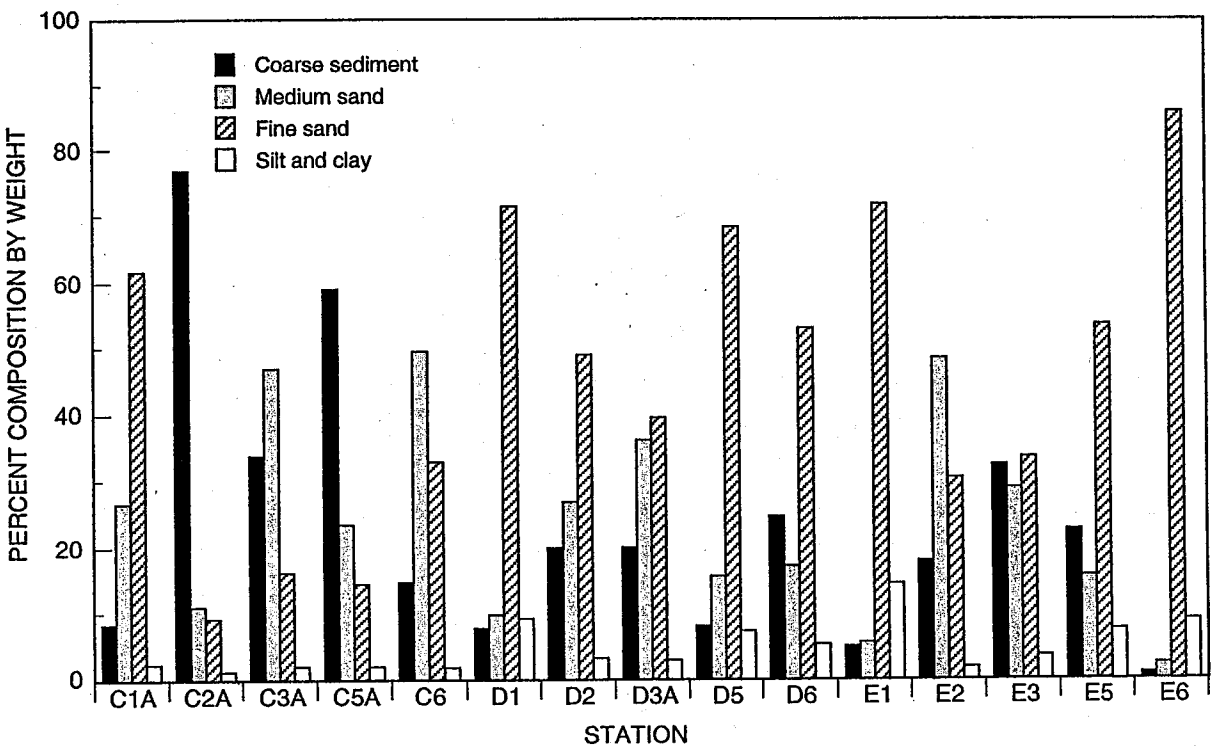


FIGURE 3. Sediment grain-size characteristics, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

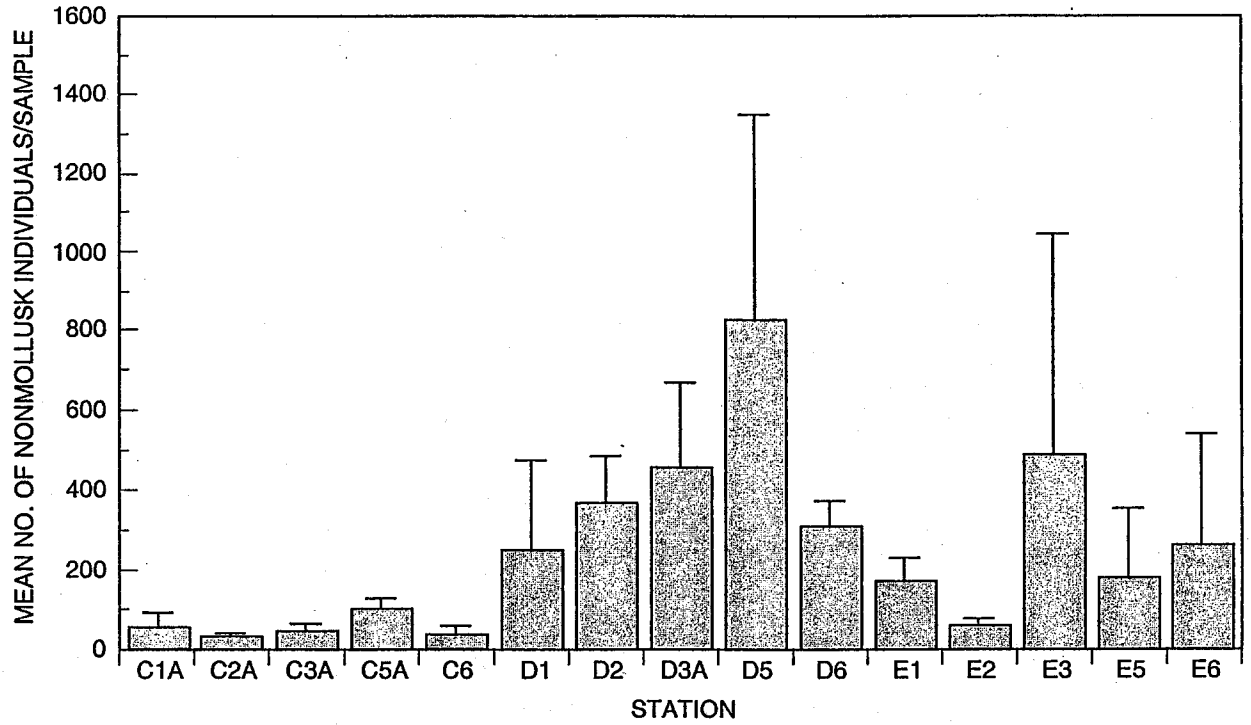


FIGURE 4. Mean (+1 SD) number of nonmollusk individuals per sample, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

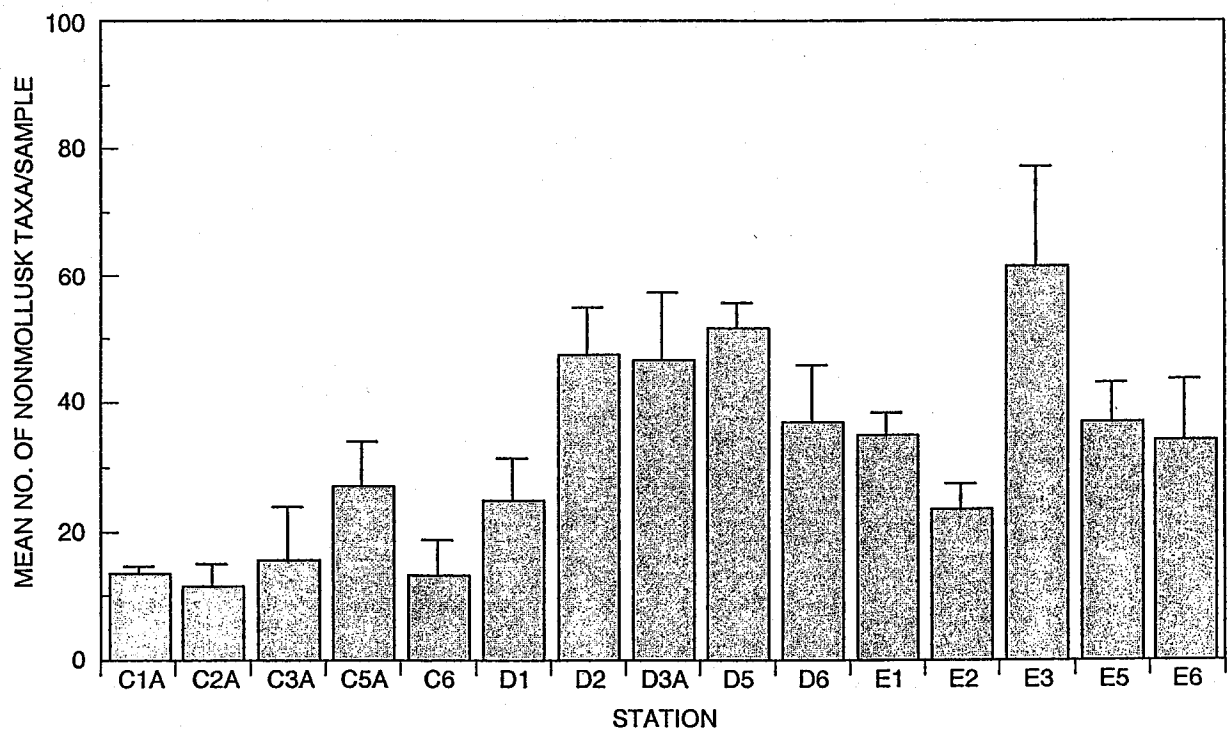


FIGURE 5. Mean (+1 SD) number of nonmollusk taxa per sample, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

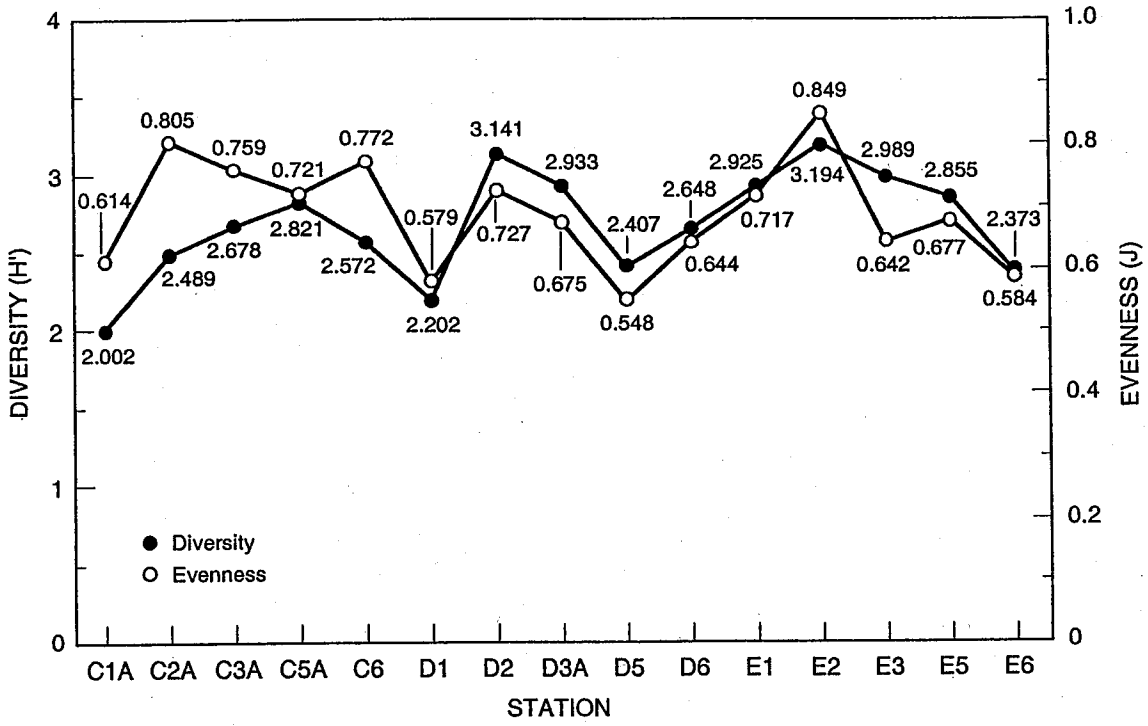


FIGURE 6. Shannon–Wiener H' diversity (ln) and evenness (J) for nonmollusks, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

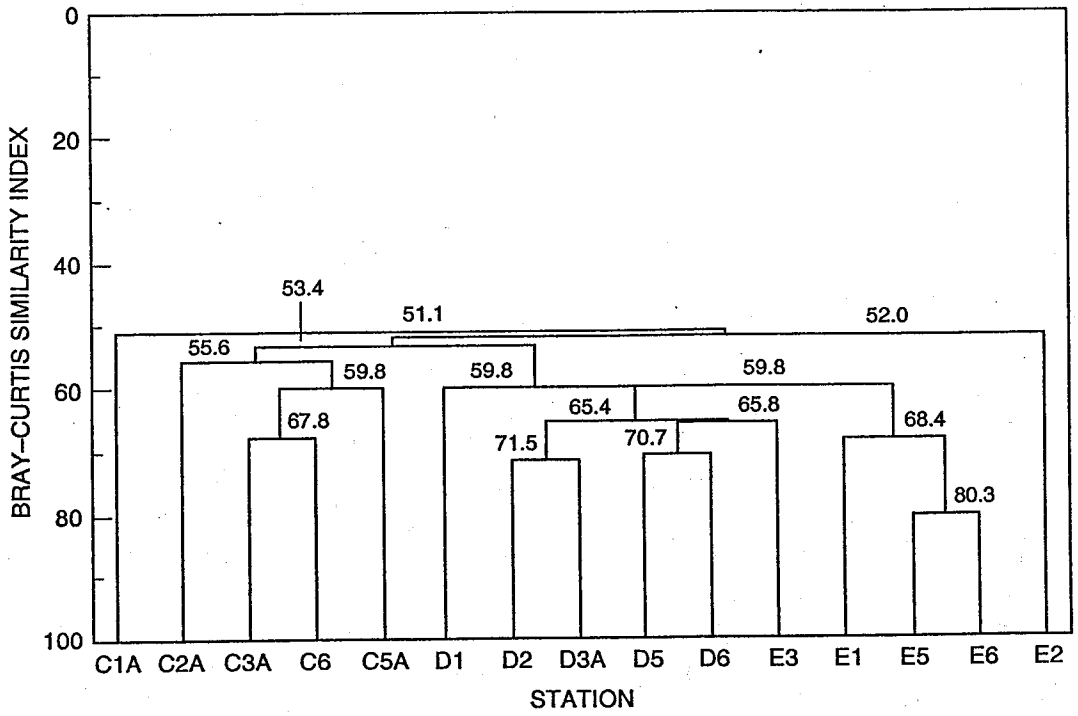


FIGURE 7. Dendrogram for double square root transformed nonmollusk data showing similarity among Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

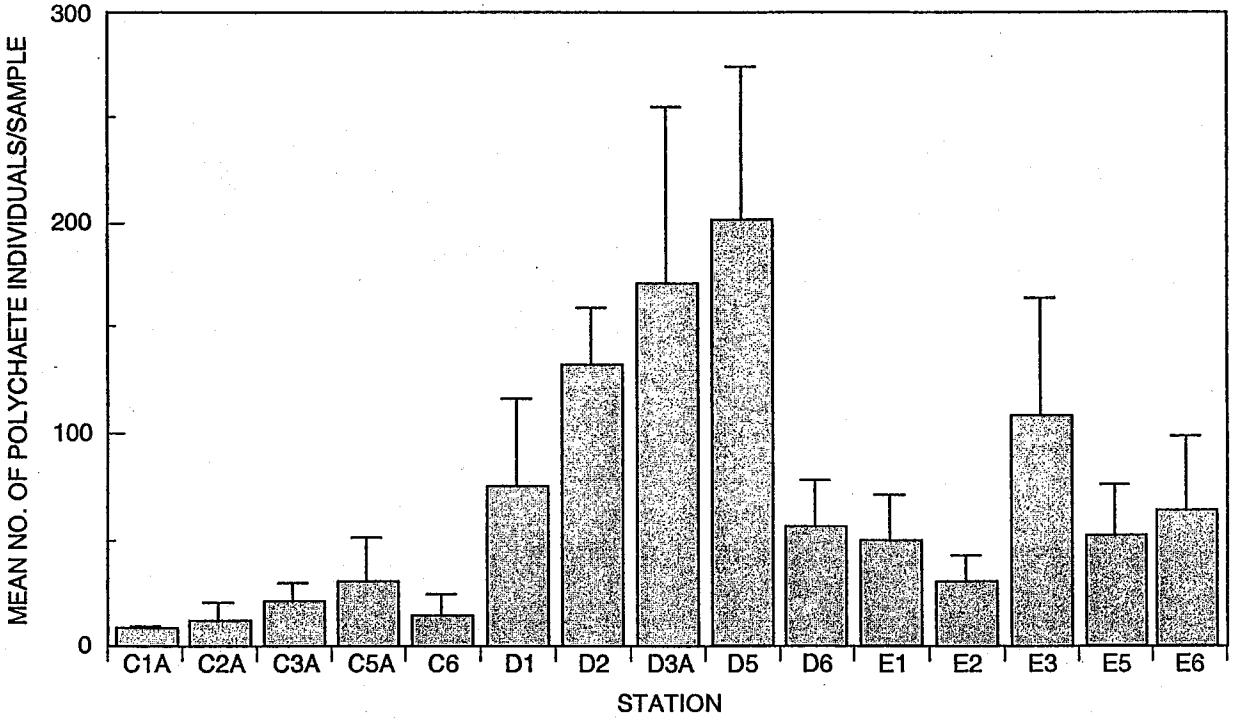


FIGURE 8. Mean (+1 SD) number of polychaete individuals per sample, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

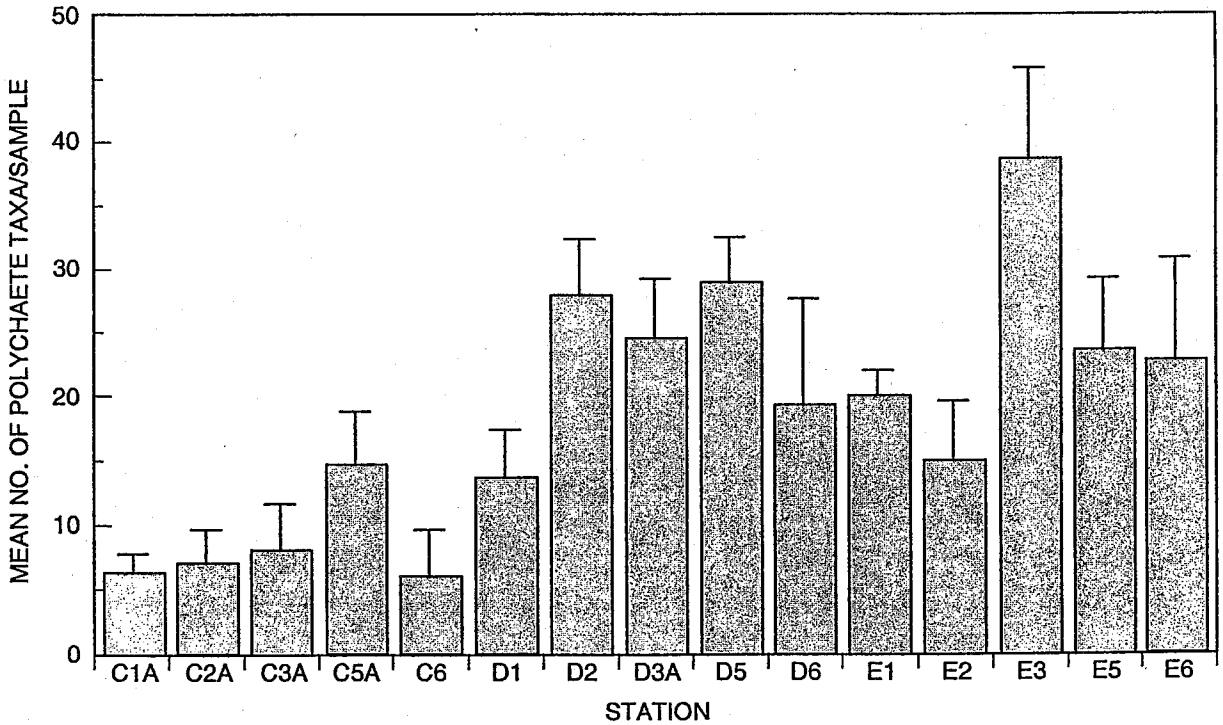


FIGURE 9. Mean (+1 SD) number of polychaete taxa per sample, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

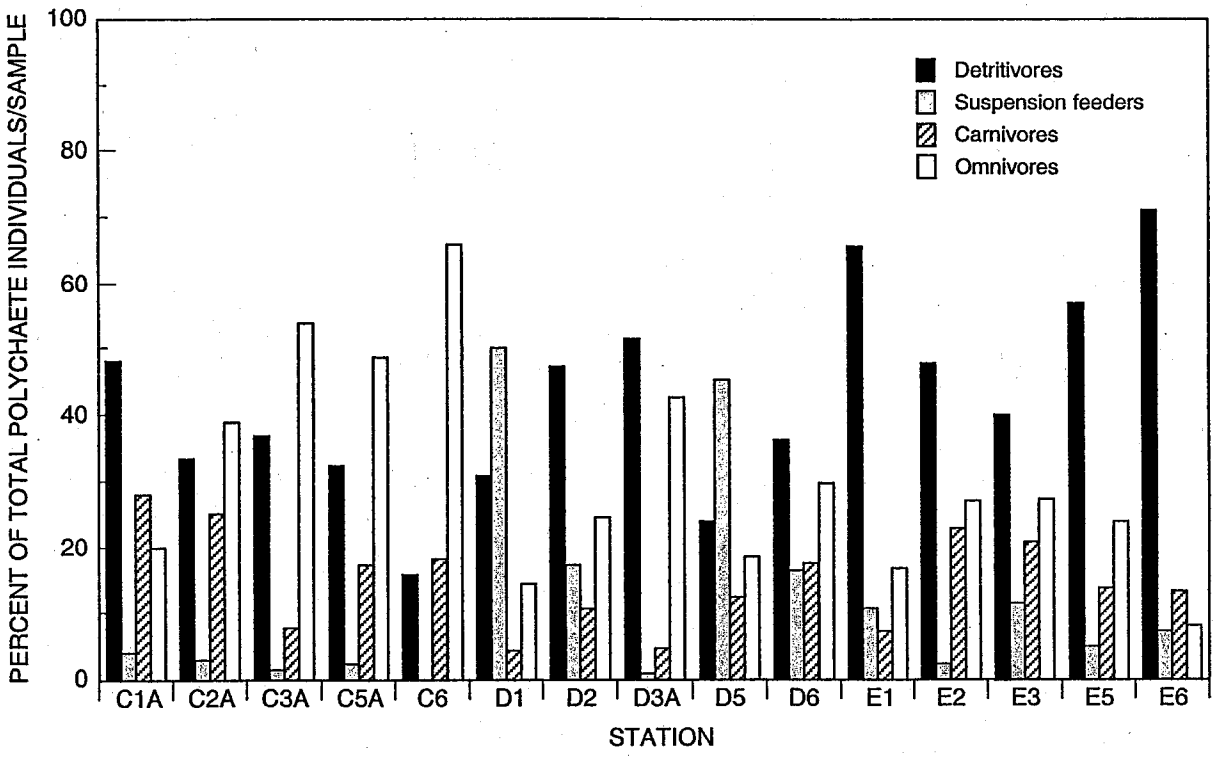


FIGURE 10. Percentage of total polychaete individuals in four trophic categories, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

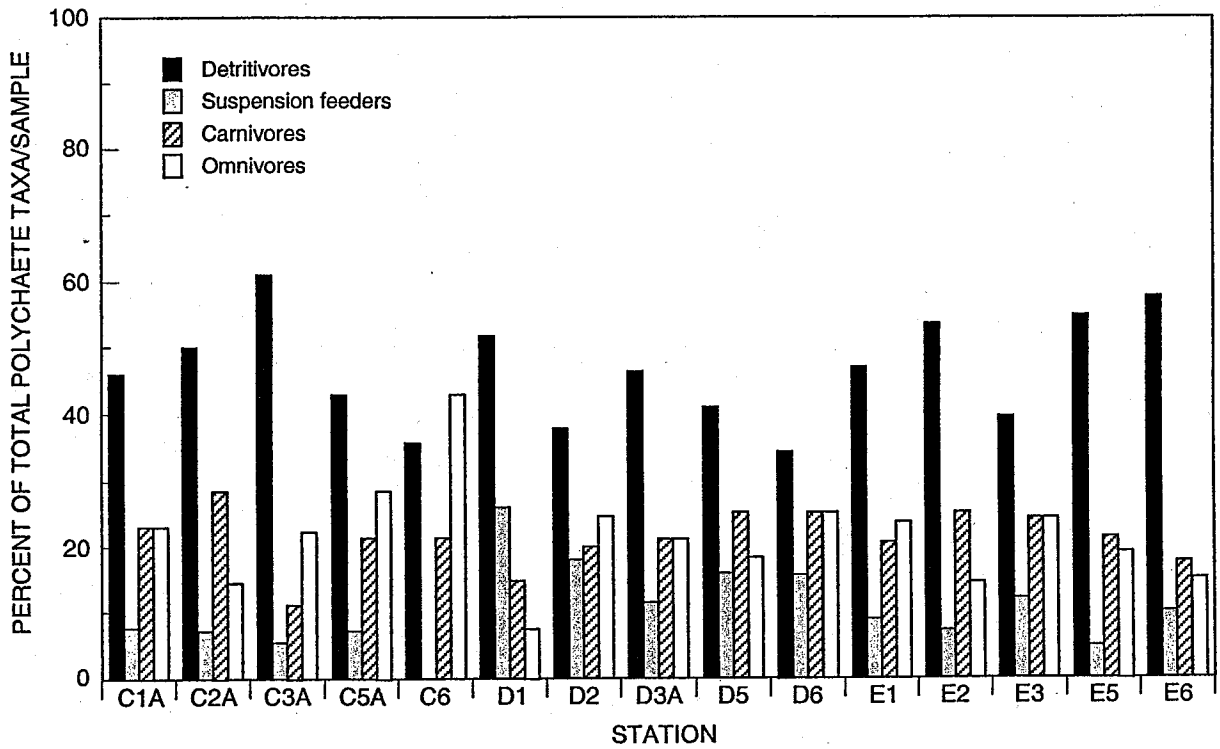


FIGURE 11. Percentage of total polychaete taxa in four trophic categories, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

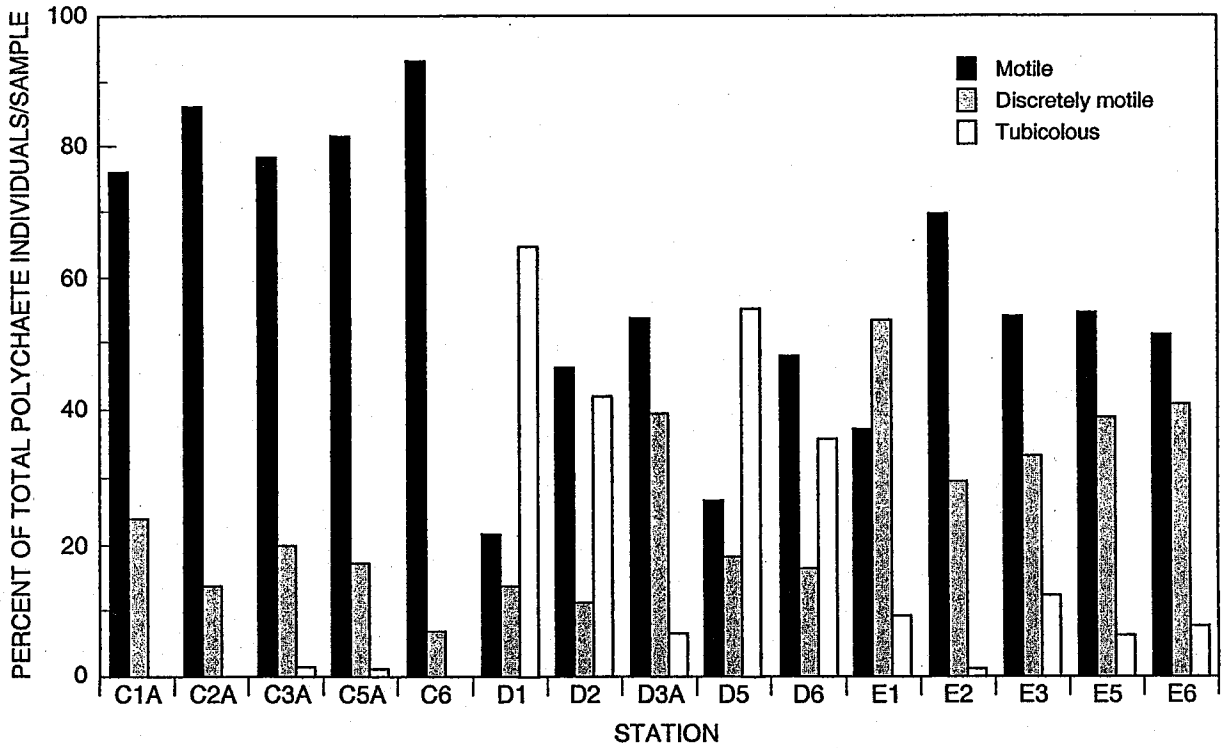


FIGURE 12. Percentage of total polychaete individuals in three motility categories, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

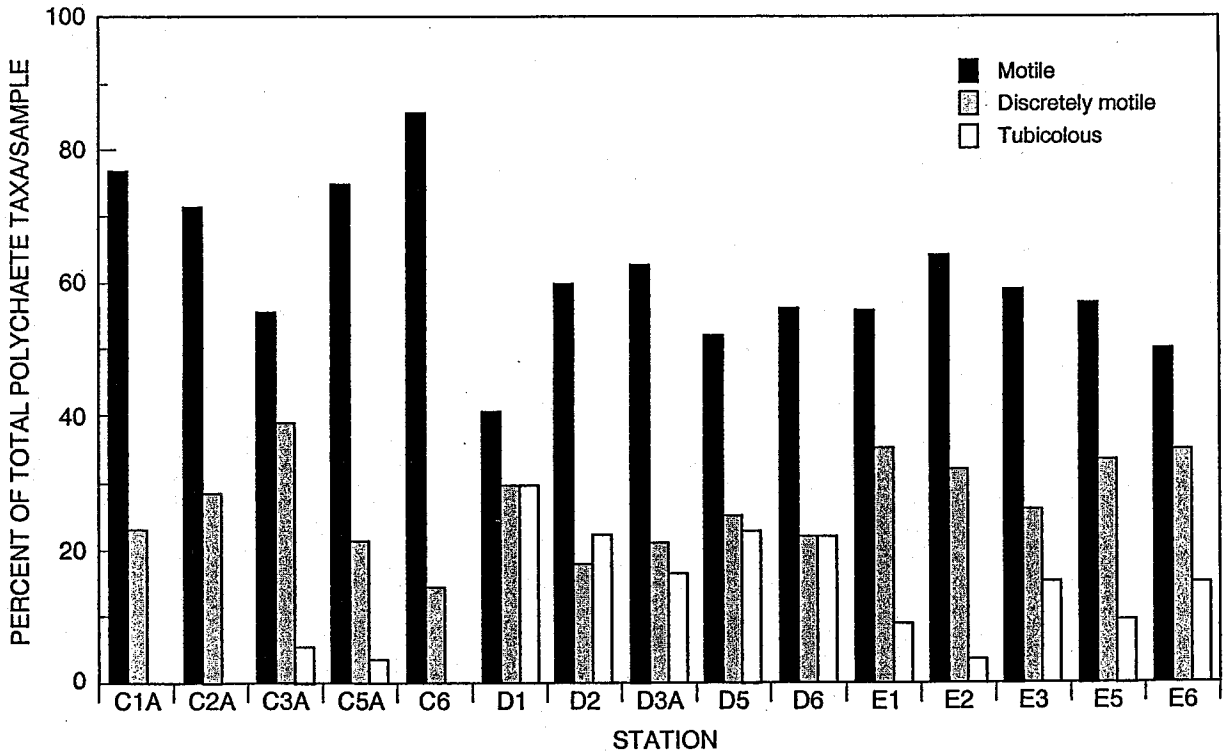


FIGURE 13. Percentage of total polychaete taxa in three motility categories, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

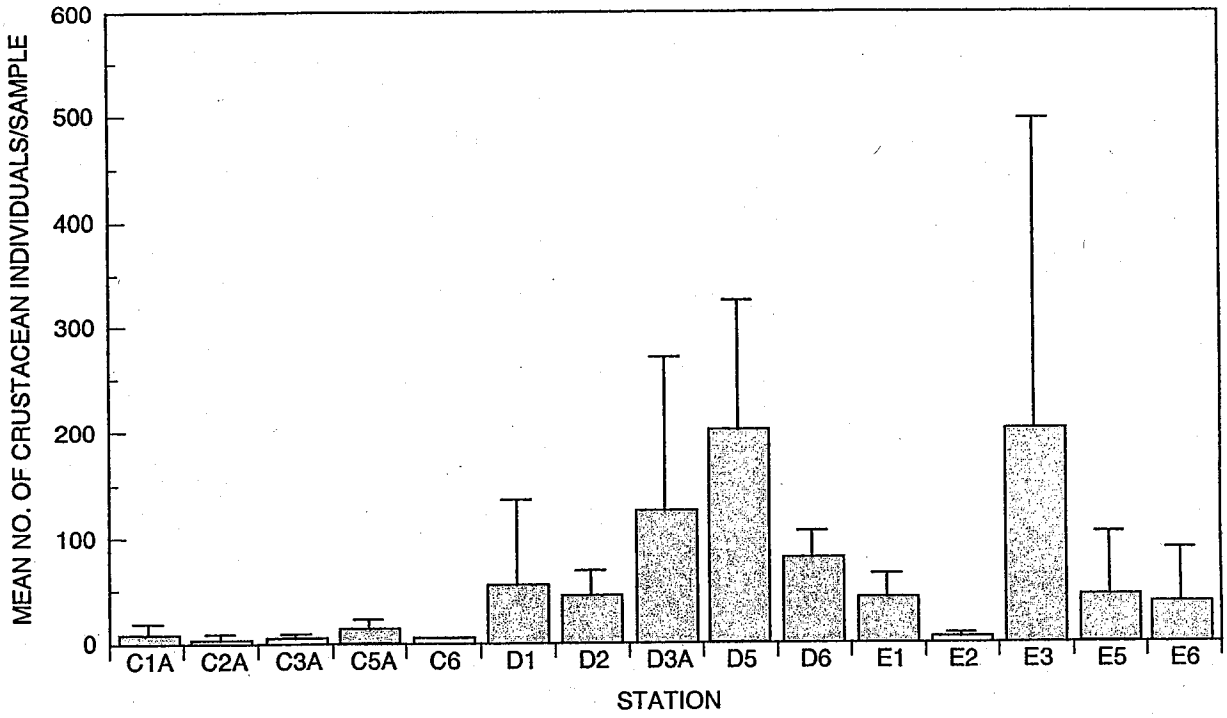


FIGURE 14. Mean (+1 SD) number of crustacean individuals per sample, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

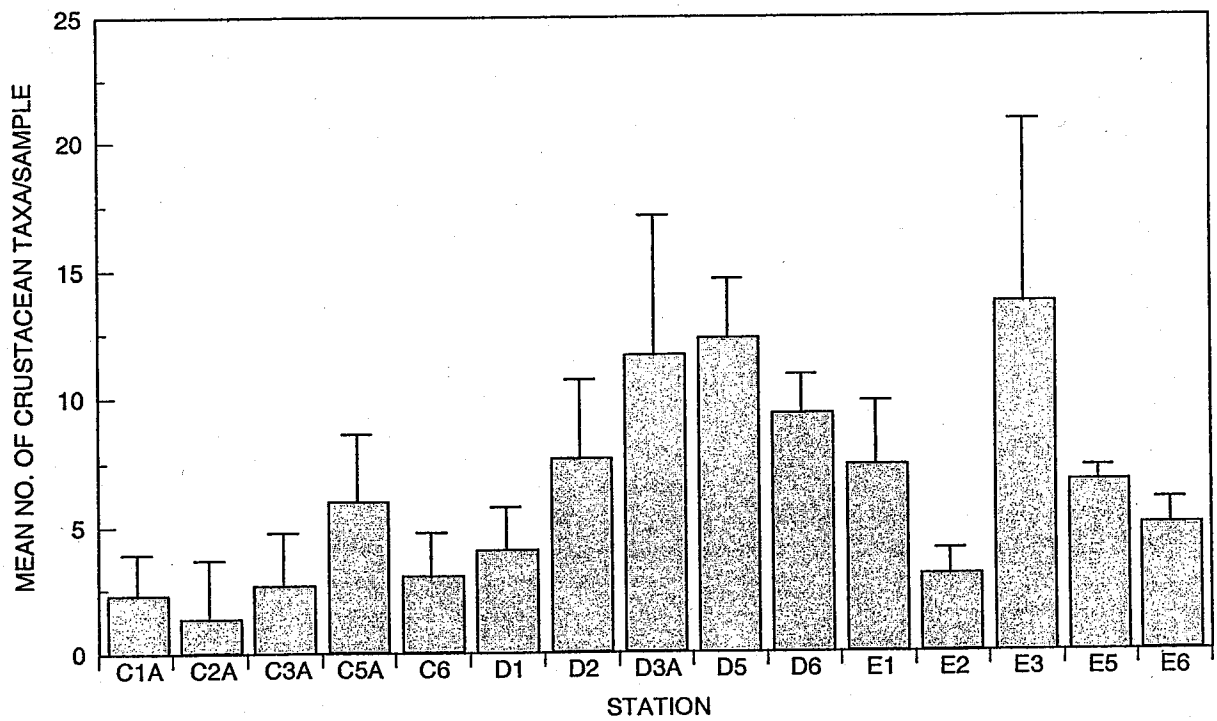


FIGURE 15. Mean (+1 SD) number of crustacean taxa per sample, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

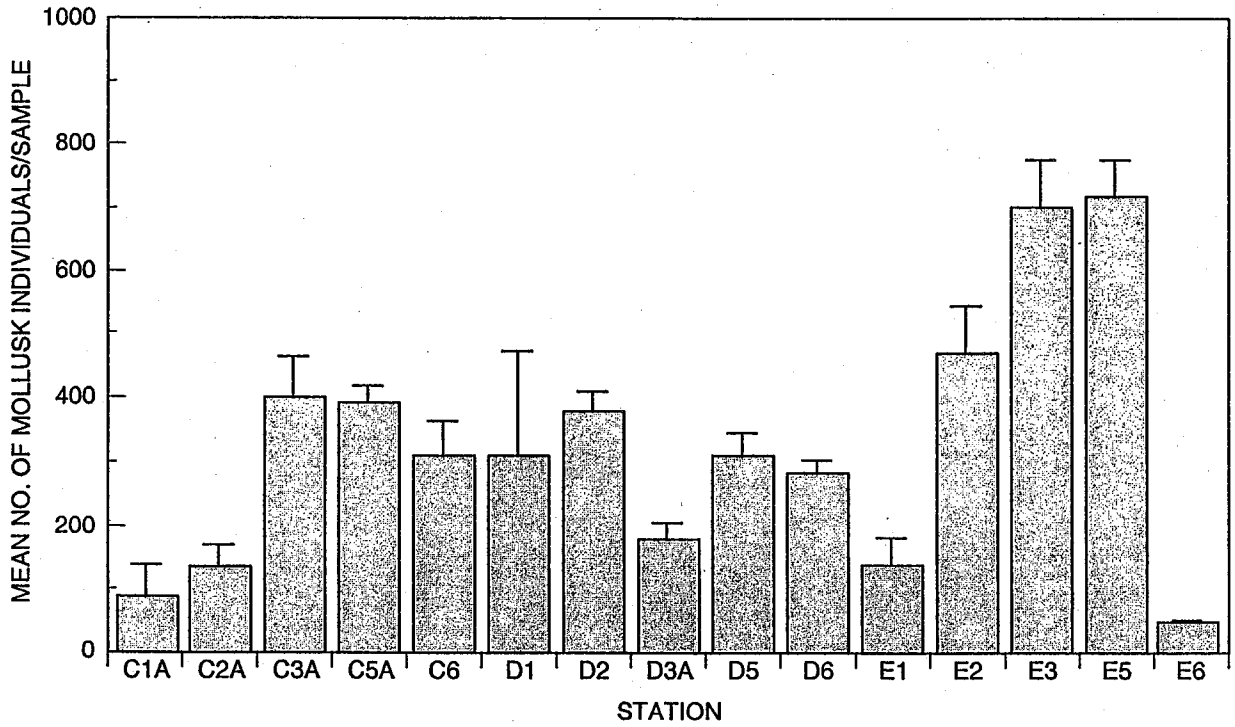


FIGURE 16. Mean (+1 SD) number of mollusk individuals per sample, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

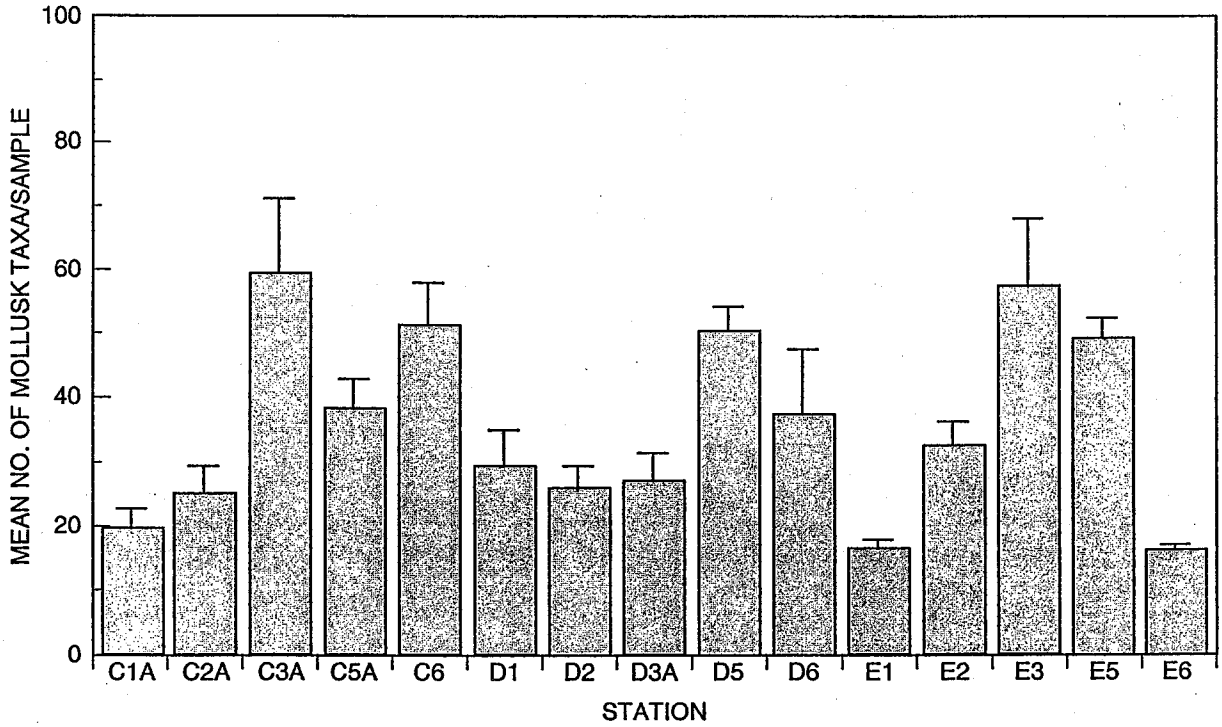


FIGURE 17. Mean (+1 SD) number of mollusk taxa per sample, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

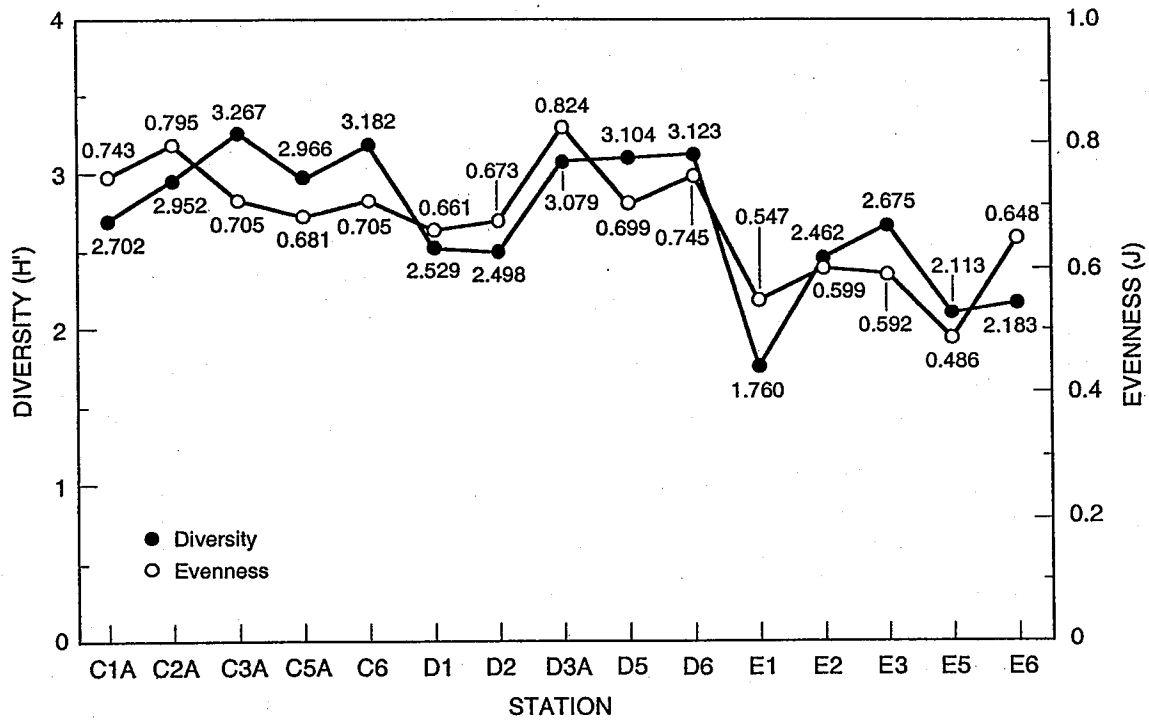


FIGURE 18. Shannon–Wiener H' diversity (ln) and evenness (J) for mollusks, Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

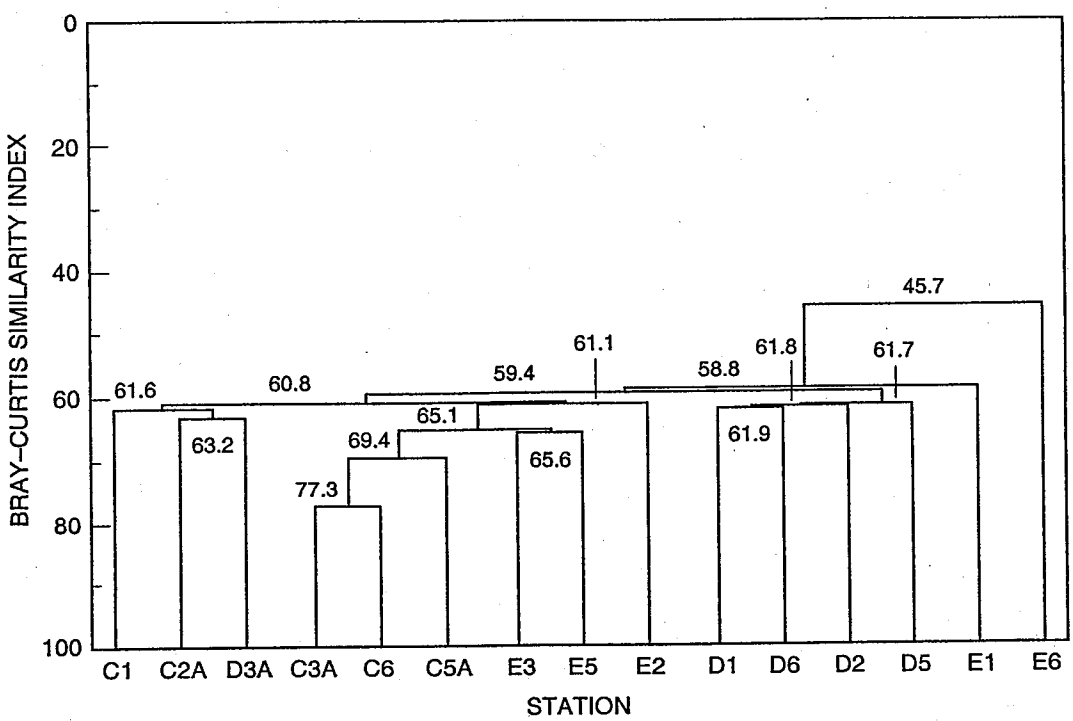


FIGURE 19. Dendrogram for double square root transformed mollusk data showing similarity among Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i, August 2002

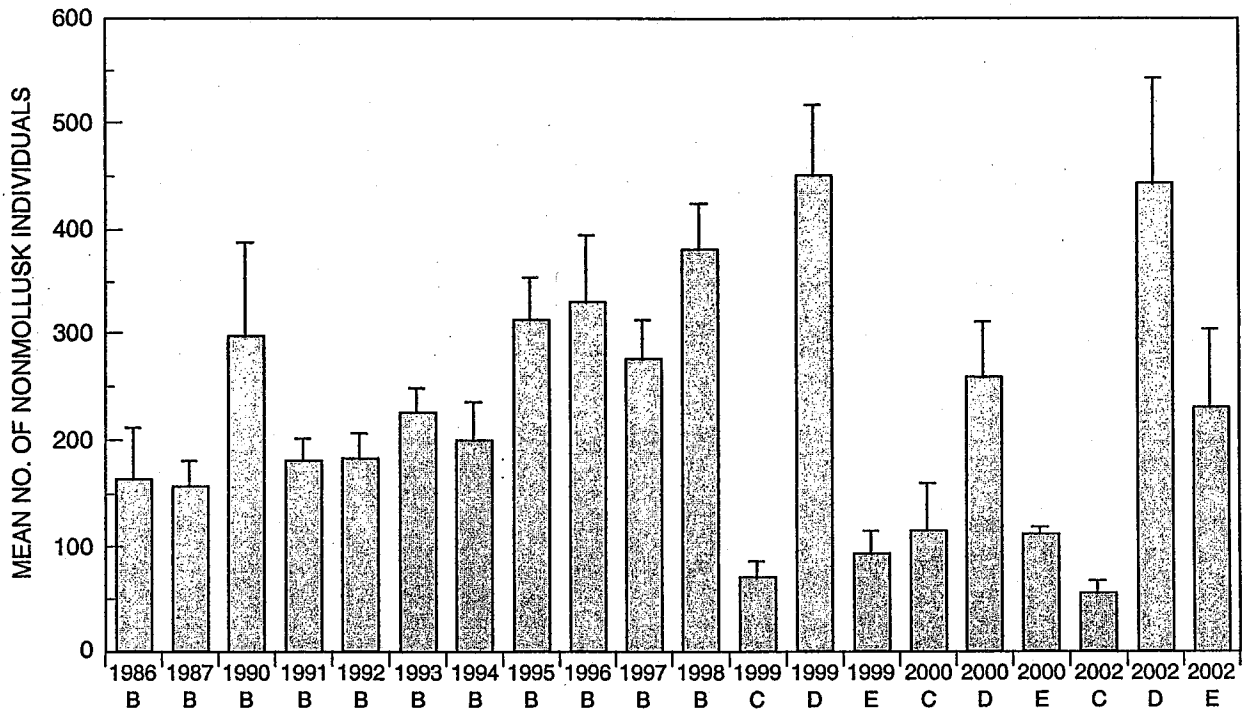


FIGURE 20. Mean (+1 SE) number of nonmollusk individuals compared among data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

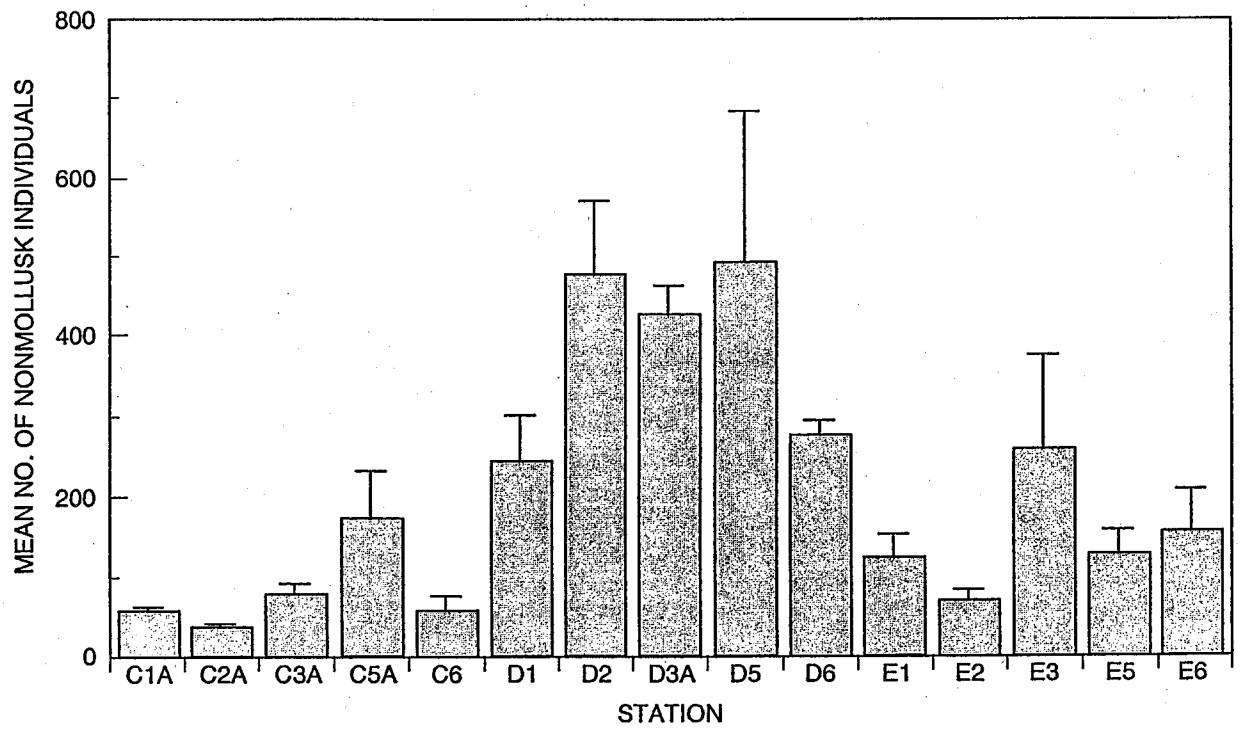


FIGURE 21. Mean (+1 SE) number of nonmollusk individuals compared among sampling stations for data collected in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

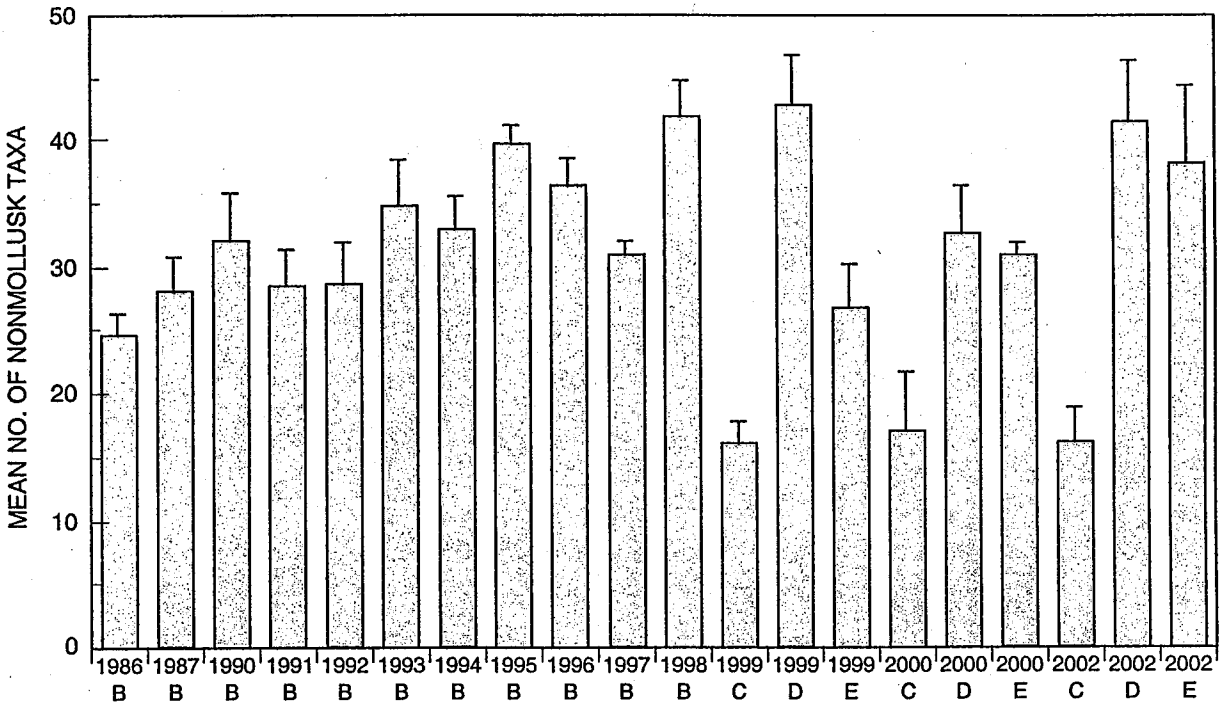


FIGURE 22. Mean (+1 SE) number of nonmollusk taxa compared among data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

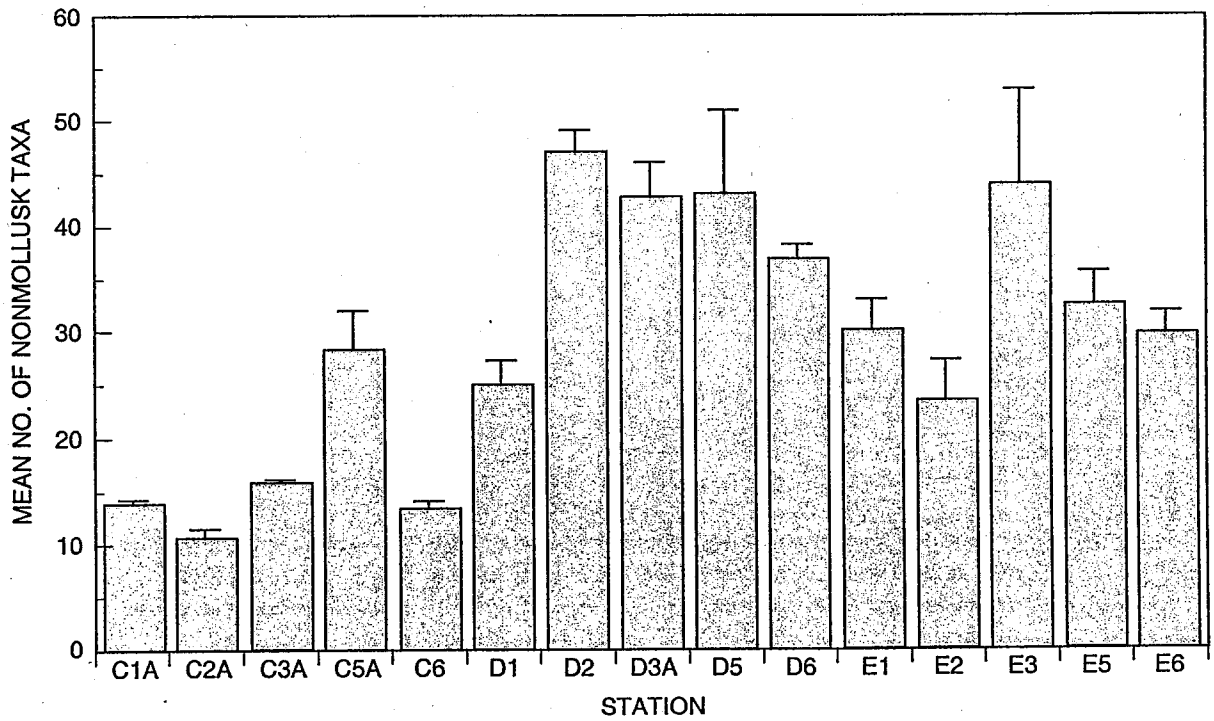


FIGURE 23. Mean (+1 SE) number of nonmollusk taxa compared among sampling stations for data collected in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

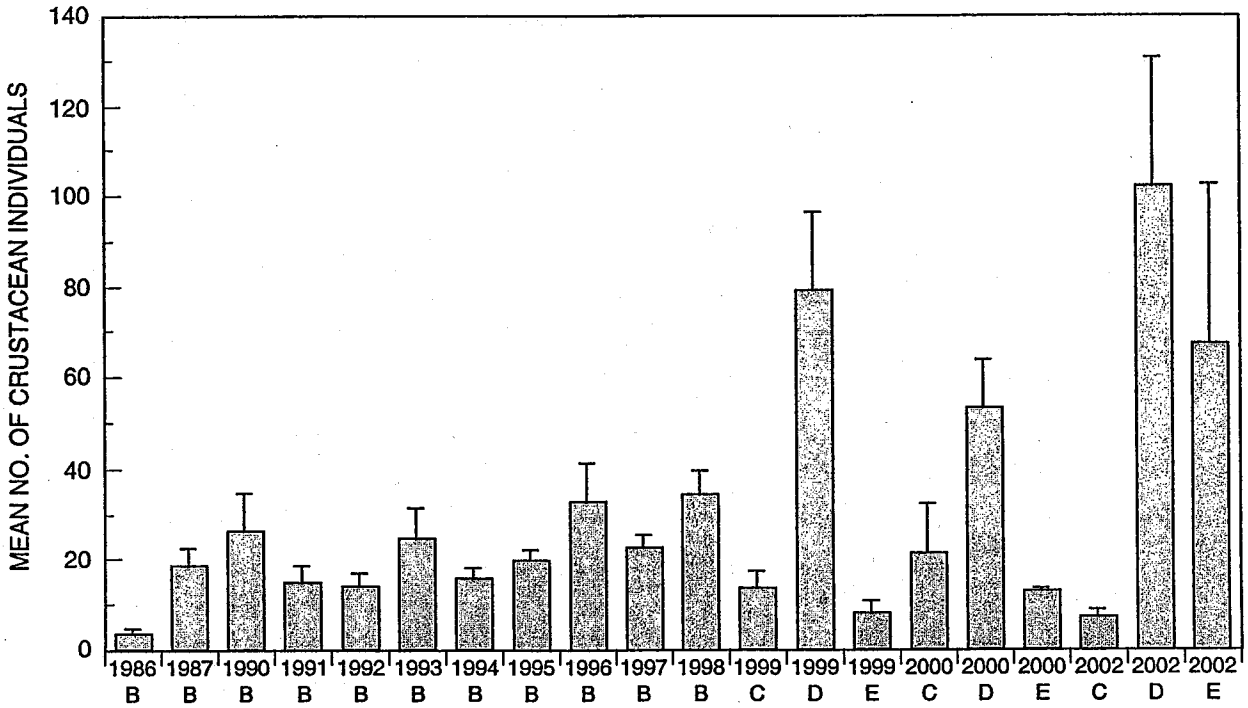


FIGURE 24. Mean (+1 SE) number of crustacean individuals compared among data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

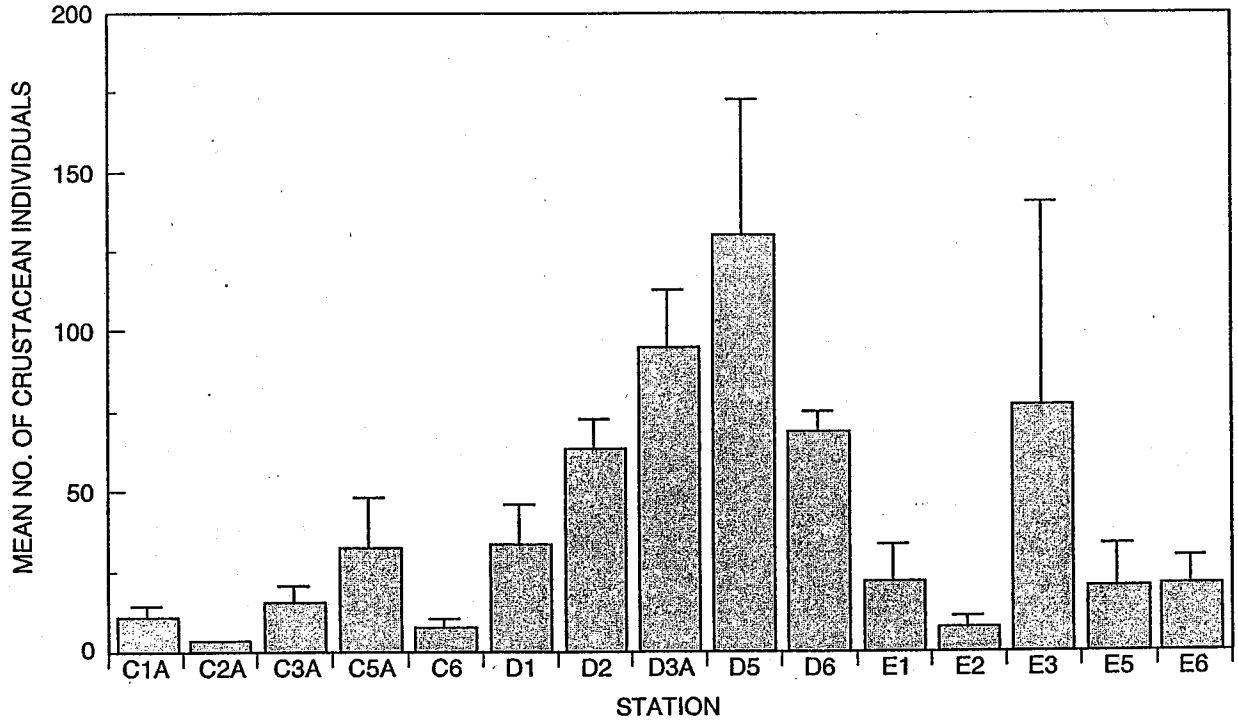


FIGURE 25. Mean (+1 SE) number of crustacean individuals compared among sampling stations for data collected in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

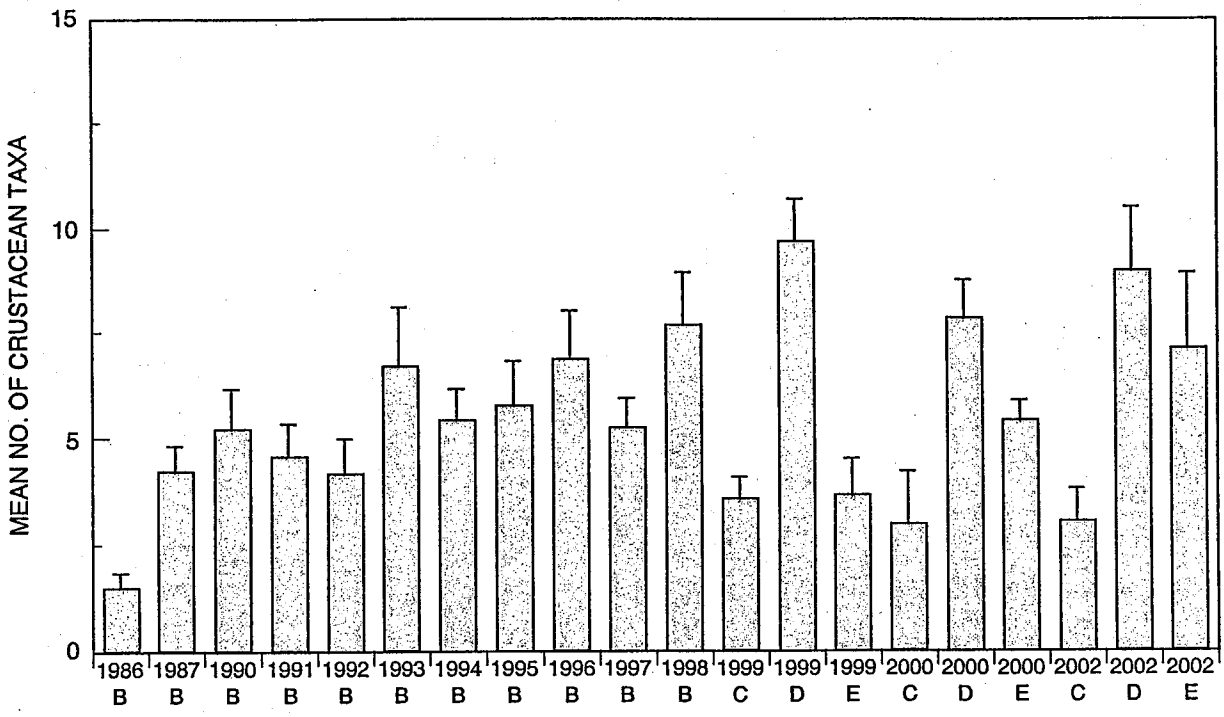


FIGURE 26. Mean (+1 SE) number of crustacean taxa compared among data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

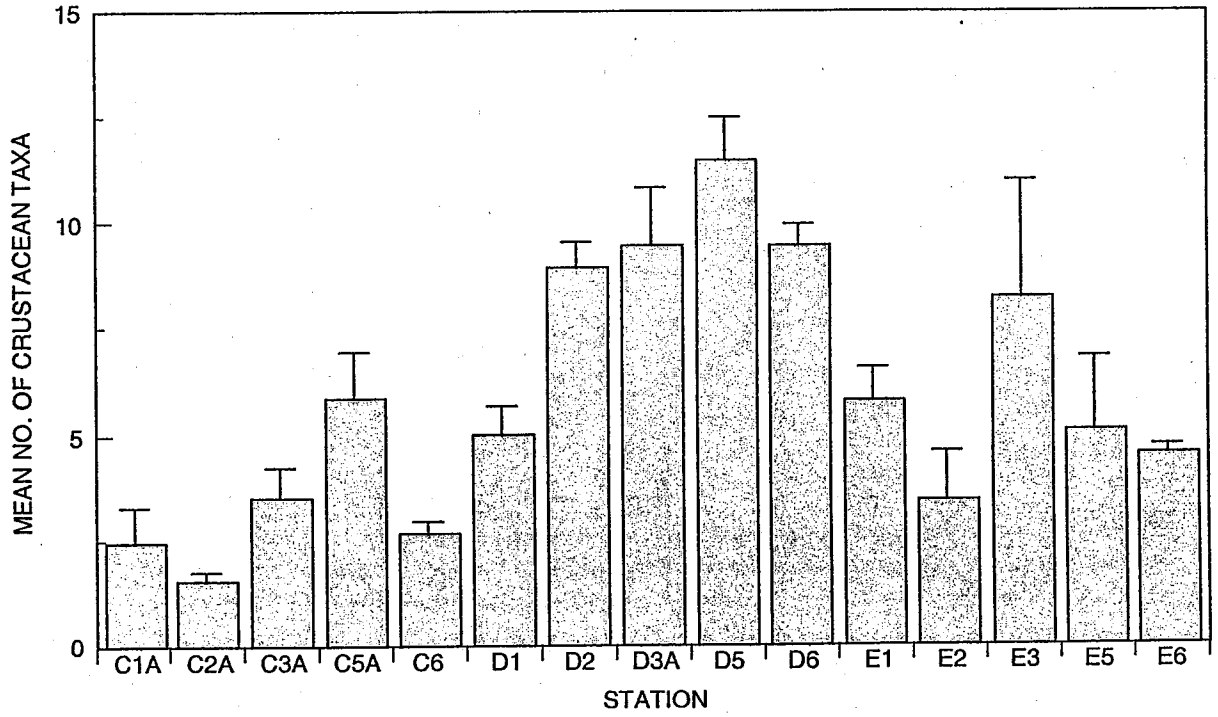


FIGURE 27. Mean (+1 SE) number of crustacean taxa compared among sampling stations for data collected in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

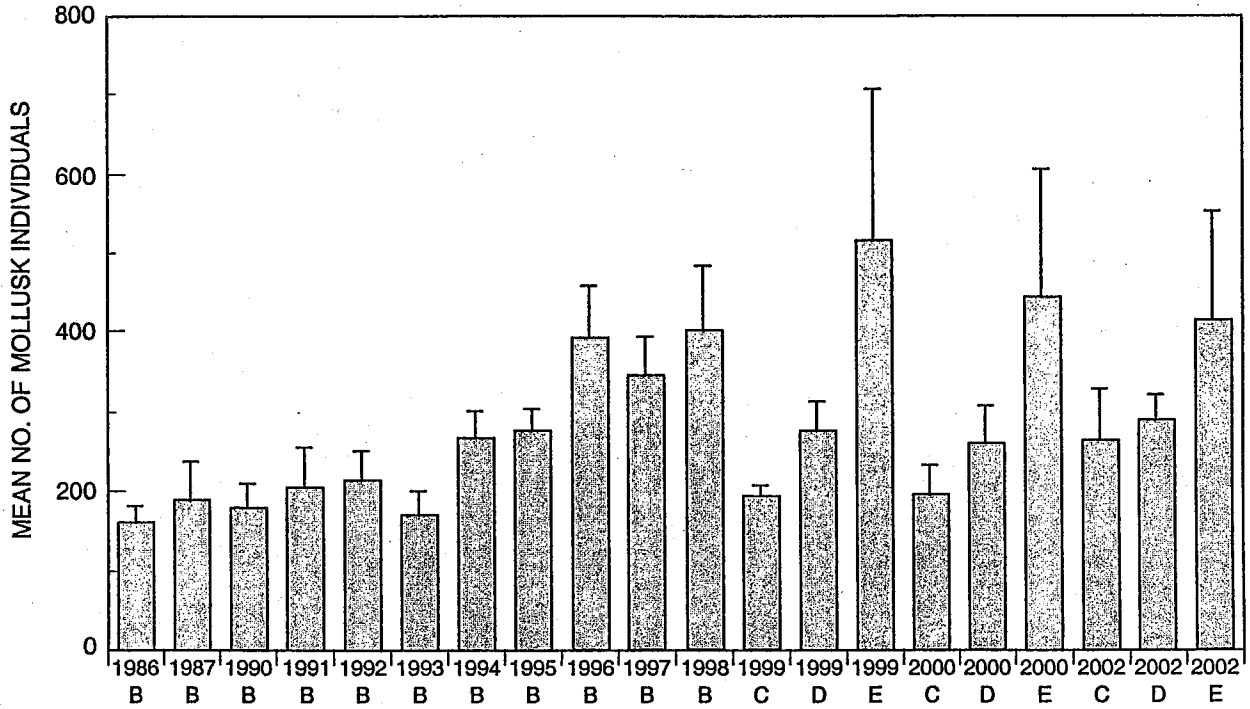


FIGURE 28. Mean (+1 SE) number of mollusk individuals compared among data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

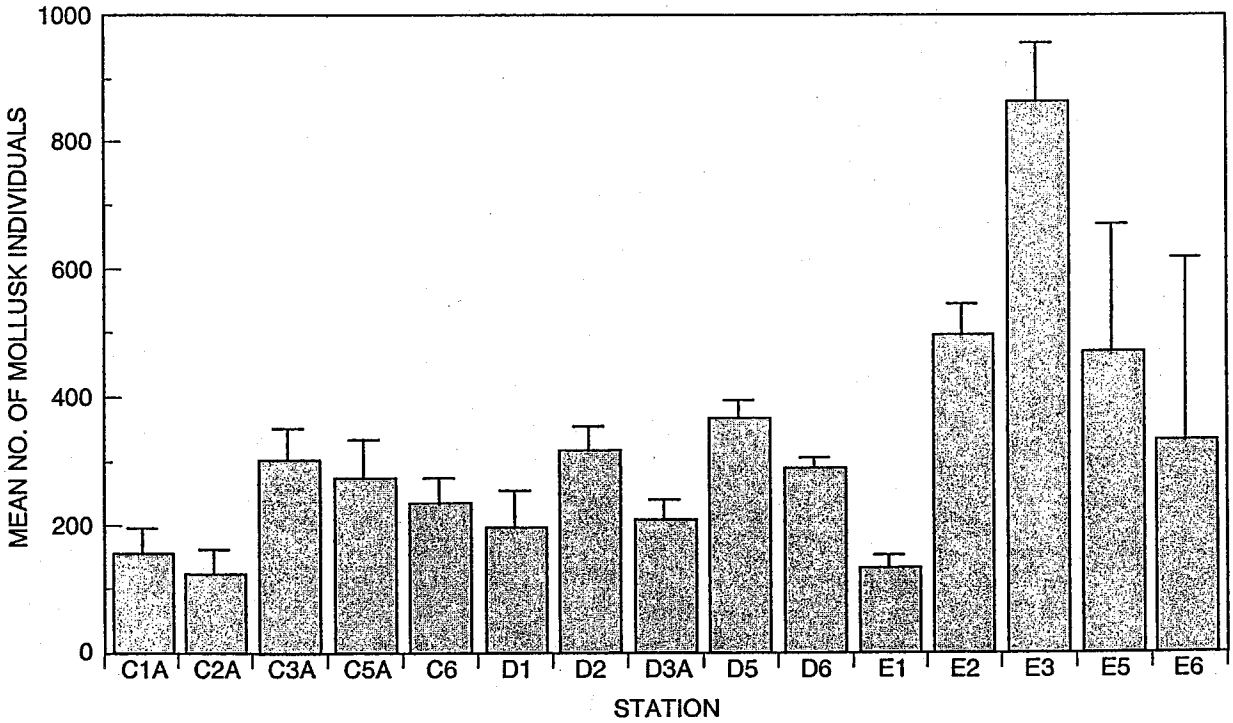


FIGURE 29. Mean (+1 SE) number of mollusk individuals compared among sampling stations for data collected in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

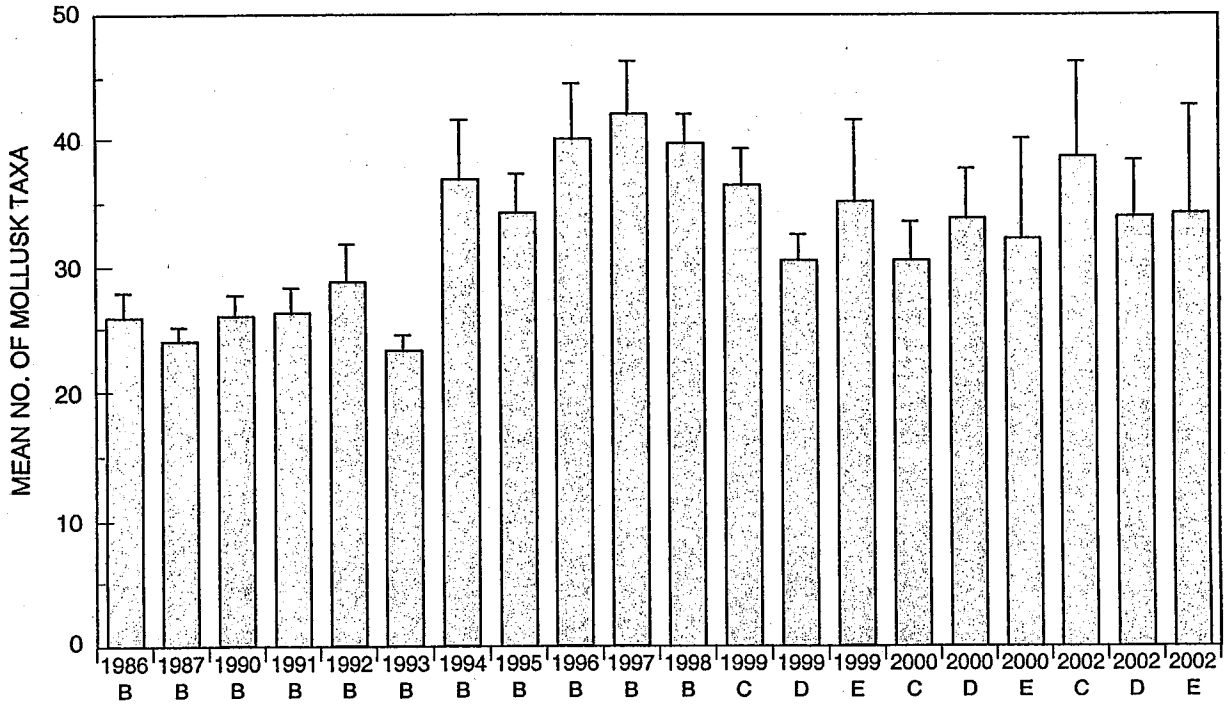


FIGURE 30. Mean (+1 SE) number of mollusk taxa compared among data collected at Transect B in 1986, 1987, and 1990 through 1998 and at Transects C, D, and E in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i

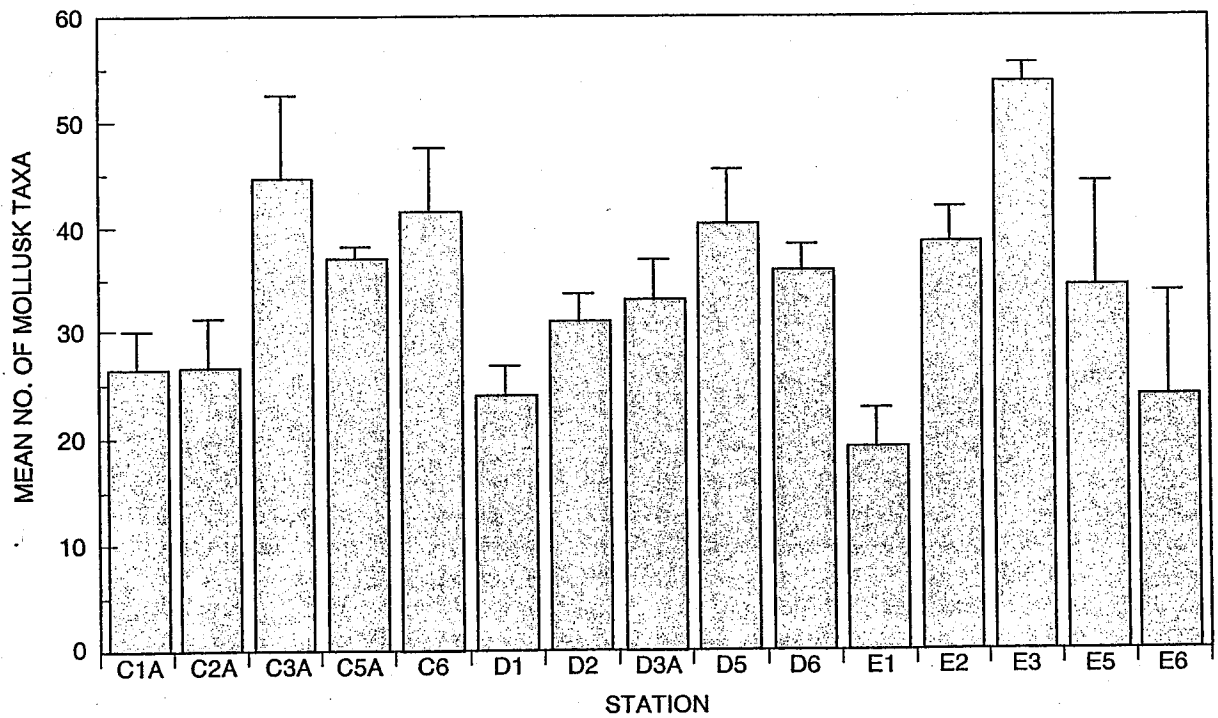


FIGURE 31. Mean (+1 SE) number of mollusk taxa compared among sampling stations for data collected in 1999, 2000, and 2002 at Sand Island Ocean Outfall sampling stations, O'ahu, Hawai'i