

CHAPTER 6

MACROFAUNAL ASSEMBLAGES

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INTRODUCTION

Macrofauna constitute a myriad of small-bodied (>1.0 mm in any one dimension) invertebrate organisms living in or on the sediments. They are an important component of the marine ecosystem, playing an important role through their feeding and burrowing (bioturbation) activities, stabilization of sediments through tube-building, input of larvae into pelagic and soft-bottom ecosystems, and trophic dynamics as both prey and predator. The macrofauna, being less mobile than the larger invertebrates and fishes, more accurately reflect the changes in the physical and chemical conditions of the soft-bottom ecosystem than the more mobile organisms. Monitoring the macrofaunal community is important because these organisms live in direct contact with the sediments and often ingest sediments and suspended particulates, which may contain organic food and/or contaminants (Gray *et al.* 1992, Diener *et al.* 1995).

Soft-bottom sediments provide a long-term record of changing environmental conditions reflecting the effects created by natural or man-made disturbances. Impacts of anthropogenic inputs, particularly those of sewage outfalls, will be manifested in the soft-bottom sediments by changes in macrofaunal community structure (e.g., abundance, diversity, and biomass). The soft-bottom macrofauna represent a community where the species assemblage can reflect a gradient of response (sensitive to tolerant) in relation to environmental (man-made or natural)

stresses (Pearson and Rosenberg 1978, Thompson *et al.* 1987, Gray 1989, Weston 1990, Ferraro *et al.* 1991, Warwick and Clark 1993, 1994, Diener *et al.* 1995, Sheppard 1995).

The macrofaunal assemblages of Los Angeles Harbor have been well documented by baseline studies since the mid-1970's (HEP 1976a, 1976b, 1980, 1983; SCOSC 1979, 1982; MEC 1988). When comparing the dominant species in the Harbor from historical records (Reish 1959, HEP 1980 and 1983, SCOSC 1982, MEC 1988) and from previous EMD surveys (CLA, EMD 1994-2006), it is apparent that the abundant species are composed of a core group of dominant organisms that vary in proportion from year to year. Some of these species include the amphipod *Amphidentopus oculatus*, the bivalve *Theora lubrica*, and polychaetes *Chaetozone corona*, *Cossura* spp. (*C. candida* and *C. sp. A* SCAMIT), *Monticellina sibilina*, *Mediomastus* spp., *Petaloclymene pacifica*, and *Paraprionospio pinnata*. Improvements in taxonomy that have occurred since samples were first collected and identified in 1954 have resulted in the identification of multiple species once considered as the same species. These include *Cossura* spp. (*Cossura candida* and *Cossura sp. A* SCAMIT), *Monticellina sibilina* (*Tharyx parvus*, *Tharyx tessellata*, *Tharyx* sp., and *Monticellina tessellata*), *Mediomastus* spp. (*Capitula ambiseta*, *Mediomastus ambiseta*, and *Mediomastus californiensis*), *Petaloclymene pacifica* (Maldanidae sp. A, Maldanidae sp. 1, and *Euchlymene* sp.), and *Scoletoma*

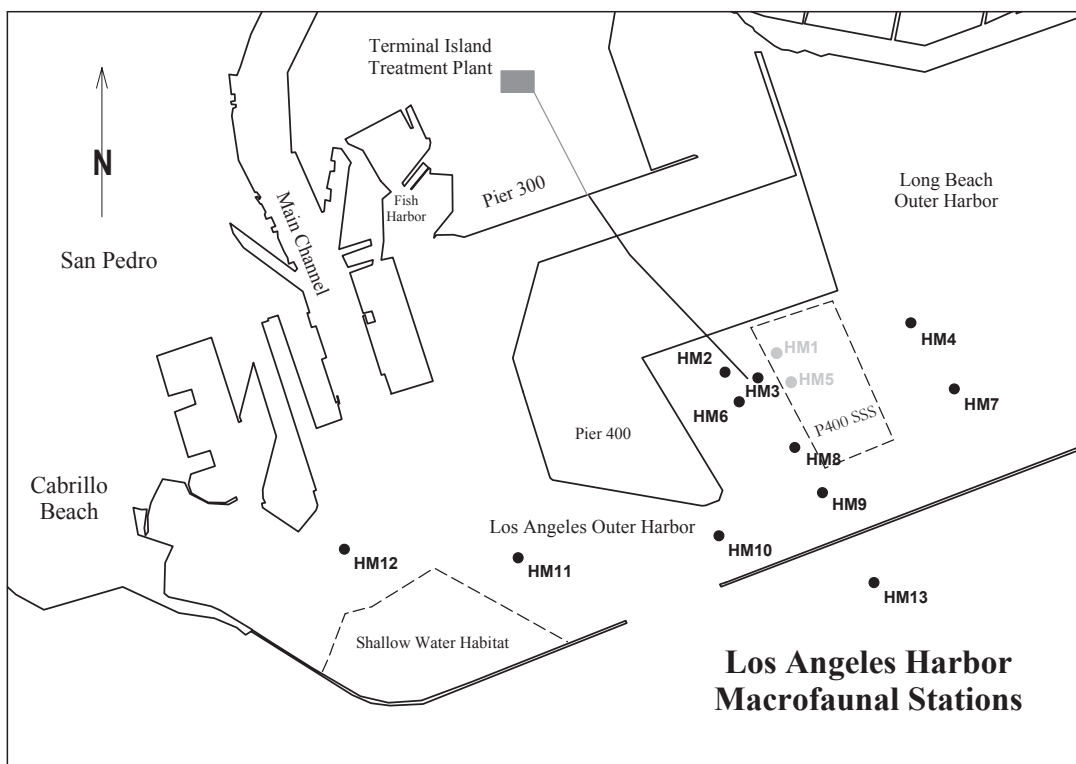


Figure 6-1. Macrofauna sampling stations in Los Angeles Harbor. Abandoned stations are depicted in gray.

sp. A (Harris) [*Lumbrineris* sp. A (Harris), *Lumbrineris* spp. and *Lumbrineris* Group III] and *Scoletoma* sp. B (Harris) [*Lumbrineris* sp. B (Harris), *Lumbrineris* spp. and *Lumbrineris* Group III].

Environmental Impact Reports have utilized these baseline surveys in assessing the potential impacts associated with the Pier 300/400 Implementation Project (PIP) (ACE 1992), the TIWRP [on September 7, 2007, following the completion of the major operational upgrade of the Advanced Wastewater Treatment Facility (AWTF), the official name of the Terminal Island Wastewater Reclamation Plant (TIWRP)] Outfall Modernization Project (ES 1994) and the Port of Los Angeles Channel Deepening Project (ACE 2000a, 2000b, 2003). Some of the relevant construction activities at the Los Angeles Harbor are summarized below (for details, see Chapter One of this report):

- Pier 300 dredge and fill activities smothered infauna (MEC 1988) in the mid-1980's.

- Pier 400 dredge and fill activities (July 1996 - April 2000) again smothered infauna with greatest impacts in 1997, followed by rapid recovery (CLA,EMD 1998-2003).
- The Channel Deepening Project (Oct. 2000-Dec. 2003) of Los Angeles Harbor filled the northern side with few impacts to Outer Harbor infauna near TIWRP Outfall (direct observations).
- Pier 400 Submerged Storage Site (P400 SSS) construction activities in 2002-2003, impacts reported herein, created limited station access.
- During 2003, access to the required TIWRP NPDES sampling stations HM1 and HM5 were permanently lost due to the deposition of dredged sediments into the P400 SSS.
- Dredge and fill operations associated with P400 SSS persisted in 2004 and 2005 as witnessed by direct observations of both the activity and

distinct, new sedimentary layers of different color on the upper surface of samples as they were collected.

- Continued progression of deposition of dredged Los Angeles Harbor sediments and removal of these stored sediments as fill material for continuing, albeit intermittent over the 2006-2007 biennium, Los Angeles Harbor construction projects.

As required by the Los Angeles Regional Water Quality Control Board (LARWQCB), the macrofauna in the vicinity of the TIWRP Outfall are to be monitored to determine impacts that may have occurred due to the discharge of tertiary effluent. Due to dredge and fill activities associated with Pier 300/400, major disruptions occurred in the original 1993 NPDES-required permit sampling program. Following approval by the LARWQCB in September 1995, an Interim Monitoring Program was initiated (see Chapter 1). With completion of the new TIWRP terminus and the initiation of effluent discharge into the new area of the Outer Harbor next to the southeast face of Pier 400 in July 1996, the TIWRP marine monitoring program was modified to accurately assess environmental impacts that may occur at this discharge point. With the approval of the LARWQCB in July 1996, the Post-Pier 400 Monitoring Program was implemented in August 1996 (see Chapter 1).

Since the 1996 summer survey, with the exception of the 1998 and 2003 summer surveys [due to the Southern California Bight 1998 (Bight '98) and 2003 (Bight '03) Regional Monitoring Surveys' receiving water sample resource exchange], the Los Angeles Harbor Annual Assessment Reports (CLA, EMD 1997-2006) have been based on the Post-Pier-400 Monitoring Program. This second Biennial Assessment Report (see Chapter 1) is presented and based on requirements set forth in the most recent NPDES permit (NPDES NO. CA0053856) adopted in 2005.

MATERIALS AND METHODS

SAMPLE COLLECTION

Single macrofaunal grab samples were collected annually at 11 NPDES sites HM1 – HM13 from the Outer Los Angeles Harbor and outside the breakwater (Figure 6-1). Stations HM1 and HM5 have been permanently excluded from the sample array since winter 2003 as they are inaccessible due to construction of the P400 SSS (see Chapter 1, CLA, EMD 2004). For 2006, the annual collections occurred on August 3 and 10. For 2007, the collections occurred on July 31 and August 2. All infauna and sediment samples were collected from the M/V Marine Surveyor. Station locations were positioned using GPS coordinates and Maptech Offshore Navigator version 5.04 navigational software. Station locations, coordinates, depths, and grab attributes, such as sediment odor, color, and composition, were recorded in the Field Data System (FDS) software.

All samples of infauna and sediment were collected with a modified Van Veen grab sampler (Word 1976), which sampled an approximate surface area of 0.1 m², following guidelines provided in SCBPP 1994, SCBRMP 1998, and SCBRMP 2003. Acceptable samples were required to have minimal surface disturbance with no leakage, canting, or washing and a penetration depth greater than 10 cm (SCBPP 1994, SCBRMP 1998, 2003). The Van Veen was placed onto a specially designed sample-washing table and assessed for sample acceptability; those with minimal surface disturbance were retained. If the sample was accepted, the inside of the Van Veen was rinsed for adhering sediments. The sample was washed carefully with seawater from a hose fan-spray (to avoid animal fragmentation) through a 1.0-mm mesh screen. The material retained on the screen was placed into a 1-liter Nalgene container; any animals adhering to the screen were carefully removed with forceps and added to the container. Containers were filled to no more than two-thirds volume with sample material to allow for proper fixation of animals. A 0.2% solution of propylene phenoxytol was initially added to each container to

relax the animals in order to prevent fragmentation during preservation. After a minimum of 30 minutes, the sample was preserved in a 10% buffered seawater-formalin solution. All containers were labeled on both the inside and outside and transported to the laboratory in plastic crates.

LABORATORY ANALYSIS

Samples were re-screened and transferred to 70% ethanol for storage and sample processing after a minimum of 48 hours in formalin. Samples were sorted using stereoscopic dissection microscopes into six basic taxonomic groups: polychaetes, crustaceans, molluscs, echinoderms, ophiuroids, and miscellaneous (other invertebrate phyla). To increase sorting efficiency for samples having large clumps of ophiuroids, only the disks were sorted from the debris for identification. Each sorted sample was checked to determine if a minimum of 95% of all organisms were removed. If less than 95% of the individuals had been removed, then the sample was completely resorted. All individuals were identified to species or lowest possible taxon. To ensure taxonomic consistency, the identifications of organisms collected were compared with the laboratory voucher collection. All questionable identifications or unknowns were sent to specialists for confirmation or identification. Specialists are recognized experts and usually are members of the Southern California Association of Marine Invertebrate Taxonomists (SCAMIT). Additional QA/QC included standardization of identification with accepted taxonomic designations of SCAMIT to ensure consistency with other marine monitoring programs in southern California (SCAMIT 1994, 2001).

COMMUNITY PARAMETERS

Simple community parameters, i.e., total number of species (S), total number of individuals (N), Margalef's species richness (d), Pielou's evenness (J'), Shannon-Wiener index of diversity (H'), and Simpson's dominance ($1-\lambda'$) were calculated for

each individual sampling event. These concepts and calculations are presented in Magurran (1988). Additionally, a suite of phylodiversity indices (Clarke and Gorley 2006, Clarke and Warwick 1999, Clarke and Warwick 2001) including variations of taxonomic distinctness and phylogenetic diversity were also calculated. Each of these phylodiversity indices are a more accurate representation of biodiversity than traditional diversity indices due to their incorporation of the cladistic or phylogenetic structure of the sample (community). For further explanation see Appendix B. The phylodiversity indices, as well as all graphics derived from them, require the construction of an appropriate (species relevant), comprehensive 'master species list' of which the given sampling events are compared. This list was created from the EMD database using data restricted to the Los Angeles Harbor from the inception of the TIWRP Receiving Water Monitoring Program in 1993 to the present. All community parameters, traditional diversity indices, and phylodiversity indices were calculated in Primer v6 (Clarke and Gorley 2006).

SPECIES ASSEMBLAGE ANALYSIS

The benthic macrofaunal community, represented by the 22 (11 per year) sampling events, was initially analyzed using a particular methodology of cladistics called parsimony analysis of endemism (PAE). PAE uses a parsimony algorithm in order to obtain area or site cladograms based on the taxa (descriptors) inhabiting the areas under scrutiny (monitoring stations). This was applied to both the binary (presence/absence) and the abundance data captured via step-matrices. The cladograms were generated using both the branch and bound algorithm for the smaller data sets (13 or fewer objects) and the heuristic search, Tree-Bisection and Reconnection (TBR) algorithm for the larger data sets (14 or more objects) from the computer program PAUP* [Phylogenetic Analysis Using Parsimony (*and other methods)] Version 4.0b10 (Swofford 2000).

From the PAE (cladistic) analyses, the patristic distance (branch length) values, which are properties

of the cladograms, were used as the nucleus from which non-metric multi-dimensional scaling (NMDS) analyses were conducted. Patristic distances were chosen as it has been shown that pairwise similarity or distance is underestimated by the conventionally used phenetic distance methods (e.g., Bray-Curtis). Pairwise comparisons using cladistic methods, which include all changes (including homoplasy or lack-of-fit) along the branches, is a better estimator or representation of the data (Smith 1994). This was first underscored by Farris (1979) showing that both distance and character information are better retained by phylogenetic than by phenetic classifications. See Appendix B for expanded details regarding the various methodologies utilized herein.

Additionally, a novel and prototypical multivariate ordination method, evolutionary principal components analysis (EPCA), was applied to the data set. EPCA functions by reconstructing shared states via squared-change parsimony, then performing Principal Components Analysis (PCA) on the vectors of change along each branch of the cladogram. Hence, the ordination acts directly upon the tree or cladogram. Most ordination techniques are based on phenetic similarity or dissimilarity indices. However, using the information from a parsimony or cladistic analysis to guide an ordination allows the ordination to maximize the shared-derived or synapomorphic differences among objects, rather than some arbitrary static property of the data such as variance, which is conventionally used in PCA. This approach (EPCA) gives insight, by capturing the most change in the system, not available using standard multivariate ordinations. EPCA and PCA calculations were carried out in the Rhetenor module within Mesquite 1.05 (Maddison and Maddison 2005).

Finally, it is well established in the literature that communities, as well as the distribution of species in communities are hierarchical and nested (O'Neill *et al.* 1986, Allen and Starr 1982); therefore, this sharing of characteristics (species) leads to the non-independence of the observations under study. Thus many theories and statistical models conventionally

used in ecological studies are in need of revision (Legendre and Legendre, 1998). In order to associate or correlate the limited abiotic data (sediment granulometry) with the station relationships derived from the infauna data and to factor or partition out any hierarchical auto-correlation [in other words, the non-independence of the data due to communities in different regions sharing species (Fox *et al.* 2000), or spatial auto-correlation (Legendre and Legendre, 1998)], the method of independent contrasts was utilized using the PDAP:PDTREE module in Mesquite 1.05 (Midford *et al.* 2002). Independent contrasts calculate contrasts between pairs of stations along the nodes to the termini of the cladogram. These contrasts are calculated vertically, down the branches at every node linking stations exhibiting immediate common biological response (similar infaunal community structure in response to similar abiotic spatiotemporal structure), essentially removing the aforementioned causes of non-independence and creating values representing independent events. If two traits are correlated (e.g., silt and sand), then a large calculated contrast with one trait in a given node should be associated with a large contrast in the other (Gittleman and Luh 1994). A known cladogram is essential to using independent contrast methodology.

Using the BIO-ENV routine, Spearman rank correlational coefficients were generated in an iterative fashion by simultaneous matching of the biotic patristic distance and normalized abiotic Euclidean distance triangular (pair-wise) matrices to determine a subset of environmental variables that best 'explain' the community topology. Primer v6 was used for all multivariate NMDS and BIO-ENV treatments (Clarke and Gorley 2006). All NMDS analyses were carried out with 1,111 restarts in order to keep from being trapped in local sub-optimal minima. The BIO-ENV routine was executed using default settings of a maximum of five variables and ten restarts.

Environmental (sediment chemistry and granulometry) data and individual taxa were then mapped onto the macrofauna community cladograms using Mesquite version 1.05 (Maddison

and Maddison 2005). The mirror-tree capability facilitated the elucidation of patterns, or lack thereof, associated with particular taxa and/or environmental data with those of the species assemblage cladograms.

In addition to the cladograms showing the relationships of the objects or stations (Q-analysis), cladograms of species groups showing the association or co-occurrence of these descriptors or species with one another (R-analysis, Legendre and Legendre 1998) were also produced for all infaunal organisms. This parsimony analysis of co-occurring species has been coined "PACOS" herein. All analyses were performed with the computer program PAUP* - Phylogenetic Analysis Using Parsimony (* and other methods) version 4.0b10 (Swofford 2000).

All taxa, with the exception of supraspecific taxa (possibly representing more than a single species) were used in the analyses regardless of their occurrence or abundance rarity.

See Appendix B for remaining methodological details.

RESULTS

COMMUNITY PARAMETERS

The total number of species (S), total number of individuals (N), Margalef's species richness (d), Pielou's evenness (J'), Shannon-Wiener index of diversity (H'), Simpson's dominance ($1-\lambda'$), Benthic Response Index (BRI), and phylodiversity indices [taxonomic diversity (Δ), taxonomic distinctness (Δ^*), average taxonomic distinctness (Δ^+), total taxonomic distinctness ($S\Delta^+$), variation in taxonomic distinctness (Λ^+), average phylogenetic diversity (Φ^+), and total phylogenetic diversity ($S\Phi^+$)] are summarized for the 2006-2007 biennial surveys in Table 6-1.

2006-2007 Biennium

There were 4,895 individuals comprising 236 taxa (both species and unique supraspecific taxa) collected within 22 sampling events at 11 stations for the 2006-2007 biennial sampling period (Table 6-1). Separation of years for comparison with the previous annual report revealed that 2006 had 2,172 individuals, 2007 had 2,723. Similarly, taxa richness was highest in 2007 with 199, followed by 179 in 2006.

The ten most abundant species of the 2006-2007 biennium were *Cossura* sp. A (262=5.4%), *Streblosoma* sp. B (211=4.3%), *Scleroplax granulata* (198=4.0%), *Amphidentopus oculus* (176=3.6%), *Pinnixa franciscana* (161=3.3%), *Scoletoma* sp. A (159=3.2%), *Neotrypaea gigas* (155=3.2%), *Spiophanes berkeleyorum* (150=3.1%), *Nuculana taphria* (150=3.1%), and *Amphiodia urtica* (142=2.9%). There were 131 taxa (55.5%) that had abundances of five or less. The fifteen most widely occurring taxa were *Pista wui*, *Scoletoma* sp. A, and *Streblosoma* sp. B, all occurring 21 out of 22 times, followed by *Spiophanes berkeleyorum* (20), *Tubulanus polymorphus*, *Theora lubrica*, *Paraprionospio pinnata*, and *Scleroplax granulata* (19), *Amphiodia urtica*, *Cossura* sp. A, *Spiochaetopterus costarum*, *Terebellides californica*, *Listriella goleta*, *Neotrypaea gigas*, and *Pinnixa franciscana* all with 18. There were 155 taxa (65.7%) that occurred five or less times.

In 2006, the ten most abundant species were *Cossura* sp. A (152=6.9%), *Streblosoma* sp. B (143=6.6%), *Monticellina siblina* (87=4.0%), *Spiophanes berkeleyorum* (83=3.8%), *Scleroplax granulata* (81=3.7%), *Scoletoma* sp. A (74=3.4%), *Pista wui* (70=3.2%), *Amphiodia urtica* (67=3.1%), *Neotrypaea gigas* (63=2.9%), and *Terebellides californica* (47=2.2%). The most widely occurring species were *Streblosoma* sp. B, *Scoletoma* sp. A, *Pista wui*, *Tubulanus polymorphus* collected 11 out of 11 times, and *Spiophanes berkeleyorum*, *Terebellides californica*, and *Spiochaetopterus costarum* collected 10 out of 11 times.

In 2007, the eleven most abundant species were *Amphidentopus oculus* (161=5.9%), *Nuculana taphria* (130=4.8%), *Pinnixa franciscana* and *Scleroplax granulata* (117=4.3%), *Cossura* sp. A (110=4.0%), *Theora lubrica*

Table 6-1. Los Angeles Harbor 2006-2007 biennium community parameters for combined fish and megainvertebrates. Community parameters: total number of species (S), total number of individuals (N), Margalef's species richness (d), Pielou's evenness (J'), Shannon-Wiener index of diversity (H'), Simpson's dominance ($1-\lambda'$), Benthic Response Index (BRI), and phylodiversity indices [taxonomic diversity (Δ), taxonomic distinctness (Δ^*), average taxonomic distinctness (Δ^+), total taxonomic distinctness ($S\Delta^+$), variation in taxonomic distinctness (Λ^+), average phylogenetic diversity (Φ^+), and total phylogenetic diversity ($S\Phi^+$)].

	S	N	d	J'	H'(loge)	$1-\lambda'$	Δ	Δ^*	Δ^+	$S\Delta^+$	Λ^+	Φ^+	$S\Phi^+$	BRI
HM2 2006	52	158	10.07	0.84	3.34	0.95	71.06	75.01	83.99	4367.69	497.55	46.56	2420.89	32.67
HM2 2007	79	411	12.96	0.83	3.63	0.95	80.06	84.04	86.83	6859.68	452.32	42.66	3370.37	18.73
HM3 2006	55	232	9.91	0.85	3.39	0.94	70.00	74.13	81.40	4476.94	543.78	43.51	2393.30	9.74
HM3 2007	56	142	11.10	0.92	3.69	0.97	87.15	89.75	89.22	4996.40	380.80	50.66	2836.75	8.30
HM4 2006	58	281	10.11	0.83	3.36	0.94	74.76	79.40	82.92	4809.45	522.51	44.63	2588.78	15.66
HM4 2007	51	165	9.79	0.88	3.45	0.96	80.72	84.25	85.48	4359.67	481.94	47.31	2413.04	30.13
HM6 2006	43	136	8.55	0.87	3.29	0.95	73.59	77.68	84.36	3627.55	499.36	47.11	2025.60	15.13
HM6 2007	56	193	10.45	0.86	3.45	0.95	80.18	84.31	84.92	4755.44	508.02	43.98	2463.06	11.68
HM7 2006	53	149	10.39	0.89	3.55	0.96	80.56	83.71	85.78	4546.09	486.70	47.87	2536.91	9.10
HM7 2007	33	128	6.60	0.74	2.60	0.86	75.75	88.35	89.39	2949.98	369.86	54.19	1788.21	24.03
HM8 2006	64	253	11.39	0.78	3.24	0.92	70.00	76.46	81.70	5229.02	525.99	44.62	2855.84	21.28
HM8 2007	82	316	14.07	0.83	3.64	0.94	83.99	88.94	86.42	7086.30	465.65	41.37	3392.53	2.80
HM9 2006	54	134	10.82	0.92	3.68	0.97	87.48	89.85	85.88	4637.50	476.35	46.81	2527.64	12.53
HM9 2007	69	340	11.67	0.82	3.46	0.93	83.72	89.99	87.24	6019.66	427.10	46.99	3242.37	12.91
HM10 2006	77	277	13.51	0.86	3.73	0.95	87.71	92.03	88.28	6797.75	400.62	45.97	3539.83	29.48
HM10 2007	84	427	13.70	0.85	3.76	0.96	87.91	91.59	87.73	7369.43	431.10	43.64	3665.83	0.23
HM11 2006	53	189	9.92	0.86	3.40	0.95	80.87	85.01	87.47	4635.82	440.31	49.72	2635.16	14.07
HM11 2007	80	312	13.76	0.81	3.55	0.94	81.35	86.33	86.97	6957.61	441.84	46.73	3738.76	10.19
HM12 2006	50	180	9.44	0.85	3.31	0.95	72.44	76.25	84.43	4221.36	481.99	48.32	2415.86	16.29
HM12 2007	34	111	7.01	0.89	3.12	0.95	72.01	75.85	81.12	2758.10	551.18	49.05	1667.54	11.40
HM13 2006	87	298	15.10	0.88	3.94	0.97	70.27	72.29	79.45	6912.09	525.37	41.95	3649.80	27.76
HM13 2007	102	300	17.71	0.90	4.17	0.98	81.82	83.52	86.24	8796.57	449.36	43.04	4390.51	27.98

(96=3.5%), *Neotrypaea gigas* (92=3.4%), *Scoletoma* sp. A (85=3.1%), *Streblosoma* sp. B (68=2.5%), *Spiophanes berkeleyorum* (67=2.5%), and *Listriella goleta* (51=1.9%). The most widely occurring species (10 out of 11 times) were *Amphideutopus oculatus*, *Pinnixa franciscana*, *Scleroplax granulata*, *Theora lubrica*, *Neotrypaea gigas*, *Scoletoma* sp. A, *Streblosoma* sp. B, *Spiophanes berkeleyorum*, *Listriella goleta*, *Pista wui*, *Paraprionospio pinnata*, *Notomastus* sp. A, and *Phoronis* sp.

Ordinated by the total number of species, the biennial samples having the five highest values were HM13 2007 (102), HM13 2006 (87), HM10 2007 (84), HM8 2007 (82), and HM11 2007 (80). The samples with the lowest number of species were HM7 2007 (33), HM12 2007 (34), and HM6 2006 (43).

The total number of species or taxa between 2006 and 2007 was similar, with an average of 59 species per station in 2006 and 66 in 2007. The average number of individuals was also relatively similar over the two-year sampling period with an average of 208 individuals per station and 250 individuals per station in 2006 and 2007, respectively.

TRADITIONAL DIVERSITY INDICES

All traditional diversity indices, generally tracked taxa richness with values from Station HM13 located outside the breakwater exhibiting the highest values (Table 6-1).

PHYLODIVERSITY INDICES

Two members of the phylodiversity index suite, total taxonomic distinctness ($s\Delta+$) and total phylogenetic diversity ($s\Phi+$), have even greater tracking performance than those of the traditional path with the total number of species as shown by extremely high Pearson Product-Moment Correlation Coefficients (PPMCC) derived from the Independent Contrasts module within Mesquite, $r = 0.99$ and 0.97 , respectively, and low two-tailed

p -values of 0.0 and 1.5×10^{-13} , respectively. The remaining phylodiversity indices depart dramatically in traction with taxa richness as low PPMCC and high p -values (values not shown herein are available by request from EMD upon request). The phylodiversity indices along with most traditional indices (Table 6-1) show a general pattern of the communities outside the breakwater being slightly more biodiverse than that seen inside the breakwater.

BRI

The Benthic Response Index (BRI) (Smith *et al.* 2001) was calculated pursuant to NPDES NO. CA0053856, Footnote 7. According to Smith *et al.* 2001, BRI values ranging from 0 to 33 suggest reference conditions, a range between 34 and 43 (loss in biodiversity; lower value represents threshold where 25% of species occurring at reference sites are not encountered), a range between 44 and 73 (loss in community function; lower value represents threshold where 90% and 75% of echinoderms and arthropods, respectively, were excluded), and a range between 72 and 100 (defaunation; lower value represents threshold where 90% of the species found at reference sites were excluded). Although the values are established for harbors, the response levels employed were originally developed for mainland shelf application and are currently being refined for bays and harbors. Nonetheless, they serve only as approximate perturbational response ranges to discriminate samples based on a subset of a priori species selections and scorings.

The BRI values ranged from 0.23 to 32.67. Hence, according to Smith *et al.* (2001) we can assume that all of our samples exist in the reference condition realm.

As in previous reports and most other community analyses, a characteristic species abundance pattern emerged: only a minor subset of species are highly abundant and/or widely occurring, a few species possess moderate to high abundance, and the majority of species are represented by very few

or by single individuals. The shape of the species rank-abundance curve for all infaunal data seems to mimic the axiomatic logistic-J distribution (Dewdney 2003), with a few highly abundant, widely occurring species, followed by a very long tail of exclusively distributed (rare and often hierarchically nested) taxa.

PARSIMONY ANALYSES AND ORDINATIONS

All available taxa and all sampled stations were used in the biennial cladistic analyses. A single (most parsimonious) tree (Figure 6-2) resulted from the biennial analysis. The tree possessed a tree length of 697.94, a consistency index of 0.2943 (maximal value = 1.00), and a retention index of 0.3840 (maximal value = 1.00). One of the most conspicuous groupings, revealed by the cladogram (Figure 6-2), was that the two most species-rich samples from Station HM13 with the highest sand fraction outside the breakwater, used as the outgroup, remained well removed from the stations found within the Harbor.

Dissecting the ingroup, reveals a terminal clade composed of samples from stations HM9 and HM10. Both stations are the deepest infauna stations found at a depth of 24 meters. The main body of the cladogram bordered by Stations HM8 2006 and HM3 2007 are all found between 11 and 17 meters. Superimposed upon this general depth pattern is an obvious increase in like-station groupings relative to recent reports. For example, both HM10 samples group together, HM9 samples group “paraphyletically” within the same apical subclade, both samples from Station HM11 are only 3 nodes removed, the two samples from Station HM12 form a common clade, as does the two samples from Station HM4, the two samples from HM2 form a “paraphyletic” group two nodes removed, and as previously stated the two samples from Station HM13 form a “monophyletic” outgroup.

The samples from Outfall Station HM3 do not group very closely to each other, even though both samples possessed near average species richness

values with HM3 2006 and HM3 2007 containing 55 and 56 species, respectively.

Direct character mapping of the species back onto the cladogram reveals that the majority of the species occur with rather “homoplasious” distributions as indicated by the relatively low consistency index. Despite this situation there are some examples of species with perfect fits to the cladogram such as *Cylichna diegensis* found exclusively at Stations HM10 2006 and HM10 2007, and *Foxiphalus obtusidens*, *Glottidia albida*, *Mooreonuphis nebulosa*, *Owenia fusiformis*, and *Scoloplos acmeceps*, all functioning as “synapomorphies” grouping the outgroup station samples HM13 2006 and HM13 2007 together.

The patristic distance (branch-lengths derived from the cladogram) of the PAE pair-wise matrix was subject to 3-D non-metric multi-dimensional scaling (NMDS) to develop patterns that may otherwise be latent (Figure 6-3).

The expanded view of the 3-D cube of Figure 6-3 illustrates the configuration of the community and reiterates the cladogram sample event relationships with similar depth and station grouping fidelity as evidenced by the proximity of similar station samples.

The novel utilization of parsimony for an R-mode analysis proved very informative regarding the distributions and associations of the various species. The PACOS cladogram was rooted with two outgroups devoid of any species (Lundberg rooting). Several very similar, equally-parsimonious PACOS cladograms were generated with a tree length of 383, a very low consistency index of 0.0574, but a very high retention index (a measure of branch support) of 0.7144. A single cladogram (Figure 6-4) was randomly chosen to present. The circular cladogram reveals three interesting areas of species groupings. The first group of interest appearing as a fan of taxa located to the left bordered by *Zeuxo normani* and *Odostomia (Evalea)* sp. are the taxa mainly found at HM13 during 2007. The second clade of interest resembles a small curved rake with short branch lengths on the right side of the

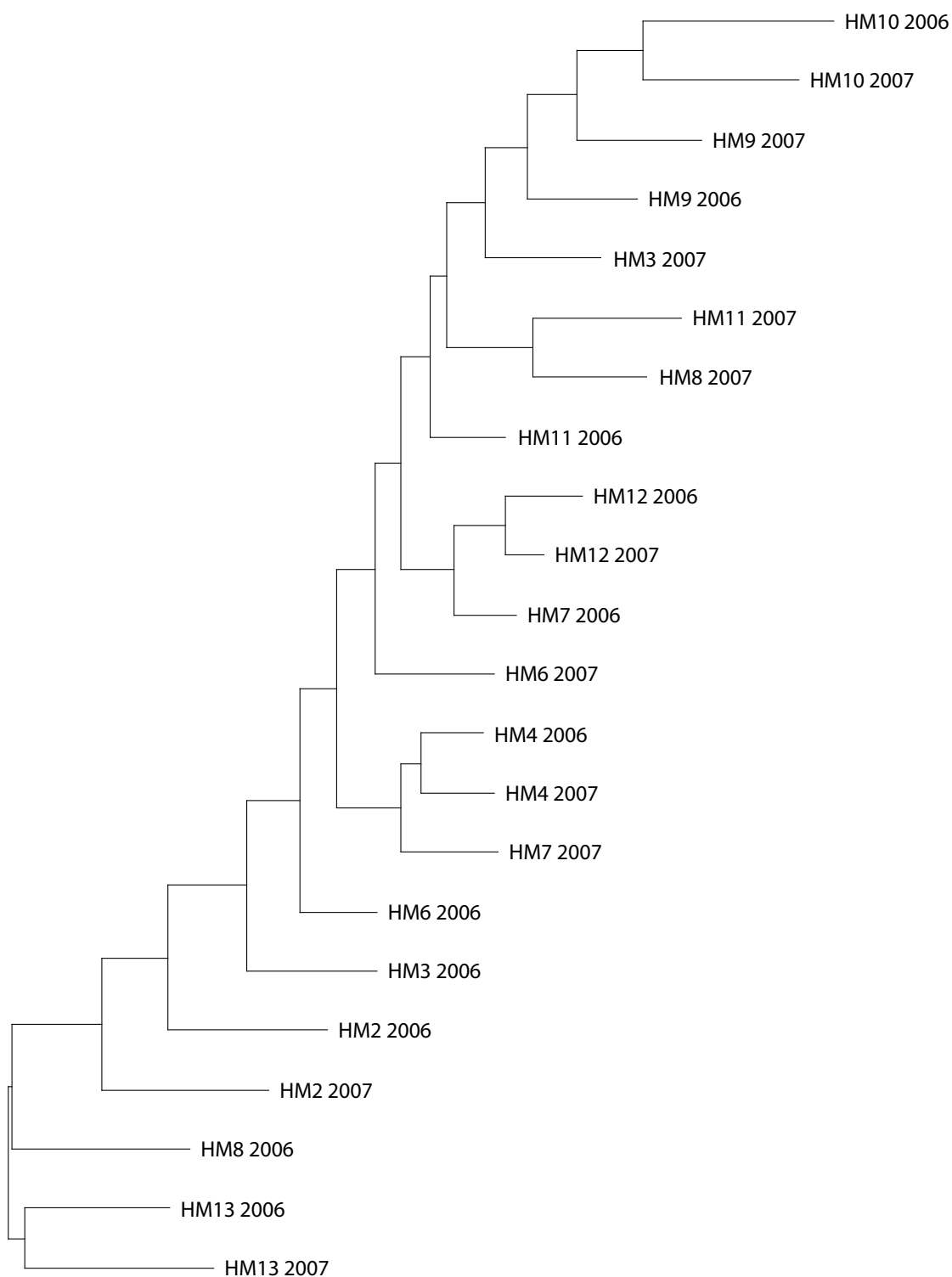


Figure 6-2. Parsimony analysis of endemicity (PAE) cladogram for the 2006-2007 biennial monitoring stations.

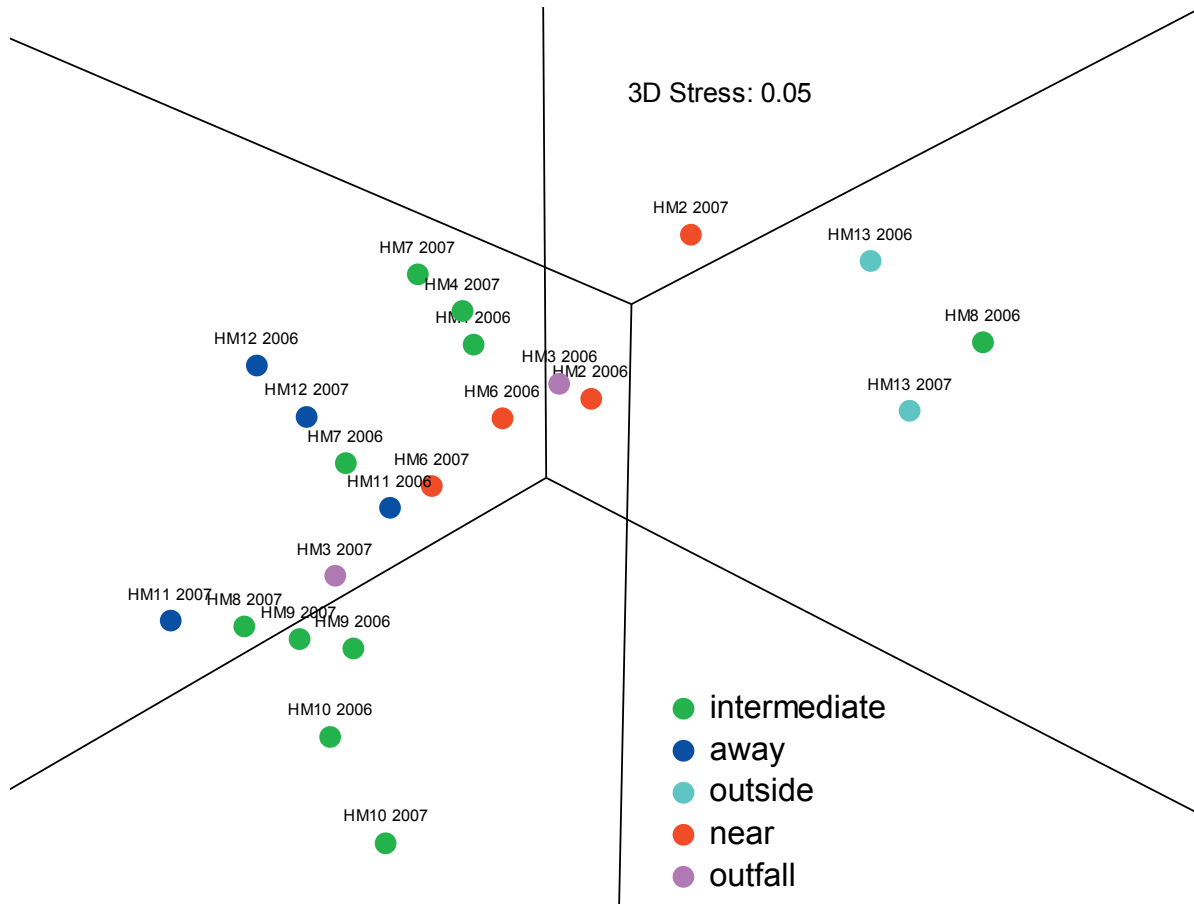


Figure 6-3. Expanded non-metric multi-dimensional scaling (NMDS) using patristic distances derived from the PAE cladogram. Locations are depicted as factors in color.

cladogram. Bordered by *Alcyonidium* sp. A and *Syllis* (*Ehlersia*) *heterochaeta*, this group is composed of species mainly found at station HM13 during 2006, located outside of the breakwater. The other clade with many nested subclades located at the bottom of cladogram bordered by *Prionospio* (*Minuspio*) *lighti* and *Ampelisca cristata microdentata*, is composed of the most widely occurring species.

ANALYSIS OF THE BIOLOGIC COMMUNITY AND ENVIRONMENTAL VARIABLES

The matching of the normalized Euclidean distance abiotic/environmental matrix with the patristic distance pair-wise biotic matrix performed with the BIO-ENV routine in Primer v6 (Clarke and Gorley 2006) identified percent silt, sand, nickel, and depth

as the highest correlating variable combination ($r=0.730$).

Additionally, a principal components analysis (PCA) was conducted upon the PAE cladogram with the sediment, depth, and chemical constituent data. The ordination (Figure 6-5) showing the greatest spatial dispersion and topological congruence with the PAE cladogram was with the sediment granulometry data (clay, silt, and sand fractions). Character loadings on the first four principal component axes were 31.45%, 17.11%, 11.58%, and 10.40%, respectively. Independently mapping the sand fractions (Figure 6-5) readily shows higher percentages were found outside the Harbor at Station HM13. Undoubtedly, the difference in the micro-topography is largely responsible for the difference in the composition of the species assemblages found in these two different areas. Independent contrasts (Pearson Product-

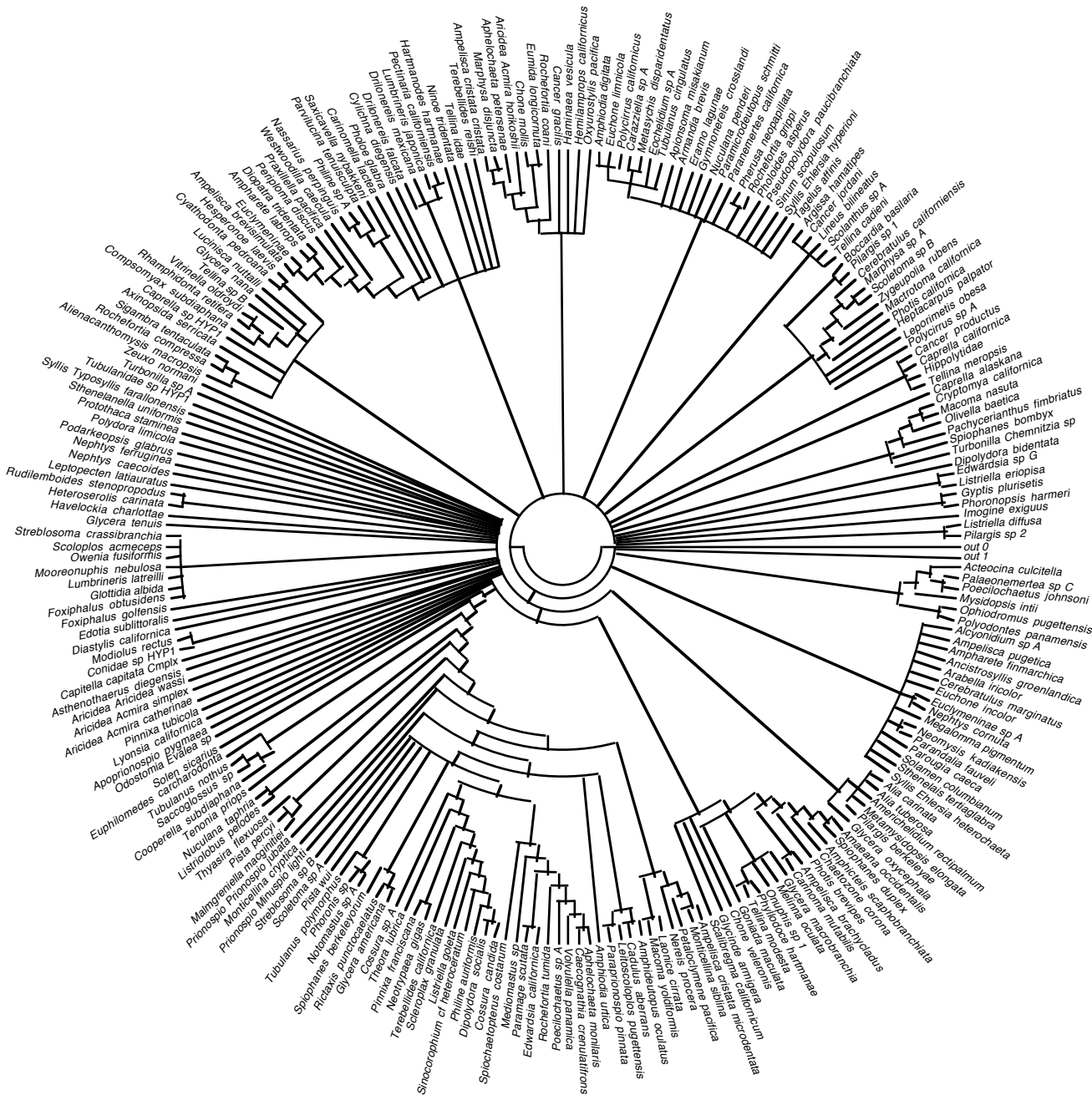


Figure 6-4. Parsimony analysis of co-occurring species (PACOS) cladogram showing the taxa relationships based on where they co-occurred during the 2006-2007 sampling period.

Moment Correlations) of the sediment variables through the cladogram resulted in clay and silt highly correlated with an r -value of 0.71 with total organic carbon (TOC) most highly correlated with silt with an r -value of 0.53. Independent contrasts between TOC and nickel, copper, chromium, zinc, and mercury were highly correlated with r -values of 0.96, 0.94, 0.94, 0.93, and 0.84, respectively, and all with highly significant two-tailed p -values. Finally,

the PCA and EPCA of all of the biodiversity indices (not shown herein) grouped the samples outside of the Harbor together due to the generally higher number of species, abundance, and elevated phylogenetic diversity values.

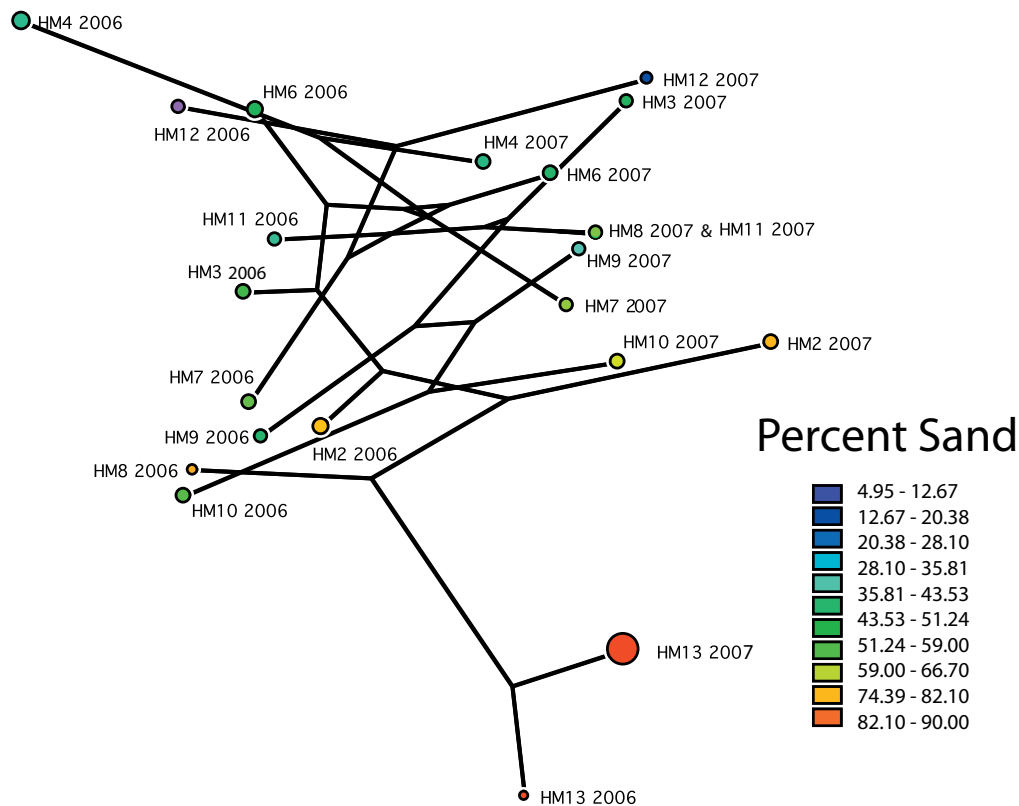


Figure 6-5. Principal components analysis of abiotic data onto the PAE cladogram with sand fractions mapped on.

DISCUSSION

The majority of the biological assessments made were based on the use of parsimony as an optimality criterion in order to determine the best fit of the data. All multivariate analyses were based on the results of this method, commonly used in phylogenetic classification. The phylogenetic procedure of grouping according to synapomorphy corresponds to expressing distance information as a path-length distance, while phenetic clustering expresses distance information through clustering levels. It is impossible for a clustering-level distance to fit distance data better than the best-fitting path-length distance. Classifications are most natural and have greatest information content per taxon, when they allow description of data in the fewest symbols. Most parsimonious trees have highest information content, are most natural, allow data to be completely summarized by the most succinct diagnoses, minimize exceptions to such complete diagnoses,

and permit the greatest number of predictions between adjacent taxa or objects. There is no justification for a phenetic approach (Farris 1979), since the phylogenetic or cladistic system contains greater information than either characters and similarities, while at the same time better reflecting relationships. Two-dimensional (2D) and three-dimensional (3D) Non-Metric Multidimensional Scaling (NMDS) outputs were assessed according to stress value, object ordination, rotational projection, and various factor (environmental, taxa richness, phylodiversity, etc.) overlays.

The advantage of using additive trees - which cladograms derived from parsimony analyses are - in ecological studies is that branch lengths are directly proportional to the changes or observations derived from the cladistic analyses. Hence, a quick perusal of any cladogram herein allows one to quickly assess species richness or diversity by looking at the relative length of the branches (Figure 6-2).

Although PAE is richly cited and formalized in the systematic literature by Rosen (1988) and Rosen and Smith (1988), the seminal work, ignored in the systematic literature, was in fact applied to marine infaunal data for eco-monitoring purposes from European waters two years earlier (Lamshead and Paterson 1986, Lamshead 1986).

Further justification for the use of PAE is the fact that communities and the species they contain are typically nested and cladistics is the dominant method in systematics for parsing out nested subsets of character distributions. See Appendix B for a more thorough methodological and theoretical discourse regarding the methodologies utilized herein.

Despite that the total number of taxa over the two-year period was a healthy 236, the macrofaunal communities sampled in the Outer Los Angeles Harbor in 2006 and 2007 had relatively depressed numbers of taxa with 179 and 199, respectively. The total number of taxa collected in 2005 (251 taxa) and 2004 (236) had continued to increase from 2002 (226), 2001 (219), and 2000 (236) since the depressed values found in 1996 – 1997, with 181 and 199 taxa, respectively. 2004 and 2005 continued to show a progression of recovery since the major disturbance created by Pier 300/400 construction activities in 1995-1996 (CLA, EMD 1996-1997). The total number of species decreased in 2003 (160) as a result of sedimentation from dredge and fill operations associated with P400 SSS construction, but its effects were still manifested in 2004 and 2005 as indicated by the cacophony of station relationships and their masked abiotic variable patterns. Although, the number of taxa did decrease during this biennium, the cladogram, NMDS, and PCA ordinations showed greater site and station grouping fidelity than the previous report. This suggests greater site fidelity by the macrofauna due to an increase in environmental stability (assumed less sediment smothering due to decreased construction activities) and possibly the beginning of community recovery.

The continued occurrence of a core set of abundant species in Outer Los Angeles Harbor (refer to

above-mentioned list in results section and previous reports) is due to the fact that all of these species commonly occur in nearshore southern California coastal waters (the species pool). *Theora lubrica*, the exotic transport from Asia, continues to be an abundant infaunal organism collected in Outer Los Angeles Harbor (CLA, EMD 1998-2006). During 2004 and 2005 this species ranked first, while in 2003 it ranked third in abundance. Over the 2006-2007 biennium, *T. lubrica* ranked third in occurrence, but down to tenth in abundance. When excluding these non-indigenous exceptions, the benthic macrofauna of Outer Los Angeles Harbor is similar in species composition to the open coast benthic macrofauna found outside the Harbor on the San Pedro Shelf (MEC 1988, ACE 1992) and Outer Long Beach Harbor (MBC 1984).

Impacts created by dredging and fill operations since 1994 on the abundance of these dominant species has been temporary, since many of these local species found in the Outer Harbor or nearby communities reproduce throughout the year or have extended reproductive periods (Reish 1982). With the completion of dredging operations for Pier 400 in April 2000, the successful settlement of larvae and migration of adults should have been uninterrupted (Maurer *et al.* 1981a, 1981b, 1982). However, with construction of the P400 SSS coupled to future deposition and/or removal from this site, infaunal recolonization will continue to be disrupted.

In summary, many analytical methods were applied to the data set this year. Parsimony analyses of the stations revealed station groupings underscoring the distinct species assemblages found outside of the Harbor relative to those within. Traditional diversity indices, as well as newly developed phylodiversity indices capturing the phylogenetic and trophic structure of the communities, revealed higher values at station HM13 outside the Harbor relative to those sampled within. The two samples from Station HM3, the closest station to the TIWRP Outfall, by not grouping together and by having near average values of taxa, abundance, and diversity indices, in concert with reference condition BRI scores further suggests the effluent from TIWRP is having little to

no observable effect on the benthic community.

Non-metric multidimensional scaling derived from the cladogram's branch lengths and subsequent multivariate analyses matching this biotic pattern to the abiotic variables identified percent silt, sand, nickel, and depth as the highest correlating combination of variables ($r=0.730$). These results complement the aforementioned pairwise Independent Contrasts (Pearson Product-Moment Correlations) of the sediment variables through the cladogram resulted in clay and silt highly correlated with an r -value of 0.71 with total organic carbon (TOC) most highly correlated with silt with an r -value of 0.53. Independent contrasts between TOC and nickel, copper, chromium, zinc, and mercury were highly correlated with r -values of 0.96, 0.94, 0.94, 0.93, and 0.84, respectively, and all with highly significant two-tailed p -values. Conducting various principal component analyses with different sets of abiotic variables onto the infauna-derived PAE cladogram resulted in groupings relatively congruent with the topology of the cladogram. The PCA of all abiotic variables with sediment fractions mapped onto the cladogram mirrored the biotic pattern the closest. The final PCA derived from the entire suite of diversity and phylodiversity indices (not shown herein) generally grouped the samples from station HM13 outside the breakwater away from the stations within the Harbor, with the highest values from the diversity indices recorded from the samples collected at station HM13.

Hence, the array of analyses applied to the data all lead to similar conclusions, namely, that the species assemblage or community pattern represented by the cladogram, was structured from a combination or interplay of sediment granulometry, depth, and the chemical constituents found therein.

Extensive re-suspension and subsequent sedimentation has occurred in the Outer Los Angeles Harbor with similar past construction events (SCOSC 1982, HEP 1983). With the completion of dredging and fill activity in the Outer Los Angeles Harbor for Pier 400, a continuing impact on the Post-Pier 400 monitoring stations around the TIWRP outfall is still

being noted, most notably from P400 SSS activity. Despite these intermittent impacts the composition of the macrofaunal community collected appears to be stabilizing with a healthy number of 236 taxa reported for the biennium despite the slightly reduced number of species reported in 2006 (179) and 2007 (199). With recovery from the impacts caused by the construction activities related to Pier 300/400 continuing to progress, coupled to current P400 SSS activity resulting in the actual loss or exclusion of near-outfall stations HM1 and HM5, the message or signal that has been obtained from the most recent data analysis may only represent an intermittent improvement in time and may degrade with future construction activity. Hence, these results may not be fully informative relative to the objective of the Post-Pier 400 Monitoring Program: to investigate the potential effects of the effluent discharged from the TIWRP on the surrounding infaunal communities in Outer Los Angeles Harbor.

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