

MEIOFAUNA ABUNDANCE AND DISTRIBUTION IN CHESAPEAKE BAY:
RELATIONSHIPS WITH ENVIRONMENTAL STRESSORS, SEDIMENT
TOXICITY AND MACROFAUNA

A Thesis
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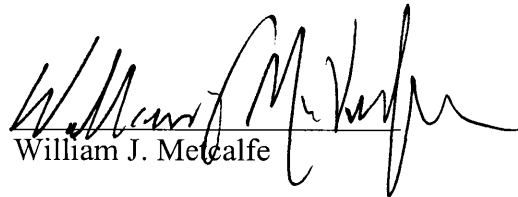
The Faculty of the School of Marine Science
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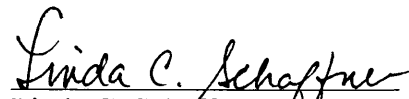
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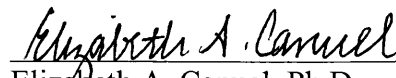

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TABLE OF CONTENTS

AKNOWLEDGMENTS.....	iii
INDEX OF FIGURES	v
INDEX OF TABLES.....	vi
ABSTRACT	vii
INTRODUCTION	9
HYPOTHESES	13
METHODS	
Initial site characterization and study site descriptions	14
Field Sampling.....	18
Subsampling of Cores.....	19
Sediment toxicity testing	21
Data analysis, statistical methods and calculation of the B-IBI	22
RESULTS	
Sediment Toxicity Testing.....	26
Environmental characteristics	26
Meiofauna abundances and community composition.....	38
Linking Biotic and Environmental Variables	48
Relationships with the B-IBI.....	49
DISCUSSION	
Anthropogenic effects on meiofauna community structure.....	57
The Nematode:Copepod Ratio	60
Linking Meiofauna Community Structure to Environmental Variables.....	60
SUMMARY	62
SOURCES OF DATA	63
LITERATURE CITED.....	64
VITA.....	69

INDEX OF FIGURES

Figure 1. Map of Chesapeake Bay showing study sites sampled in 2003.....	17
Figure 2. Projection of sampling sites on the first plane of a PCA based on the historic water quality variables and data found in Table 1.....	29
Figure 3. Projection of sampling sites on the first plane of a PCA based on the measured habitat parameters and data found in Table 2.....	32
Figure 4. Projection of sampling sites on the first plane of a PCA based on the watershed land use variables and data found in Table 3.	35
Figure 5. Abundances of nematode individuals/ 1.13 cm ² averaged over site/strata.....	40
Figure 6. Abundances of harpacticoid copepod individuals/ 1.13 cm ² averaged over site/strata..	41
Figure 7. Abundances of benthic foraminifera individuals/ 1.13 cm ² averaged over site/stratum.....	42
Figure 8-12. Ordination plots of non-metric Multi-dimensional Scaling of square root transformed meiofauna abundance data from 2003 sampling sites..	43-47
Figure 13. Correlation of nematode abundance and average B-IBI score by site showing means and standard error bars for abundance and B-IBI score	52
Figure 14. Correlation of copepod abundance and average B-IBI score by site showing means and standard error bars for abundance and B-IBI score	53
Figure 15. Correlation of foraminifera abundance and average B-IBI score by site showing means and standard error bars for abundance and B-IBI score	54
Figure 16. Average ratio of nematodes to harpacticoid copepods by site/stratum in order of increasing B-IBI score (increasing benthic integrity).....	56

INDEX OF TABLES

Table 1. Eigenvectors and historical water quality variables associated with Figure 2...	30
Table 2. Matrix of historical water quality data used in Fig. 2.....	31
Table 3. Eigenvectors and measured variables associated with Figure 3.	33
Table 4. Matrix of measured habitat property data used in Fig. 3.....	34
Table 5. Eigenvectors and land cover classes associated with Figure 4.	36
Table 6. Matrix of watershed land use data used in Fig. 4.	37
Table 7. Summary of regression results for each parameter versus average B-IBI score by site	51

ABSTRACT

Macrofauna-based biocriteria to assess impairment in aquatic communities are well-developed and have been widely accepted as useful for coastal monitoring programs worldwide. Meiofauna-based methods are not as well developed, but meiofauna are intimately associated with sediments through their life cycles and are functionally important. Thus, an understanding of meiofauna relationships with environmental quality is also important. Relationships between the abundance and composition of major meiofauna taxa for two shallow water habitat types (protected, with muddy sediment; exposed, with sandy sediment) were investigated along gradients associated with changing land use, sediment contamination and environmental stressors in Chesapeake Bay. Principal component analysis shows that urbanization, eutrophication and sediment contamination affect shallow water sites in the lower Chesapeake Bay, Virginia ecosystem. Multidimensional scaling ordination of meiofauna community data reveals gradients associated with human activities and major habitat types. Both sediment enrichment (high percent organic carbon and percent nitrogen) and sediment toxicity were associated with shifts in meiofauna community composition in muddy sediment. Benthic Foraminifera, known to be pollution sensitive, were rare or absent in collections from sites with sediment enrichment or toxicity. Nematodes were abundant at a site with enrichment, but not at a site with significant sediment toxicity. Major meiofauna taxa also differed clearly between protected and exposed sites, with greater abundances in collections from mud versus sand sediment. Results of analyses matching biotic to environmental patterns point to the importance of regional historic salinity and chlorophyll-a levels in addition to other habitat properties, including sediment organic carbon, total nitrogen and sediment toxicity as predictors of meiofauna community structure. The Benthic Index of Biotic Integrity (B-IBI) developed for Chesapeake Bay based on macrofauna was negatively correlated with nematode abundance at muddy sites when a site with significant sediment toxicity was excluded. There were no other significant relationships between meiofauna metrics and the B-IBI. The ratio of nematodes to copepods was not effective for discriminating relationships among sites relative to anthropogenic effects.

**MEIOFAUNA ABUNDANCE AND DISTRIBUTION IN CHESAPEAKE BAY:
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INTRODUCTION

Benthic meiofauna are important components of coastal and estuarine ecosystems. As grazers of microalgae and bacteria, meiofauna have been shown to influence primary production, nutrient cycling and other benthic metabolic processes (Carman *et al.*, 1996, 1997, 2000; Manini *et al.*, 2000; Pinckney *et al.*, 2003).

Organic matter (and nutrients) grazed by meiofauna are assimilated, or egested. Energy from assimilated materials is fixed and incorporated as net production, or respired. When an animal dies, remineralized nutrients become available for microbial processes and primary production (Coull, 1999).

Because of the short generation times of meiofauna (weeks to months), these processes may result in a relatively rapid cycling of nutrients through the meiobenthos. Utilization of microalgae, microbes and detritus by benthic meiofauna facilitates energy and nutrient transfer to higher trophic levels in benthic food webs (Coull *et al.*, 1995; Aarnio *et al.*, 1996; Street *et al.*, 1998; Kovac *et al.*, 2001 French *et al.*, 2001; Leguerrier *et al.*, 2003). Thus, the effects of human-induced disturbances on meiofauna should be understood and their effects minimized in order to retain these important ecosystem services.

Previous investigations have suggested that meiofauna and macrofauna may show similar responses to human disturbances of aquatic environments (Coull & Chandler, 1992; Peterson *et al.*, 1996; Warwick *et al.*, 1990; Schratzberger *et al.*, 2001). Based on a review of the literature, Peterson *et al.* (1996) argue that macrofaunal and meiofaunal communities exhibit repeatable patterns of response to environmental stressors, which are generally detectable at high taxonomic levels

(even phyla). Thus, echinoderms and crustaceans, especially amphipods and some harpacticoid copepods, are highly sensitive to toxic chemicals in their environment and these groups typically show large declines in abundance due to sediment toxicity. In contrast, polychaetes, oligochaetes, and nematodes are not especially sensitive to toxic chemicals. These groups tend to include species with opportunistic life histories and appropriate feeding types (especially nonselective deposit feeders) that render them capable of utilizing organic materials associated with organic enrichment. Consequently, these taxa typically show substantial increases under organic pollution settings where oxygen depletion is not a factor (Peterson *et al.*, 1996).

The potentially opposing effects of organic pollution and sediment toxicity on different groups of benthic meiofauna and macrofauna make ordination techniques of benthic community analysis effective in discriminating the effects of environmental stressors at higher levels of taxonomic classification, including the phylum level for macrofauna (Warwick and Clarke, 1993). It also suggests a means of isolating different causal mechanisms in studies of pollution involving both toxicant and nutrient stressor effects.

The use of biocriteria-based monitoring for detecting and understanding environmental stressor effects is increasing. Methods based on macrofauna are the best-developed and have been widely accepted as useful for many coastal monitoring programs world wide (Diaz and Rosenberg, 1995; Netto, 1999; Warwick, 2001; Dornie, 2003; Arana *et al.*, 2005). Numerous studies have shown that macrofauna respond predictably and repeatedly to a diverse range of natural and anthropogenic stresses (Weisberg *et al.*, 1997). Although the use of macrofaunal criteria has been

successful for characterizing environmental conditions at local scales, natural variation in macrofauna community structure with changing salinity, sediment granulometry, temperature and depth, can confound the accuracy of regional-scale studies. The Benthic Index of Biotic Integrity (B-IBI) developed for Chesapeake Bay accounts for these natural habitat variations by defining habitat-specific reference conditions at sites free of anthropogenic stress and assigning categorical values for various macrofaunal metrics by which sites under investigation can be compared (Weisberg *et al.*, 1997). This approach is advantageous to measuring levels of ambient contaminants because chemical monitoring misses many of the human-induced perturbations that impair uses of aquatic systems (Karr and Dudley, 1981). Habitat alteration, reduced flow, and alteration in energy supplies to support marine communities are examples of stressors that degrade integrity but are not detected by physical and chemical monitoring.

Methods to use meiofauna to assess the impacts of anthropogenic stressors are not as well developed relative to methods using macrofauna; currently available meiofauna based methods are only applicable in sandy beach habitats experiencing organic enrichment (Coull and Chandler 1992). Raffaelli and Mason (1981) first proposed use of the meiofaunal nematode to copepod (Ne/Co) ratio, based on the argument that nematodes are more pollution tolerant than copepods. Several authors argued that the index, as proposed, is not universally applicable to all habitats (Coull *et al.*, 1981; Lamshead, 1984; Moore and Pearson, 1986). Warwick (1981) suggests refinements based on metabolic requirements including only the copepods that forage interstitially and in the same manner as nematodes. Shiells and Anderson (1985) also

suggest that only interstitial forms be included in the calculation. Peterson *et al.* (1996) argues that the method could be useful if the differential response of major (even phylum level) meiofaunal taxa to various pollutant stressors, such as sediment toxicants and organic loading, were better understood.

For the present study we investigate relationships between the abundance and composition (major taxa) of meiofauna for two shallow water habitat types along gradients of changing land use, sediment contamination and other environmental stressors in Chesapeake Bay. We chose to conduct this study in shallow water habitats because of their close proximity to potential point and non-point sources, and thus their high level of exposure to a diverse array of human activities. Previous studies have shown the importance of hydrodynamic regime and grain size related factors for both meiofauna and macrofauna, so our sites included relatively protected muddy habitats and relatively exposed sandy habitats. We also investigated relationships between aspects of meiofauna community structure (abundance at the level of order and the nematode:copepod ratio) versus the Benthic Index of Biotic Integrity (B-IBI), which provides an estimate of benthic community integrity based on the macrofauna. To date there have been few unified assessments of environmental quality using both meiofauna and macrofauna techniques and we are aware of no other studies linking meiofauna abundance and composition and macrofauna community integrity in an estuary. The overall goal of our work is to improve the utility of biocriteria-based tools for the enhanced preservation, management and restoration of Chesapeake Bay and other estuarine ecosystems.

HYPOTHESES

The following null hypotheses guide the research:

H1_o: No significant relationships will be detected between metrics of meiofauna community health (relative abundances of the major meiofauna taxa and total meiofauna, ratio of nematodes to copepods) and B-IBI values.

H2_o: No significant relationships will be detected between metrics of meiofauna community health (relative abundances of the major meiofauna taxa and total meiofauna, ratio of nematodes to copepods) and sediment toxicity as indicated by an acute toxicity test.

METHODS

Initial site characterization and study site descriptions

In order to characterize meiofauna community structure in soft-sediment habitats along gradients of human activities and environmental quality, it was necessary to establish sites that spanned from relatively low-impact to severely impacted areas of Chesapeake Bay. Environmental data for potential field sites were explored using databases available through the Chesapeake Bay Program's (CBP) monitoring program (<http://www.chesapeakebay.net/monprgms.htm>), the U.S. Environmental Protection Agency's Environmental Monitoring and Assessment Program (EMAP; <http://www.epa.gov/emap/>), EPA's Middle Atlantic Integrated Assessment Program (MAIA; <http://www.epa.gov/maia>), and the Virginia Department of Environmental Quality (VADEQ; http://gisweb.deq.virginia.gov/monapp/mon_data_retrieval_app.html#). These data mostly come from areas in deeper waters than were sampled in this study and reflect water quality on a regional scale.

Each potential sampling site was visited during late spring-early summer 2003 to characterize salinity, bathymetry, sediment particle size, organic and chlorophyll-a content, physical exposure, and tidal regimes. The presence of oyster reefs or submerged aquatic vegetation was also examined in order to define the distribution of soft sediments relative to other bottom types and the spatial extent of the proposed sampling sites (shallow subtidal, ≤ 1 m at mean low water, MLW) prior to initiating the field sampling programs. In addition, any available benthic community or environmental data for the candidate sampling sites were also considered.

Based on the site assessments, five sampling sites (Sarah Creek, Severn River/Thorntons Creek, Back River (NASA/Langley), Chisman Creek, and Elizabeth River) were chosen to represent a continuum from relatively low-impact to severely impacted shallow subtidal soft-sediment habitats (Fig. 1). The Severn River/Thorntons Creek complex (ST) is located within a relatively undeveloped watershed. Sediment from the muddy ST site has previously been used to culture amphipods in our laboratory with no adverse effects (Schaffner, personal observation). Sarah Creek (SA), a subtributary of the lower York River, supports a marina located at the mouth of the creek and is bordered by primarily residential and agricultural development along the shoreline of the headwaters. Tributyltin (10-40 ng/L) has been detected in the water column annually between 1986 and 1996 at the mouth of Sarah Creek and is likely associated with sediments in greater concentrations (Hall *et al.* 2000). No historical documentation of pollution in the headwaters of Sarah Creek has been recorded although personal communication with residents suggests heavy agricultural spraying and cattle farming in the watershed as possible sources of nutrients or other chemicals to the system. The headwaters of Chisman Creek (CH) border a previous EPA Superfund site that has undergone remediation. The Chisman Creek Superfund Site holds an estimated 500,000 tons of fly ash from Virginia Power's Yorktown Power Station in underground borrow pits. Heavy metals, arsenic, beryllium, chromium, copper, molybdenum, and selenium were found to have leached from the pits, contaminating groundwater, surface water, sediments, and soil. The site was included on the National Priorities List (NPL) on September 1, 1983. EPA conducted a five-year review in 1996 and determined that

the remedial actions were operating properly (NPL Fact Sheet - CHISMAN CREEK). The Back River (LA) was selected as a potentially degraded site because of its highly developed watershed, which includes residential and commercial activities, as well as a military installation and government research center (NASA/Langley). There are more than 40 sources of possible contamination at the two facilities including petroleum, oils and lubricants, fuels, solvents, paints, pesticides, photographic chemicals, polychlorinated biphenyls (PCBs), polycyclic hydrocarbons (PAHs), heavy metals, scrap materials, used batteries, printed circuit board plating wastes and polychlorinated terphenyls (NPL Fact Sheet - LANGLEY AIR FORCE BASE/NASA LANGLEY RESEARCH CENTER). Remediation was conducted in 1999 and included dredging and excavation of sediments upstream of the muddy habitat site used for this study. The southern branch of the Elizabeth River (ER) has a highly industrialized watershed, extensive shipping activities and history of severe sediment contamination from polycyclic aromatic hydrocarbons (PAHs), pentachlorophenol (PCP), polychlorinated dibenzodioxins (PCDDs), polychlorinated dibenzofurans (PCDFs), and metals contamination (arsenic, chromium, and zinc) (Walker, 2001). The muddy site is located at the previously closed Atlantic Wood Industries, Inc. facility, which was used predominately for creosote and pentachlorophenol wood preserving purposes during its history of operation from 1926 to 1992.

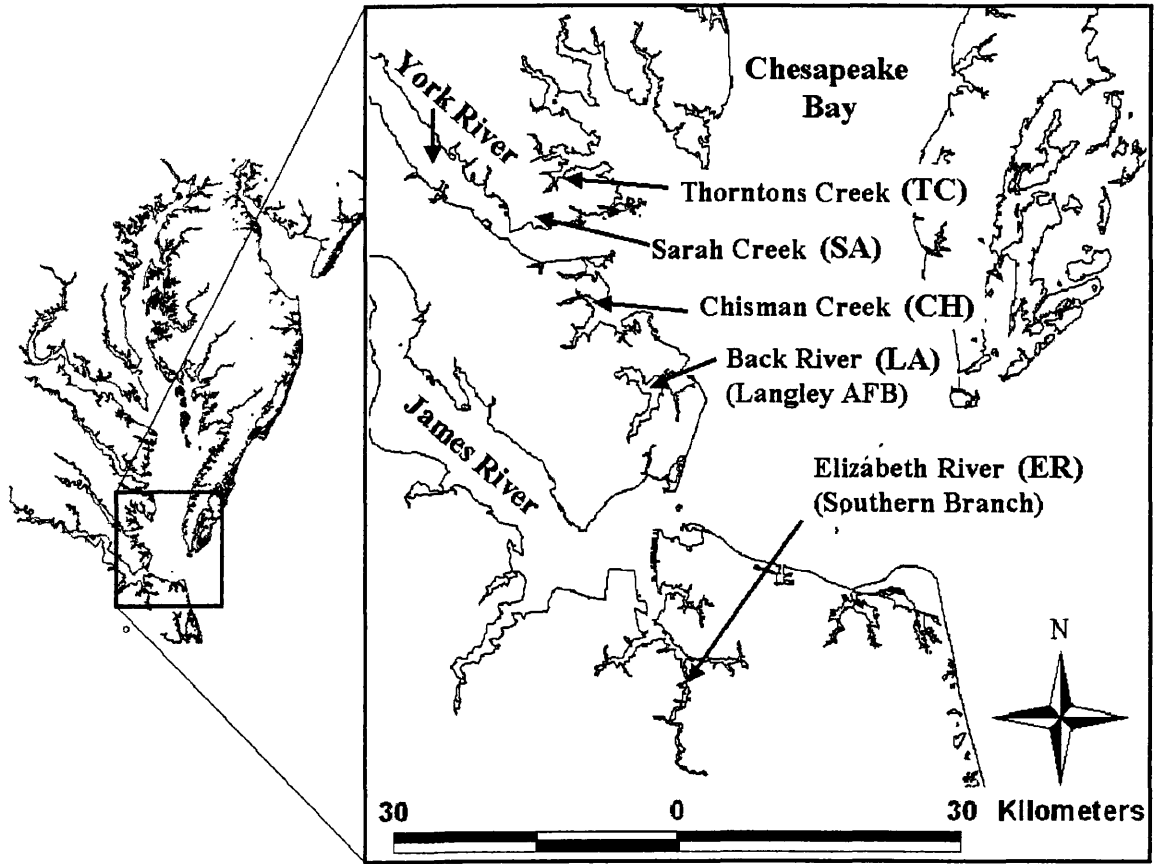


Figure 1. Map of Chesapeake Bay showing study sites sampled in 2003.

Field Sampling

Following site selection, individual stations were randomly selected within pre-determined near-field (muddy) and far-field (sandy) strata delineated on the basis of potential impacts from upland activities, sediment type and exposure to physical energy (i.e. waves, flow regime). Sampling was restricted to a relatively narrow salinity range (12-18 ppt) to minimize the effects of salinity variation on benthic community structure. Near-field sites were typically located within tidal creeks or protected bays that were somewhat embedded within the upland region. They tended to be depositional regions, protected from wave-exposure and characterized by fine, organic rich sediment. Far-field sites were located within 1 km of the near-field sites, and often much closer, and were typically located along an exposed shoreline. As a result, the potential for wave disturbance of sediments was greater and sediment was primarily sand with low organic content. For each stratum within a site there were nine individual stations established randomly within the depth range (0.5 - 0.75 m MLW). The numbers of samples needed was based on a priori consideration of the likely variance structure for the various sample types and the power need to detect meaningful differences among sites and strata. Sampling occurred during summer because it is the index period for the B-IBI (defined as July 15 through September 30; Weisberg, 1997). Each site was visited once during 2003.

Large acrylic cores (13.3 cm i.d. by 40 cm) were used to collect sediment to a depth of 25 cm. The overlying water (15 cm) was retained and cores were sealed at both ends, kept cool and secured for transport back to the lab (ER, LA and ST, only). Cores from ER, ST and LA were stored overnight, employed in non-destructive

benthic metabolism/flux studies on the following day and stored overnight again before processing. Cores from SA and CH were processed in the field on the day of sampling.

Subsampling of Cores

Cores were subsampled for grain size, total organic carbon (TOC), total nitrogen (TN), sediment chlorophyll-a, phaeophytin and meiofauna analyses prior to sieving the sediments for macrofauna. For particle size distribution and TOC and TN analyses, a pre-cut 60 mL syringe was used to collect sediment to a depth of 11.5 cm at SA and CH sites. At LA, ER and ST additional sediment characterization cores were taken directly adjacent to the large acrylic cores for determination of TOC and TN content. Sediment characterization cores were collected to a depth of 25 cm adjacent to the large acrylic cores and subsectioned for analyses of TOC and TN. Sediment particle size distribution was determined following standard protocol (modification of Plumb, 1981). Sediment was analyzed for carbon and nitrogen content using a Fisons CHN analyzer (Model EA1108) after removing inorganic carbon with 10% hydrochloric acid (Hedges and Stern, 1984) and using acetanilide as a standard. Chlorophyll-a and phaeophytin content were sampled in triplicate using a pre-cut 5 mL Fortuna syringe (1.2 cm i.d.) inserted in the top 3 cm of each core. The sample was divided into 3 depth sections: 0-1, 1-2, and 2-3 cm. Triplicate samples for each of three depth subsections were composited in a centrifuge tube, extractant added and frozen for at least 24 hours. Following extraction, samples were centrifuged, filtered (Gelman PTFE, 0.45 μ M), and analyzed using a Shimadzu UV-1601 spectrophotometer before and after adding 0.15 mL 10% HCl to each sample.

Chlorophyll-a and phaeophytin concentrations were calculated using the equations of Lorenzen (1967).

A meiofauna subsample was taken from each core to a depth of 5 cm using a pre-cut 5 mL Fortuna syringe (1.2 cm i.d.). Meiofauna were fixed and stored in 3% buffered formalin and filtered seawater solution prior to further analysis. Meiofauna were then extracted from sediments using Ludox® colloidal silica solution following a protocol by Burgess (2001) and stained with rose bengal. The percent of meiofauna extracted was calculated for each sample as the number extracted by the sol divided by the total number found in the sol and the pellet. The total efficiency of all extractions was estimated to be 99.1 plus or minus 0.3% (Appendix 1). These findings are in accordance with those of Burgess: 96.8 plus or minus 3.9% for the total meiofaunal abundance. Meiofauna were sorted to the level of major taxonomic groups (copepods, nematodes, nauplii, turbellarians, foraminifera, ostracods, mites, and newly settled clams and polychaetes) using a dissecting microscope.

Prior to sieving, cores were divided into two depth horizons (0-5, >5 cm) to allow determination of macrofaunal vertical distribution patterns. Each horizon was gently washed over a 500 μ m screen and the fraction retained on the screen was fixed and then stored in 10% buffered formalin with rose bengal stain added to aid in subsequent sorting. Organisms were subsequently identified to the lowest possible taxonomic level, which generally resulted in species-level identification. Biomass was determined as ash-free dry weight (550 °C for 4 hrs.).

Sediment toxicity testing

Acute sediment toxicity was determined using standard methods with the estuarine amphipod *Leptocheirus plumulosus* (ASTM E 1367-92). Sediments for toxicity testing were collected from each stratum at each of the five sites by scraping an aliquot of sediment from the top 3-5 cm at each sampling station into mason jars using a nylon spoon. The aliquots were composited within each site to represent average toxicity for a stratum. Sediments for control treatments and amphipods for the tests were collected live from Queens Creek in New Quarter Park (Williamsburg, VA), grown in culture following standardized protocol (Schaffner, personal communication) and handled as follows. One liter glass mason jars (10.0 cm diameter) were used as test chambers. Test sediments were thoroughly homogenized and a 2 cm deep aliquot of sediment was added to each test chamber. Test chambers were then filled so that 8 cm filtered seawater overlay the test sediment. Aeration was provided to the test chambers through clean glass pipettes at least 2 cm from the sediment surface. After overnight equilibration of the test chambers, 15 test amphipods were randomly distributed to each chamber. Amphipods were removed from the culture sediment by a combination of elutriation, wet sieving and pipetting. Active, healthy amphipods were selected and randomly distributed among dishes containing 150 ml of filtered seawater. Amphipods were added to test chambers without disruption of the sediment by placing a polyethylene disk on the water surface, and pouring amphipods from the sorting dish over the disk into the test chamber. A random sample of 20 animals was sacrificed on day 1 of testing to provide a size range of test amphipods. Animals used in this experiment ranged from

3 to 5 mm measured from the base of the antennae to the end of the third pleon segment along the dorsal surface. Amphipods that had not burrowed into test sediment after 10 minutes were removed and replaced with healthy animals unless animals were observed emerging in an avoidance response. Toxicity testing was terminated after ten days by sieving amphipods from test sediments using a 0.5 mm mesh screen. Results were reported as average percent survival following 10-day exposure.

Data analysis, statistical methods and calculation of the B-IBI

To better link the observed meiofauna community variables to environmental variables, historical water quality, watershed land use and measured habitat parameters were compiled. Historical parameters selected for investigation included Chesapeake Bay Region of Concern (ROC) (http://www.chesapeakebay.net/pubs/subcommittee/tsc/toxics/pdf%20finals/toxics_2000.pdf), the historic mean, low, high and range of selected water quality variables (bottom water DO, DIP, NO_x, NH₄⁺, salinity and surface water chl-a) and % of recorded events where bottom water DO concentrations were > 5mg/L from January 1993 to April 2003. Measured habitat parameters included in the analyses were sediment toxicity index (% survival of *L. plumulosus* following 10-d exposure), sand, silt and clay (% by wt.), chlorophyll-a (µg/cm²), phaeophytin (µg/cm²), molar C:N, sediment TOC (% dry wt.), sediment TN (% dry wt.), chl-a:phaeo, salinity (ppt) and water temperature at time of sampling. To determine percent land use in the watershed of each site, watersheds were first delineated using U.S. Geological Survey Digital Ortho Quarter Quads (DOQQs) and Arcview 3.2 (ESRI). Watersheds were

converted to shapefiles and layered over the National Land Cover Dataset (NLCD) for eastern Virginia (Zone 60). The “Clip” and “Return.Area” calculator functions were then used to extract the spatial information for each watershed. Watershed land use parameters recorded were: percent low (20-49% impervious surface), medium (50-79% impervious surface) and high (80-100% impervious surface) intensity development, developed open space, barren, forested, farmland, and wetlands in each watershed. See Appendix 2 for definitions of land cover classes.

Site and stratum characteristics were explored using Principal Components Analyses (PCA) of historical, measured and watershed datasets using the software PRIMER (Clarke and Warwick, 2001). Historical, measured and watershed matrix data were normalized by subtracting the means and dividing by the standard deviations over all samples for a parameter so that all environmental metrics are of potentially equal importance in determining the principal components. Results were displayed individually in ordination plots using Euclidian distance. Historical water quality, measured and watershed datasets were analyzed individually to determine the principal components structuring meiofauna communities on regional and local scales, as well as the relative importance of various watershed activities.

The data on meiofauna abundance by major taxa for each station were analyzed by multivariate classification and ordination techniques using PRIMER software. Data were square root transformed to weight in favor of species present in low abundances so that the multivariate pattern would not be driven entirely by highly abundant taxa (e.g. nematodes) (Clarke and Warwick, 2001). An among-sites similarity matrix was produced from square root transformed abundance data using

the Bray-Curtis similarity measure. The matrix was subjected to hierarchical agglomerative clustering using group average sorting and depicted by Multidimensional Scaling Ordination (MDS). One-way and two-way nested Analysis of Similarity (ANOSIM) tests (Clarke and Warwick, 1994) were used to determine the significance of faunal differences between sites and between strata.

Relationships between the community-level patterns discerned from biotic collections and distributions of major taxa were compared by plotting patterns of major taxa abundance relative to the two-dimensional MDS configuration. The PCA results for measured, historical and watershed datasets were compared to the faunal MDS configuration to obtain visual correlations with major axes. The biological-environmental linkage (BIO-ENV) procedure was used to select “best fitting” subsets of abiotic variables that maximized rank Spearman correlation between similarity matrices of square root transformed meiofauna abundances by core and all possible dissimilarity matrices composed of subsets of historic water quality and site characterization data assembled using Euclidian distance. Clarke and Ainsworth (1993) describe the approach in detail.

For the B-IBI, the appropriate habitat index (high mesohaline mud or high mesohaline sand) was applied to each macrofauna sample (Weisburg *et al.* 1997, Alden *et al.*, 2002; Llansó, 2002). The B-IBI was calculated for each station (faunal sample) and then averaged by strata within sites. Scores were classified according to the Chesapeake Bay Program (CBP) as meets goal (≥ 3.0), marginal (2.7-2.9), degraded (2.1-2.6) or severely degraded (≤ 2).

Both univariate and multivariate approaches were used to investigate relationships between meiofauna, environmental characteristics, sediment toxicity and benthic community integrity as measured by the B-IBI. In addition to the aforementioned multivariate techniques, analysis of variance (ANOVA) was run using the SAS® System for Statistical Analysis software to investigate differences in toxicity among strata. Regression analyses were run using SAS® to investigate relationships between meiofauna abundances and average B-IBI scores or measured habitat properties. For ANOVA and regression analyses, data were arcsin transformed to meet the assumptions of normality and homogeneity of variance. Normality was tested using the Shapiro-Wilk statistic and homogeneity of variance was tested using the Levine statistic and by physical inspection of boxplots.

RESULTS

Sediment Toxicity Testing

Sediment toxicity was significantly higher at the ER near-field stratum at relative to other sites/strata ($p < .0001$, $F = 9.96$, $N = 55$) (Appendix 3). Percent survival of *L. plumulosus* in ER near-field test chambers was zero at the end of the 10-d exposure and emergence of test animals was noted beginning on day 1 of the experiment. A posteriori contrast using Least Square Means indicated % survival of *L. plumulosus* at ER-N to be significantly different from all other sites and control ($p < .0001$ for all comparisons) (Appendix 3). Survival of *L. plumulosus* in all remaining test chambers was not significantly different from control ($p > .05$) and averaged between 80 and 100%.

Environmental characteristics

Principal components analysis of historical water quality data shows that nutrients, salinity, chlorophyll-a and DO conditions account for 88.3% of the observed variation in regional water quality, with PC1 accounting for 68.1% of the variation (Fig. 2; Table 1, Appendix 3). York River (SA) and Elizabeth River (ER) have the highest historical maxima and ranges of ammonia and phosphate concentrations, the lowest minimum NO_x concentrations, the lowest maximum DO concentrations and the highest chlorophyll-a maxima and ranges. Mean and maximum levels of salinity are highest at the York River and Elizabeth River monitoring stations (Table 1); these sites have positive loadings on PC1 (x-axis). High chlorophyll-a values and low DO values indicate eutrophication as a potential

source of regional water quality impairment at SA and ER sites. The large range in ammonia, phosphate and chl-a concentrations indicates variability and the potential importance of episodic events. The remaining stations (Mobjack Bay; Poquoson River and Back River) experience relatively lower maxima and ranges of ammonia and phosphate concentrations. DO reaches higher maximum concentrations and salinity levels are lower on average at Mobjack Bay, Poquoson River and Back River water quality monitoring stations. DO conditions account for an additional 20.2% of the observed variation among stations along PC2 (Fig. 2; Table 1).

PCA of measured habitat parameters arrayed the sites along a gradient of sediment grain-size, chlorophyll-a and phaeophytin concentrations and accounted for 70% of sample variation, with PC1 accounting for 48.1% of the variation and PC2 accounting for 22.0% of the variation. (Fig. 3; Table 2). Sampling sites are divided on PC1 into near-field and far-field groups respectively. ST near-field is grouped with far-field sites because sediment particle size analysis revealed a relatively high % sand. The sites are arrayed on PC 2 according to sedimentary chl-a and phaeophytin concentrations.

PCA of watershed land use arrayed the sites along gradients of industrial and agricultural development and accounted for 93% of the sample variation, PC1 accounting for 85% of the variation (Fig. 4; Table 3). ST is isolated by PCs 1 and 2 as the area with the least developed watershed characterized by high % forest and % wetlands. CH and SA are separated from ST and are characterized by relatively higher agricultural development on PC2. ER and LA are separated from the

aforementioned study locations on PC1 and are characterized by high industrial watershed development.

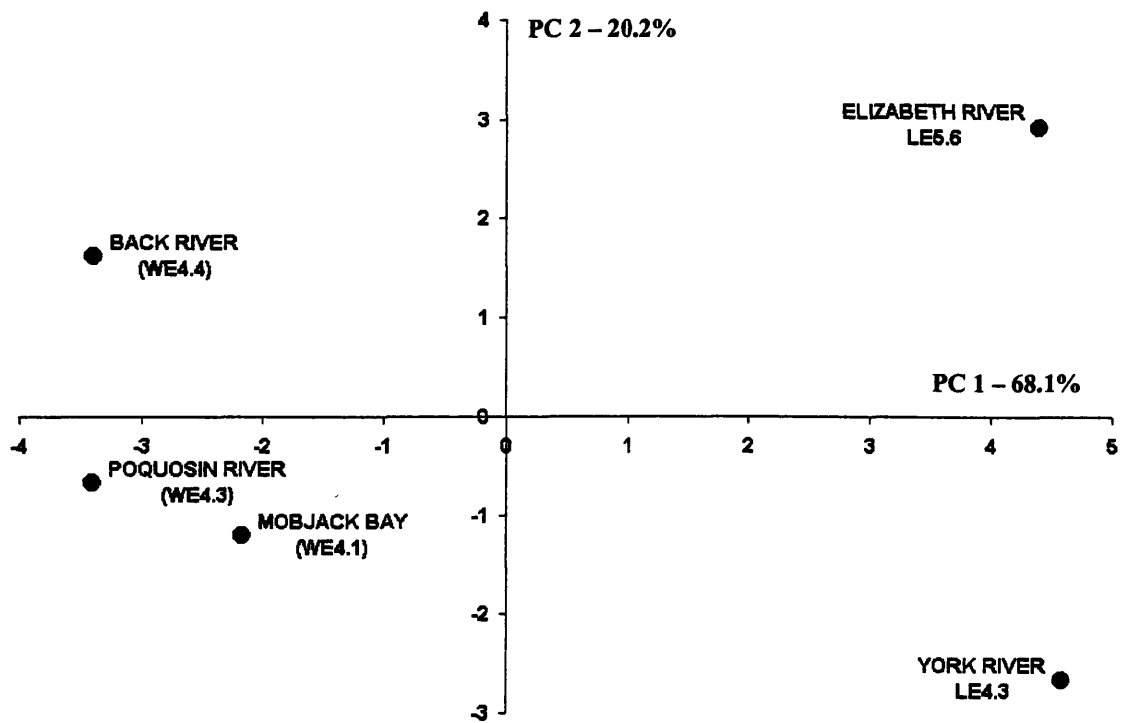


Figure 2. Projection of sampling sites on the first plane of a PCA based on the historic water quality variables and data found in Table 1.

Table 1. Eigenvectors and historical water quality variables associated with Figure 2.

Eigenvectors					
(Coefficients in the linear combinations of variables making up PC's)					
Variable	PC1	PC2	PC3	PC4	PC5
DO (mg/L) MAX	-0.241	-0.025	-0.045	0.054	0.087
DO (%>5mg/L)	-0.216	0.179	-0.145	-0.036	-0.027
DO (mg/L) RANGE	-0.047	-0.393	-0.284	0.156	-0.275
DO (mg/L) MIN	-0.042	0.399	0.277	-0.142	0.141
Chl-a (ug/L) MIN	0.008	-0.263	-0.54	0.295	0.421
NH4 (ug/L) MIN	0.112	-0.339	0.321	0.085	0.33
PO4 (ug/L) MIN	0.13	-0.321	0.309	0.091	-0.182
CBP ROC? 0=no, 1=yes,	0.144	0.324	-0.246	0.025	-0.135
SAL (PPT) RANGE	0.145	-0.242	-0.15	-0.556	-0.119
SAL (PPT) MIN	0.161	0.17	0.206	0.58	-0.001
Chl-a (ug/L) MEAN	0.181	0.214	-0.33	-0.034	0.101
NOx (ug/L) MEAN	0.212	0.167	-0.218	-0.034	-0.046
NOx (ug/L) RANGE	0.225	-0.161	0.007	-0.089	0
NOx (ug/L) MAX	0.225	-0.159	0.007	-0.087	0.241
PO4 (ug/L) MEAN	0.225	0.145	-0.104	0.091	0.043
NH4 (ug/L) MEAN	0.229	0.13	-0.096	0.055	-0.007
Chl-a (ug/L) RANGE	0.235	0.06	0.087	-0.167	0.187
Chl-a (ug/L) MAX	0.236	0.055	0.076	-0.162	0.436
NH4 (ug/L) MAX	0.239	-0.021	0.002	-0.158	-0.119
SAL (PPT) MAX	0.239	-0.017	0.078	0.127	-0.077
NH4 (ug/L) RANGE	0.239	-0.016	-0.002	-0.16	-0.151
NOx (ug/L) MIN	0.239	0.029	0.052	0.131	-0.193
PO4 (ug/L) MAX	0.24	-0.041	-0.038	0.099	-0.346
PO4 (ug/L) RANGE	0.24	-0.036	-0.045	0.098	0.193
SAL (PPT) MEAN	0.24	0.027	0.03	0.13	-0.098

Table 2. Matrix of historical water quality data used in Fig. 2. CBP ROC = Chesapeake Bay Program Region of Concern.

REGION	MOBJACK	YORK	POQUOSON	BACK	ELIZABETH
CBP ROC? 0=no, 1=yes,	0.00	0.00	0.00	0.00	1.00
DO (%>5mg/L)	95.39	70.87	98.03	98.68	86.29
DO (mg/L) MAX	13.50	12.40	13.79	13.60	12.39
DO (mg/L) MIN	1.30	0.44	1.20	4.73	3.60
DO (mg/L) RANGE	12.20	11.96	12.59	8.87	8.79
NH4 (ug/L) MEAN	1.37	4.85	1.12	0.94	7.26
NH4 (ug/L) MAX	12.22	23.21	6.41	8.14	22.07
NH4 (ug/L) MIN	0.05	0.29	0.05	0.05	0.00
NH4 (ug/L) RANGE	12.17	22.93	6.36	8.09	22.07
NOx (ug/L) MEAN	1.60	2.76	1.04	0.72	5.03
NOx (ug/L) MAX	23.07	44.29	15.25	12.66	32.14
NOx (ug/L) MIN	0.01	0.29	0.02	0.02	0.29
NOx (ug/L) RANGE	23.06	44.00	15.23	12.64	31.86
PO4 (ug/L) MEAN	0.13	0.54	0.13	0.10	0.87
PO4 (ug/L) MAX	0.95	3.63	0.87	0.31	3.30
PO4 (ug/L) MIN	0.01	0.07	0.01	0.01	0.00
PO4 (ug/L) RANGE	0.94	3.57	0.86	0.30	3.30
SAL (PPT) MEAN	19.84	22.78	19.98	19.88	22.82
SAL (PPT) MAX	24.61	30.60	24.82	24.75	29.70
SAL (PPT) MIN	8.10	13.80	12.16	12.23	15.00
SAL (PPT) RANGE	16.51	16.80	12.66	12.52	14.70
Chl-a (ug/L) MEAN	8.01	8.13	7.74	7.38	9.78
Chl-a (ug/L) MAX	35.60	62.00	22.83	34.15	64.60
Chl-a (ug/L) MIN	0.80	0.69	1.00	0.00	0.50
Chl-a (ug/L) RANGE	34.80	61.31	21.83	34.15	64.10

Source: Chesapeake Bay Program's (CBP) monitoring program
(www.chesapeakebay.net/monprgms.htm)

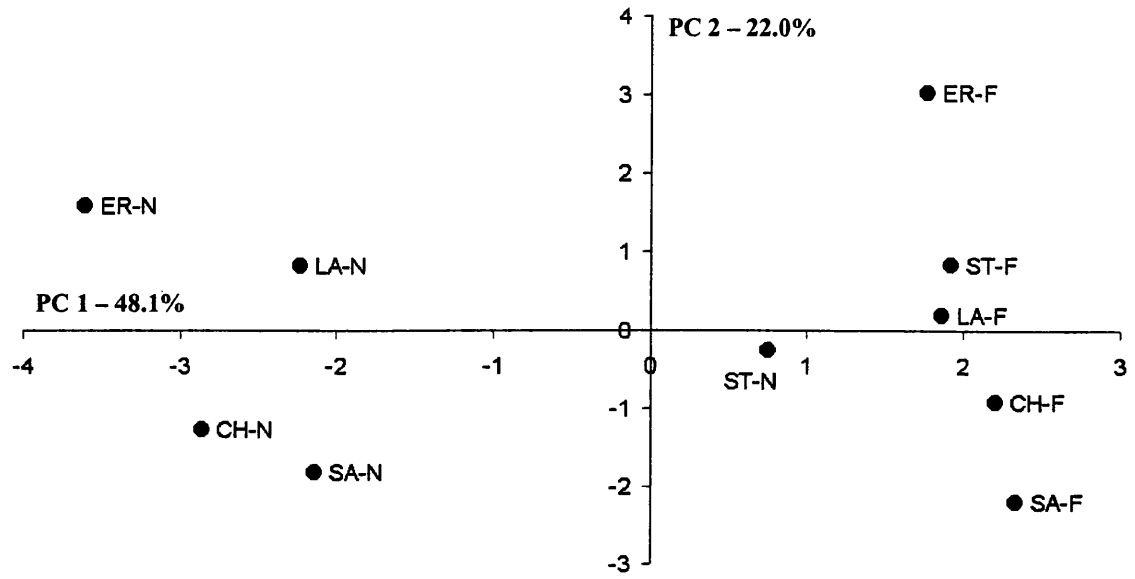


Figure 3. Projection of sampling sites on the first plane of a PCA based on the measured habitat parameters and data found in Table 2.

Table 3. Eigenvectors and measured variables associated with Figure 3.

<u>Eigenvectors</u>					
(Coefficients in the linear combinations of variables making up PC's)					
Variable	PC1	PC2	PC3	PC4	PC5
per_N	-0.401	-0.088	0.051	-0.114	-0.103
per_silt	-0.389	-0.045	-0.215	0.036	-0.152
per_clay	-0.386	-0.072	-0.21	0.054	0.012
per_C	-0.348	0.119	0.361	-0.017	0.018
molar C:N	-0.258	0.336	0.386	-0.138	0.008
measured water temp (deg C)	-0.182	0.341	-0.321	0.541	-0.278
Phaeo	0.089	-0.343	0.28	-0.163	-0.832
chl a:phaeo	0.094	0.475	-0.278	-0.328	-0.385
Chl_a	0.154	0.535	-0.094	-0.337	-0.02
Tox_Score	0.223	-0.271	-0.504	-0.066	-0.051
measured salinity (psu)	0.272	0.191	0.243	0.646	-0.19
per_sand	0.393	0.055	0.216	-0.043	0.097

Table 4. Matrix of measured habitat property data used in Fig. 3. ST= Severn River/Thorntons Creek, SA=Sarah Creek, CH=Chisman Creek, LA= Langley AFB/ Back River, ER=Elizabeth River (SW Branch). 01=near-field stratum, 02=far-field stratum. 01-09=sampling station. Tox Score = % survival of *L plumulosus* after 10-d exposure. Far-field = silt/clay content 0-40% by weight. Near-field = silt/clay content > 40% by weight. Sand = >63 μm , Silt = 63-4 μm , Clay = <4 μm particle size using the Wentworth scale.

Label	Tox Score	per_sand	per_silt	per_clay	measured salinity (psu)	measured water temp (deg C)	Chl_a	Phaeo	chl a:phaeo	per_N	per_C	molar C:N
CH0101	90.67	9.43	56.42	34.15	4.00	29.00	14.40	15.42	0.95	0.26	3.32	14.98
CH0201	94.67	97.46	0.01	2.53	19.00	26.00	53.97	11.33	5.64	0.02	0.16	9.28
ER0101	0.00	38.11	38.90	22.99	15.80	28.90	101.82	23.48	4.48	0.33	11.13	39.09
ER0201	86.67	88.16	7.42	4.41	15.70	29.00	402.28	4.80	639.38	0.03	0.47	19.60
LA0101	88.00	8.95	60.63	30.43	17.20	32.20	74.18	2.43	273.13	0.24	3.04	14.59
LA0201	92.00	92.94	5.54	1.52	18.80	28.90	141.95	4.73	33.94	0.02	0.18	9.96
SA0101	96.00	25.75	47.85	26.40	7.00	27.00	1.00	38.35	0.03	0.33	3.89	13.65
SA0201	97.33	98.31	0.46	1.23	19.00	26.50	4.40	174.02	0.02	0.06	0.15	8.37
ST0102	94.67	73.15	8.44	18.41	17.10	28.60	95.34	6.90	14.29	0.06	0.70	12.78
ST0201	88.00	94.78	0.78	4.45	17.80	28.50	186.46	1.89	222.82	0.01	0.16	12.16

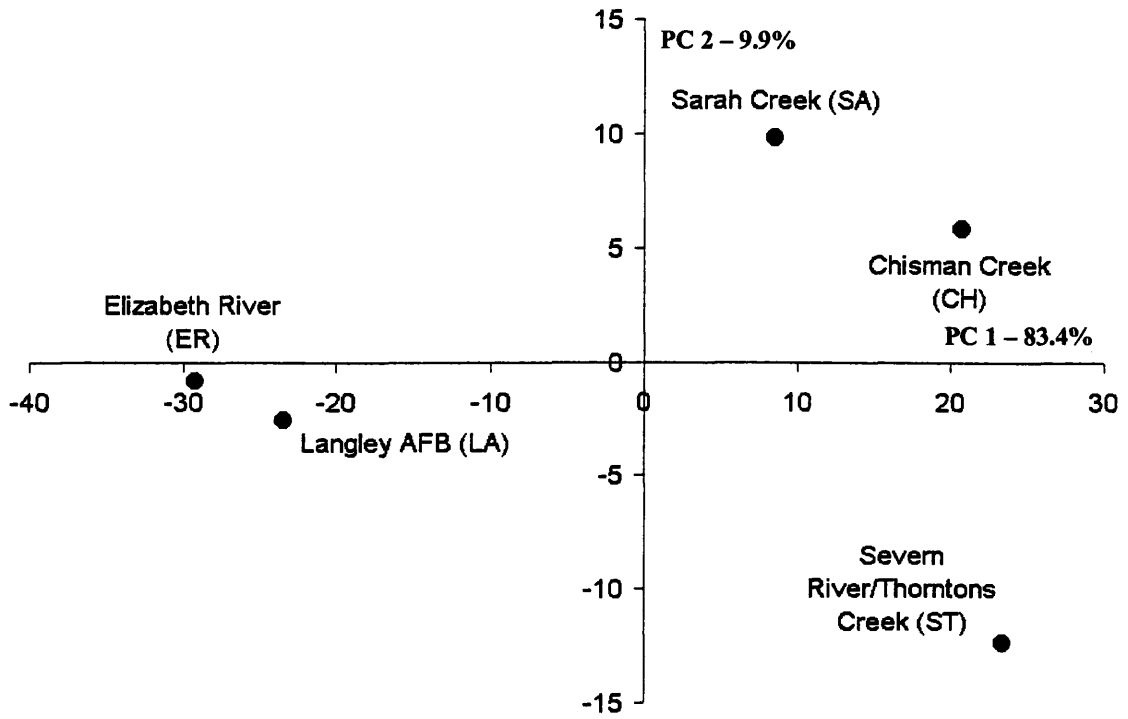


Figure 4. Projection of sampling sites on the first plane of a PCA based on the watershed land use variables and data found in Table 3.

Table 5. Eigenvectors and land cover classes associated with Figure 4.

<u>Eigenvectors</u>					
(Coefficients in the linear combinations of variables making up PC's)					
Variable	PC1	PC2	PC3	PC4	PC5
% Developed Low Intensity	-0.464	-0.018	-0.351	-0.55	0.499
% Developed Open Space	-0.284	0.244	-0.109	0.793	0.366
% Developed Medium Intensity	-0.225	-0.032	-0.105	0.009	0.159
% Developed High Intensity	-0.089	-0.035	-0.049	-0.07	-0.199
% Natural Barren	0.042	0.035	-0.032	-0.041	-0.423
% Farmland	0.105	0.495	0.732	-0.222	0.34
% Wetlands	0.13	-0.821	0.351	0.11	0.347
% Forest	0.785	0.132	-0.437	-0.03	0.37

Table 6. Matrix of watershed land use data used in Fig. 4. CH = Chisman Creek. ER = Elizabeth River. LA = Langley AFB. SA = Sarah Creek. ST = Thorntons Creek

Label	% Developed Open Space	% Developed Low Intensity	% Developed Medium Intensity	% Developed High Intensity	% Natural Barren	% Forest	% Farmland	% Woodlands
CH	9.04	6.29	1.77	0.32	3.65	57.20	17.09	4.64
ER	18.05	28.33	12.27	4.82	1.17	13.49	15.56	6.31
LA	21.93	21.94	11.19	3.89	1.08	17.98	13.02	8.97
SA	11.96	5.30	2.51	0.36	2.69	40.43	30.66	6.09
ST	2.37	1.25	0.49	0.16	2.75	51.67	17.19	24.12

Meiofauna abundances and community composition

Nematodes averaged between 92 and 1725 individuals per cm² at near and far-field sites (Fig. 5). Densities were highest at SA near-field and lowest by an order of magnitude at ER near-field, a site characterized by significant sediment toxicity (Table 2). Copepods averaged between 1 and 34 individuals per cm² at near and far-field sites (Fig. 6). Generally, copepod abundances were highest in fine-grained near-field sediments and lowest in coarse far-field sediments. Foraminifera averaged between 0.5 and 21 individuals per cm² at near and far-field sites (Fig. 7). Foram abundances were lowest at SA and CH in both near-field and far-field strata and the range of abundances did not differ greatly between strata.

Multi-Dimensional Scaling of square root transformed meiofauna abundances by station groups the near-field collections according to the type and intensity of disturbance, while far-field collections show relatively little dissimilarity (Fig. 8). Near-field collections group the ST, LA and CH near-field sites together intermediately, SA near-field sites most separated from the ER near-field sites. Careful inspection of the MDS reveals separation of near-field and far-field meiofauna communities within most sites in addition to clustering within the near-field sites themselves.

Taxa specific comparisons are apparent when abundances for nematodes, copepods, harpacticoid nauplii and benthic foraminifera are superimposed over the MDS plot (Fig. 9-12). Nematodes can be seen to exhibit highest abundances in SA-N, decrease in LA-N, ST-N, and CH-N and are virtually absent ER-N. Results of ANOVA using log transformed abundances of nematodes indicate significant

differences between near-field and far-field strata with elevated nematode abundances occurring in muddy near-field sediments ($p=0.0012$, $F=11.24$, $N=88$) (Appendix 3). Relative to the environmental characteristics (Tables 1-3) nematodes were most abundant in environmentally stressed fine-grained sediments associated with residentially and agriculturally developed watersheds characterized by low DO events and less abundant in coarse-grained sediments.

Harpacticoid copepods (Fig. 10) reach highest abundances in muddy near-field sediments (LA-N, ST-N, and CH-N) low abundances at SA-N. Results of ANOVA using $\log(n+1)$ transformed abundances of copepods indicate significant differences between near-field and far-field strata with elevated copepod abundances occurring in muddy near-field sediments ($p<0.0001$, $F=27.21$, $N=88$) (Appendix 3). A pattern similar to that of the copepod taxa can be seen in the harpacticoid nauplii abundance data (Fig. 11). Numbers of nauplii are heavily skewed toward near-field habitat.

Benthic Foraminifera exhibited site-specific variation in abundance, being present at CH, ER and ST sites and virtually absent at ER and SA sites (Fig. 12). The range of abundance was comparable for near-field and far-field strata.

Average Nematode Abundance

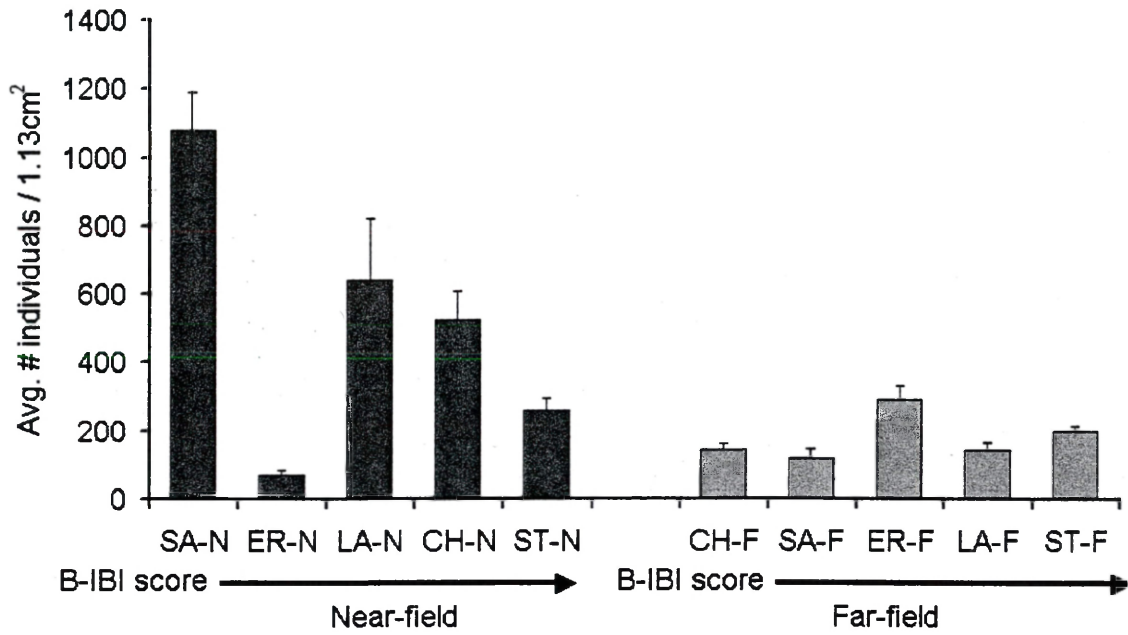


Figure 5. Abundances of nematode individuals/ 1.13 cm² averaged over site/stratum. Sampling sites are arrayed in order of increasing B-IBI score (increasing benthic integrity) at near-field and at far-field strata. Error bars are standard error (SE).

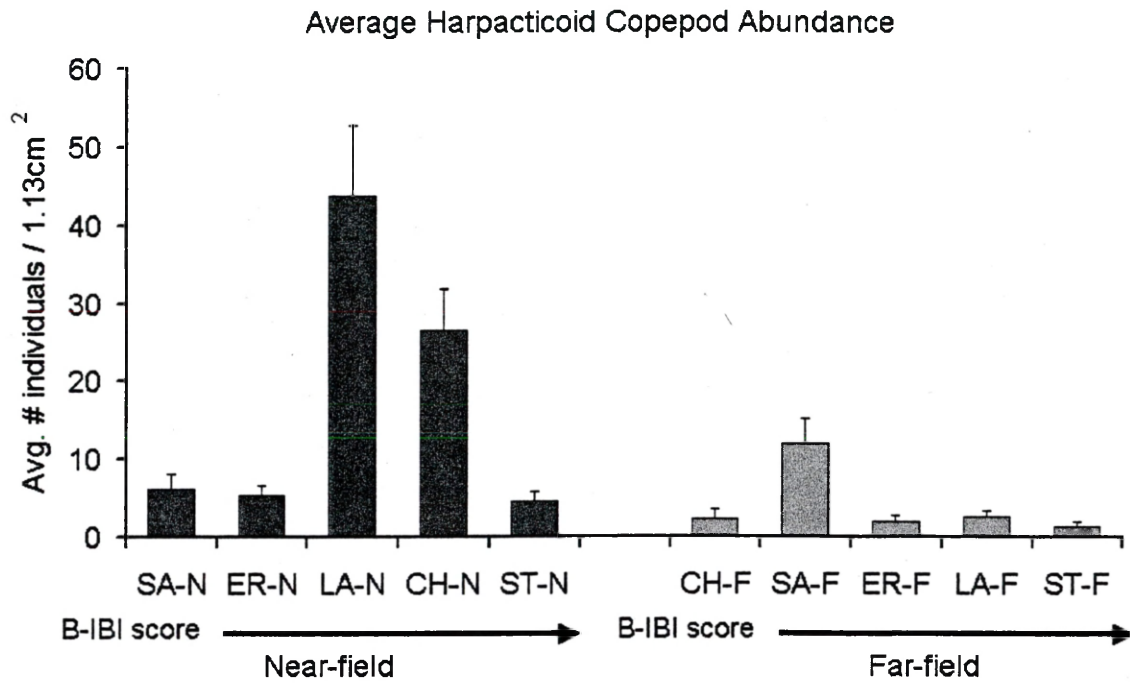


Figure 6. Abundances of harpacticoid copepod individuals/ 1.13 cm² averaged over site/stratum. Sampling sites are arrayed in order of increasing B-IBI score (increasing benthic integrity) at near-field and at far-field strata. Error bars are standard error (SE).

Average Benthic Foraminifera Abundance

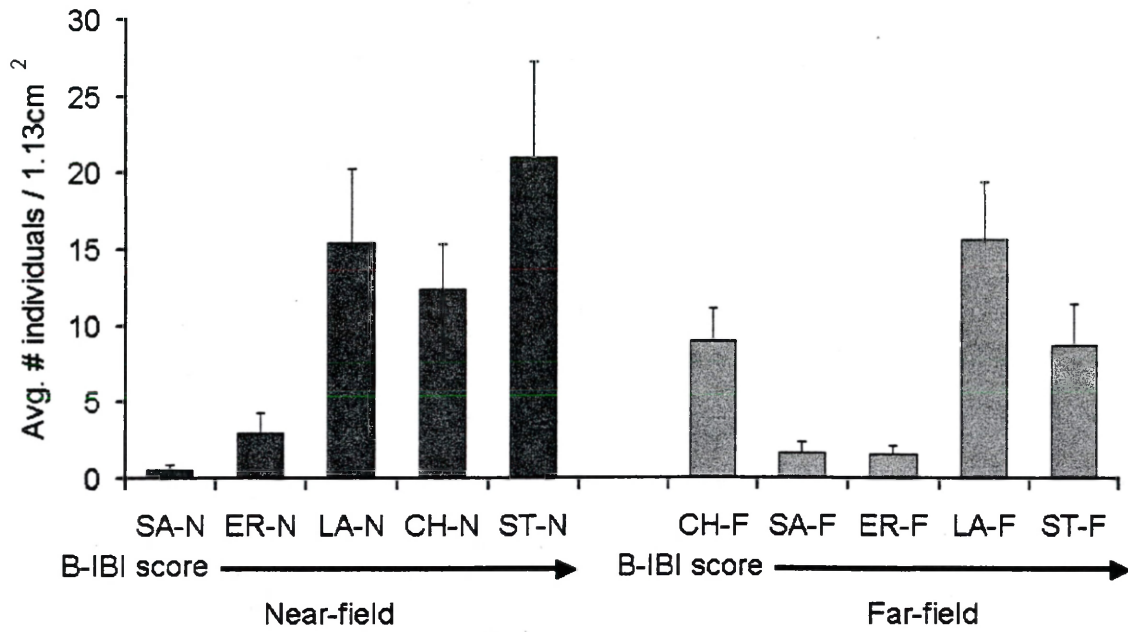


Figure 7. Abundances of benthic foraminifera individuals/ 1.13 cm² averaged over site/stratum. Sampling sites are arrayed in order of increasing B-IBI score (increasing benthic integrity) at near-field and at far-field strata. Error bars are standard error (SE).

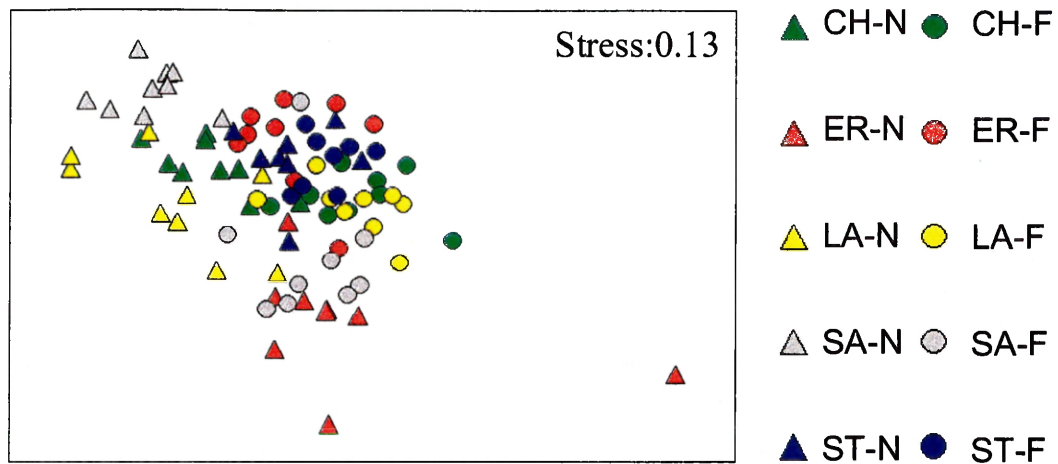


Figure 8. Ordination plots of non-metric Multi-dimensional Scaling of square root transformed meiofauna abundance data from 2003 sampling sites. Taxa included in the analysis: nematodes, harpacticoid copepods, harpacticoid nauplii, ostracods, mites, turbellarians and forams.

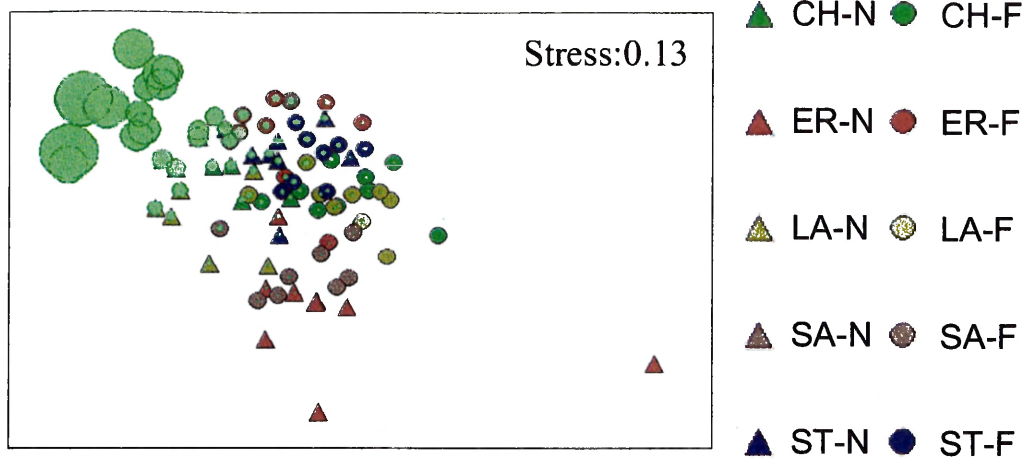


Figure 9. Ordination plots of non-metric Multi-dimensional Scaling of square root transformed meiofauna abundance data from 2003 sampling sites. Taxa included in the analysis: nematodes, harpacticoid copepods, harpacticoid nauplii, ostracods, mites, turbellarians and forams. Superimposed over the MDS plot are relative nematode abundances allowing taxa specific comparisons among stations.

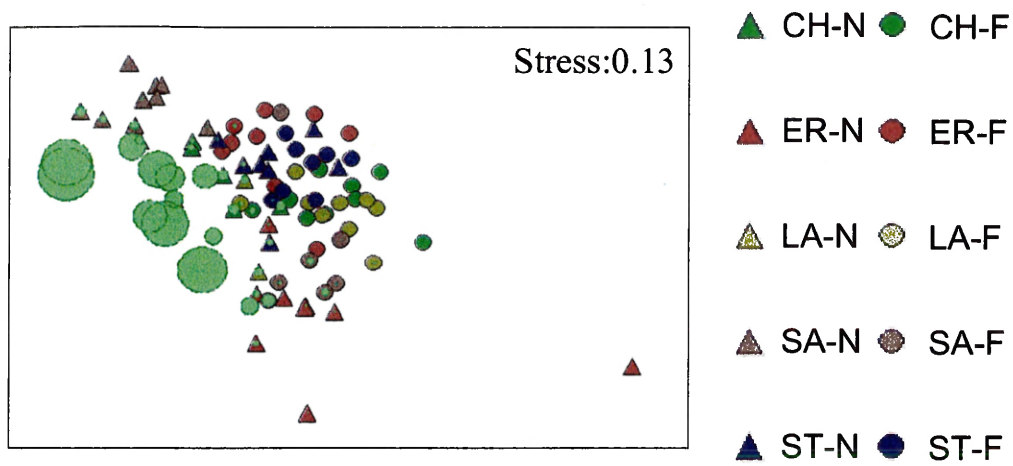


Figure 10. Ordination plots of non-metric Multi-dimensional Scaling of square root transformed meiofauna abundance data from 2003 sampling sites. Taxa included in the analysis: nematodes, harpacticoid copepods, harpacticoid nauplii, ostracods, mites, turbellarians and forams. Superimposed over the MDS plot are relative copepod abundances allowing taxa specific comparisons among stations.

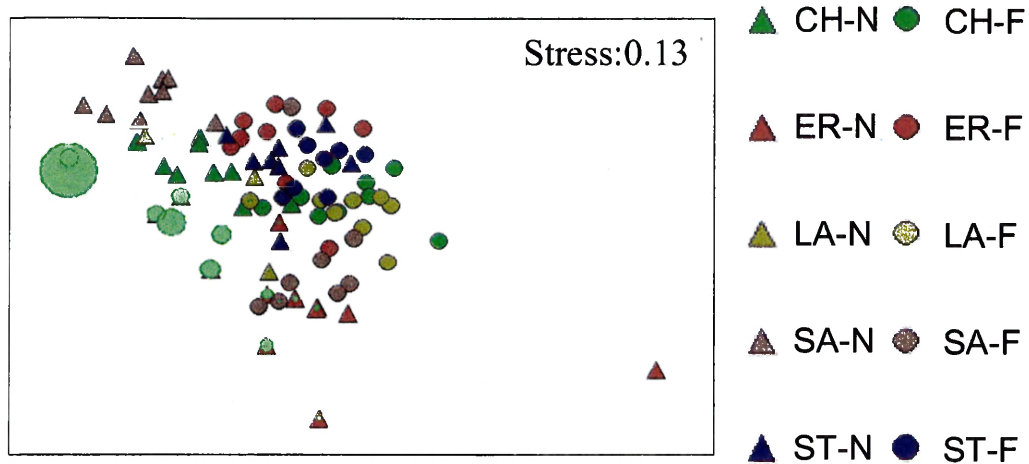


Figure 11. Ordination plots of non-metric Multi-dimensional Scaling of square root transformed meiofauna abundance data from 2003 sampling sites. Taxa included in the analysis: nematodes, harpacticoid copepods, harpacticoid nauplii, ostracods, mites, turbellarians and forams. Superimposed over the MDS plot are relative copepod nauplii abundances allowing taxa specific comparisons among stations.

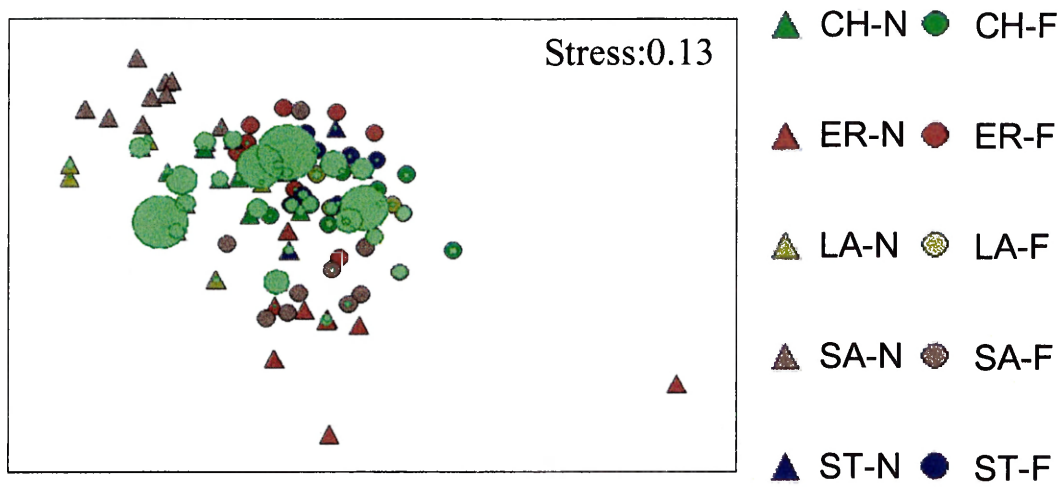


Figure 12. Ordination plots of non-metric Multi-dimensional Scaling of square root transformed meiofauna abundance data from 2003 sampling sites. Taxa included in the analysis: nematodes, harpacticoid copepods, harpacticoid nauplii, ostracods, mites, turbellarians and forams. Superimposed over the MDS plot are relative foraminifera abundances allowing taxa specific comparisons among stations.

Results of ANOSIM tests of square root transformed meiofauna abundances by core reveal significant differences in meiofauna community structure among near-field sites (Global R = 0.49, significance level of sample statistic: 0.1%; Appendix 3). Differences in meiofauna community structure among far-field stations exist, but to a weaker degree (Global R = 0.25, Significance level of sample statistic: 0.1%). The separations between near-field and far-field strata as indicated by ANOSIM (Global R = 0.24, Significance level of sample statistic: 0.1%) were also relatively weak, which suggests that further taxonomic resolution could improve our understanding of the effects of environmental stressors on meiofauna community structure (Appendix 3).

Linking Biotic and Environmental Variables

The biological-environmental linkage procedure (BIO-ENV) procedure allows comparison of the biological and environmental data. The procedure was used to select the “best fitting” abiotic variable subsets which maximized rank correlation between a similarity matrix of square root transformed meiofauna abundances by core and all possible (dis)similarity matrices of the historic water quality parameters presented in Table 1. The same procedure was run a second time, this time to correlate the observed meiofauna community structure with measured site characterization metrics and to compare the relative strength of historic factors vs. habitat properties in structuring the meiofauna communities at these sites. Site characterization metrics included all variables presented in Table 2.

Subsets of historical water quality variables that best group the regions in a manner consistent with the faunal pattern, incorporate salinity (max, mean, range), water column chlorophyll-a (max), NO_x (min), NH₄⁺ (min) and DO (max) ($\rho_w = 0.13$; Appendix 3). Measured variables that best grouped the sites in a manner consistent with the faunal pattern are sediment %TOC and %TN, molar C:N, sediment toxicity and percent farmland ($\rho_w = 0.54 - 0.56$; Appendix 3). These results highlight the relatively strong influence of local sediment-associated factors, rather than regional water quality in shaping meiofauna community structure.

Relationships with the B-IBI

Based on the average B-IBI, the degree of degradation of macrofauna community integrity was SA-N > ER-N > LA-N > CH-N > ST-N for near-field sites and CH-F > SA-F > ER-F > LA-F > ST-F for far-field sites. At the far-field sites CH and SA both scored as “severely degraded” while ER and LA had high percentages of stations with “marginal” B-IBI scores. The degraded B-IBI scores at SA and CH far-field and SA near-field are driven by high total abundances of macrofauna with a high percentages (>25%) of individuals classified as pollution indicative taxa. The values of these metrics and comparisons with the measured environmental parameters suggest that organic enrichment of the sediment at non-toxic levels may be the primary cause of the degraded macrobenthic community. The degraded B-IBI rankings for the near-field sites are also consistent with the results of the PCA of historical nutrient loadings for the York River (SA) and Elizabeth River (ER), which

are characterized by high nutrient concentrations, high chl-a and salinity levels (Fig. 3).

At near-field sites, average nematode abundance declines linearly ($R^2=0.9427$, $p=0.0291$) with increasing average B-IBI score when the ER-N site with significant sediment toxicity was excluded from the dataset (Fig. 13, Table 4). In the far-field no relationship is observed between nematode abundance and B-IBI scores ($p>.05$).

Table 7. Summary of regression results for each parameter versus average B-IBI score by site. n.s.= not significant.

Elizabeth River Excluded					
Strata	Parameter	n	r²	p	Slope
Near-field	Average Nematode Abundance	4	0.94	0.029	-730.87
Near-field	Average Copepod Abundance	4	0.00	n.s.	n.s.
Near-field	Average Ne/Co Ratio	4	0.56	n.s.	n.s.
Near-field	Average Foraminifera Abundance	4	0.75	n.s.	n.s.
Far-field	Average Nematode Abundance	4	0.44	n.s.	n.s.
Far-field	Average Copepod Abundance	4	0.31	n.s.	n.s.
Far-field	Average Ne/Co Ratio	4	0.41	n.s.	n.s.
Far-field	Average Foraminifera Abundance	4	0.42	n.s.	n.s.

Elizabeth River Included					
Strata	Parameter	n	r²	p	Slope
Near-field	Average Nematode Abundance	5	0.37	n.s.	n.s.
Near-field	Average Copepod Abundance	5	0.00	n.s.	n.s.
Near-field	Average Ne/Co Ratio	5	0.41	n.s.	n.s.
Near-field	Average Foraminifera Abundance	5	0.69	0.079	17.76
Far-field	Average Nematode Abundance	5	0.34	n.s.	n.s.
Far-field	Average Copepod Abundance	5	0.35	n.s.	n.s.
Far-field	Average Ne/Co Ratio	5	0.46	n.s.	n.s.
Far-field	Average Foraminifera Abundance	5	0.10	n.s.	n.s.

Average Nematodes vs. Average B-IBI

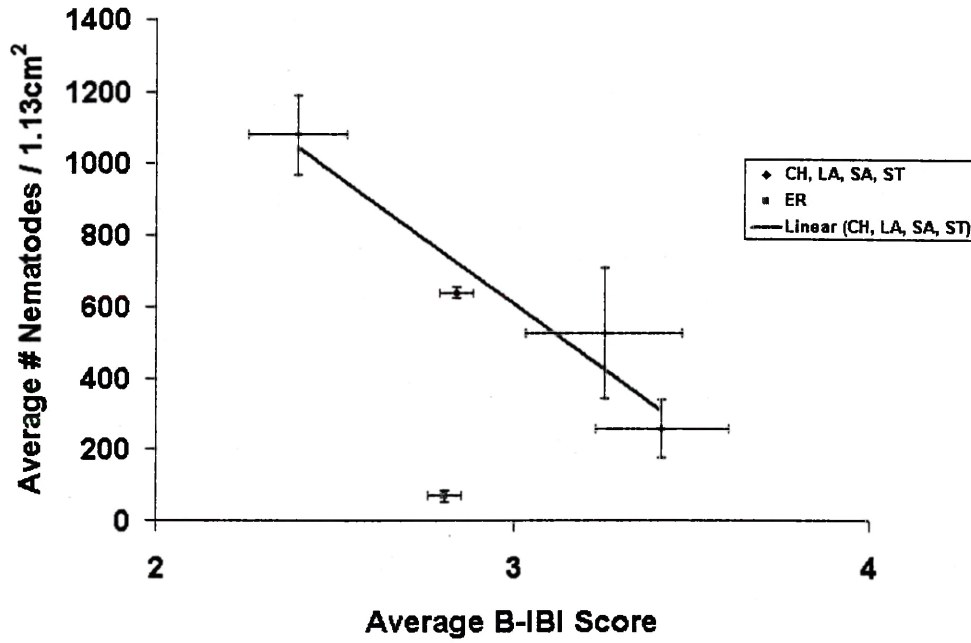


Figure 13. Correlation of nematode abundance and average B-IBI score by site showing means and standard error bars for abundance and B-IBI score. Error bars are standard error (SE).

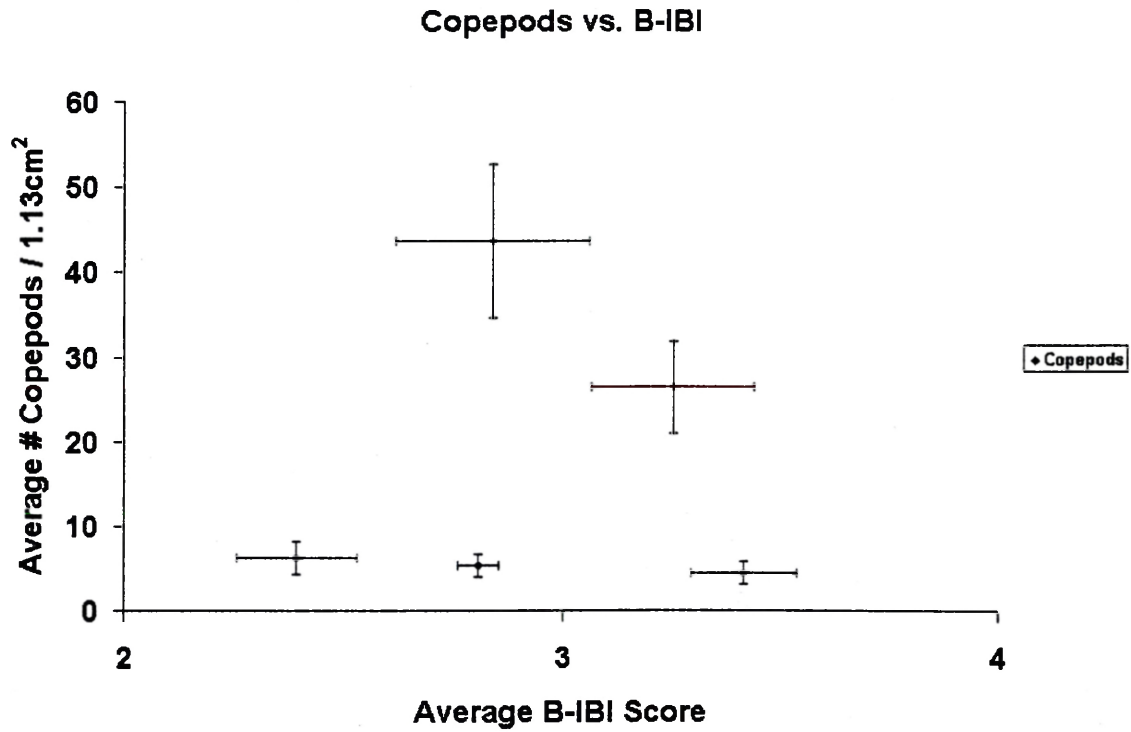


Figure 14. Correlation of copepod abundance and average B-IBI score by site showing means and standard error bars for abundance and B-IBI score. Error bars are standard error (SE).

Forams vs. B-IBI

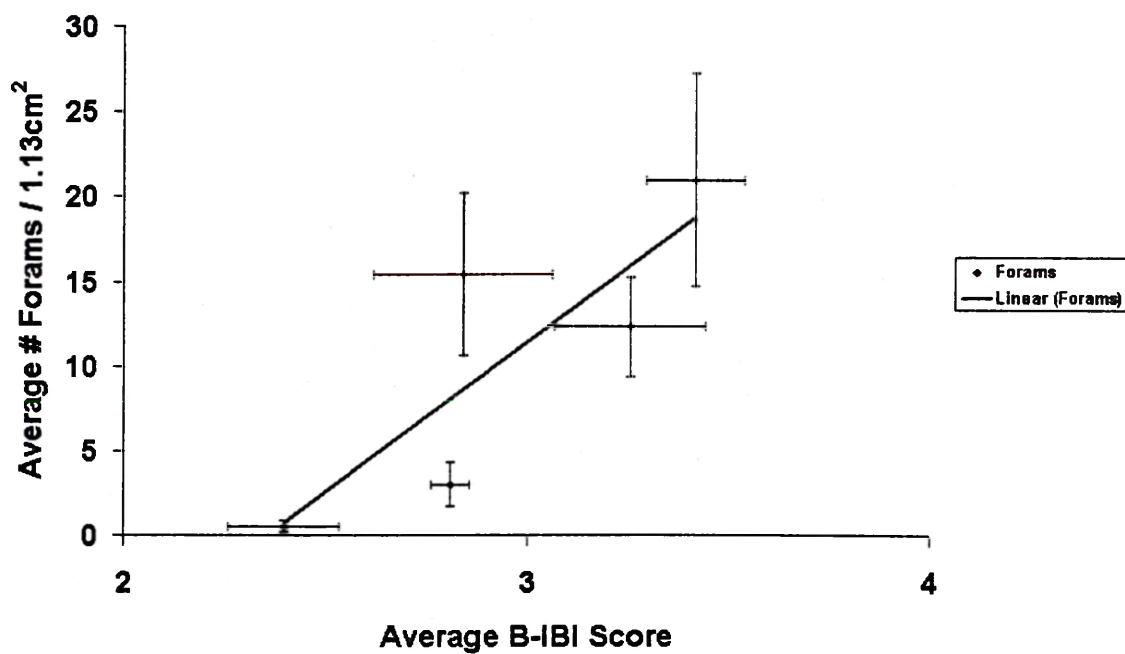


Figure 15. Correlation of foraminifera abundance and average B-IBI score by site showing means and standard error bars for abundance and B-IBI score. Error bars are standard error (SE).

At near-field sites copepod abundance did not vary linearly with increasing B-IBI value (Fig. 14, Table 4). In the far-field no relationship was observed between copepod abundance and B-IBI scores. No relationship was observed between Ne/Co and B-IBI scores in near or far-field strata (Fig. 16). Results of a linear regression analysis between average foram abundance and average B-IBI score indicate a trend but results are not significant ($p=0.079$; Fig. 15, Table 4).

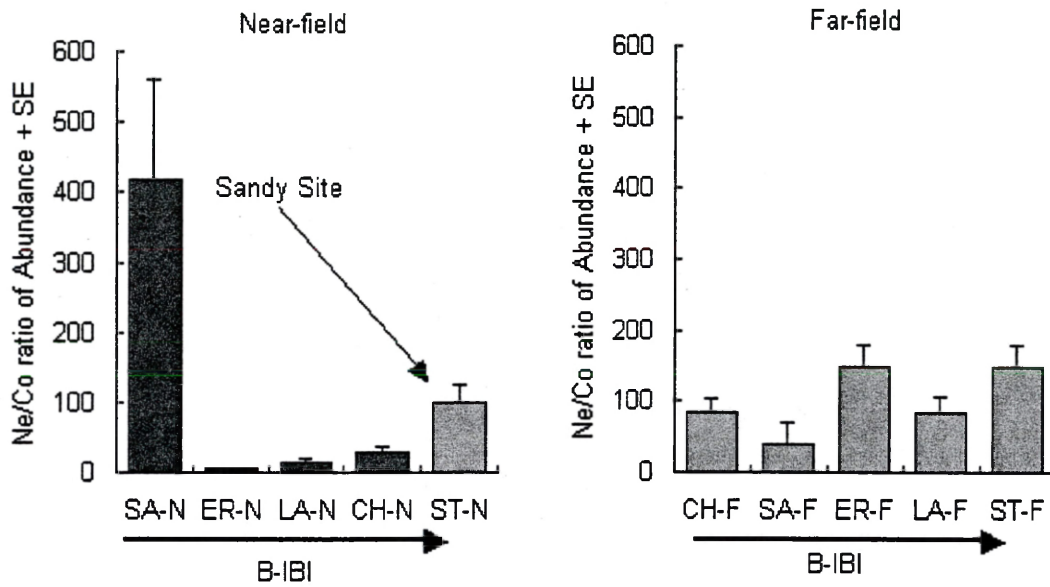


Figure 16. Average ratio of nematodes to harpacticoid copepods by site/stratum in order of increasing B-IBI score (increasing benthic integrity). Error bars are standard error (SE).

DISCUSSION

Anthropogenic effects on meiofauna community structure

Warwick (1988) suggests that anthropogenic effects modify benthic community composition at relatively high taxonomic levels, while natural environmental variables influence the fauna more by species replacement. Consistent with this generalization, our results demonstrate that meiofauna assemblages of shallow water habitats of lower Chesapeake Bay show shifts in meiofauna community composition, especially the relative abundances of nematodes and benthic Foraminifera in response to anthropogenic alterations of estuarine habitat quality. We also demonstrate shifts in community structure at the major taxa level associated with environmental variation indicative of near versus far-field site settings, especially with respect to sediment %TOC, %TN and grain size. Significant sediment toxicity is associated with a depauperate meiofauna.

Nematode abundance varied predictably along a disturbance gradient revealed by historic and measured water and sediment quality parameters, thus, my results are consistent with those of previous investigators who show that nematodes generally increase in abundance along gradients of increasing organic enrichment unless sediment toxicity is a factor (Raffaelli 1987, Higgins and Thiel 1988, Essink & Keindel 1998).

Based on the findings of Peterson *et al.* (1996) I predicted that harpacticoid copepods would be sensitive to disturbance gradients in the environment, but I was unable to document a response for harpacticoids as a group to the documented stressor gradient as indexed by the B-IBI among sites for either the near or far-field

sites. Others have shown that harpacticoid copepod taxa have several different life styles in the sediments, which affect their susceptibility to pollution (Raffaelli, 1987). Interstitial harpacticoids are considered very sensitive to environmental perturbations, especially those associated with organic-rich sediments, due to clogging of the sediment interstices. Non-interstitial harpacticoids, especially several epibenthic species and some burrowing forms, can withstand stressed conditions and are sometimes even capable of rapid increases in abundance in organic-rich environments (Marcotte and Coull, 1974). Identification of specific groups of copepods was beyond the scope of the present investigation. Further investigation of harpacticoid guild structure might be necessary to identify possible effects of anthropogenic alterations of habitat. Taxonomic resolution beyond Order requires careful handling and discrimination of harpacticoid specimens and diminishes the attractiveness and ease of using of meiobenthos as a pollution indicator relative to the use of macrobenthos.

It is well known that many species of forams are sensitive to pollution (Shari. *et al.*, 1991; Yanko and Flexer, 1992; Yanko *et al.*, 1994; Alve 1995; Alve and Olsgard, 1999; Debenay *et al.*, 2001). My results for benthic Foraminifera are in line with those of other authors who concluded that forams are very sensitive to pollution, thus they should provide a useful proxy for disturbance in environments affected by anthropogenic activities (Du Chatelet *et al.*, 2004).

The linear relationship between the B-IBI and nematode abundance is not significant when the ER site with high sediment toxicity is included. Schaffner *et al.* (in progress) have shown that the average B-IBI does not adequately reflect the

effects of sediment toxicity in Elizabeth River near-field sites. During Summer 2003, only four species of macrofauna were found at the ER near-field site and they were primarily omnivorous or carnivorous. Very low species richness at this site is consistent with high sediment toxicity, while the moderate abundances and biomasses recorded may be explained by the ability of a few species to benefit from the eutrophic conditions of the estuary. Evidence suggests that microalgae were proliferating (chl-a levels averaged 402.3 mg m⁻² at ER-N, Table 2) in the region, even in the presence of significant sediment contamination. The interacting effects of sediment toxicity and environmental stressors resulted in a marginally degraded benthic community as indexed by the B-IBI. Thus, Schaffner *et al.* have hypothesized that there is a significant interaction between stressors -- the presence of a benthic microalgal mat supported by high nutrient loading may effectively buffer some macrofauna from the effects of toxic sediments.

In the far-field, physical energy results in a coarser-grained habitat where the negative effects of sediment toxicity are likely to be minimized. The B-IBI was initially developed for use in deeper waters with physical energy regimes different than those at the shallow water stations sampled in this study and it may be that at these shallow water far-field sites the generalized B-IBI metrics are confounded by the effects of localized physical disturbance. Meiofauna abundances were generally low and physical forces and sediment grain size may primarily structure communities of exposed, sandy, shallow water regions unless low oxygen conditions prevail.

The Nematode:Copepod Ratio

The ratio of nematodes to copepods was driven primarily by nematode abundance at the sites studied. The toxic sediments of the Elizabeth River near-field had little effect on the Ne/Co ratio relative to low-impact sites because sediment toxicity acted to greatly reduce abundances of both nematodes and copepods alike. The incorporation of sediment toxicity testing into future meiobenthic pollution studies could account for some of the seemingly incompatible findings previously reported with regard to the nematode to copepod ratio that could be the result of toxic sediment.

Linking Meiofauna Community Structure to Environmental Variables

Results of ANOSIM indicated differences in the assemblages of meiofauna communities among near-field sites were greater than among those of far-field sites and a weak assemblage difference was detected between near-field and far-field strata. Differences in community composition at near-field sites were driven primarily by changes in the abundances of nematodes and Foraminifera. Our results suggest that reduced abundances of forams at ER and SA combined with high nematode abundance at SA-N and low nematode abundance at ER-N provides a means of discriminating between the effects of nutrient stressors and sediment contamination. Near-field sediments with high nematode abundances and low forams abundances may be indicative of sediment organic enrichment while sediments with low abundances of both nematodes and forams may be indicative of sediment toxicity. The higher degree of separation between meiofauna communities at near-field stations may be indicative of the role of sediments, particularly fine-grained silts

and clays, in sequestering contaminants, which in turn strongly affect community composition at near-field sites.

On regional and historical scales, results of the BIO-ENV procedure suggest chlorophyll-a, salinity, NO_x and NH_4^+ levels are weakly predictive of meiofauna community structure in shallow water areas. While the Spearman correlation coefficients for the historical water quality data were weak in general ($\rho_w = .13$), it should be noted that the water quality data were obtained from the CBP monitoring database and generally characterizes waters deeper than were actually sampled in this study. However, historical chlorophyll-a levels in the region can be considered a proxy for the cumulative effects of nutrient loadings, water residence time, biological activity and a myriad of other complex interactions that contribute to overall ecosystem health. Comparison of the habitat and historic ρ_w values obtained using the BIO-ENV procedure indicate the relatively stronger influence of habitat properties, such as sediment organic carbon, sediment nitrogen and sediment toxicity, rather than historic variables for shaping meiofauna community structure. These findings are in line with those of Giere (1994) who reported that meiofaunal abundance is known to correlate with organic carbon content from shallow water to the deep sea. These results are also consistent with those of Fenchel and Finlay (2004) whose neutral community model postulates that for small species (<1mm) with large population sizes, high rates of dispersal and low rates of extinction, habitat properties alone are needed to explain the presence of a given organism and historical factors are less important.

SUMMARY

Multivariate analyses of historical and measured sediment and water quality and land use parameters, and the Benthic Index of Biotic integrity show that the sites under investigation span a range of anthropogenic influence from highly impacted to relatively pristine. Meiofauna community structure changes at higher taxonomic levels along gradients of sediment toxicity and environmental stress, indicated by changes in land use and sediment organic carbon and nitrogen content. Meiofauna abundance is severely depressed when sediment toxicity is significant. Nematodes increased in abundance and Foraminifera decrease in abundance with increasing environmental stress in the absence of significant sediment toxicity. Sediment grain size is also important for meiofauna community structure – both nematode and copepod abundances were significantly elevated in muddy versus sandy habitats. Average nematode and foram abundances correlated with the B-IBI based on macrofauna metrics. Further discrimination of harpacticoid copepods and other meiofauna taxa will be required in order to determine if they are useful as indicators of human alterations of benthic habitat.

SOURCES OF DATA

Chesapeake Bay Program's (CBP) monitoring program:
www.chesapeakebay.net/monprgms.htm

U.S. Environmental Protection Agency's Environmental Monitoring and Assessment Program: EMAP; www.epa.gov/emap/

EPA's Middle Atlantic Integrated Assessment Program: MAIA; www.epa.gov/maia

Virginia Department of Environmental Quality:
http://gisweb.deq.virginia.gov/monapp/mon_data_retrieval_app.html#

NPL Fact Sheet – Chisman Creek
<http://www.epa.gov/superfund/sites/nplfs/fs0302756.pdf>

NPL Fact Sheet - Atlantic Wood Industries, Inc:
<http://www.epa.gov/superfund/sites/nplfs/fs0302836.pdf>

NPL Fact Sheet - Langley Air Force Base / NASA Langley
Research Center
<http://www.epa.gov/superfund/sites/nplfs/fs0303768.pdf>

Methods for Calculating the Chesapeake Bay B-IBI
<http://www.baybenthos.versar.com/docs/ChesBayBIBI.PDF>

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