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Robert M. Cerrato
School of Marine and Atmospheric Sciences, Stony Brook University, robert.cerrato@stonybrook.edu

Alison M. Flanagan
School of Marine and Atmospheric Sciences, Stony Brook University, alison.flanagan@stonybrook.edu

Roger D. Flood
School of Marine and Atmospheric Sciences, Stony Brook University, roger.flood@stonybrook.edu

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By

Robert M. Cerrato
Alison M. Flanagan
Roger D. Flood

Marine Sciences Research Center
School of Marine and Atmospheric Sciences
Stony Brook University
Stony Brook, NY 11794-5000

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ABSTRACT

High-resolution backscatter and bathymetric maps created by multibeam and sidescan sonar surveys were used to identify five different seafloor bottom types within Haverstraw Bay. Grab samples were collected within these areas to characterize sediment properties and macrofauna. Selected sampling locations were revisited and seafloor images were obtained with an HD underwater camera. Multivariate analysis was used to identify the most important factors explaining variations in community structure. Results indicated that categorical variables defining bottom types, grain size, and water depth can explain about 42% of community structure variation. In addition, shell length data collected for *Rangia cuneata*, an introduced species, indicated that successful spawning and recruitment occurred for this species during 2011, 2012, and 2013. An attempt to relate 2012-2014 hydrophone location data for Atlantic and Shortnose sturgeon to identified bottom types did not produce clear bottom preferences.

INTRODUCTION

Maps generated by acoustic surveys are incredibly useful, enabling large areas to be surveyed at fine resolution in relatively short periods of time; however, these maps are not sufficient for predicting bottom characteristics or the distribution of benthic communities, and at least one ground truth stage is required to link the acoustic maps with environmental and biological assemblages. Acoustic surveys can distinguish areas of different bottom character, but determining that those sites are, for example, sea-grass beds, rocky substrates, rippled sands, or muddy surfaces requires verification by direct sampling. Knowing the type of bottom present is an important indicator of the benthic community that may be present, but benthic communities are highly variable and cannot be accurately predicted based on bottom type alone. In addition, geophysical features detectable by acoustic surveys that appear to characterize distinct sedimentary regions are not necessarily biologically relevant (Brown *et al.*, 2002).

The principal objective of this study was to collect and analyze sediment and faunal ground truth samples in Haverstraw Bay. Sampling locations were determined by visual examination of high resolution backscatter and bathymetric maps created by multibeam and side scan sonar surveys. The multibeam sonar survey was conducted as part of a separate task, and these maps are not part of the current report. Ground truth data were analyzed in order to describe the environment and fauna in Haverstraw Bay, and to determine how well collected environmental data can explain benthic community structure. GIS data were also used to explore a possible relationship between the ground truth results and sturgeon tracking data collected by the Hudson River Fisheries Unit of the New York State Department of Environmental Conservation (NYSDEC). Funding for this study was provided by an Environmental Benefits Project from NYSDEC.

METHODS

Study Area and Sampling Locations

This study was carried out in the Haverstraw Bay portion of the Hudson River from approximately Stony Point in the north to Croton Point in the south (Figure 1). Stratification of the bay into initial bottom type provinces was conducted by visual examination of preliminary

300 kHz multibeam backscatter data collected by Roger Flood (SoMAS) and 100 KHz sidescan sonar mosaics for Area B3 collected as part of the Hudson River Mapping Program (R. Bell, W.B.F. Ryan, S.M. Carbotte, F.O. Nitsche, Lamont-Doherty Earth Observatory of Columbia University, NY). In this process, acoustic backscatter was taken as a proxy for bottom type, and visual examination suggested the presence of six regions or provinces of homogeneous bottom type (Figure 2). These six provinces were arbitrarily assigned a letter code from A-F. Ten grab sampling stations were randomly positioned within each province using the “Create Random Points” tool in ArcGIS 10 (ESRI, Redlands CA) (Figure 2a), with two exceptions. Province F was small relative to the other bottom types, and only two grab samples were collected within it. Province A was larger than other bottom types, and eleven samples were collected within it. In determining sampling locations, stations within 100 m of a boundary between bottom types or of another station were deleted and replaced by another randomly selected location. The former was to minimize the possibility of inadvertently drifting across a boundary while sampling or sampling in an ecotone or transitional region between provinces. The latter was to maintain independence between sampling stations and to insure that the sampling results represented the full range of variability within a province.

A subsequent comparison of the grab sampling locations with a more complete, processed version of the 300 kHz backscatter data was carried out after grab samples were collected, but before any data analysis. This visual inspection indicated that several province boundaries required adjusting (Figure 2b). These adjustments had several consequences. Stations C03 and C04 were clearly within province A and not province C. While the sample identifiers were not changed, these two samples were assigned to province A for analysis. Several other stations (C02, C05, D07, E05, E06) were located closer (< 100 m) to a boundary than initially planned, and therefore, possibly within an ecotone between bottom types. These stations were included in all analyses anyway, although they may have increased the variability of some of the results.

Sediment and Fauna Sampling

Bottom samples for sediments and fauna were collected on October 3-4, 2013 using a modified van Veen grab (0.04 m^2). A total of 53 samples were collected. Subsamples of sediments for grain size were drawn from each grab sample. The remaining sediment was washed through a 0.5 mm sieve for fauna. All material left on the sieve was preserved in 10% buffered formalin and stained with rose bengal. Faunal samples were rewashed in the lab and transferred to 70% ethanol before sorting and identification. Individual organisms were identified to species level whenever possible and the total for each taxon enumerated. Unless otherwise noted, all abundances in this report are expressed as the number of individuals per sample (i.e., per 0.04 m^2).

Sediment grain size analysis following methodology in Folk (1974) was used to estimate percent composition by weight of major size-fractions (gravel, sand, silt, clay). Samples were initially partitioned into three size-fractions by adding 50 ml of a 1% Calgon solution to the sample, mixing to disaggregate the particles in the sample, and wet sieving with distilled water through a combination of 2 mm and 63 micron sieves. The >2 mm (gravel) and 2 mm-63 micron (sand) fractions were placed in a drying oven at 60^o C for at least 48 hours to obtain dry weights. Water containing the <63 micron fraction (silt-clay or mud) was brought up to 1000 ml total volume by adding distilled water in a graduated cylinder, mixed thoroughly, and subsampled with a 20 ml pipette at a depth of 20 cm, 20 seconds after mixing to obtain an estimate of silt-clay. A clay sample was obtained from a second 20 ml pipette sample collected at a depth of 10 cm, 2 hours and 3 minutes after mixing. Pipette samples were placed in a drying oven at 60^o C for at least 48 hours to obtain dry weight estimates of the silt-clay and clay fractions. Weight estimates included a correction for the amount of Calgon introduced to the samples. Silt content was estimated from the difference in weight between the silt-clay and clay fractions.

Bottom images were collected by revisiting at least two sampling locations in provinces A-E on October 10, 2013 and deploying a Seatrex HD (Ocean Systems Inc., Everett WA) industrial grade underwater point of view camera mounted on a tripod. Distance from the camera to the sediment surface had to be decreased to 25 cm because of very high turbidity in the study area, and image size was 14 x 24.5 cm, comparable in size to the dimensions of the modified van Veen grab (20 x 20 cm) used to collect faunal and grain-size samples. For each video, VLC Media Player (VideoLAN, Paris, France) was used to extract a still frame for inclusion in this report.

Data Entry and Summary

Data were entered into Microsoft Excel spreadsheets, and faunal data were summarized by using PC-ORD (MJM Software Design, Gleneden Beach, OR). This summary and subsequent data analyses required assigning a unique 6-character code for each species. This was created in most cases by using the first 3 characters in both the genus and species name. Faunal data at each sampling station were summarized by calculating the abundance (total number of individuals per grab), species richness S (number of species per grab), Shannon diversity ($H' = -\sum p_i ln p_i$) where p_i is the proportion of individuals of each species, and equitability ($E = H'/lnS$). Equitability ranges from 0 to 1 and measures how evenly individuals are distributed among the S species present. A geodatabase of the data and GIS maps displaying selected data were created in ArcGIS version 10.2.2 (ESRI, Redlands CA). All data were imported into the GIS directly from the Excel spreadsheets.

Multivariate Analysis

Data were analyzed by redundancy analysis (RDA), a multivariate direct gradient technique that explicitly incorporates environmental variables in the analysis of the faunal data. RDA, first suggested by Rao (1964), is a technique that combines ordination of sample sites based on species abundance data with regression on the environmental data in order to examine the relationship between community structure and environmental variables (Jongman *et al.*, 1995). By examining the environmental and biological data simultaneously, this analysis depicts the trends in the species data that are related to the selected environmental data. RDA is based on Euclidean distance, which is not the most appropriate resemblance measure for species data, since it incorrectly interprets shared species absences between samples as similarities. In order to circumvent this shortcoming, abundance data were Hellinger transformed by taking the square root of relative abundances of each species in a sample (Legendre and Gallagher, 2001). This transformation focuses the analysis on compositional differences, reduces the influence of the most abundant species, and combined with Euclidean distance, has been shown to produce good representations of ecological data (Legendre and Gallagher, 2001).

A parsimonious set of significant environmental variables was identified by sequentially adding variables in a forward selection process (Jongman et al., 1995). Candidate variables included water depth, grab penetration depth, apparent RPD depth, percent gravel, sand, mud, and categorical variables identifying each province. At each step in the process, the environmental variable explaining the largest amount of faunal variability is selected, and its effect is removed before the next best fitting variable is considered. Variables identified by forward selection were trimmed back to a smaller set by the AICc stopping criterion (Burnham and Anderson 2002). AICc is the small sample, bias adjusted version of the Akaike Information Criterion (AIC). The use of AICc applies an information-theoretic approach to statistical modeling that overcomes problems associated with multiple significance testing (Burnham and Anderson 2014). Although a not entirely correct interpretation (see Burnham and Anderson 2002), AIC can be considered a measure that assesses the tradeoff between fit and complexity among models. In application, the model with the smallest AIC or AICc is chosen over the set of models considered (Hastie et al. 2009). In the current analysis, categorical province variables were also combined into smaller sets (e.g., A&E combined, B&D combined, etc.) and evaluated by the AICc criterion to insure that the smallest number of distinct provinces was selected. RDA was carried out using Canoco 4.5 (ter Braak and Smilauer 2002).

RESULTS

General Description of the Environmental and Faunal Characteristics of the Study Area

Sediments in the study area were diverse but were most often characterized by high percent mud contents (Figures 3-4). Of the 53 samples, 39 had mud contents greater than 50%, while there were only 7 samples with gravel exceeding 50% and 3 samples with sand exceeding 50%. Water depths at sampling stations ranged from 2.8 to 19.9 m. During the period of grab sample collection (October 3-4, 2013), salinities at the bottom ranged from about 10-15 and at the surface from 6.5-7.5. Temperatures ranged from 20-21° C at the bottom and 21-22° C at the surface. The modified van Veen grab penetrated to its maximum depth of 10 cm for 35 of the 53 samples and rarely penetrated less than 5 cm (8 samples). The depth of the apparent redox potential discontinuity (RPD) varied between 0 and 2.5 cm. Field and grain size data tabulated by sample are contained in Appendices 1 and 2, respectively.

A total of 5,640 animals representing 25 taxa were collected in the 53 samples. Average abundance in the 53 samples was 106.4 individuals per sample (2,660 per m^2). Of the 25 taxa, 20% were polychaetes, 16% were molluscs, 44% were crustaceans, and the remainder (20%) was distributed among five other groups (Table 1). Numerical dominants included the amphipod *Melita nitida* (969 individuals), the bivalve *Rangia cuneata* (828 individuals), the polychaete *Hypaniola grayi* (564 individuals), oligochaetes (501 individuals), the amphipod *Leptocheirus plumulosus* (409 individuals), the barnacle *Balanus amphitrite* (343 individuals), the polychaete *Neanthes (Nereis) succinea* (331 individuals), the bivalve *Mytilopsis leucophaeata* (319 individuals), the polychaete *Boccardia ligerica* (263 individuals), the polychaete *Scolecolepides viridis* (250 individuals), chironomid larvae (199 individuals), Nemertinea sp (198 individuals), and the amphipod *Corophium* sp (136 individuals). These 13 taxa represented about 94% of the total number of individuals collected, and no other taxon had an average abundance greater than

2 per sample (>106 individuals). Faunal data listed by sample and bottom type province are tabulated in Appendices 3 and 4.

a) Province A

Thirteen samples were collected in this bottom type (A01-11, C03-04). Province A was one of four shallow areas (A, C, E, F) sampled (Figure 5), and sampling stations within this bottom type had a mean water depth of 3.9 m $\pm$ 0.4 sd. The van Veen grab penetrated to its maximum depth (10 cm) for all samples except one (C04), where it penetrated to 7 cm (Figure 6). Average RPD depth was 1.1 cm $\pm$ 0.5 sd (Figure 7). Sediments were muddy (silt-clay mean = 85.9% $\pm$ 11.9 sd) (Figure 8) and cohesive, but with an uncompacted surface layer about 1 cm thick. The gravel fraction (mean = 3.1% $\pm$ 5.1 sd) of the sediments consisted mainly of shell hash and pieces of organic debrii (e.g., wood). A small amount of sand was also present (mean = 11.1% $\pm$ 11.2 sd). The sediment surface was flat, easily resuspended, with pieces of shell visible (Figure 9). The siphons of live *Rangia* were apparent, along with grooves leading up to the siphons suggesting recent lateral movement by some individuals.

Faunal abundances ranged from 56 to 174 individuals per sample and species richness varied from 6 to 11 species per sample. Mean abundance was 91.5 $\pm$ 39.7 (sd) individuals per sample (Figure 10), and mean species richness was 9.4 $\pm$ 1.7 (sd) species per sample (Figure 11). A total of 18 species were collected. The most abundant taxa was the wedge clam *Rangia cuneata*, and it represented 28.3% of the total number of individuals in the samples. Other abundant species included the polychaete *Hypaniola grayi* (24.0%), the amphipod *Leptocheirus plumulosus* (13.4%), chironomid larvae (10.2%), the spionid polychaete *Scolecolepides viridis* (5.6%), the dreissenid bivalve *Mytilopsis leucophaeata* (4.0%), nemerteans (4.0%) and oligochaetes (3.8%), the slender isopod *Cyathura polita* (1.8%), the clam worm *Neanthes succinea* (1.8%), and the amphipod *Melita nitida* (1.0%) (Table 2). Mean Shannon diversity was 1.65 $\pm$ 0.25 (sd) (Figure 12), and mean equitability was 0.75 $\pm$ 0.10 (sd) (Figure 13).

b) Province B

Ten samples were collected in this province (B01-B10). Province B was one of two deeper areas (B, D) on the west side of the bay. Water depths averaged 10.3 m $\pm$ 2.5 sd. All grab samples penetrated to their maximum depth of 10 cm. Average RPD depth was 1.3 cm $\pm$ 1.5 sd. This area had one sample with 3.3% gravel, but no other sample had a gravel content exceeding 0.4%. Samples were largely mud (mean silt-clay = 90.3% $\pm$ 6.3), with a small amount of sand (9.3% $\pm$ 5.7). The sediment surface was flat, featureless, and non-cohesive (Figure 14), with an occasional small piece of shell, wood, leaf, or anthropogenic debris (coal) remaining in the grab sample after sieving with a 0.5 mm screen.

The fauna in Province B was depauperate compared to the other regions in the study area, including one sample with no macrofauna (B03) and one with a single species (B02). Faunal abundances varied from 0 to 75 individuals per sample. Species richness ranged from 0 to 7 species per sample. Mean abundance was only 18.8 $\pm$ 24.2 (sd) individuals per sample and mean species richness was 3.7 $\pm$ 2.2 (sd) species per sample. A total of 9 taxa were collected.

Eight of these represented > 1% of the total fauna: the gastropod *Hydrobia* sp (43.6%), oligochaetes (12.8%), the wedge clam *Rangia cuneata* (13.8%), nemerteans (11.2%), the spionid polychaete *Scolecolepides viridis* (9.0%), the capitellid polychaete *Notomastus* sp (4.8%), the slender isopod *Cyathura polita* (3.2%), and the polychaete *Hypaniola grayi* (1.1%). Chironomid larvae (0.5%) was the only remaining taxa found in this province. Province B was the only area with a mean Shannon diversity below 1 (0.93 ± 0.67 sd) (Figure 12). Mean equitability was 0.65 ± 0.42 (sd) (Figure 13).

c) Province C

This province is a relict oyster reef habitat, characterized by a silt layer overlying oyster shells (Figure 15) with cohesive sand or mud sediments below the shells. Eight samples were collected in this province (C01-02, C05-10), because as indicated earlier, samples C03-C04 were reassigned to Province A after examining a more complete, processed version of the 300 kHz backscatter data. Water depths ranged from 2.8 to 4.7 m. The grab sampler penetration depth was shallow (3.4 cm ± 1.2 sd), and average RPD depth was 0.1 cm ± 0.4 sd. Sediment grain size was highly variable, ranging from 12.2-92.3% gravel and shell, 4.4-37.8% sand, and 3.3-58.2% silt-clay. Average gravel (with shell), sand, and mud contents were 52.0% ± 21.8 (sd), 26.8% ± 10.6, 21.2% ± 17.8, respectively.

Mean abundance and species richness was higher than other provinces in the study area. Mean abundance was only 300.6 ± 263.9 (sd) individuals per sample and mean species richness was 12.6 ± 2.1 (sd) species per sample. Abundances ranged from 95 to 901 individuals per sample, accounting for the high standard deviation, and species richness ranged from 10 to 16 species per sample. A total of 19 taxa were collected. The most abundant taxa included the amphipod *Melita nitida* (37.5%), oligochaetes (12.0%), the barnacle *Balanus amphitrite* (11.9), the spionid polychaete *Boccardia ligerica* (9.9%), the clam worm *Neanthes succinea* (8.8%), the dreissenid bivalve *Mytilopsis leucophaeata* (6.3%), the tubicolous amphipod *Corophium* sp (5.0%), the spionid polychaete *Scolecolepides viridis* (2.8%), and the ribbed mussel *Geukensia demissa* (1.9%). Mean Shannon diversity was 1.79 ± 0.17 (sd), and mean equitability was 0.71 ± 0.07 (sd).

d) Province D

Province D was a second deeper area (along with B) on the west side of the bay. Ten samples were collected (D01-D10). Water depths averaged 11.0 ± 4.6 (sd) meters. The van Veen grab penetrated to its maximum depth (10 cm) for all samples except two (D02, D03) where it penetrated to 8 cm. Average RPD depth was 1.1 cm ± 1.1 sd. Stations in this province were muddy but with noticeable pieces of coarser material, such as shells, shell hash, gravel, coarse sand, boiler slag, coal, wood, and leaves (Figure 16). Average gravel (and shell, slag, etc.) content was 14.0% ± 21.6 sd. Mean sand and mud contents were 20.6% ± 21.4 and 65.4% ± 29.8, respectively.

Like province B, this deeper area had low faunal abundance and species richness. Average abundance was 25.8 ± 25.1 individuals per sample, and average species richness was 6.4 ± 3.8 species per sample. Sample D01 had no macrofauna present. Faunal abundances varied from 0 to 87 individuals per sample. Species richness ranged from 0 to 12 species per sample. A total of 17 species were collected, a value almost twice as large as province B and comparable to the other provinces in the study area. Numerically abundant taxa included the bivalve *Rangia* cuneata (24.8%), the spionid polychaete *Scolecolepides viridis* (13.6%), oligochaetes (12.0%), the slender isopod *Cyathura polita* (9.7%), nemertineans (9.7%), chironomid larvae (7.4%), the polychaete *Hypaniola grayi* (4.7%), the clam worm *Neanthes succinea* (4.3%), the capitellid polychaete *Notomastus* sp (3.9%), the mud crab *Rhithropanopeus harrisii* (3.1%), the barnacle *Balanus amphitrite* (2.3%), and the dreissenid bivalve *Mytilopsis leucophaeata* (1.9%). Mean Shannon diversity was 1.42 ± 0.64 (sd), and mean equitability was 0.78 ± 0.29 (sd). So, despite the low abundances, this province had the highest evenness in the study area.

e) Province E

Ten samples were collected in this province (E01-E10). This province was located on the east side of the river adjacent to Croton Point. Water depths averaged 3.6 m ± 0.2 sd. Grab samples penetrated to a depth of 8.2 cm ± 2.4 (sd). Average RPD depth was 1.3 cm ± 0.7 sd. Samples were a mixture of sand (38.1% ± 11.6 sd) and mud (mean silt-clay = 54.1% ± 19.9), with a small amount of gravel and shell (7.8% ± 10.7). The exception to this pattern was E10 with a gravel content of 35.3% and almost no mud (5.8%). Sediments were cohesive with small shell hash, *Rangia* shell pieces, and siphons of live individuals apparent on the surface (Figure 17).

Faunal abundances ranged from 87 to 214 individuals per sample and species richness varied from 9 to 16 species per sample. Mean abundance was 135.1 ± 44.3 (sd) individuals per sample, and mean species richness was 12.3 ± 2.6 (sd) species per sample. A total of 21 species were collected. The wedge clam *Rangia* cuneata was the most abundant taxa present, representing 25.0% of the individuals collected. Additional abundant species included the amphipod *Leptocheirus plumulosus* (18.2%), the polychaete *Hypaniola grayi* (11.2%), the dreissenid bivalve *Mytilopsis leucophaeata* (6.7%), nemerteans (6.6%) and oligochaetes (5.8%), the clam worm *Neanthes succinea* (4.7%), the spionid polychaete *Scolecolepides viridis* (4.6%), the amphipod *Melita nitida* (3.7%), chironomid larvae (3.6%), the barnacle *Balanus amphitrite* (3.3%), the ribbed mussel *Geukensia demissa* (1.3%), and the tubicolous amphipod *Corophium* sp (1.1%). Mean Shannon diversity was 1.89 ± 0.42 (sd), and mean equitability was 0.76 ± 0.14 (sd).

f) Province F

Because of its small size, only two grab samples and no bottom images were collected in province F. The samples had similar van Veen grab penetration depths (8.0 cm), RPD depths (1 cm), and water depths (4.0 and 3.7 m), but differed considerably in sediment grain size. Sample F01 had 76.1% gravel and oyster shells, while F02 was 90.5% mud with a small amount of fine shell hash. Abundant taxa in F01 included oligochaetes (31.8%), the clam worm *Neanthes succinea* (26.1%), and the dreissenid bivalve *Mytilopsis leucophaeata* (19.3%), while the polychaete *Hypaniola grayi* (56.5%) and the bivalve *Rangia cuneata* (29.2%) were abundant in F02.

Although averages for this province were included in all tables and figures, the large differences between the abiotic and biotic characteristics of these two samples indicate that this province was not adequately described by two samples. As a result, this province was excluded from the multivariate analysis presented below.

Multivariate Analysis

Forward selection RDA resulted in identifying and retaining 6 environmental variables based on the AICc stopping criterion: the categorical variables for Provinces A&E combined, B, C, D, and the continuous variables water depth and percent sand (Figure 18). These environmental variables explained 42.1% of the total variability in community structure (Table 3). The selection of most province variables indicated that community structure differed in a manner consistent with differences in the backscatter data collected by the multibeam sonar. A total of 97.8% of the explained species-environment relationship was contained in the first four ordination axes (Figure 18), with most of that explained variation (80.9%) in the first two axes. Because of the high degree of explained variance in the first two axes, the interpretation of results presented below will focus on these axes (Figure 18a).

The RDA ordination triplot in Figure 18 shows the relationship between community structure and the final set of environmental variables. In this ordination diagram, points represent the community structure at each station; those that plot close to one another have similar species composition while points far apart are dissimilar. The larger black triangles and black arrows represent categorical and quantitative environmental variables, respectively. The black triangles are located at the centroid of the samples belonging to the categorical variable (e.g., the triangle labeled C is the centroid of the samples collected in province C). Envelopes corresponding in color to the province designations A&E, B, C, and D are drawn around the samples representing each of the categorical groups. The black arrows represent the direction of steepest increase for the quantitative environmental variables (water depth and percent sand). The origin is the mean of the variable and decreasing values for the quantitative environmental variable extend through the origin in the direction opposite the head of the arrow. The red arrows represent the abundances of selected species whose variances are well explained by the RDA analysis. Sample points can be orthogonally projected onto the arrow of a species or environmental variable (i.e., the direction of the projected point is perpendicular to the arrow); this projection approximately orders the samples from the largest to the smallest value for that variable.

The first two ordination axes contain most (80.9%) of the explained variation in community structure (Figure 18a). Province C samples are distinct and strongly separated along the first axis from samples in other areas. Provinces B and D are distinguished from the remaining provinces on the basis of greater water depth and lower percent sand. They appear to overlap in the plane formed by ordination axes 1 and 2, but separate from one another along axes 3 &4. Although samples in provinces A and E displayed considerable faunal variability, especially along the first ordination axis, model selection analysis using the AICc criterion did not justify separating these samples into two distinct faunal assemblages. Of the 25 taxa collected, 18 were found in both provinces, only 3 were found in one but not the other province (taxa in E but not in A: *Corophium* sp, *Edotia triloba,* and *Hydrobia* sp), and the remaining 4 were not present in either province. The distributions of selected quantitative environmental variables and species are given in Figures 19-30.

Distribution and Potential Age Structure of *Rangia cuneata*

Field observations suggested that several distinct cohorts of the wedge clam *Rangia cuneata* were present in the grab samples. Shell length measurements in the lab confirmed this impression (Figure 31). Three distinct size groups were present in the population, corresponding to shell lengths of roughly 0-10 mm, 20-30 mm, and 40-50 mm. Based on the length-age relationship in Fritz et al. (1990) for Delaware Bay *Rangia cuneata*, these sizes correspond to ages 0, 1, and 2 years. In the Delaware population, each year class consisted of a mixture of spring and fall spawned individuals. Assuming that spring and fall spawning events also occur in the Hudson River, the three identified groups may also consist of a mixture of two seasonally spawned cohorts. Additionally, the small number of individuals 12-19 mm in shell length in province A could potentially represent either age 0, spring spawned individuals or age 1, fall spawned individuals. Since this species forms a winter annulus in the shell, a radial cross-section of the shell from the umbo to the margin could be used to determine age (Fritz et al. 1990). As a final note, most individuals of this species were collected on the eastern side of the bay (Figure 32). Only the age 0 class was collected in province B, two age classes were found in province C, and all three age classes were present in provinces A, D, and E (Figure 31).

Potential Sturgeon Habitat Preferences

An attempt to relate confirmed sturgeon position data to the bottom types identified in the sonar data was not definitive. GIS files containing hydrophone data locating Atlantic and Shortnose sturgeon in Haverstraw Bay was obtained from Amanda Higgs of the Hudson River Fisheries Unit of the New York State Department of Environmental Conservation. The sturgeon datasets were queried to select the time period of interest, spatially joined to the final province layer, and counts of sturgeon occurrences were standardized by dividing by the area of each bottom type. No consistent preferences for bottom type were identified across the years 2012-2014 (Figure 33) or by limiting sampling time to the fall (September-December) period, the same season as collection of the grab sample data (Figure 34).

DISCUSSION

General Description of the Sediments and Faunal Community

Both sediment and faunal characteristics varied within and among areas sampled. Sediments tended to be muddy (39 of 53 samples with >50% mud), but a few samples (14 of 53) contained substantial amounts of sand and/or gravel. Faunal abundances differed widely from 0 to 901 individuals per sample. Species richness was also highly variable, ranging from 0 to 16 species per sample. Of the 25 taxa and excluding province F, 5 (20%) were found in only one of the five areas, 6 (24%) were found in 2-3 areas, and 14 (56%) were found in 4 or more areas.

Multivariate Analysis

Multivariate analysis revealed a fairly typical faunal-environmental relationship, with 42.1% of the total variance explained by two continuous (water depth and percent sand) and four categorical (A&E, B, C, D) variables. A large fraction of that variability (26.8% of the 42.1%) was explained by dividing the study area into distinct provinces suggested by interpreting sonar backscatter data. This result agrees well with our prior studies in the Peconics Estuary, North Shore Long Island bays, and Tappan Zee (Cerrato and Holt 2008, Cerrato and Maher 2007, Maher and Cerrato 2004) where the explained faunal-environmental relationship ranged from 30-58% of the total variance. Those studies also found that variables derived from sonar data were more effective at explaining community variation than traditional variables such as grain size and water depth.

With the exception of sampling stations C03 and C04, no attempt was made to regroup stations based on their environmental or faunal characteristics. More complete processing of the multibeam sonar data indicated that C03 and C04 were assigned to the wrong province, and shifting these two stations into province A was justified. This decision was made prior to any faunal analysis. It was tempting to consider whether samples in provinces A and E were really distinct, but in the end, differences were not great enough to justify differentiating these areas.

Distribution and Potential Age Structure of *Rangia cuneata*

Rangia cuneata is an interesting species because while present in the Pleistocene, no live individuals were found along the entire East Coast of the US during the mid-1800s to mid-1900s, and it was generally listed in the technical literature as a Gulf Coast species (Hopkins and Andrews 1970). Carlton (1992) reported *Rangia* as present in the Hudson River in 1988 based on a collector (C. Letts) and suggested it was possibly introduced as larvae in ballast water. Ristich et al. (1977) collected no individuals during their extensive 1972 estuary-wide survey from New York Harbor to Poughkeepsie in 1968. Llyanso et al. (2003) collected Rangia from stations between Yonkers (river mile 17) and New Hamburg (river mile 66), demonstrating that a well-established population was present during their 2000-2001 study. In the current Haverstraw Bay study, at least three year classes were present, indicating that successful spawning and recruitment occurred during 2011, 2012, and 2013. It is possible that individuals > 35 mm were older than age 2 based on size ranges reported in Fritz et al. (1990), so successful recruitment may have extended to years even earlier than 2011. *Rangia* is a filter feeder, and so it joined the zebra mussel *Dreissena polymorpha* as recent introductions that have increased the capacity of filter feeding animals in the Hudson.

Potential sturgeon habitat preferences

No clear preferences for bottom type were identified by relating sturgeon location data to the provinces in the sonar data (Figures 33-34). The sediment and faunal characteristics of the bottom types do, however, suggest several potential habitat-related factors to consider in interpreting sturgeon movement and location patterns. The relatively low macrofaunal abundances found at provinces B and D suggest that these areas may not be particularly rich feeding areas for sturgeon, at least during the fall period when the grab samples were collected.

Province C, which had high macrofaunal abundance and species richness, also had a hard, shelly bottom (Figure 6, 15) that might present problems for sturgeon trying to feed on any abundant infaunal invertebrates (e.g., *Neanthes succinea* buried in sediments, *Melita nitida* under shells) that would be generally much smaller than the oyster shells present. Provinces A and E had substantially higher abundances of *Rangia cuneata* than the other provinces. If sturgeon prefer to feed in areas of high infaunal biomass, then these two provinces would be areas with abundant food. Data on sturgeon diet preferences coupled with the results of this ground truth study might provide information about the relative importance to sturgeon of the bottom types present in Haverstraw Bay.

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Table 1. List of species collected during Haverstraw Bay sampling.

Phylum	Subphylum/Class	Order	Family	Species
Annelida	Oligochaeta			*Oligochaete* spp.
Annelida	Polychaeta	Spionida	Spionidae	*Boccardia ligerica*
Annelida	Polychaeta	Terebellida	Ampharetidae	*Hypaniola grayi*
Annelida	Polychaeta	Phyllodocida	Nereididae	*Neanthes succinea*
Annelida	Polychaeta		Capitellidae	*Notomastus* sp.
Annelida	Polychaeta	Spionida	Spionidae	*Scolecolepides viridis*
Arthropoda	Crustacea	Amphipoda	Corophiidae	*Corophium* sp.
Arthropoda	Crustacea	Amphipoda	Gammaridae	*Gammarus daiberi*
Arthropoda	Crustacea	Amphipoda	Corophiidae	*Leptocheirus plumulosus*
Arthropoda	Crustacea	Amphipoda	Melitidae	*Melita nitida*
Arthropoda	Crustacea	Amphipoda	Oedicerotidae	*Monoculodes* sp.
Arthropoda	Crustacea	Cirripedia	Balanidae	*Balanus amphitrite*
Arthropoda	Crustacea	Decapoda	Panopeidae	*Rhithropanopeus harrisii*
Arthropoda	Crustacea	Isopoda	Anthuridae	*Cyathura polita*
Arthropoda	Crustacea	Isopoda	Idoteidae	*Edotea triloba*
Arthropoda	Crustacea	Isopoda	Sphaeromatidae	*Sphaeroma quadridentatum*
Arthropoda	Crustacea	Isopoda	Idoteidae	*Synidotea laevidorsalis*
Arthropoda	Insecta	Diptera	Chironomidae	*Chironomidae* spp. (larvae)
Mollusca	Bivalvia	Veneroida	Dreissenidae	*Mytilopsis leucophaeata*
Mollusca	Bivalvia	Mytiloida	Mytilidae	*Geukensia demissa*
Mollusca	Bivalvia	Veneroida	Mactridae	*Rangia cuneata*
Mollusca	Gastropoda	Littorinimorpha	Hydrobiidae	*Hydrobia* sp.
Platyhelminthes	Rhabditophora	Polycladida	Stylochidae	*Stylochus ellipticus*
Platyhelminthes	Turbellaria			Turbellaria sp.
Nemertea				Nemertea sp.

Table 2. Average abundance (per sample) and percent relative abundance by province

		Average Abundance (per sample)						Percent of Fauna					
Taxa	**IDCode**	**A**	**B**	**C**	**D**	**E**	**F**	**A**	**B**	**C**	**D**	**E**	**F**
Balanus amphitrite	Balamp	0.4	0.0	35.8	0.6	4.5	0.5	0.4	0.0	11.9	2.3	3.3	0.4
Boccardia ligerica	Boclig	0.7	0.0	29.8	0.0	1.2	2.0	0.8	0.0	9.9	0.0	0.9	1.6
Chironomidae spp (larvae)	Chispp	9.3	0.1	0.4	1.9	4.8	3.5	10.2	0.5	0.1	7.4	3.6	2.8
Corophium sp	Corosp	0.0	0.0	15.0	0.0	1.5	0.5	0.0	0.0	5.0	0.0	1.1	0.4
Cyathura polita	Cyapol	1.6	0.6	0.5	2.5	0.9	0.0	1.8	3.2	0.2	9.7	0.7	0.0
Edotea triloba	Edotri	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.1	0.0
Gammarus daiberi	Gamdai	0.2	0.0	1.6	0.0	0.2	0.5	0.2	0.0	0.5	0.0	0.1	0.4
Geukensia demissa	Geudem	0.2	0.0	5.6	0.1	1.7	0.5	0.2	0.0	1.9	0.4	1.3	0.4
Hydrobia sp	Hydrsp	0.0	8.2	0.0	0.2	0.7	0.0	0.0	43.6	0.0	0.8	0.5	0.0
Hypaniola grayi	Hypgra	21.9	0.2	2.6	1.2	15.1	46.5	24.0	1.1	0.9	4.7	11.2	37.3
Leptocheirus plumulosus	Lepplu	12.2	0.0	0.0	0.2	24.6	1.0	13.4	0.0	0.0	0.8	18.2	0.8
Melita nitida	Melnit	0.9	0.0	112.9	0.1	5.0	1.5	1.0	0.0	37.5	0.4	3.7	1.2
Monoculodes sp	Monosp	0.1	0.0	0.0	0.0	0.7	0.0	0.1	0.0	0.0	0.0	0.5	0.0
Mytilopsis leucophaeata	Mytleu	3.7	0.0	19.0	0.5	9.1	11.5	4.0	0.0	6.3	1.9	6.7	9.2
Nemertinea sp	Nemesp	3.7	2.1	1.6	2.5	8.9	1.0	4.0	11.2	0.5	9.7	6.6	0.8
Neanthes succinea	Neasuc	1.6	0.0	26.5	1.1	6.4	11.5	1.8	0.0	8.8	4.3	4.7	9.2
Notomastus sp	Notosp	0.1	0.9	0.0	1.0	0.6	0.0	0.1	4.8	0.0	3.9	0.4	0.0
Oligochaete spp	Olispp	3.5	2.4	36.0	3.1	7.8	17.5	3.8	12.8	12.0	12.0	5.8	14.1
Rangia cuneata	Rancun	25.8	2.6	1.8	6.4	33.8	25.0	28.3	13.8	0.6	24.8	25.0	20.1
Rhithropanopeus harrisii	Rhihar	0.5	0.0	2.0	0.8	1.2	0.5	0.5	0.0	0.7	3.1	0.9	0.4
Scolecolepides viridis	Scovir	5.2	1.7	8.4	3.5	6.2	1.0	5.6	9.0	2.8	13.6	4.6	0.8
Sphaeroma quadridentatum	Sphqua	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0
Stylochus ellipticus	Styell	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0
Synidotea laevidorsalis	Synlae	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.4	0.0	0.0
Turbellaria sp	Turbsp	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0
	Average Abundance Total	91.5	18.8	300.6	25.8	135.1	124.5						
	Number of Taxa	18	9	19	17	21	16						

Table 3. RDA results

**** Summary ****

Axes	1	2	3	4	Total variance
Eigenvalues :	0.211	0.130	0.046	0.025	1.000
Species-environment correlations :	0.920	0.893	0.751	0.611	
Cumulative percentage variance					
of species data :	21.1	34.0	38.7	41.2	
of species-environment relation:	50.1	80.9	91.9	97.8	
Sum of all eigenvalues					1.000
Sum of all canonical eigenvalues					0.421

All four eigenvalues reported above are canonical and correspond to axes that are constrained by the environmental variables.

Figure 1. Haverstraw Bay study area

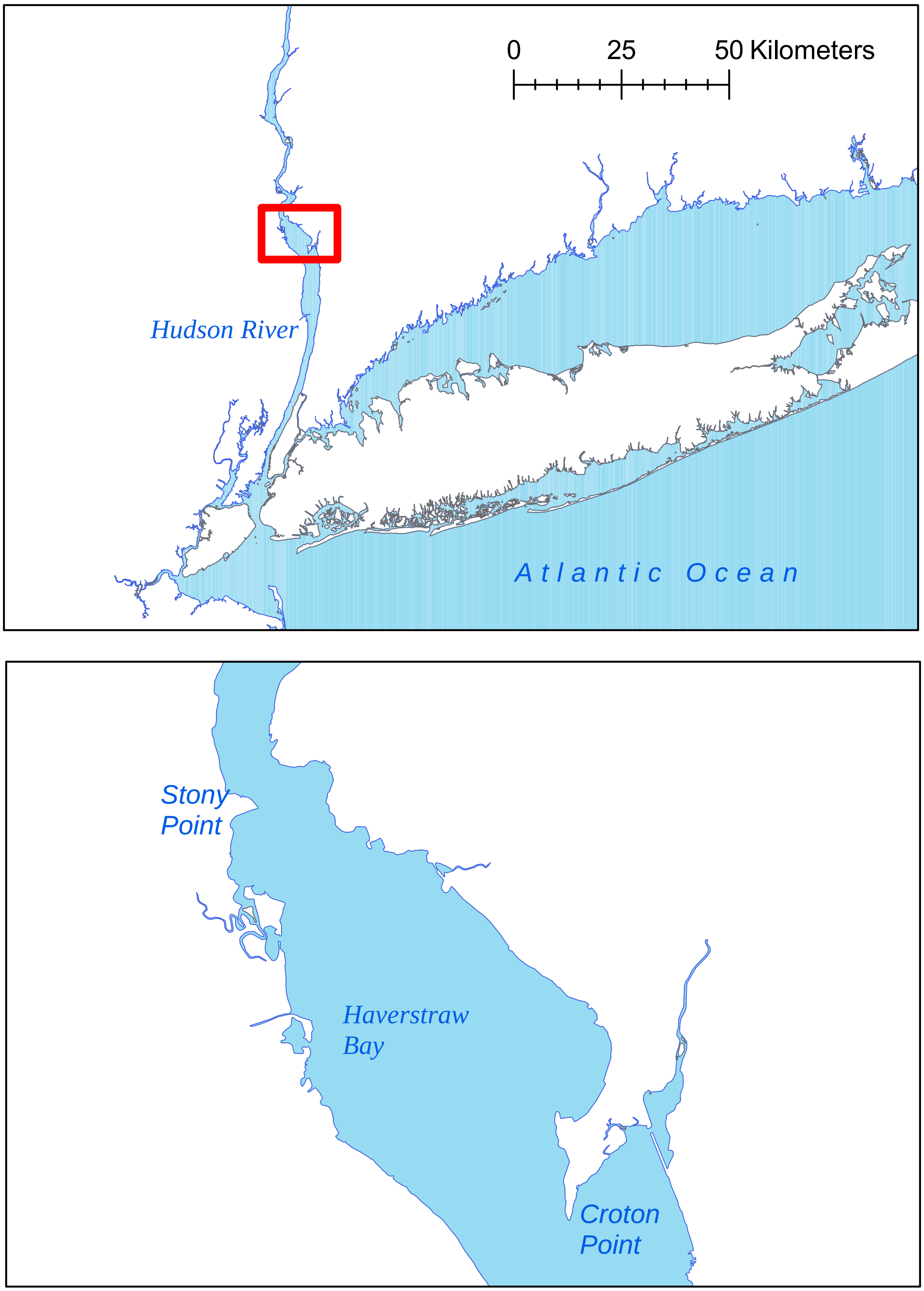


Figure 2. Initial (left) and final (right) sonar provinces with sampling stations. The left plot was based on available sonar data at the time of sample collection on October 3-4, 2013. The right plot was based on a more complete, processed version of the 300 kHz backscatter data. The newer data suggest small boundary adjustments between provinces. See text for further details.

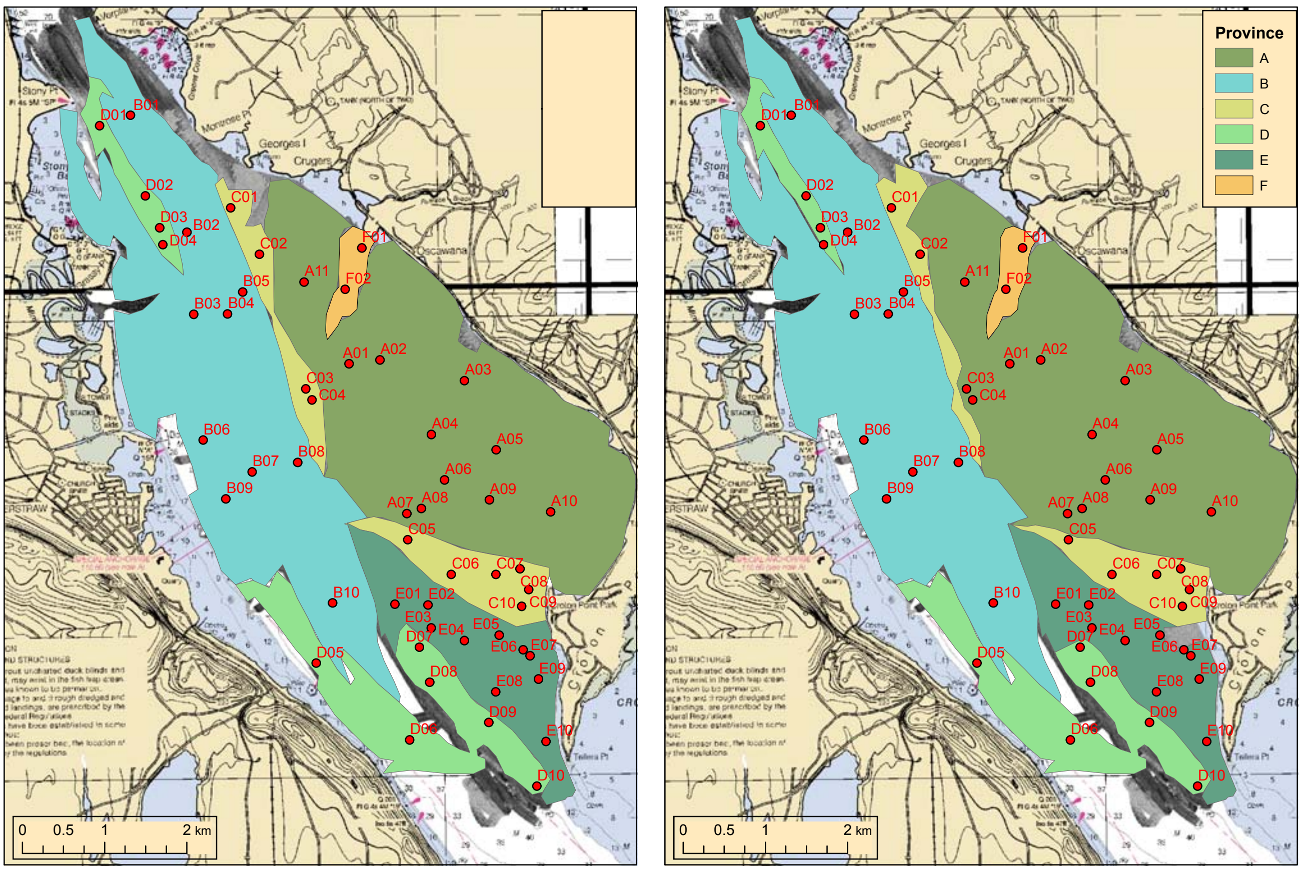


Figure 3. Sediment grain size results by province

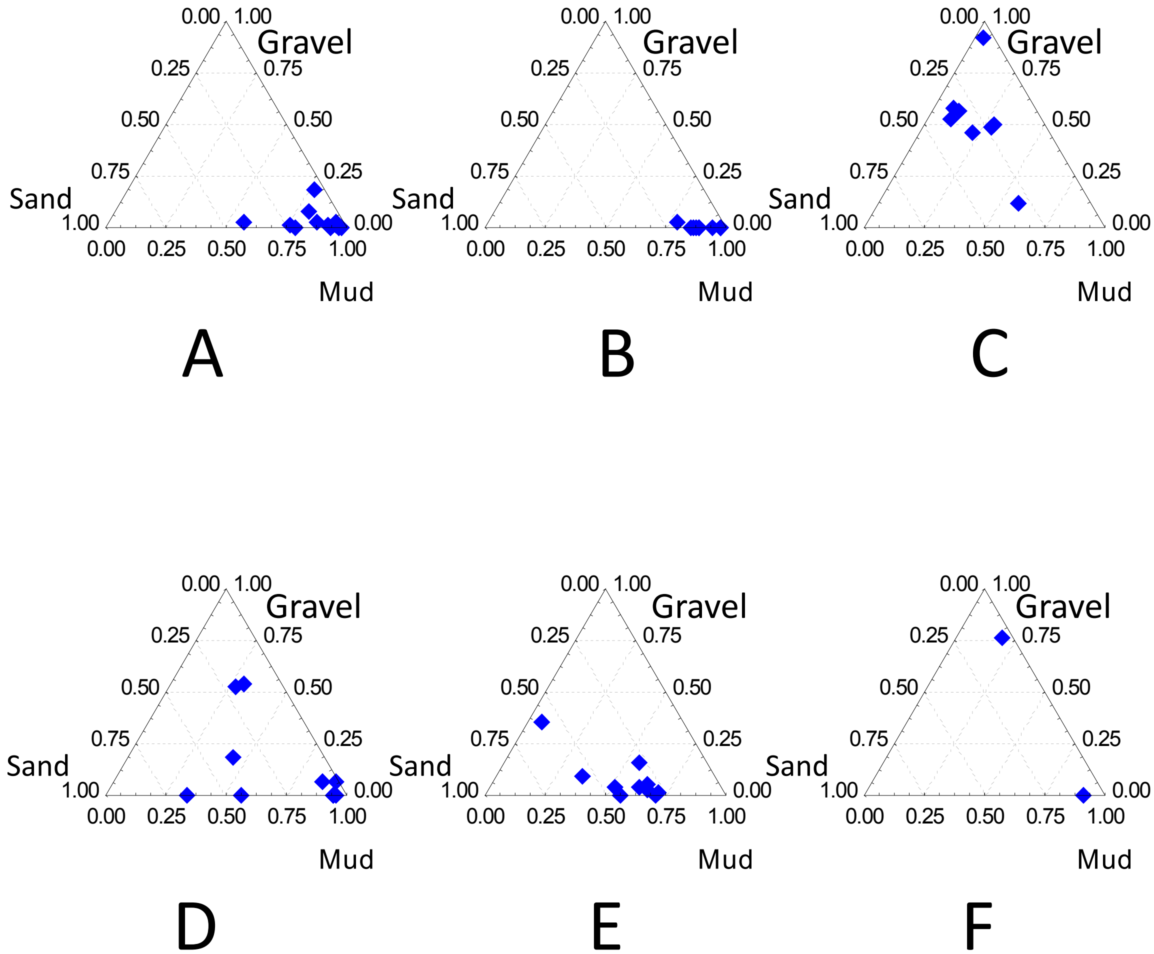


Figure 4. Sediment grain size results by sample

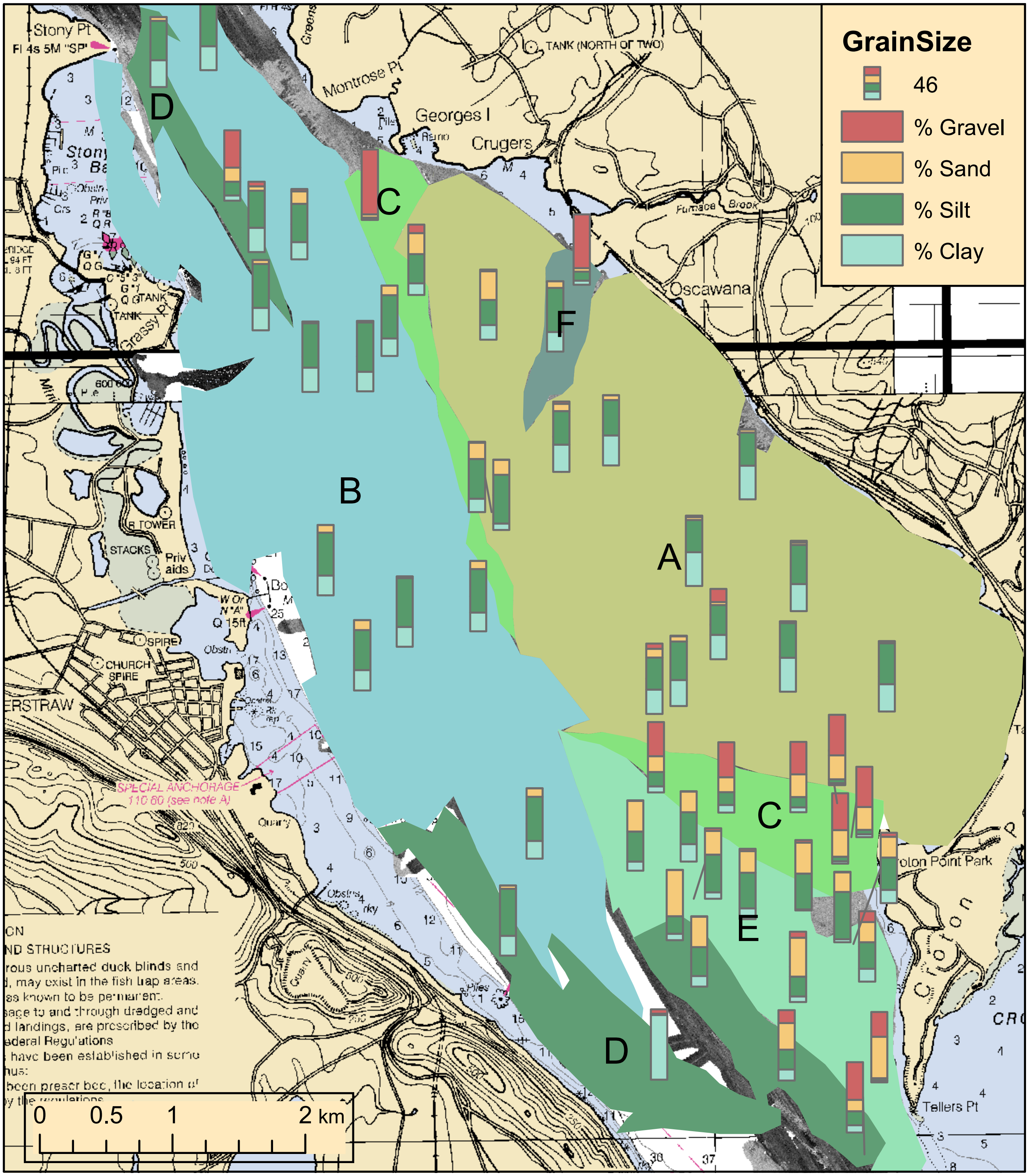


Figure 5. Water depth results by province.

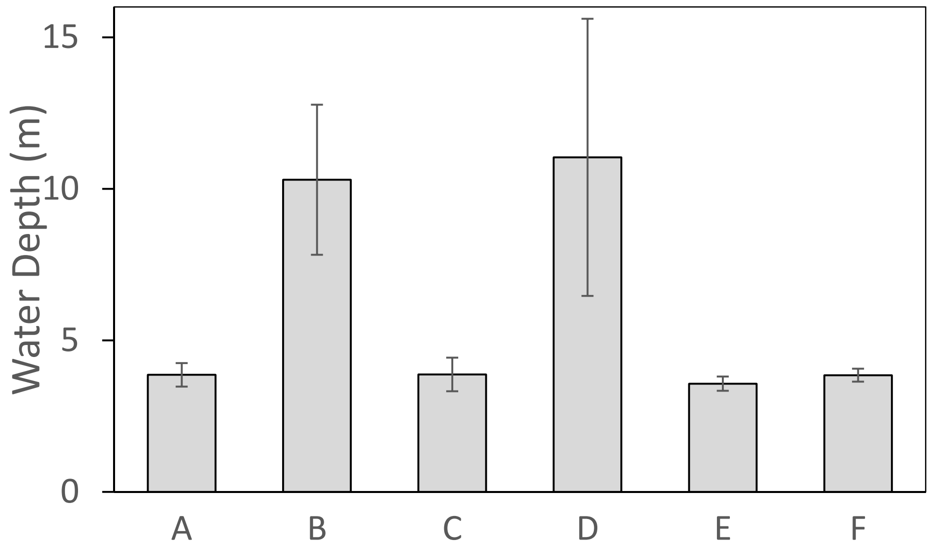


Figure 6. Grab penetration depth results by province.

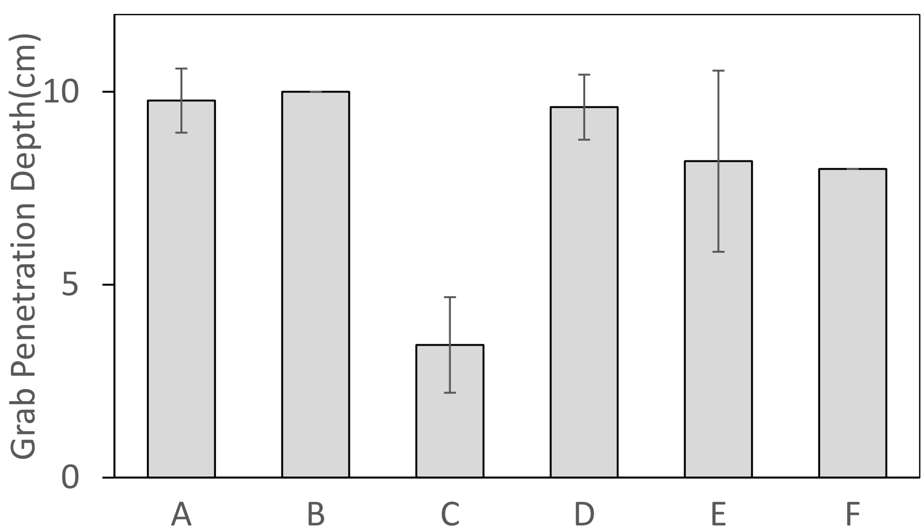


Figure 7. RPD depth results by province.

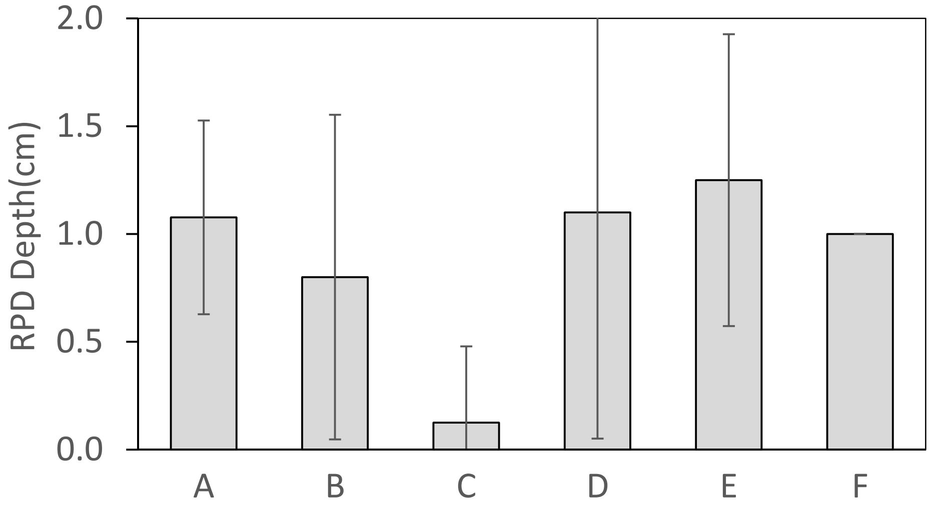


Figure 8. Grain size results by province.

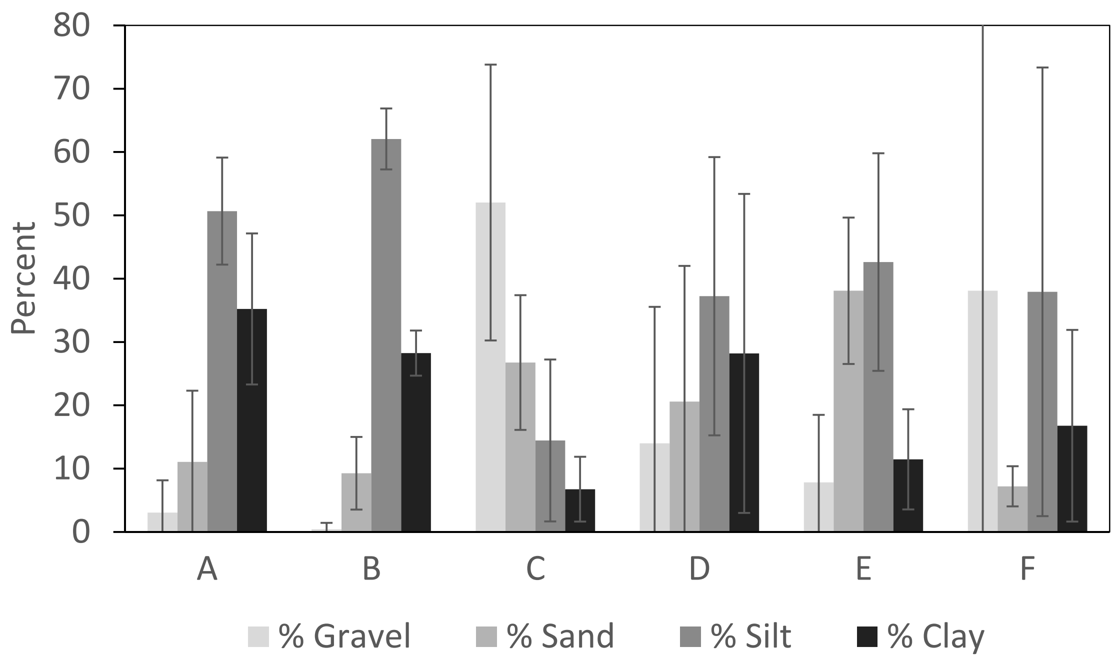
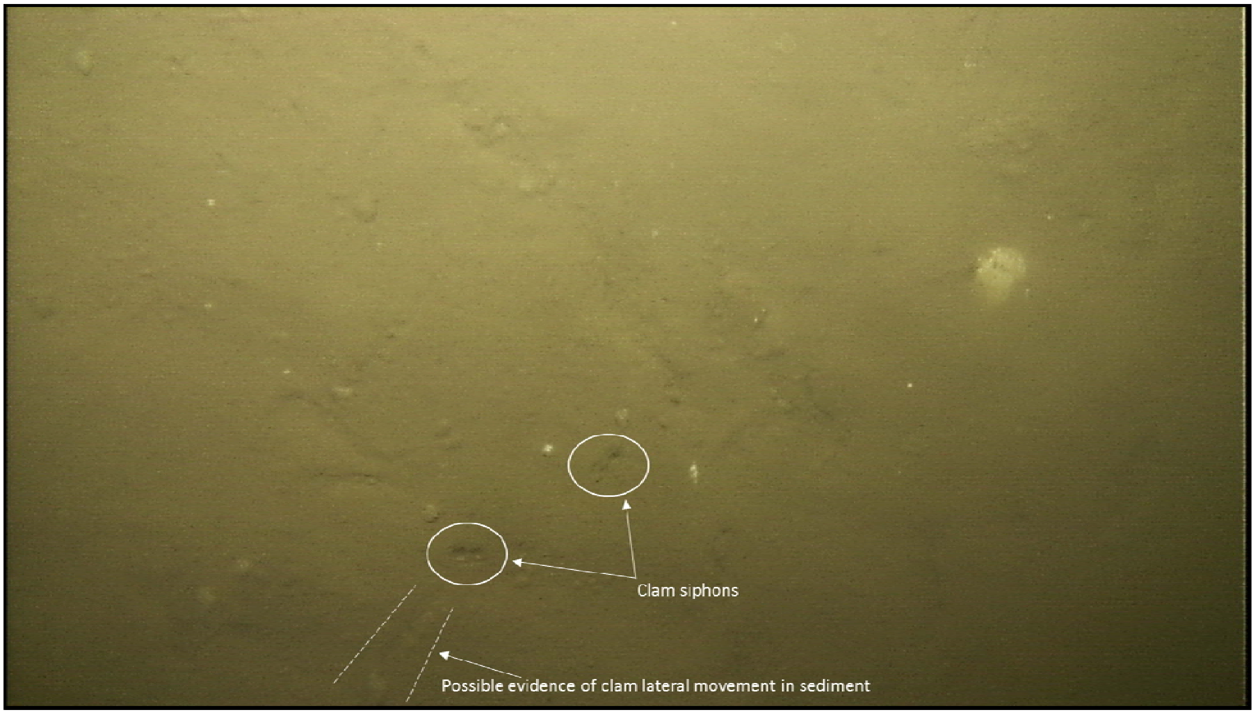


Figure 9. Sediment surface images extracted from Seatrex HD videos for station A3 and A11, respectively. Image size is 14 x 24.5 cm.



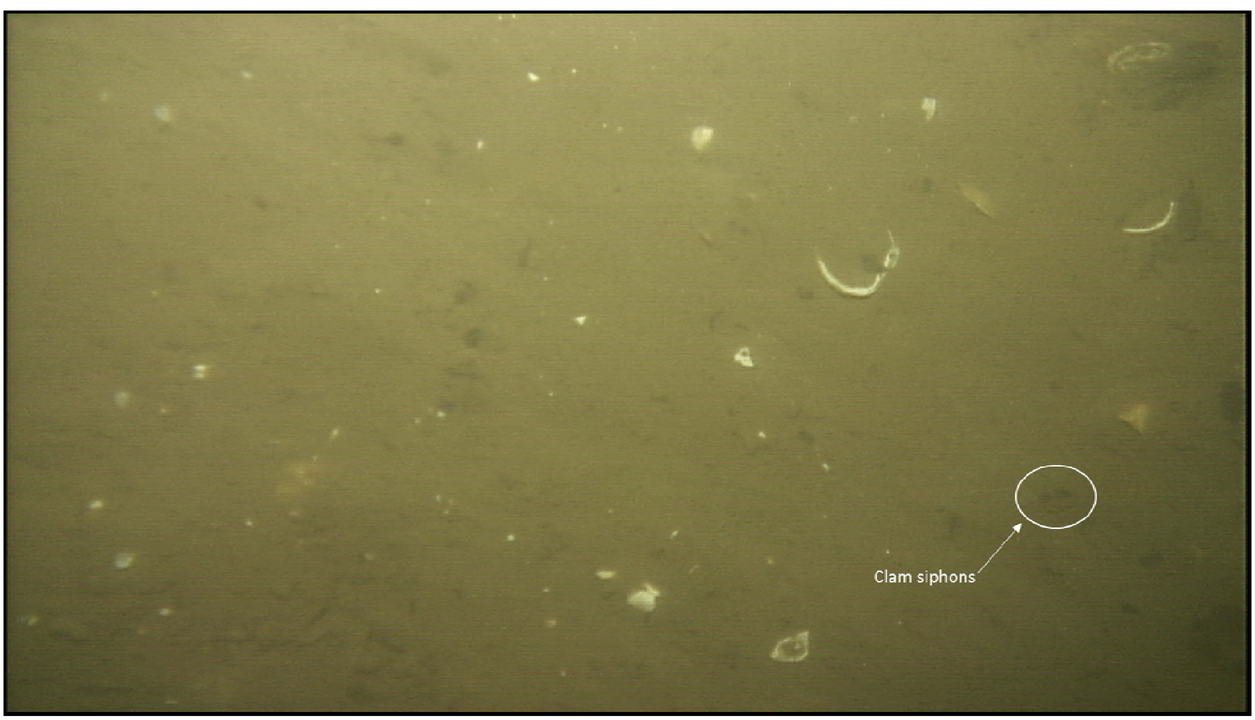


Figure 10. Abundance results by province.

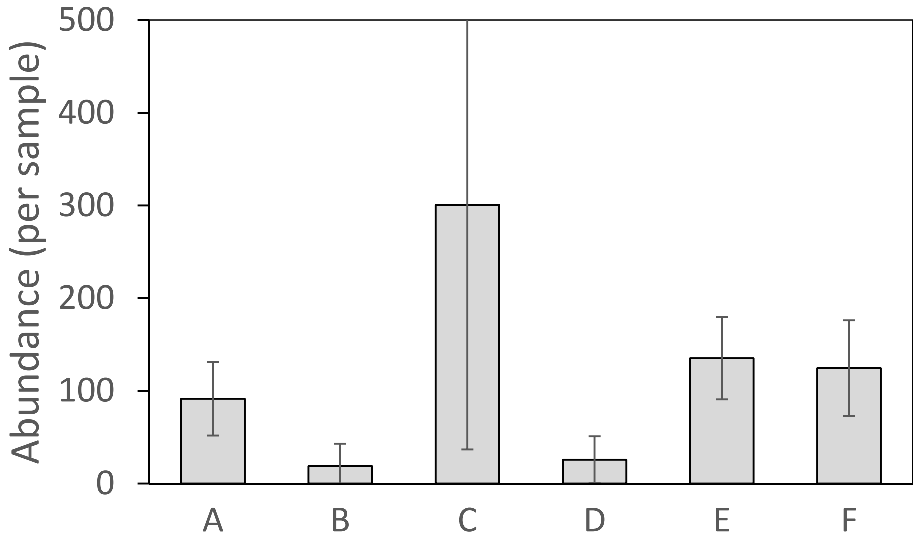


Figure 11. Species richness results by province.

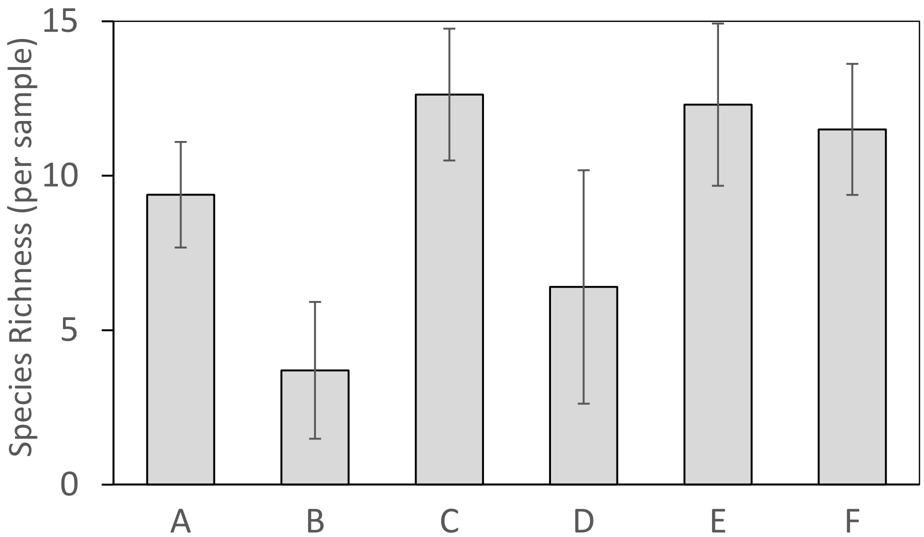


Figure 12. Shannon diversity results by province.

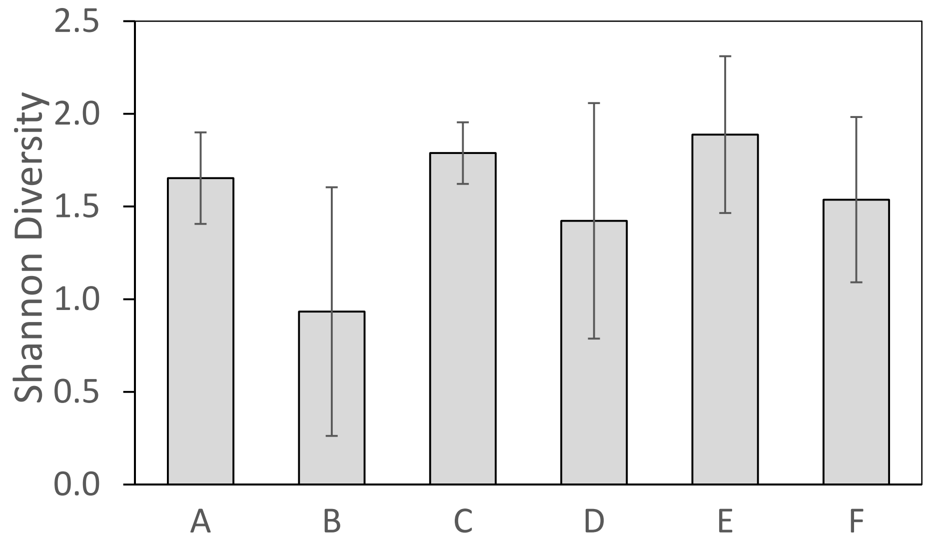


Figure 13. Equitability results by province.

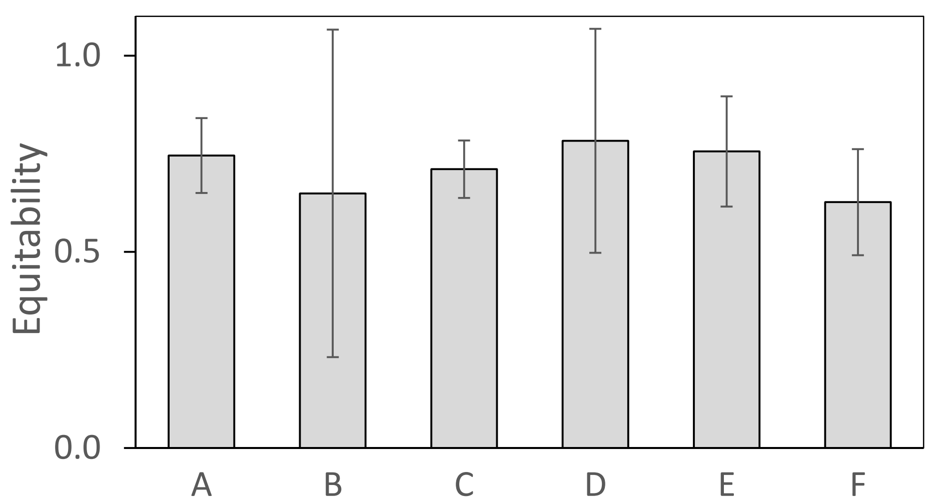


Figure 14. Sediment surface images extracted from Seatrex HD videos for station B8. Image size is 14 x 24.5 cm.

Figure 15. Sediment surface image extracted from Seatrex HD videos for station C02. Image size is 14 x 24.5 cm

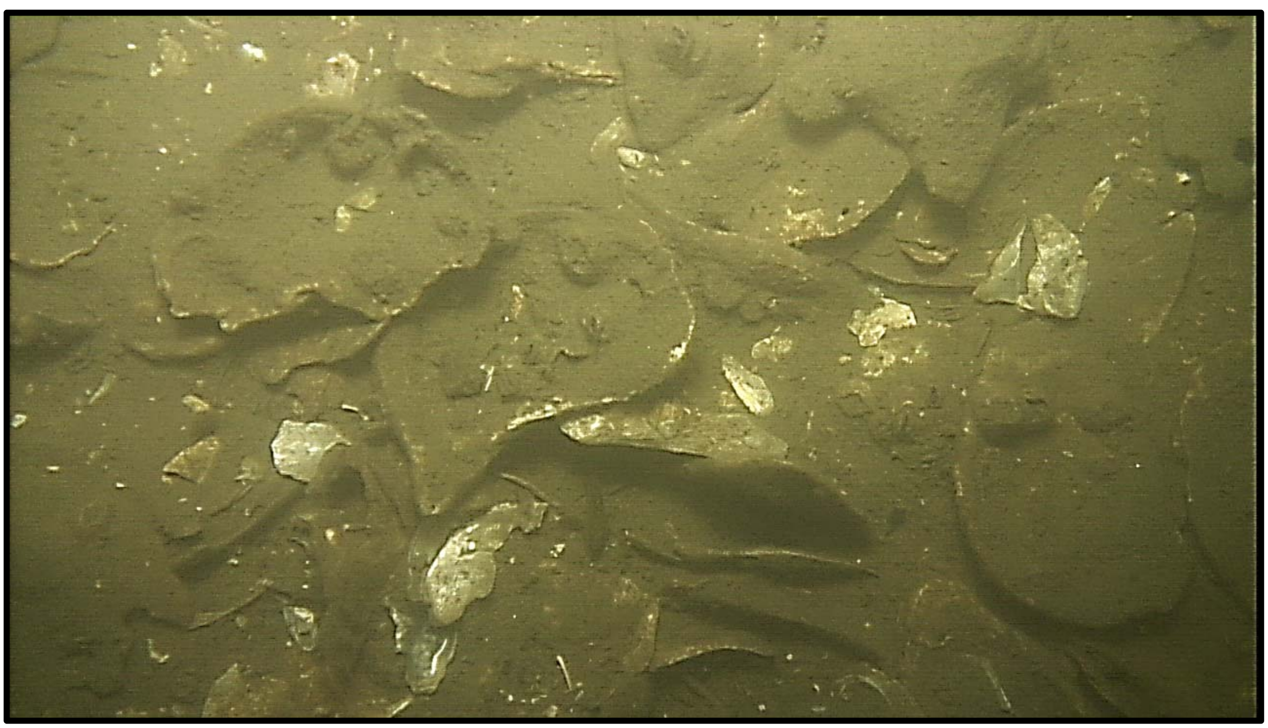


Figure 16. Sediment surface image extracted from Seatrex HD videos for station D08. Image size is 14 x 24.5 cm

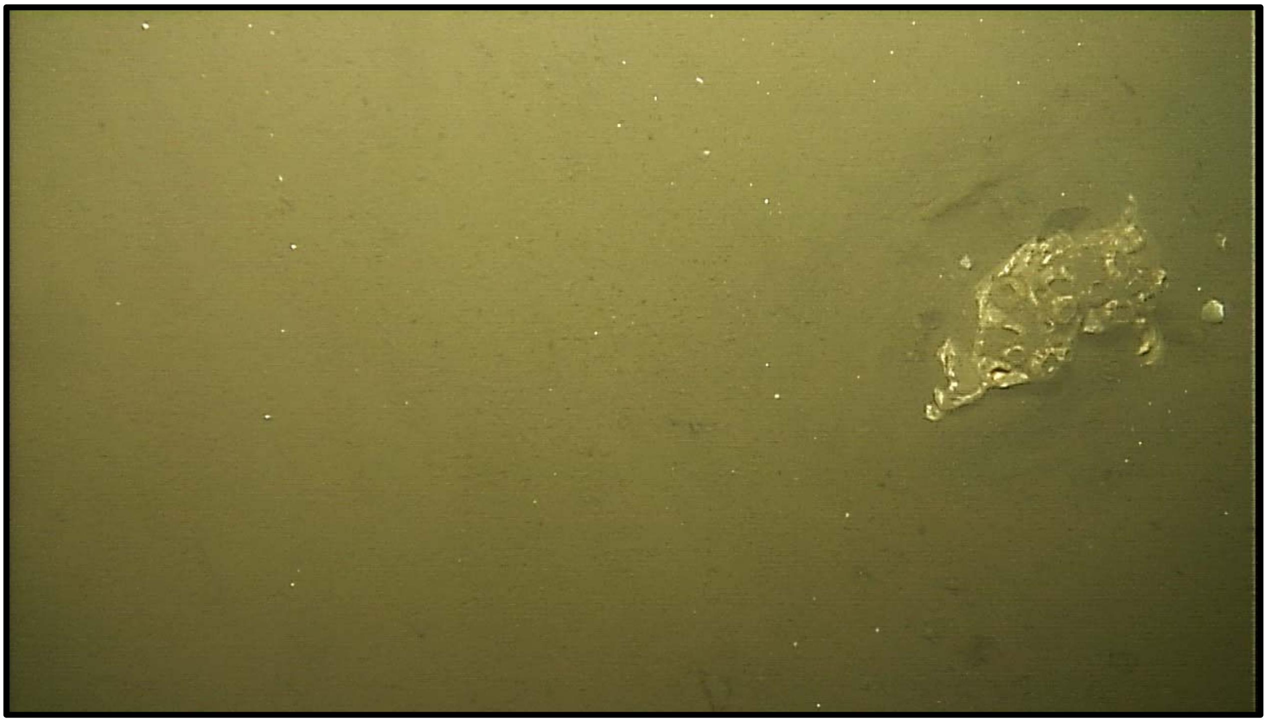


Figure 17. Sediment surface image extracted from Seatrex HD videos for station E08. Image size is 14 x 24.5 cm

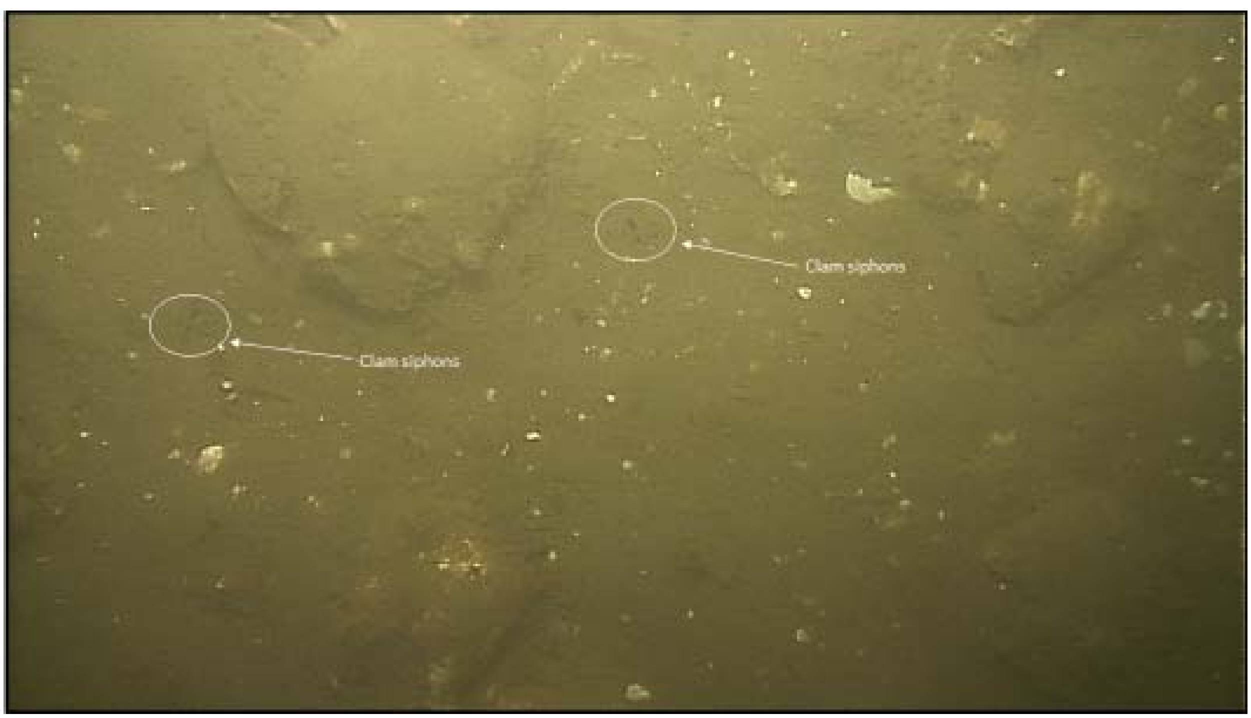


Figure 18. RDA ordination triplot results for axes 1 & 2 (a) and axes 3 & 4 (b). Eigenvalues for these axes are 0.211, 0.130, 0.046, and 0.025, respectively. Samples are colored and enclosed in envelopes based on membership in each geographic area. Sample proximity implies similarity. See Table 2 for species abbreviation codes.

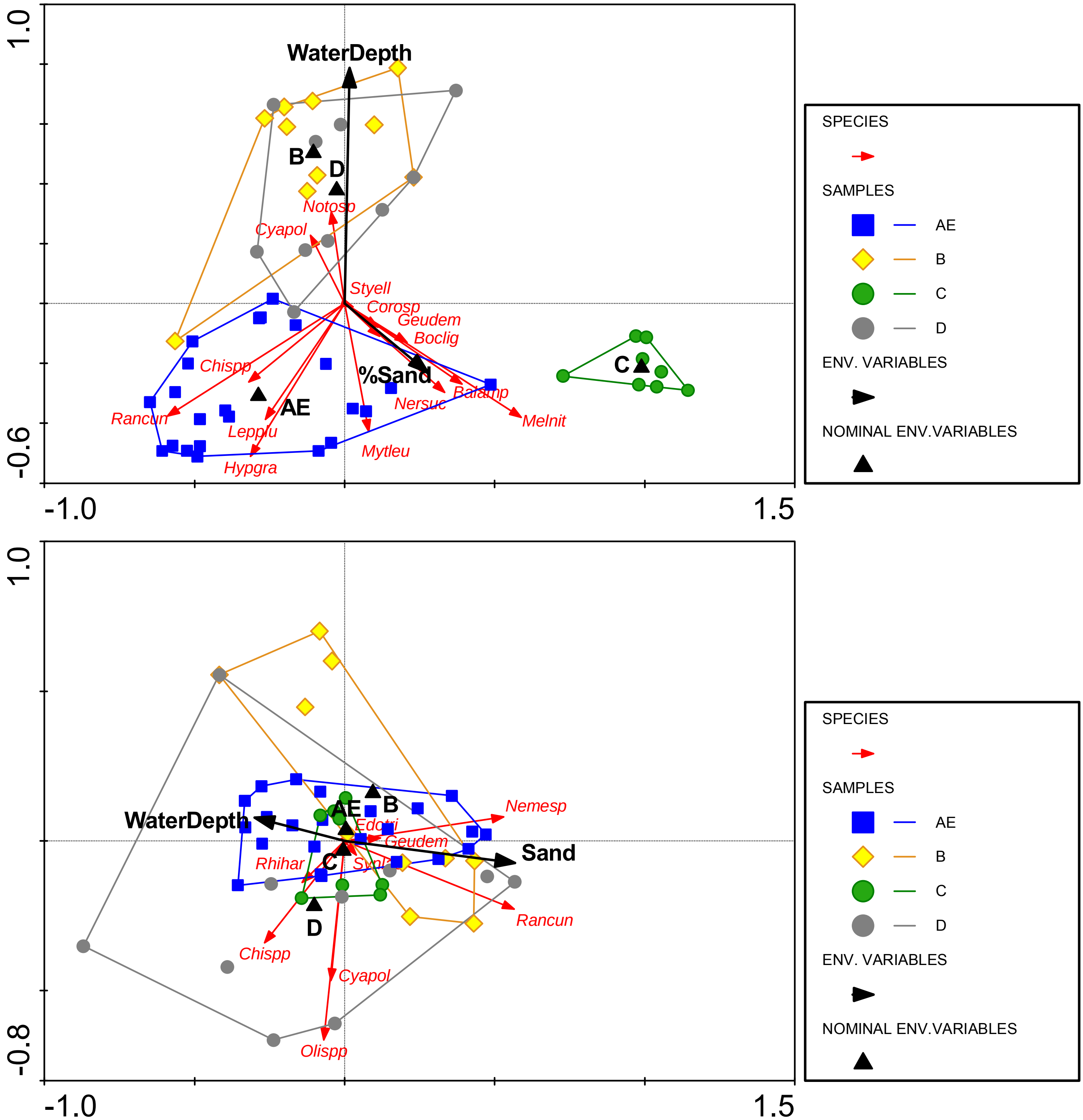


Figure 19. Sample water depths. Points represent samples and size of the point is proportional to value.

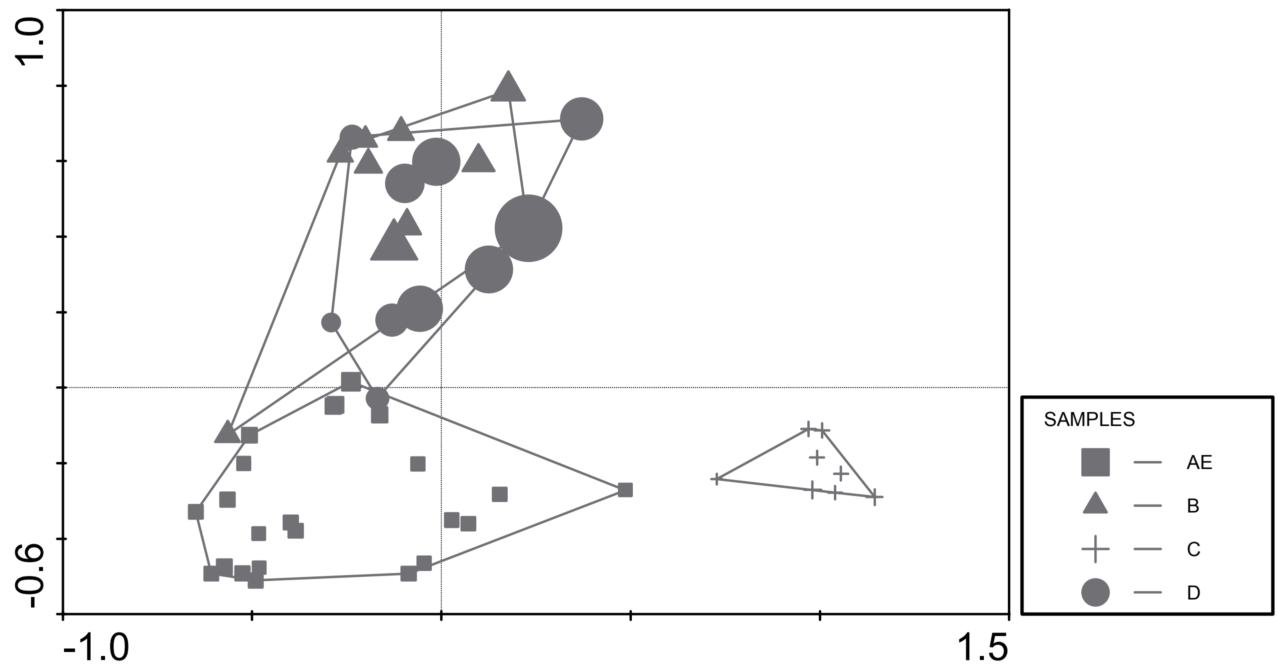


Figure 20. Sand content in samples (% by weight). Points represent samples and size of the point is proportional to value.

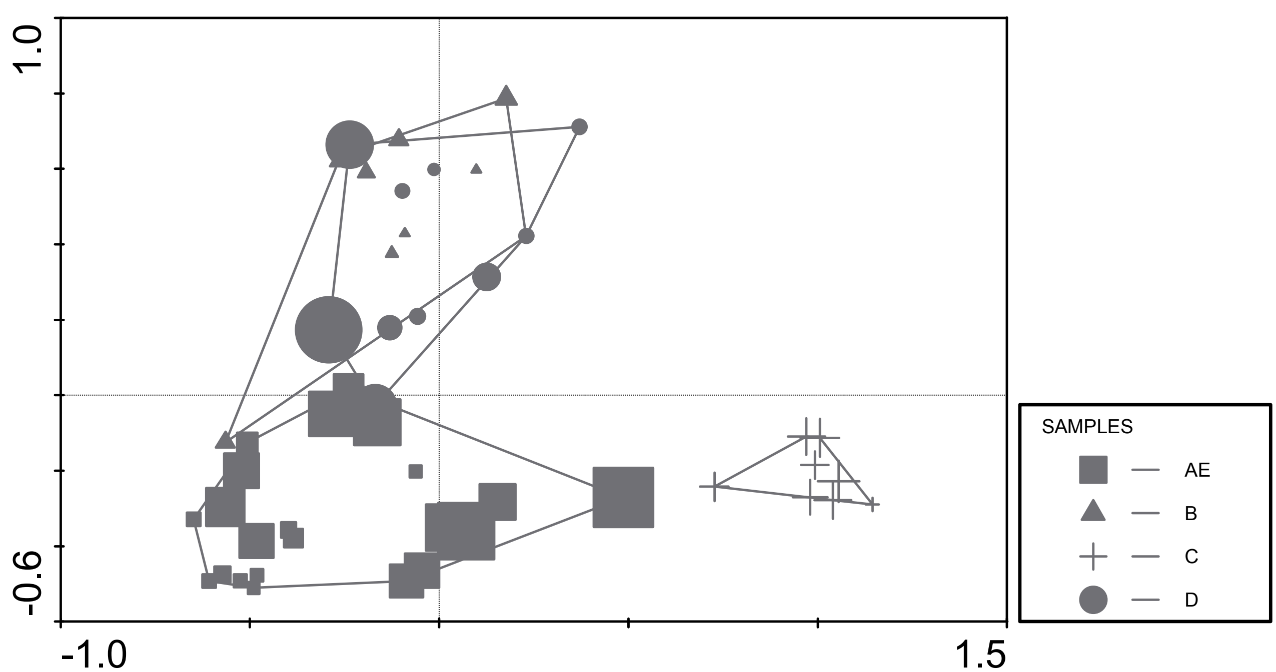


Figure 21. Relative abundance of the bivalve *Rangia cuneata.* Points represent samples. Symbol diameters are proportional to relative abundance.

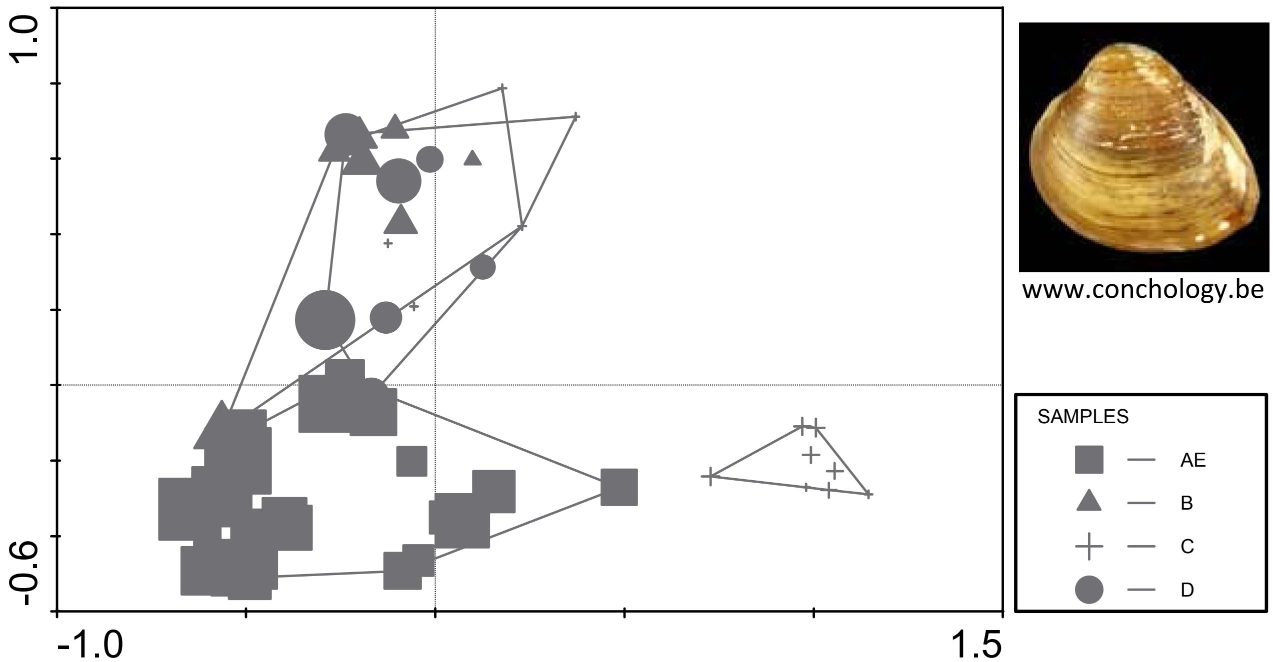


Figure 22. Relative abundance of the polychaete *Hypaniola grayi.* Points represent samples. Symbol diameters are proportional to relative abundance.

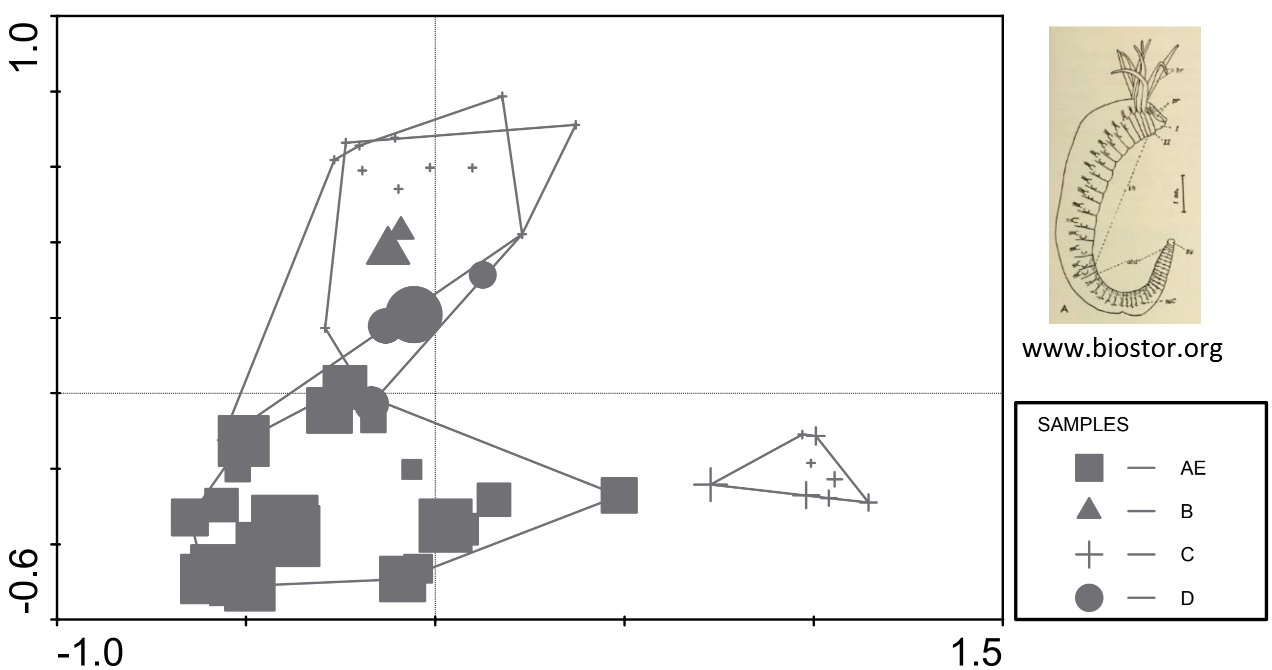


Figure 23. Relative abundance of the amphipod *Leptocheirus plumulosus.* Points represent samples. Symbol diameters are proportional to relative abundance.

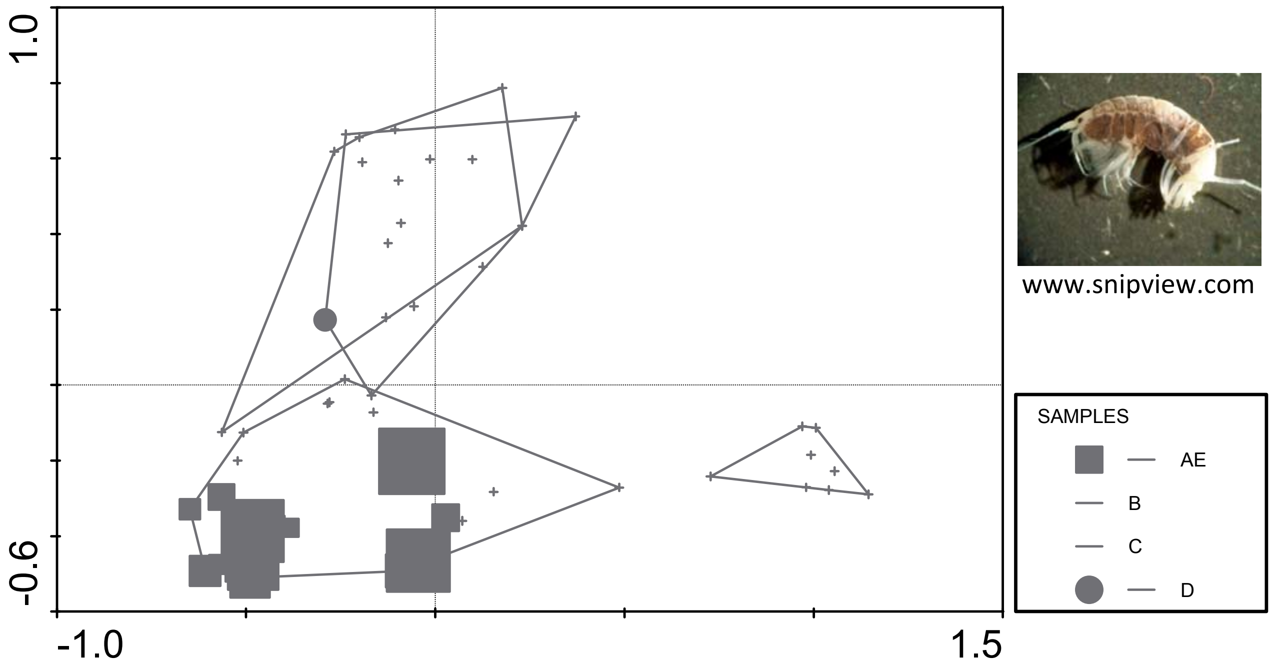


Figure 24. Relative abundance of chironomid larvae*.* Points represent samples. Symbol diameters are proportional to relative abundance.

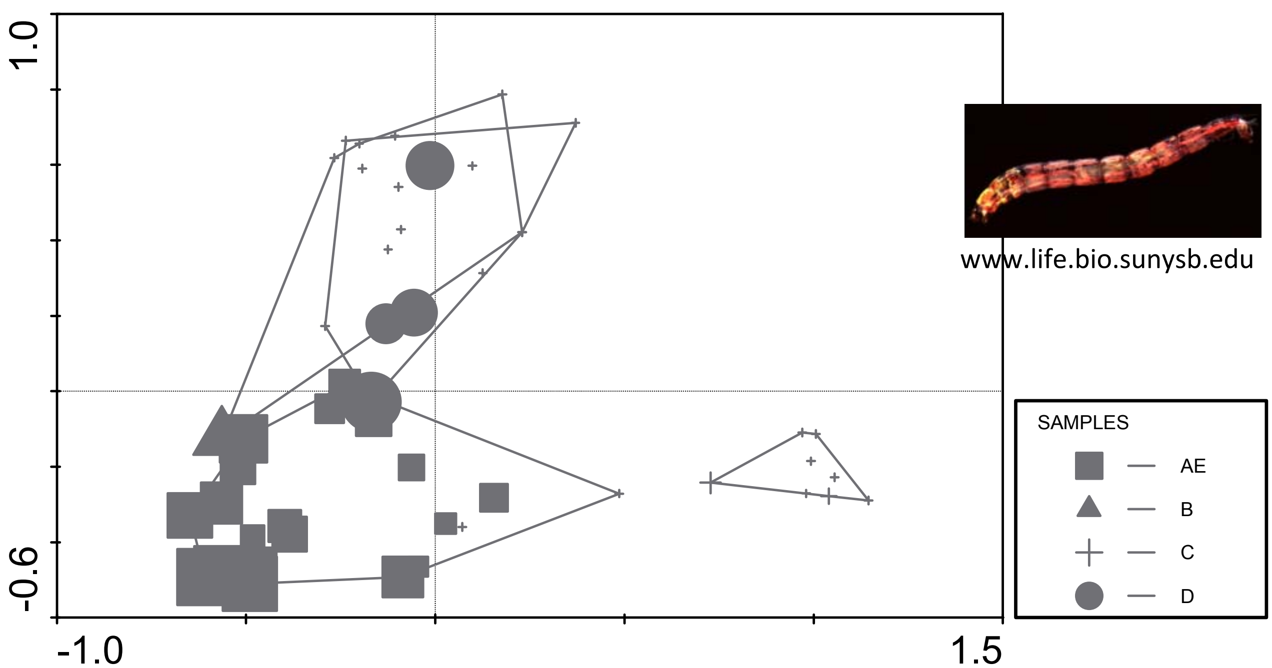


Figure 25. Relative abundance of the slender isopod *Cyathura polita.* Points represent samples. Symbol diameters are proportional to relative abundance.

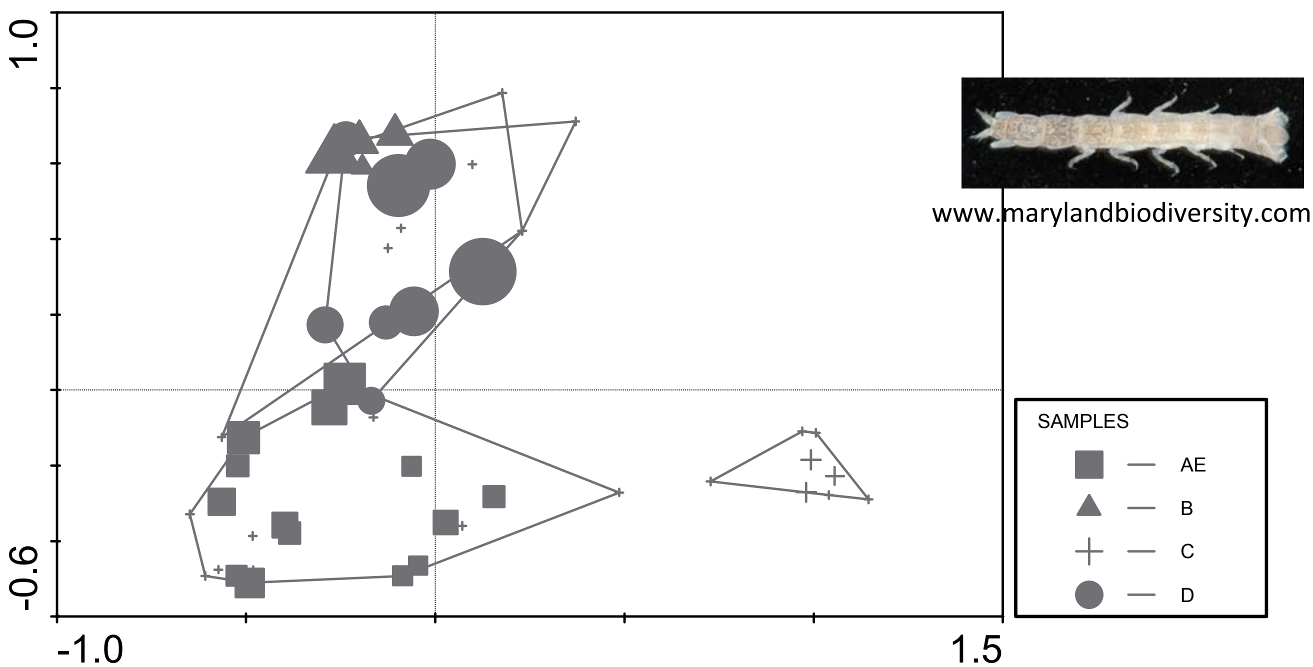


Figure 26. Relative abundance of the amphipod *Melita nitida.* Points represent samples. Symbol diameters are proportional to relative abundance.

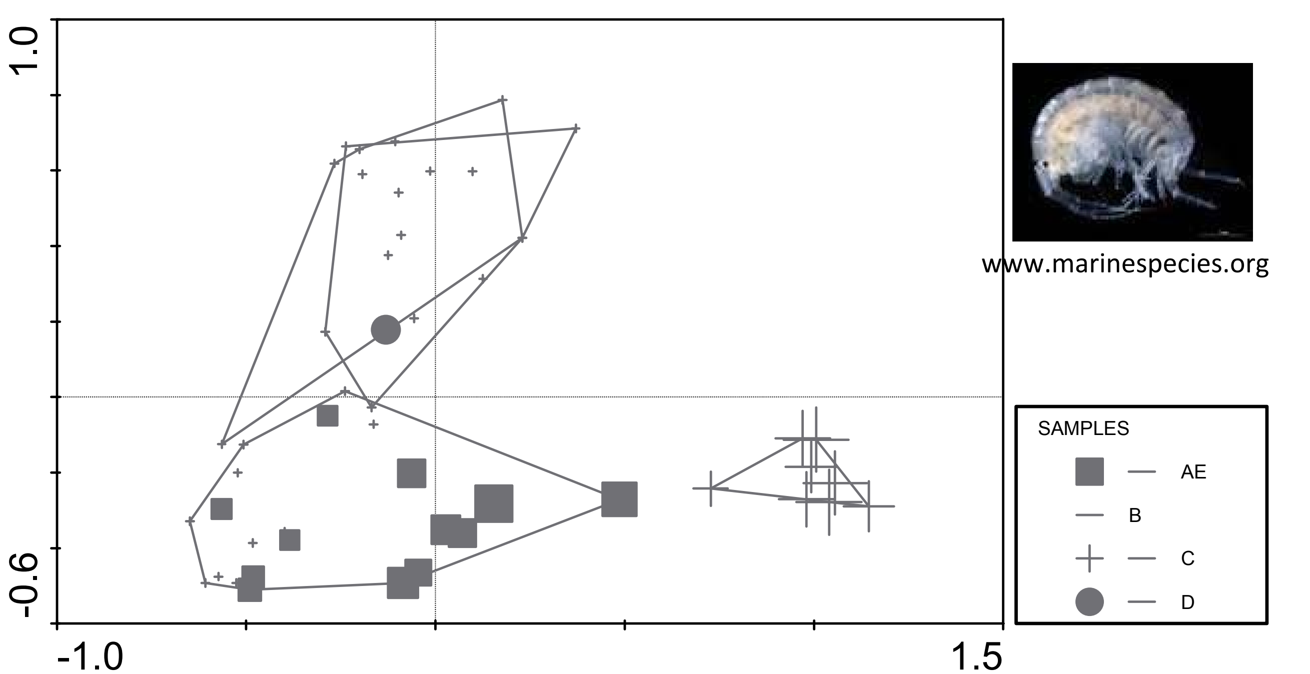


Figure 27. Relative abundance of the polychaete *Neanthes succinea.* Points represent samples. Symbol diameters are proportional to relative abundance.

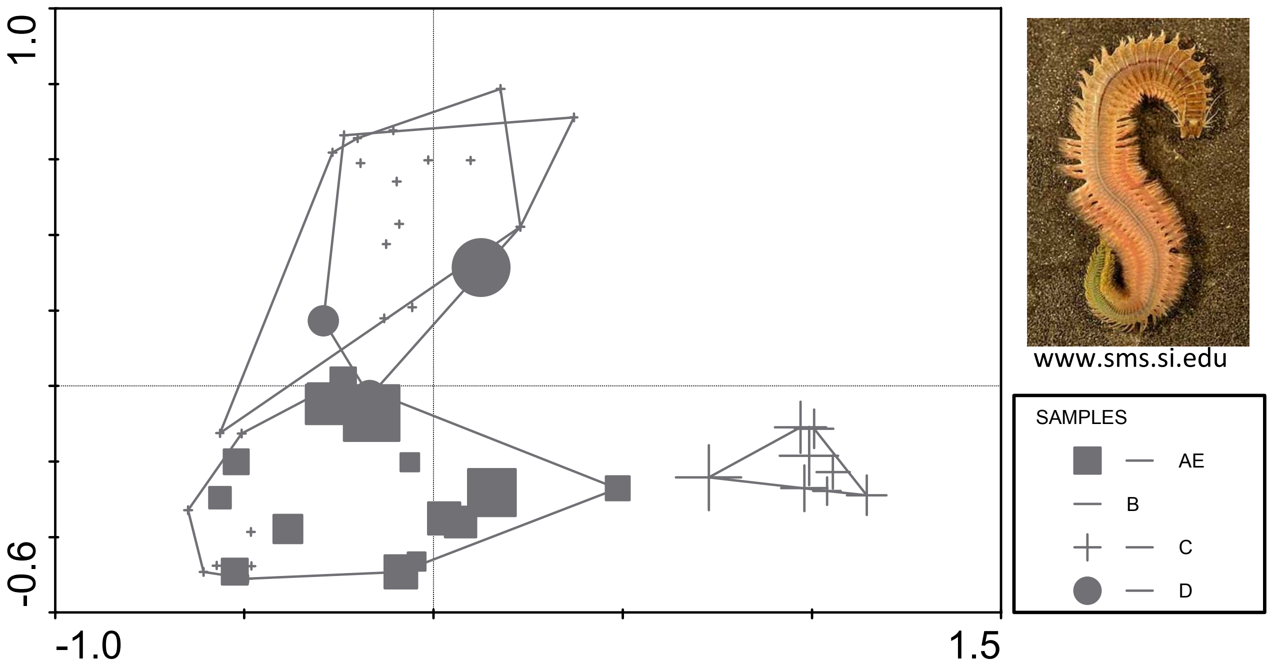


Figure 28. Relative abundance of the barnacle *Balanus amphitrite.* Points represent samples. Symbol diameters are proportional to relative abundance.

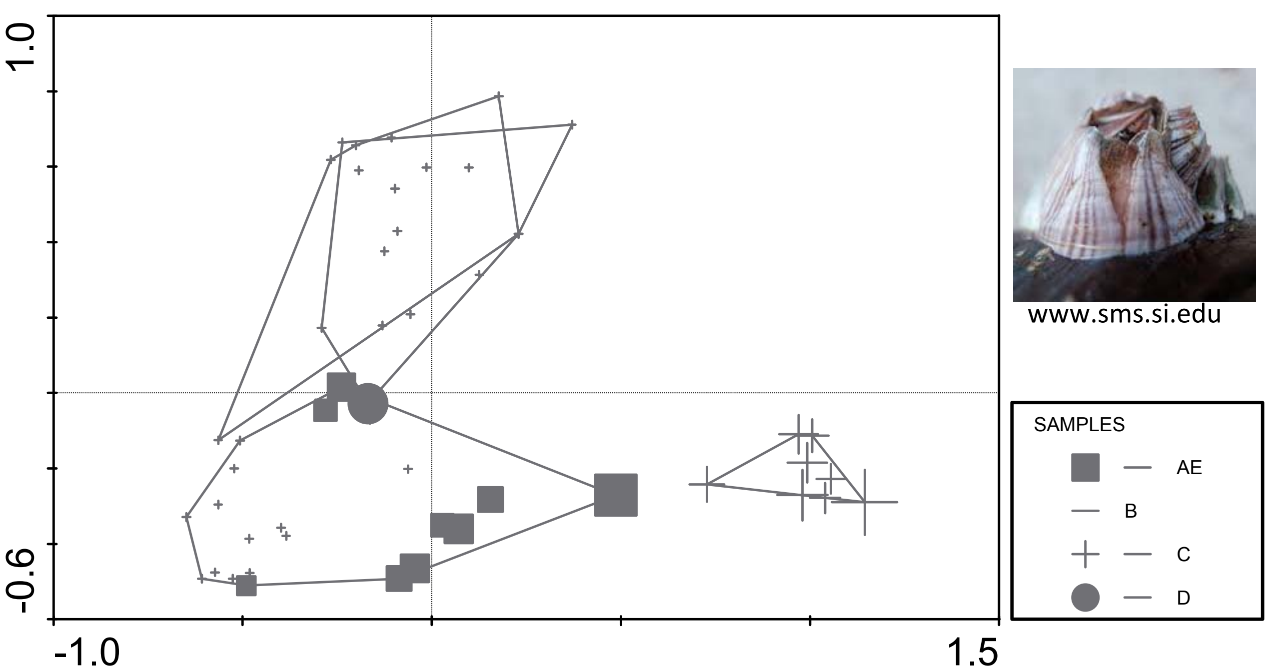
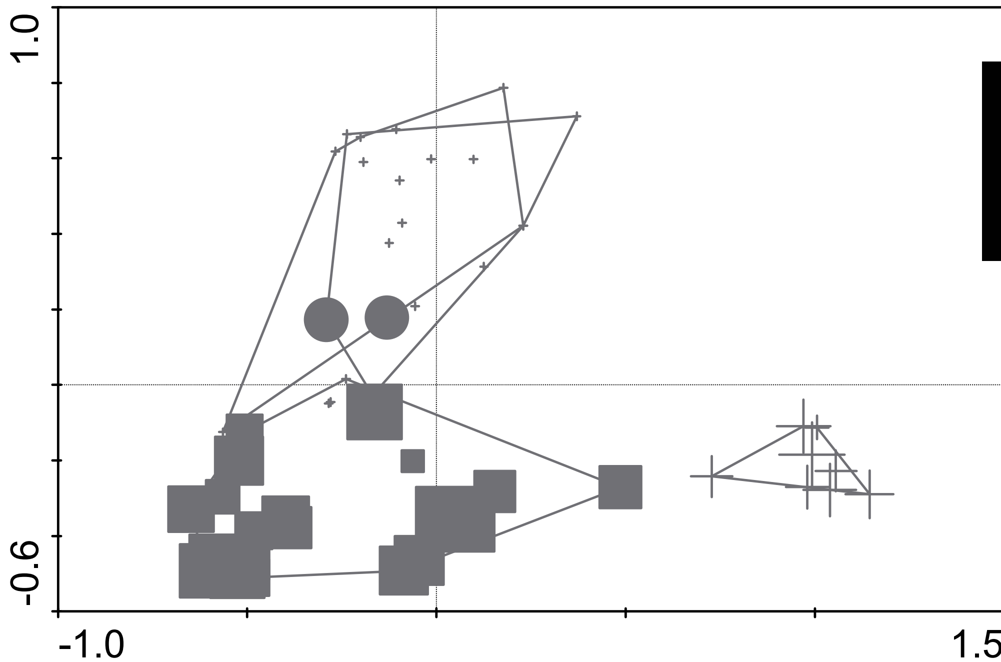
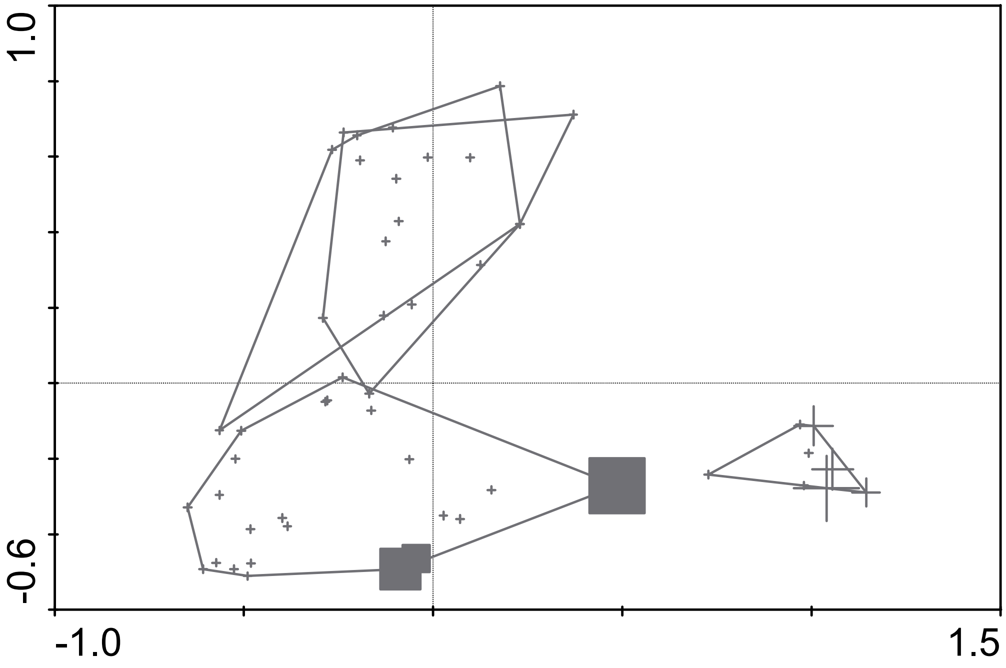


Figure 29. Relative abundance of the bivalve *Mytilopsis leucophaeata.* Points represent samples. Symbol diameters are proportional to relative abundance.




www.conchology.be

Figure 30. Relative abundance of the amphipod *Corophium* sp*.* Points represent samples. Symbol diameters are proportional to relative abundance.




www.macrofauna.cl

Figure 31. Shell length distribution of collected individuals of *Rangia cuneata*.

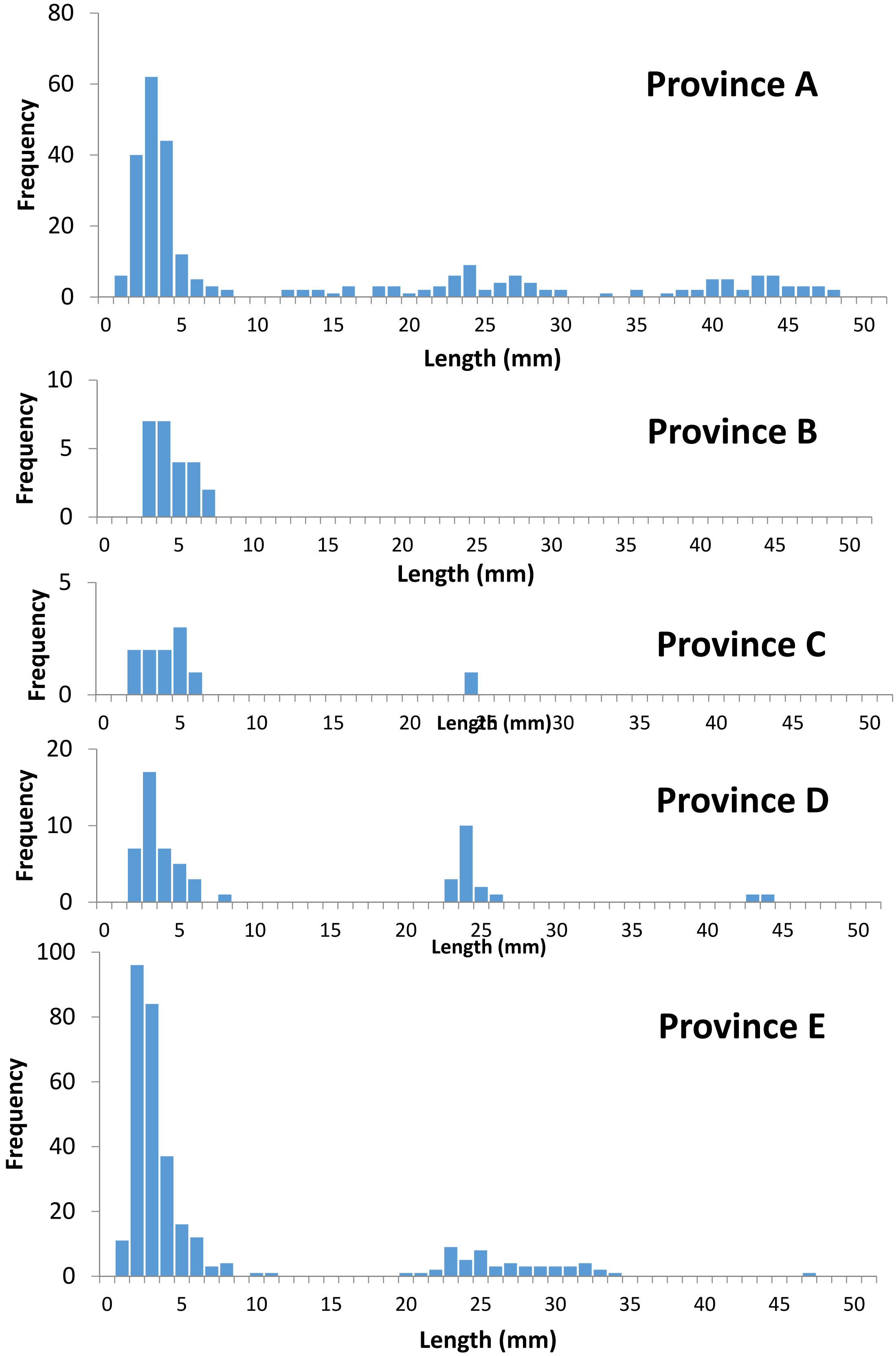


Figure 32. Distribution of collected individuals of *Rangia cuneata*.

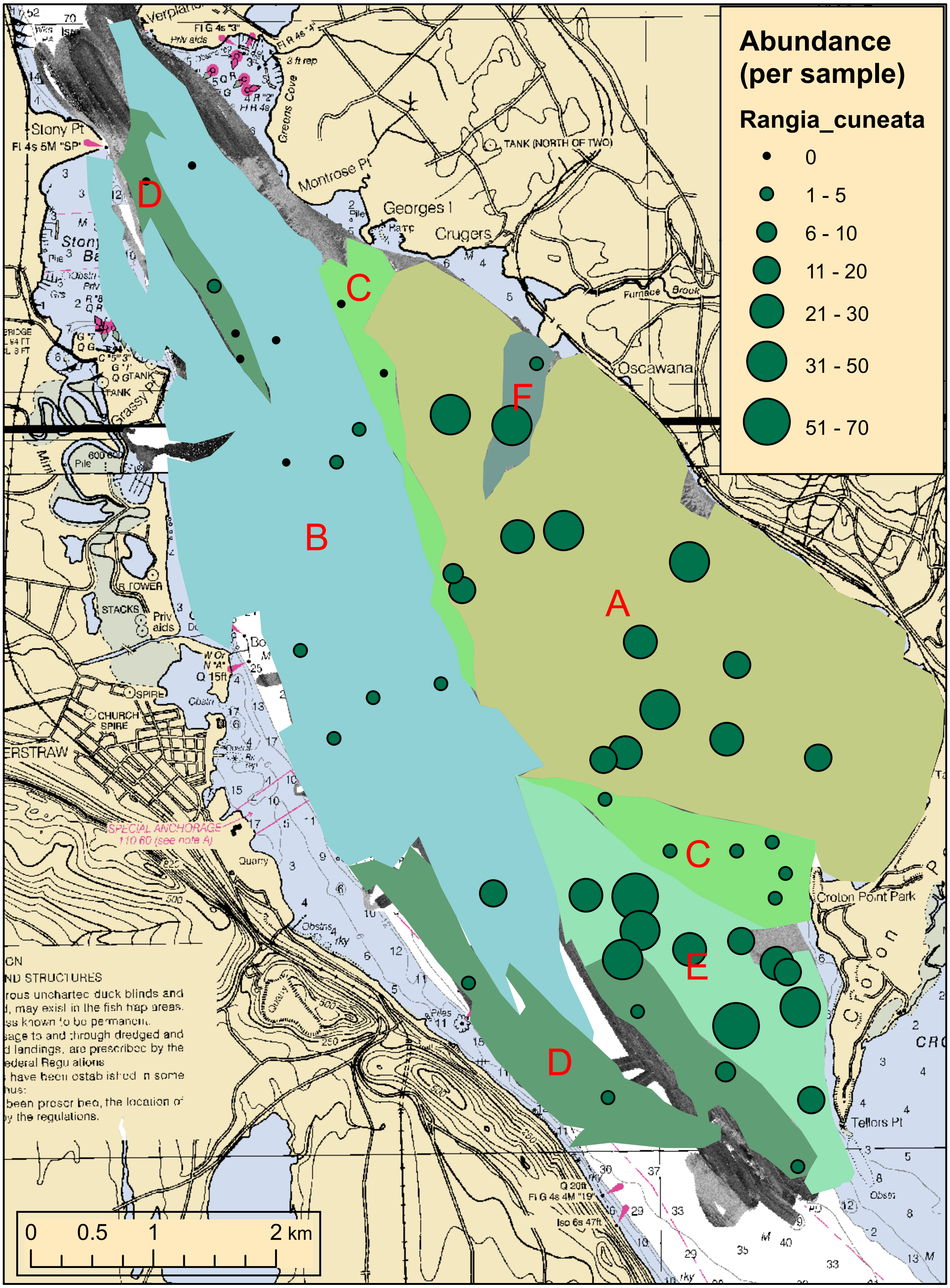


Figure 33. Sturgeon hydrophone location data by province for 2012-2014. Data from Amanda Higgs, New York State Department of Environmental Conservation.

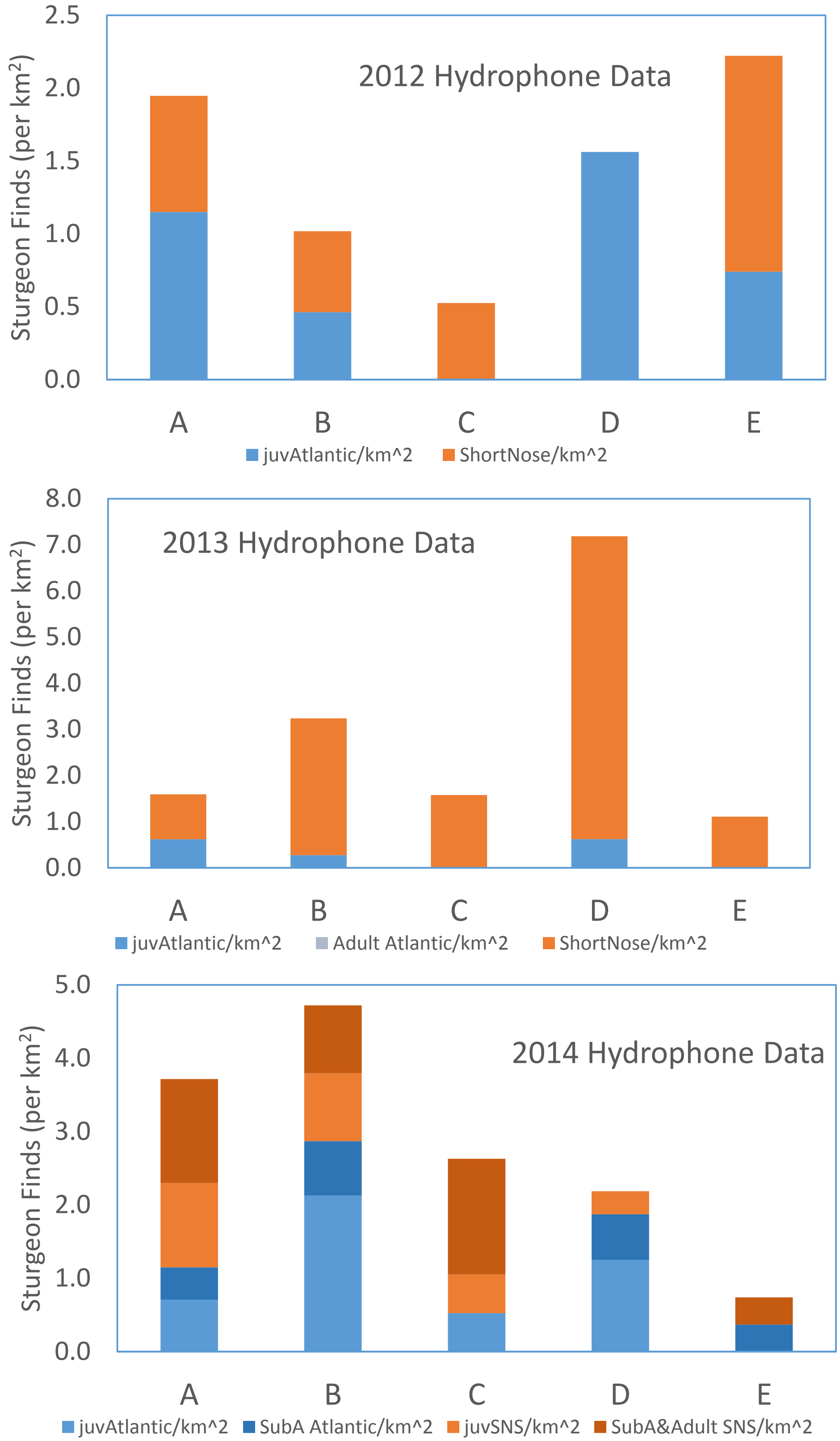
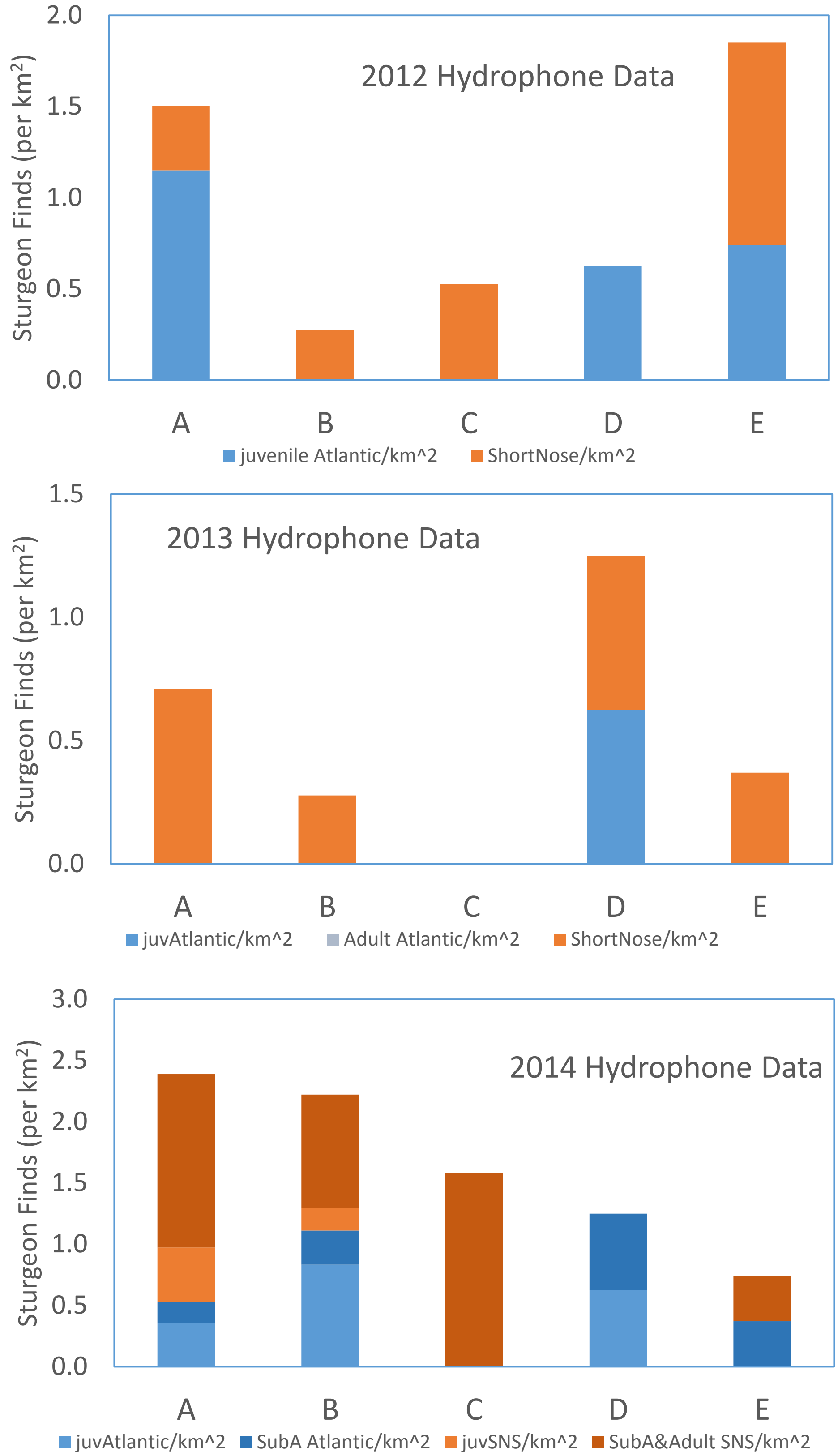


Figure 34. Fall (September-December) sturgeon hydrophone location data by province. Data from Amanda Higgs, New York State Department of Environmental Conservation.



Sample	Site	Grab depth (cm)	RPD Depth (cm)	Water Depth (m)	Latitude	Longitude	Notes
HV01	B03	10.0	0.0	12.0	41.217467	-73.952100	
HV02	D04	10.0	0.0	12.3	41.225133	-73.956450	
HV03	D03	8.0	0.0	13.2	41.227000	-73.956883	2cm mud overlying anthropogenic material (slag, etc)
HV04	D02	8.0	0.0	13.7	41.230500	-73.958917	anthropogenic material on mud
HV05	D01	10.0	2.5	19.9	41.238250	-73.965417	anthropogenic material
HV06	B01	10.0	0.0	16.1	41.239367	-73.960917	
HV07	B02	10.0	0.0	11.5	41.226467	-73.952950	S(6.6 sur, 12.0 bot), T(21.7 sur, 20.4 bot)
HV08	C01	3.0	0.0	4.4	41.229083	-73.946567	oyster shell
HV09	C02	6.5	1.0	4.7	41.223950	-73.942467	oyster shells on surface
HV10	B05	10.0	1.0	8.4	41.219833	-73.944950	mud
HV11	B04	10.0	1.0	9.8	41.217450	-73.947183	mud with almost no shell
HV12	A11	10.0	1.0	4.1	41.220850	-73.936050	Rangia
HV13	F01	8.0	1.0	4.0	41.224500	-73.927600	oyster shells, 1 Rangia
HV14	F02	8.0	1.0	3.7	41.220000	-73.930067	shell
HV15	A02	10.0	1.0	3.7	41.212217	-73.925167	Rangia
HV16	A01	10.0	2.0	3.7	41.211833	-73.929650	Rangia (small, medium, & large size classes)
HV17	C03	10.0	2.0	4.8	41.209150	-73.935967	
HV18	C04	7.0	0.5	4.3	41.207933	-73.935100	small Rangia, cohesive sediments
HV19	B08	10.0	2.0	7.8	41.201083	-73.937283	sediments not cohesive
HV20	B07	10.0	2.0	10.9	41.200100	-73.943900	
HV21	B10	10.0	5.0	9.2	41.185617	-73.932467	S(7.1 sur, 14.5 bot), T(21.9 sur, 20.2 bot) not cohesive
HV22	D05	10.0	0.5	11.1	41.179050	-73.934967	sediments not cohesive
HV23	D06	10.0	0.5	13.8	41.170517	-73.921533	
HV24	D10	10.0	2.5	9.1	41.165267	-73.903167	Rangia, slag (combusted boiler material)
HV25	E10	3.0	0.0	3.3	41.170150	-73.901767	shell with 1 medium Rangia
HV26	D09	10.0	2.0	6	41.172300	-73.910050	
HV27	D08	10.0	1.0	6.5	41.176800	-73.918533	
HV28	E08	6.0	2.0	3.5	41.175667	-73.908967	shells, Rangia
HV29	E09	8.0	1.5	3.3	41.177000	-73.902733	Rangia, cohesive sediments
HV30	E07	10.0	1.0	3.5	41.179567	-73.903917	Rangia, shells, cohesive sediments
HV31	E06	10.0	1.0	3.7	41.180233	-73.904917	Rangia, cohesive sediments
HV32	E05	10.0	2.0	3.6	41.181883	-73.908367	Rangia, shells, cohesive sediments
HV33	E04	10.0	1.0	3.6	41.181333	-73.913400	
HV34	D07	10.0	2.0	4.8	41.180667	-73.919950	
HV35	E03	8.0	1.5	3.7	41.182767	-73.918217	
HV36	E02	7.0	2.0	3.4	41.185283	-73.918633	
HV37	E01	10.0	0.5	4.1	41.185400	-73.923433	small Rangia
HV38	C05	3.0	0.0	2.8	41.192450	-73.921450	
HV39	B06	10.0	1.0	8.5	41.203650	-73.950950	S(7.5 sur, 10.6 bot), T(21.3 sur, 20.8 bot) not cohesive, plant fibers
HV40	B09	10.0	0.5	8.8	41.197167	-73.947767	noncohesive mud
HV41	C06	3.0	0.0	3.8	41.188583	-73.915200	shell overlying mud
HV42	C07	3.0	0.0	3.9	41.188533	-73.908717	shell overlying mud
HV43	C08	3.0	0.0	3.9	41.189117	-73.905233	shell
HV44	C09	3.0	0.0	3.7	41.186817	-73.903983	shell
HV45	C10	3.0	0.0	3.8	41.185017	-73.905033	
HV46	A10	10.0	1.0	3.5	41.195300	-73.900667	Rangia, mud
HV47	A09	10.0	1.0	3.7	41.196733	-73.909533	Rangia, cohesive sediments, silt on surface
HV48	A08	10.0	1.0	4	41.195850	-73.919433	Rangia
HV49	A07	10.0	1.0	4	41.195333	-73.921550	Rangia
HV50	A06	10.0	0.5	3.8	41.198983	-73.916000	Rangia
HV51	A05	10.0	1.0	3.3	41.202183	-73.908467	
HV52	A04	10.0	1.0	3.7	41.203967	-73.917833	
HV53	A03	10.0	1.0	3.6	41.209817	-73.912933	

Appendix 2 - Grain Size Summary

Sample	Site	Gravel	Sand	Silt	Clay	Mud
HV1	B3	0.0	2.6	62.8	34.5	97.4
HV2	D4	0.0	5.6	62.5	31.8	94.4
HV3	D3	6.9	6.3	52.6	34.2	86.9
HV4	D2	53.1	19.9	19.5	7.5	27.0
HV5	D1	0.3	5.3	56.0	38.4	94.4
HV6	B1	0.4	5.7	59.9	34.0	94.0
HV7	B2	3.3	18.0	54.5	24.3	78.7
HV8	C1	92.3	4.4	2.9	0.4	3.3
HV9	C2	12.2	29.7	41.7	16.5	58.2
HV10	B5	0.0	13.8	61.4	24.8	86.2
HV11	B4	0.0	1.9	70.1	28.0	98.1
HV12	A11	2.5	41.1	35.3	21.1	56.4
HV13	F1	76.1	5.0	12.9	6.1	18.9
HV14	F2	0.1	9.4	63.0	27.5	90.5
HV15	A2	0.1	6.7	50.4	42.9	93.2
HV16	A1	3.2	10.6	47.9	38.3	86.2
HV17	C3	1.1	23.2	56.6	19.1	75.7
HV18	C4	0.4	20.9	69.3	9.3	78.7
HV19	B8	0.0	11.4	61.9	26.7	88.6
HV20	B7	0.4	2.2	69.1	28.2	97.4
HV21	B10	0.0	12.0	63.0	25.0	88.0
HV22	D5	0.0	4.8	67.0	28.2	95.2
HV23	D6	6.3	1.5	0.0	92.2	92.2
HV24	D10	53.7	16.0	20.2	10.2	30.3
HV25	E10	35.3	58.9	3.5	2.3	5.8
HV26	D9	18.5	37.7	28.4	15.5	43.9
HV27	D8	0.8	43.1	41.1	15.0	56.1
HV28	E8	8.8	55.2	28.2	7.8	36.0
HV29	E9	15.5	28.7	37.6	18.2	55.8
HV30	E7	5.9	29.3	46.2	18.6	64.8
HV31	E6	0.9	27.7	67.5	4.0	71.4
HV32	E5	4.0	43.8	51.1	1.2	52.2
HV33	E4	3.1	30.9	50.6	15.3	66.0
HV34	D7	0.3	65.7	25.1	8.9	34.0
HV35	E3	3.7	33.7	53.6	9.0	62.6
HV36	E2	0.2	29.6	45.2	25.0	70.2
HV37	E1	0.8	43.3	42.8	13.1	55.9
HV38	C5	48.7	22.4	20.3	8.7	28.9
HV39	B6	0.0	10.7	61.2	28.2	89.3
HV40	B9	0.1	14.3	56.8	28.9	85.6
HV41	C6	49.7	21.3	18.4	10.5	29.0
HV42	C7	46.0	32.3	14.5	7.3	21.8
HV43	C8	57.7	33.9	5.3	3.1	8.4
HV44	C9	57.3	32.3	6.2	4.1	10.3
HV45	C10	52.4	37.8	6.3	3.5	9.8
HV46	A10	0.0	3.0	58.2	38.8	97.0
HV47	A9	0.3	2.5	49.4	47.9	97.3
HV48	A8	0.8	7.4	55.1	36.7	91.8
HV49	A7	7.5	12.4	45.9	34.3	80.2
HV50	A6	18.7	4.1	42.3	34.9	77.2
HV51	A5	2.4	3.5	55.4	38.7	94.1
HV52	A4	1.7	4.4	45.5	48.3	93.9
HV53	A3	0.9	4.2	47.3	47.5	94.9

Appendix 3 – Faunal Summary by Sample

****************************** Data Summarization ******************************

PC-ORD, 6.08
26 Mar 2015, 14:03:45
DataSummaryAllSamples

Summary of: 53 samples N = 25 species

Num.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S	E	H	D`
1	A01	3.800	8.972	95.0000	0.000	39.000	11	0.723	1.734	0.7459
2	A02	6.280	17.408	157.0000	0.000	80.000	8	0.692	1.438	0.6649
3	A03	2.240	6.900	56.0000	0.000	34.000	7	0.664	1.291	0.5957
4	A04	2.960	6.598	74.0000	0.000	24.000	8	0.783	1.629	0.7692
5	A05	2.440	5.687	61.0000	0.000	20.000	9	0.739	1.623	0.7514
6	A06	5.160	12.182	129.0000	0.000	46.000	10	0.701	1.614	0.7460
7	A07	2.920	5.715	73.0000	0.000	20.000	9	0.850	1.868	0.8129
8	A08	2.960	7.092	74.0000	0.000	25.000	6	0.828	1.483	0.7396
9	A09	4.000	7.953	100.0000	0.000	25.000	11	0.770	1.846	0.8082
10	A10	6.960	22.315	174.0000	0.000	110.000	11	0.534	1.280	0.5653
11	A11	3.680	9.419	92.0000	0.000	45.000	11	0.678	1.627	0.7084
12	B01	0.160	0.473	4.0000	0.000	2.000	3	0.946	1.040	0.6250
13	B02	0.120	0.600	3.0000	0.000	3.000	1	0.000	0.000	0.0000
14	B03	is empty								
15	B04	0.720	1.815	18.0000	0.000	8.000	5	0.880	1.417	0.7160
16	B05	0.120	0.440	3.0000	0.000	2.000	2	0.918	0.637	0.4444
17	B06	0.280	0.678	7.0000	0.000	2.000	4	0.975	1.352	0.7347
18	B07	3.000	14.379	75.0000	0.000	72.000	4	0.153	0.212	0.0779
19	B08	0.760	1.535	19.0000	0.000	5.000	6	0.944	1.691	0.8033
20	B09	0.440	1.261	11.0000	0.000	6.000	5	0.804	1.295	0.6446
21	B10	1.920	4.020	48.0000	0.000	14.000	7	0.869	1.691	0.7917
22	C01	7.640	20.147	191.0000	0.000	92.000	10	0.652	1.501	0.6930
23	C02	6.000	11.701	150.0000	0.000	44.000	12	0.787	1.956	0.8140
24	C03	1.880	3.127	47.0000	0.000	10.000	11	0.872	2.092	0.8538
25	C04	2.280	4.188	57.0000	0.000	14.000	10	0.855	1.969	0.8304
26	C05	3.800	8.196	95.0000	0.000	30.000	13	0.715	1.835	0.7814
27	C06	5.640	10.496	141.0000	0.000	34.000	12	0.778	1.934	0.8270
28	C07	8.680	16.790	217.0000	0.000	63.000	10	0.808	1.861	0.8163
29	C08	11.160	28.841	279.0000	0.000	122.000	13	0.609	1.562	0.7035
30	C09	36.040	84.186	901.0000	0.000	406.000	16	0.661	1.833	0.7505
31	C10	17.240	40.272	431.0000	0.000	181.000	15	0.674	1.825	0.7505
32	D01	is empty								
33	D02	1.080	2.361	27.0000	0.000	8.000	6	0.885	1.585	0.7764
34	D03	0.600	1.323	15.0000	0.000	5.000	6	0.902	1.617	0.7733
35	D04	0.120	0.440	3.0000	0.000	2.000	2	0.918	0.637	0.4444
36	D05	0.640	1.524	16.0000	0.000	5.000	4	0.989	1.371	0.7422
37	D06	0.840	2.095	21.0000	0.000	10.000	8	0.786	1.634	0.7211
38	D07	3.480	9.147	87.0000	0.000	46.000	12	0.704	1.750	0.6947
39	D08	0.760	1.739	19.0000	0.000	7.000	6	0.877	1.571	0.7590
40	D09	1.880	3.383	47.0000	0.000	12.000	9	0.887	1.950	0.8357
41	D10	0.920	1.681	23.0000	0.000	8.000	11	0.880	2.111	0.8318
42	E01	4.160	7.814	104.0000	0.000	30.000	9	0.881	1.935	0.8245
43	E02	3.840	13.502	96.0000	0.000	68.000	10	0.516	1.187	0.4852
44	E03	3.480	9.640	87.0000	0.000	48.000	12	0.655	1.628	0.6653
45	E04	3.960	5.877	99.0000	0.000	22.000	13	0.885	2.270	0.8754
46	E05	7.640	12.790	191.0000	0.000	56.000	14	0.833	2.198	0.8524
47	E06	6.440	8.641	161.0000	0.000	32.000	16	0.874	2.423	0.8909
48	E07	8.560	24.430	214.0000	0.000	123.000	15	0.608	1.645	0.6472
49	E08	4.800	10.476	120.0000	0.000	52.000	14	0.766	2.021	0.7771
50	E09	6.600	19.541	165.0000	0.000	92.000	8	0.637	1.326	0.6234
51	E10	4.560	6.777	114.0000	0.000	25.000	12	0.903	2.244	0.8752
52	F01	3.520	7.495	88.0000	0.000	28.000	13	0.722	1.852	0.7859
53	F02	6.440	19.954	161.0000	0.000	91.000	10	0.531	1.222	0.5913
	AVERAGES:	4.257	10.08	106.4	0.000	44.30	8.9	0.726	1.534	0.6800

1325 cells in main matrix
Percent of cells empty = 64.528
Matrix total = 0.56400E+04
Matrix mean = 0.42566E+01
Variance of totals of samples = 0.19094E+05
CV of totals of samples = 129.85%

S = Richness = number of non-zero elements in row
E = Evenness = H / ln (Richness)
H = Diversity = - sum (Pi*ln(Pi)) = Shannon`s diversity index
D = Simpson`s diversity index for infinite population = 1 - sum (Pi*Pi)
where Pi = importance probability in element i (element i relativized by row total)

****************************** Analysis completed ******************************

******************************** Species List ********************************
PC-ORD, 6.08
26 Mar 2015, 14:36:35

Matrix contents: 53 samples
by 25 species

DataSummaryBySample

Species file:
C:\Users\Bob\Documents\2013&2014Proposals\Haverstraw_SturgeonCrotonPoint\PC Ord\SpeciesList.txt

SPECIES LISTS FOR EACH SAMPLE UNIT

DataSummaryBySample
Sample unit: A01

Chispp	Chironomidae spp (larvae)	6.000
Cyapol	Cyathura polita	1.000
Hypgra	Hypaniola grayi	39.000
Lepplu	Leptocheirus plumulosus	1.000
Melnit	Melita nitida	1.000
Mytleu	Mytilopsis leucophaeata	4.000
Nemesp	Nemertinea sp	7.000
Nersuc	Neanthes succinea	3.000
Olispp	Oligochaete spp	3.000
Rancun	Rangia cuneata	25.000
Scovir	Scolecolepides viridis	5.000

DataSummaryBySample
Sample unit: A02

Boclig	Boccardia ligerica	8.000
Chispp	Chironomidae spp (larvae)	8.000
Cyapol	Cyathura polita	3.000
Hypgra	Hypaniola grayi	80.000
Mytleu	Mytilopsis leucophaeata	9.000
Olispp	Oligochaete spp	4.000
Rancun	Rangia cuneata	40.000
Scovir	Scolecolepides viridis	5.000

DataSummaryBySample
Sample unit: A03

Chispp	Chironomidae spp (larvae)	7.000
Hypgra	Hypaniola grayi	6.000
Lepplu	Leptocheirus plumulosus	1.000
Mytleu	Mytilopsis leucophaeata	3.000
Nemesp	Nemertinea sp	1.000
Rancun	Rangia cuneata	34.000
Scovir	Scolecolepides viridis	4.000

DataSummaryBySample
Sample unit: A04

Chispp	Chironomidae spp (larvae)	17.000
Hypgra	Hypaniola grayi	18.000
Lepplu	Leptocheirus plumulosus	6.000
Mytleu	Mytilopsis leucophaeata	6.000
Nemesp	Nemertinea sp	1.000
Olispp	Oligochaete spp	1.000
Rancun	Rangia cuneata	24.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: A05

Chispp	Chironomidae spp (larvae)	9.000
Gamdai	Gammarus daiberi	1.000
Hypgra	Hypaniola grayi	6.000
Lepplu	Leptocheirus plumulosus	20.000
Melnit	Melita nitida	1.000
Mytleu	Mytilopsis leucophaeata	1.000
Olispp	Oligochaete spp	2.000

Rancun	Rangia cuneata	20.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: A06

Chispp	Chironomidae spp (larvae)	21.000
Cyapol	Cyathura polita	1.000
Hypgra	Hypaniola grayi	39.000
Lepplu	Leptocheirus plumulosus	3.000
Mytleu	Mytilopsis leucophaeata	11.000
Nemesp	Nemertinea sp	2.000
Nersuc	Neanthes succinea	3.000
Olispp	Oligochaete spp	2.000
Rancun	Rangia cuneata	46.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: A07

Chispp	Chironomidae spp (larvae)	11.000
Cyapol	Cyathura polita	3.000
Geudem	Geukensia demissa	1.000
Hypgra	Hypaniola grayi	19.000
Mytleu	Mytilopsis leucophaeata	2.000
Nemesp	Nemertinea sp	7.000
Olispp	Oligochaete spp	4.000
Rancun	Rangia cuneata	20.000
Scovir	Scolecolepides viridis	6.000

DataSummaryBySample
Sample unit: A08

Chispp	Chironomidae spp (larvae)	12.000
Hypgra	Hypaniola grayi	24.000
Lepplu	Leptocheirus plumulosus	1.000
Mytleu	Mytilopsis leucophaeata	8.000
Rancun	Rangia cuneata	25.000
Scovir	Scolecolepides viridis	4.000

DataSummaryBySample
Sample unit: A09

Balamp	Balanus amphitrite	1.000
Chispp	Chironomidae spp (larvae)	21.000
Cyapol	Cyathura polita	3.000
Hypgra	Hypaniola grayi	25.000
Lepplu	Leptocheirus plumulosus	17.000
Melnit	Melita nitida	2.000
Mytleu	Mytilopsis leucophaeata	3.000
Nemesp	Nemertinea sp	1.000
Rancun	Rangia cuneata	23.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	3.000

DataSummaryBySample
Sample unit: A10

Chispp	Chironomidae spp (larvae)	4.000
Cyapol	Cyathura polita	1.000
Gamdai	Gammarus daiberi	1.000
Hypgra	Hypaniola grayi	2.000
Lepplu	Leptocheirus plumulosus	110.000
Melnit	Melita nitida	7.000
Mytleu	Mytilopsis leucophaeata	1.000
Nersuc	Neanthes succinea	1.000
Olispp	Oligochaete spp	28.000
Rancun	Rangia cuneata	13.000
Scovir	Scolecolepides viridis	6.000

DataSummaryBySample
Sample unit: A11

Balamp	Balanus amphitrite	1.000
Chispp	Chironomidae spp (larvae)	1.000

Cyapol	Cyathura polita	2.000
Hypgra	Hypaniola grayi	8.000
Melnit	Melita nitida	1.000
Nemesp	Nemertinea sp	15.000
Nersuc	Neanthes succinea	8.000
Notosp	Notomastus sp	1.000
Olispp	Oligochaete spp	1.000
Rancun	Rangia cuneata	45.000
Scovir	Scolecolepides viridis	9.000

DataSummaryBySample
Sample unit: B01

Hypgra	Hypaniola grayi	1.000
Nemesp	Nemertinea sp	1.000
Scovir	Scolecolepides viridis	2.000

DataSummaryBySample
Sample unit: B02

Notosp	Notomastus sp	3.000

DataSummaryBySample
Sample unit: B03

DataSummaryBySample
Sample unit: B04

Hypgra	Hypaniola grayi	1.000
Nemesp	Nemertinea sp	3.000
Notosp	Notomastus sp	3.000
Olispp	Oligochaete spp	8.000
Rancun	Rangia cuneata	3.000

DataSummaryBySample
Sample unit: B05

Chispp	Chironomidae spp (larvae)	1.000
Rancun	Rangia cuneata	2.000

DataSummaryBySample
Sample unit: B06

Cyapol	Cyathura polita	2.000
Nemesp	Nemertinea sp	2.000
Rancun	Rangia cuneata	1.000
Scovir	Scolecolepides viridis	2.000

DataSummaryBySample
Sample unit: B07

Hydrsp	Hydrobia sp	72.000
Nemesp	Nemertinea sp	1.000
Olispp	Oligochaete spp	1.000
Rancun	Rangia cuneata	1.000

DataSummaryBySample
Sample unit: B08

Cyapol	Cyathura polita	2.000
Nemesp	Nemertinea sp	5.000
Notosp	Notomastus sp	1.000
Olispp	Oligochaete spp	3.000
Rancun	Rangia cuneata	4.000
Scovir	Scolecolepides viridis	4.000

DataSummaryBySample
Sample unit: B09

Cyapol	Cyathura polita	1.000
Nemesp	Nemertinea sp	2.000

Olispp	Oligochaete spp	1.000
Rancun	Rangia cuneata	1.000
Scovir	Scolecolepides viridis	6.000

DataSummaryBySample
Sample unit: B10

Cyapol	Cyathura polita	1.000
Hydrsp	Hydrobia sp	10.000
Nemesp	Nemertinea sp	7.000
Notosp	Notomastus sp	2.000
Olispp	Oligochaete spp	11.000
Rancun	Rangia cuneata	14.000
Scovir	Scolecolepides viridis	3.000

DataSummaryBySample
Sample unit: C01

Balamp	Balanus amphitrite	92.000
Boclig	Boccardia ligerica	4.000
Corosp	Corophium sp	2.000
Geudem	Geukensia demissa	1.000
Hypgra	Hypaniola grayi	1.000
Melnit	Melita nitida	45.000
Mytleu	Mytilopsis leucophaeata	12.000
Nersuc	Neanthes succinea	17.000
Olispp	Oligochaete spp	16.000
Rhihar	Rhithropanopeus harrisii	1.000

DataSummaryBySample
Sample unit: C02

Balamp	Balanus amphitrite	38.000
Boclig	Boccardia ligerica	5.000
Cyapol	Cyathura polita	1.000
Geudem	Geukensia demissa	7.000
Hypgra	Hypaniola grayi	6.000
Melnit	Melita nitida	44.000
Mytleu	Mytilopsis leucophaeata	7.000
Nemesp	Nemertinea sp	2.000
Nersuc	Neanthes succinea	20.000
Olispp	Oligochaete spp	1.000
Rhihar	Rhithropanopeus harrisii	4.000
Scovir	Scolecolepides viridis	15.000

DataSummaryBySample
Sample unit: C03

Balamp	Balanus amphitrite	2.000
Boclig	Boccardia ligerica	1.000
Chispp	Chironomidae spp (larvae)	2.000
Cyapol	Cyathura polita	4.000
Geudem	Geukensia demissa	1.000
Hypgra	Hypaniola grayi	8.000
Nemesp	Nemertinea sp	10.000
Nersuc	Neanthes succinea	1.000
Rancun	Rangia cuneata	8.000
Rhihar	Rhithropanopeus harrisii	2.000
Scovir	Scolecolepides viridis	8.000

DataSummaryBySample
Sample unit: C04

Balamp	Balanus amphitrite	1.000
Chispp	Chironomidae spp (larvae)	2.000
Cyapol	Cyathura polita	3.000
Hypgra	Hypaniola grayi	11.000
Monosp	Monoculodes sp	1.000
Nemesp	Nemertinea sp	4.000
Nersuc	Neanthes succinea	5.000
Rancun	Rangia cuneata	13.000
Rhihar	Rhithropanopeus harrisii	3.000
Scovir	Scolecolepides viridis	14.000

DataSummaryBySample

Sample unit: C05

Balamp	Balanus amphitrite	9.000
Chispp	Chironomidae spp (larvae)	1.000
Geudem	Geukensia demissa	1.000
Hypgra	Hypaniola grayi	8.000
Melnit	Melita nitida	8.000
Mytleu	Mytilopsis leucophaeata	4.000
Nemesp	Nemertinea sp	1.000
Nersuc	Neanthes succinea	30.000
Olispp	Oligochaete spp	29.000
Rancun	Rangia cuneata	1.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	1.000
Styell	Stylochus ellipticus	1.000

DataSummaryBySample
Sample unit: C06

Balamp	Balanus amphitrite	19.000
Boclig	Boccardia ligerica	1.000
Cyapol	Cyathura polita	1.000
Geudem	Geukensia demissa	3.000
Melnit	Melita nitida	34.000
Mytleu	Mytilopsis leucophaeata	19.000
Nemesp	Nemertinea sp	2.000
Nersuc	Neanthes succinea	34.000
Olispp	Oligochaete spp	18.000
Rancun	Rangia cuneata	1.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	8.000

DataSummaryBySample
Sample unit: C07

Balamp	Balanus amphitrite	27.000
Boclig	Boccardia ligerica	1.000
Melnit	Melita nitida	63.000
Mytleu	Mytilopsis leucophaeata	18.000
Nemesp	Nemertinea sp	6.000
Nersuc	Neanthes succinea	38.000
Olispp	Oligochaete spp	43.000
Rancun	Rangia cuneata	2.000
Rhihar	Rhithropanopeus harrisii	2.000
Scovir	Scolecolepides viridis	17.000

DataSummaryBySample
Sample unit: C08

Balamp	Balanus amphitrite	22.000
Boclig	Boccardia ligerica	3.000
Corosp	Corophium sp	8.000
Gamdai	Gammarus daiberi	1.000
Geudem	Geukensia demissa	2.000
Hypgra	Hypaniola grayi	2.000
Melnit	Melita nitida	122.000
Mytleu	Mytilopsis leucophaeata	2.000
Nemesp	Nemertinea sp	2.000
Nersuc	Neanthes succinea	23.000
Olispp	Oligochaete spp	84.000
Rancun	Rangia cuneata	3.000
Scovir	Scolecolepides viridis	5.000

DataSummaryBySample
Sample unit: C09

Balamp	Balanus amphitrite	55.000
Boclig	Boccardia ligerica	120.000
Chispp	Chironomidae spp (larvae)	2.000
Corosp	Corophium sp	96.000
Gamdai	Gammarus daiberi	7.000
Geudem	Geukensia demissa	19.000
Hypgra	Hypaniola grayi	3.000
Melnit	Melita nitida	406.000
Mytleu	Mytilopsis leucophaeata	72.000
Nersuc	Neanthes succinea	27.000
Olispp	Oligochaete spp	67.000

Rancun	Rangia cuneata	4.000
Rhihar	Rhithropanopeus harrisii	2.000
Scovir	Scolecolepides viridis	15.000
Sphqua	Sphaeroma quadridentatum	3.000
Turbsp	Turbellaria sp	3.000

DataSummaryBySample
Sample unit: C10

Balamp	Balanus amphitrite	24.000
Boclig	Boccardia ligerica	104.000
Corosp	Corophium sp	14.000
Cyapol	Cyathura polita	2.000
Gamdai	Gammarus daiberi	5.000
Geudem	Geukensia demissa	12.000
Hypgra	Hypaniola grayi	1.000
Melnit	Melita nitida	181.000
Mytleu	Mytilopsis leucophaeata	18.000
Nersuc	Neanthes succinea	23.000
Olispp	Oligochaete spp	30.000
Rancun	Rangia cuneata	3.000
Rhihar	Rhithropanopeus harrisii	5.000
Scovir	Scolecolepides viridis	6.000
Styell	Stylochus ellipticus	3.000

DataSummaryBySample
Sample unit: D01

DataSummaryBySample
Sample unit: D02

Cyapol	Cyathura polita	8.000
Hypgra	Hypaniola grayi	1.000
Nersuc	Neanthes succinea	6.000
Rancun	Rangia cuneata	1.000
Rhihar	Rhithropanopeus harrisii	5.000
Scovir	Scolecolepides viridis	6.000

DataSummaryBySample
Sample unit: D03

Chispp	Chironomidae spp (larvae)	2.000
Cyapol	Cyathura polita	2.000
Hypgra	Hypaniola grayi	5.000
Olispp	Oligochaete spp	4.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: D04

Olispp	Oligochaete spp	2.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: D05

Cyapol	Cyathura polita	4.000
Olispp	Oligochaete spp	5.000
Rancun	Rangia cuneata	4.000
Scovir	Scolecolepides viridis	3.000

DataSummaryBySample
Sample unit: D06

Chispp	Chironomidae spp (larvae)	3.000
Cyapol	Cyathura polita	3.000
Nemesp	Nemertinea sp	1.000
Notosp	Notomastus sp	1.000
Olispp	Oligochaete spp	10.000
Rancun	Rangia cuneata	1.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: D07

Cyapol	Cyathura polita	5.000
Geudem	Geukensia demissa	1.000
Hydrsp	Hydrobia sp	2.000
Lepplu	Leptocheirus plumulosus	2.000
Mytleu	Mytilopsis leucophaeata	4.000
Nemesp	Nemertinea sp	7.000
Nersuc	Neanthes succinea	3.000
Notosp	Notomastus sp	5.000
Olispp	Oligochaete spp	6.000
Rancun	Rangia cuneata	46.000
Scovir	Scolecolepides viridis	5.000
Synlae	Synidotea laevidorsalis	1.000

DataSummaryBySample
Sample unit: D08

Cyapol	Cyathura polita	1.000
Nemesp	Nemertinea sp	4.000
Notosp	Notomastus sp	2.000
Olispp	Oligochaete spp	1.000
Rancun	Rangia cuneata	4.000
Scovir	Scolecolepides viridis	7.000

DataSummaryBySample
Sample unit: D09

Balamp	Balanus amphitrite	6.000
Chispp	Chironomidae spp (larvae)	12.000
Cyapol	Cyathura polita	1.000
Hypgra	Hypaniola grayi	4.000
Nemesp	Nemertinea sp	5.000
Nersuc	Neanthes succinea	2.000
Olispp	Oligochaete spp	1.000
Rancun	Rangia cuneata	6.000
Scovir	Scolecolepides viridis	10.000

DataSummaryBySample
Sample unit: D10

Chispp	Chironomidae spp (larvae)	2.000
Cyapol	Cyathura polita	1.000
Hypgra	Hypaniola grayi	2.000
Melnit	Melita nitida	1.000
Mytleu	Mytilopsis leucophaeata	1.000
Nemesp	Nemertinea sp	8.000
Notosp	Notomastus sp	2.000
Olispp	Oligochaete spp	2.000
Rancun	Rangia cuneata	2.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: E01

Chispp	Chironomidae spp (larvae)	7.000
Hypgra	Hypaniola grayi	3.000
Mytleu	Mytilopsis leucophaeata	9.000
Nemesp	Nemertinea sp	17.000
Nersuc	Neanthes succinea	22.000
Notosp	Notomastus sp	5.000
Olispp	Oligochaete spp	5.000
Rancun	Rangia cuneata	30.000
Scovir	Scolecolepides viridis	6.000

DataSummaryBySample
Sample unit: E02

Chispp	Chironomidae spp (larvae)	6.000
Cyapol	Cyathura polita	1.000
Hydrsp	Hydrobia sp	4.000
Hypgra	Hypaniola grayi	3.000

Monosp	Monoculodes sp	1.000
Mytleu	Mytilopsis leucophaeata	6.000
Nemesp	Nemertinea sp	4.000
Nersuc	Neanthes succinea	2.000
Rancun	Rangia cuneata	68.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: E03

Chispp	Chironomidae spp (larvae)	9.000
Cyapol	Cyathura polita	2.000
Hydrsp	Hydrobia sp	2.000
Hypgra	Hypaniola grayi	7.000
Lepplu	Leptocheirus plumulosus	4.000
Melnit	Melita nitida	1.000
Monosp	Monoculodes sp	1.000
Mytleu	Mytilopsis leucophaeata	2.000
Nemesp	Nemertinea sp	8.000
Nersuc	Neanthes succinea	1.000
Rancun	Rangia cuneata	48.000
Scovir	Scolecolepides viridis	2.000

DataSummaryBySample
Sample unit: E04

Balamp	Balanus amphitrite	3.000
Chispp	Chironomidae spp (larvae)	3.000
Cyapol	Cyathura polita	1.000
Geudem	Geukensia demissa	4.000
Hypgra	Hypaniola grayi	8.000
Melnit	Melita nitida	10.000
Mytleu	Mytilopsis leucophaeata	4.000
Nemesp	Nemertinea sp	13.000
Nersuc	Neanthes succinea	14.000
Olispp	Oligochaete spp	2.000
Rancun	Rangia cuneata	22.000
Rhihar	Rhithropanopeus harrisii	3.000
Scovir	Scolecolepides viridis	12.000

DataSummaryBySample
Sample unit: E05

Balamp	Balanus amphitrite	4.000
Chispp	Chironomidae spp (larvae)	2.000
Cyapol	Cyathura polita	3.000
Hypgra	Hypaniola grayi	56.000
Lepplu	Leptocheirus plumulosus	10.000
Melnit	Melita nitida	9.000
Mytleu	Mytilopsis leucophaeata	22.000
Nemesp	Nemertinea sp	12.000
Nersuc	Neanthes succinea	9.000
Notosp	Notomastus sp	1.000
Olispp	Oligochaete spp	27.000
Rancun	Rangia cuneata	20.000
Rhihar	Rhithropanopeus harrisii	2.000
Scovir	Scolecolepides viridis	14.000

DataSummaryBySample
Sample unit: E06

Balamp	Balanus amphitrite	5.000
Chispp	Chironomidae spp (larvae)	16.000
Corosp	Corophium sp	5.000
Cyapol	Cyathura polita	1.000
Hydrsp	Hydrobia sp	1.000
Hypgra	Hypaniola grayi	32.000
Lepplu	Leptocheirus plumulosus	17.000
Melnit	Melita nitida	9.000
Monosp	Monoculodes sp	2.000
Mytleu	Mytilopsis leucophaeata	10.000
Nemesp	Nemertinea sp	5.000
Nersuc	Neanthes succinea	8.000
Olispp	Oligochaete spp	3.000
Rancun	Rangia cuneata	24.000
Rhihar	Rhithropanopeus harrisii	5.000
Scovir	Scolecolepides viridis	18.000

DataSummaryBySample
Sample unit: E07

Balamp	Balanus amphitrite	10.000
Chispp	Chironomidae spp (larvae)	2.000
Corosp	Corophium sp	2.000
Cyapol	Cyathura polita	1.000
Geudem	Geukensia demissa	7.000
Hypgra	Hypaniola grayi	10.000
Lepplu	Leptocheirus plumulosus	123.000
Melnit	Melita nitida	7.000
Mytleu	Mytilopsis leucophaeata	14.000
Nemesp	Nemertinea sp	12.000
Nersuc	Neanthes succinea	1.000
Olispp	Oligochaete spp	4.000
Rancun	Rangia cuneata	19.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: E08

Balamp	Balanus amphitrite	6.000
Boclig	Boccardia ligerica	1.000
Edotri	Edotea triloba	2.000
Geudem	Geukensia demissa	4.000
Hypgra	Hypaniola grayi	8.000
Melnit	Melita nitida	5.000
Monosp	Monoculodes sp	3.000
Mytleu	Mytilopsis leucophaeata	14.000
Nemesp	Nemertinea sp	8.000
Nersuc	Neanthes succinea	5.000
Olispp	Oligochaete spp	7.000
Rancun	Rangia cuneata	52.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	4.000

DataSummaryBySample
Sample unit: E09

Chispp	Chironomidae spp (larvae)	3.000
Gamdai	Gammarus daiberi	2.000
Hypgra	Hypaniola grayi	13.000
Lepplu	Leptocheirus plumulosus	92.000
Mytleu	Mytilopsis leucophaeata	5.000
Nemesp	Nemertinea sp	6.000
Olispp	Oligochaete spp	5.000
Rancun	Rangia cuneata	39.000

DataSummaryBySample
Sample unit: E10

Balamp	Balanus amphitrite	17.000
Boclig	Boccardia ligerica	11.000
Corosp	Corophium sp	8.000
Geudem	Geukensia demissa	2.000
Hypgra	Hypaniola grayi	11.000
Melnit	Melita nitida	9.000
Mytleu	Mytilopsis leucophaeata	5.000
Nemesp	Nemertinea sp	4.000
Nersuc	Neanthes succinea	2.000
Olispp	Oligochaete spp	25.000
Rancun	Rangia cuneata	16.000
Scovir	Scolecolepides viridis	4.000

DataSummaryBySample
Sample unit: F01

Balamp	Balanus amphitrite	1.000
Boclig	Boccardia ligerica	2.000
Chispp	Chironomidae spp (larvae)	5.000
Corosp	Corophium sp	1.000
Geudem	Geukensia demissa	1.000
Hypgra	Hypaniola grayi	2.000
Melnit	Melita nitida	3.000

Mytleu	Mytilopsis leucophaeata	17.000
Nersuc	Neanthes succinea	23.000
Olispp	Oligochaete spp	28.000
Rancun	Rangia cuneata	3.000
Rhihar	Rhithropanopeus harrisii	1.000
Scovir	Scolecolepides viridis	1.000

DataSummaryBySample
Sample unit: F02

Boclig	Boccardia ligerica	2.000
Chispp	Chironomidae spp (larvae)	2.000
Gamdai	Gammarus daiberi	1.000
Hypgra	Hypaniola grayi	91.000
Lepplu	Leptocheirus plumulosus	2.000
Mytleu	Mytilopsis leucophaeata	6.000
Nemesp	Nemertinea sp	2.000
Olispp	Oligochaete spp	7.000
Rancun	Rangia cuneata	47.000
Scovir	Scolecolepides viridis	1.000

*********************** Lists completed. Normal exit. ***********************
26 Mar 2015, 14:36:35

Appendix 4 – Faunal Summary by Province

************************ Output from program SUMMARY ************************
PC-ORD, 6.08
26 Mar 2015, 15:10:05

Data Summary By Province

Compact format data file:
C:\Users\Bob\Documents\2013&2014Proposals\Haverstraw_SturgeonCrotonPoint\PC Ord\PCOrdDataCompact.txt
Species file:
C:\Users\Bob\Documents\2013&2014Proposals\Haverstraw_SturgeonCrotonPoint\PC Ord\SpeciesList.txt

Matrix size: 53 sample (rows)
25 species (columns)

Subgroup: Prov A

Summary of 13 sample N= 18 species

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S	E	H`
1	A01	5.278	9.098	95.00	0.00	39.0	11	0.723	1.734
2	A02	8.722	17.59	157.0	0.00	80.0	8	0.692	1.438
3	A03	3.111	6.957	56.00	0.00	34.0	7	0.664	1.291
4	A04	4.111	6.702	74.00	0.00	24.0	8	0.783	1.629
5	A05	3.389	5.769	61.00	0.00	20.0	9	0.739	1.623
6	A06	7.167	12.35	129.0	0.00	46.0	10	0.701	1.614
7	A07	4.056	5.831	73.00	0.00	20.0	9	0.850	1.868
8	A08	4.111	7.188	74.00	0.00	25.0	6	0.828	1.483
9	A09	5.556	8.110	100.0	0.00	25.0	11	0.770	1.846
10	A10	9.667	22.49	174.0	0.00	110.	11	0.534	1.280
11	A11	5.111	9.532	92.00	0.00	45.0	11	0.678	1.627
12	C03	2.611	3.215	47.00	0.00	10.0	11	0.872	2.092
13	C04	3.167	4.285	57.00	0.00	14.0	10	0.855	1.969
AVERAGES:		5.08	9.16	91.46	0.00	37.8	9.4	0.745	1.653

Number of cells in main matrix = 234
Percent of cells empty = 47.863
Matrix total = 1.1890E+03
Matrix mean = 5.0812E+00
Variance of totals of sample = 1.5753E+03

S = Richness = number of non-zero elements in row
E = Evenness = H / ln (Richness)
H = Diversity = - sum (Pi*ln(Pi))
where Pi = importance probability in element i (element i
relativized by row total)

Summary of 18 species N= 13 sample

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S
1	Balamp	0.385E+00	0.650E+00	0.5000E+01	0.000E+00	0.200E+01	4
2	Boclig	0.692E+00	0.221E+01	0.9000E+01	0.000E+00	0.800E+01	2
3	Chispp	0.931E+01	0.686E+01	0.1210E+03	0.100E+01	0.210E+02	13
5	Cyapol	0.162E+01	0.145E+01	0.2100E+02	0.000E+00	0.400E+01	9
7	Gamdai	0.154E+00	0.376E+00	0.2000E+01	0.000E+00	0.100E+01	2
8	Geudem	0.154E+00	0.376E+00	0.2000E+01	0.000E+00	0.100E+01	2
10	Hypgra	0.219E+02	0.212E+02	0.2850E+03	0.200E+01	0.800E+02	13
11	Lepplu	0.122E+02	0.301E+02	0.1590E+03	0.000E+00	0.110E+03	8
12	Melnit	0.923E+00	0.193E+01	0.1200E+02	0.000E+00	0.700E+01	5
13	Monosp	0.769E-01	0.277E+00	0.1000E+01	0.000E+00	0.100E+01	1
14	Mytleu	0.369E+01	0.371E+01	0.4800E+02	0.000E+00	0.110E+02	10
15	Nemesp	0.369E+01	0.473E+01	0.4800E+02	0.000E+00	0.150E+02	9
16	Neasuc	0.162E+01	0.250E+01	0.2100E+02	0.000E+00	0.800E+01	6
17	Notosp	0.769E-01	0.277E+00	0.1000E+01	0.000E+00	0.100E+01	1
18	Olispp	0.346E+01	0.752E+01	0.4500E+02	0.000E+00	0.280E+02	8
19	Rancun	0.258E+02	0.121E+02	0.3360E+03	0.800E+01	0.460E+02	13
20	Rhihar	0.462E+00	0.967E+00	0.6000E+01	0.000E+00	0.300E+01	3
21	Scovir	0.515E+01	0.367E+01	0.6700E+02	0.100E+01	0.140E+02	13
AVERAGES:		0.508E+01	0.561E+01	0.6606E+02	0.667E+00	0.201E+02	6.8

Subgroup: Prov B

Summary of 10 sample N= 9 species

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S	E	H`
1	B01	0.4444	0.5546	4.000	0.00	2.00	3	0.946	1.040
2	B02	0.3333	0.6383	3.000	0.00	3.00	1	0.000	0.000
3	B03	is empty							
4	B04	2.000	2.236	18.00	0.00	8.00	5	0.880	1.417
5	B05	0.3333	0.4907	3.000	0.00	2.00	2	0.918	0.637
6	B06	0.7778	0.8474	7.000	0.00	2.00	4	0.975	1.352
7	B07	8.333	15.37	75.00	0.00	72.0	4	0.153	0.212
8	B08	2.111	2.064	19.00	0.00	5.00	6	0.944	1.691
9	B09	1.222	1.492	11.00	0.00	6.00	5	0.804	1.295
10	B10	5.333	5.319	48.00	0.00	14.0	7	0.869	1.691
AVERAGES:		2.09	2.90	18.80	0.00	11.4	3.7	0.649	0.933

Number of cells in main matrix = 90
Percent of cells empty = 58.889
Matrix total = 1.8800E+02
Matrix mean = 2.0889E+00
Variance of totals of sample = 1.8730E+03

S = Richness = number of non-zero elements in row
E = Evenness = H / ln (Richness)
H = Diversity = - sum (Pi*ln(Pi))
where Pi = importance probability in element i (element i relativized by row total)

Summary of 9 species N= 10 sample

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S
3	Chispp	0.100E+00	0.316E+00	0.1000E+01	0.000E+00	0.100E+01	1
5	Cyapol	0.600E+00	0.843E+00	0.6000E+01	0.000E+00	0.200E+01	4
9	Hydrsp	0.820E+01	0.226E+02	0.8200E+02	0.000E+00	0.720E+02	2
10	Hypgra	0.200E+00	0.422E+00	0.2000E+01	0.000E+00	0.100E+01	2
15	Nemesp	0.210E+01	0.233E+01	0.2100E+02	0.000E+00	0.700E+01	7
17	Notosp	0.900E+00	0.129E+01	0.9000E+01	0.000E+00	0.300E+01	4
18	Olispp	0.240E+01	0.392E+01	0.2400E+02	0.000E+00	0.110E+02	5
19	Rancun	0.260E+01	0.422E+01	0.2600E+02	0.000E+00	0.140E+02	7
21	Scovir	0.170E+01	0.211E+01	0.1700E+02	0.000E+00	0.600E+01	5
AVERAGES:		0.209E+01	0.423E+01	0.2089E+02	0.000E+00	0.130E+02	4.1

Subgroup: Prov C

Summary of 8 sample N= 19 species

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S	E	H`
1	C01	10.05	20.30	191.0	0.00	92.0	10	0.652	1.501
2	C02	7.895	11.86	150.0	0.00	44.0	12	0.787	1.956
3	C05	5.000	8.287	95.00	0.00	30.0	13	0.715	1.835
4	C06	7.421	10.65	141.0	0.00	34.0	12	0.778	1.934
5	C07	11.42	17.02	217.0	0.00	63.0	10	0.808	1.861
6	C08	14.68	29.06	279.0	0.00	122.	13	0.609	1.562
7	C09	47.42	84.98	901.0	0.00	406.	16	0.661	1.833
8	C10	22.68	40.65	431.0	0.00	181.	15	0.674	1.825
AVERAGES:		15.8	27.9	300.6	0.00	122.	12.6	0.711	1.788

Number of cells in main matrix = 152
Percent of cells empty = 33.553
Matrix total = 2.4050E+03
Matrix mean = 1.5822E+01
Variance of totals of sample = 6.9625E+04

S = Richness = number of non-zero elements in row
E = Evenness = H / ln (Richness)
H = Diversity = - sum (Pi*ln(Pi))
where Pi = importance probability in element i (element i relativized by row total)

Summary of 19 species N= 8 sample

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S
1	Balamp	0.358E+02	0.266E+02	0.2860E+03	0.900E+01	0.920E+02	8
2	Boclig	0.298E+02	0.510E+02	0.2380E+03	0.000E+00	0.120E+03	7
3	Chispp	0.375E+00	0.744E+00	0.3000E+01	0.000E+00	0.200E+01	2
4	Corosp	0.150E+02	0.331E+02	0.1200E+03	0.000E+00	0.960E+02	4
5	Cyapol	0.500E+00	0.756E+00	0.4000E+01	0.000E+00	0.200E+01	3
7	Gamdai	0.162E+01	0.277E+01	0.1300E+02	0.000E+00	0.700E+01	3
8	Geudem	0.562E+01	0.672E+01	0.4500E+02	0.000E+00	0.190E+02	7
10	Hypgra	0.262E+01	0.292E+01	0.2100E+02	0.000E+00	0.800E+01	6
12	Melnit	0.113E+03	0.131E+03	0.9030E+03	0.800E+01	0.406E+03	8
14	Mytleu	0.190E+02	0.224E+02	0.1520E+03	0.200E+01	0.720E+02	8
15	Nemesp	0.162E+01	0.200E+01	0.1300E+02	0.000E+00	0.600E+01	5
16	Neasuc	0.265E+02	0.715E+01	0.2120E+03	0.170E+02	0.380E+02	8
18	Olispp	0.360E+02	0.276E+02	0.2880E+03	0.100E+01	0.840E+02	8
19	Rancun	0.175E+01	0.149E+01	0.1400E+02	0.000E+00	0.400E+01	6
20	Rhihar	0.200E+01	0.169E+01	0.1600E+02	0.000E+00	0.500E+01	7
21	Scovir	0.838E+01	0.659E+01	0.6700E+02	0.000E+00	0.170E+02	7
22	Sphqua	0.375E+00	0.106E+01	0.3000E+01	0.000E+00	0.300E+01	1
23	Styell	0.500E+00	0.107E+01	0.4000E+01	0.000E+00	0.300E+01	2
25	Turbsp	0.375E+00	0.106E+01	0.3000E+01	0.000E+00	0.300E+01	1
AVERAGES:		0.158E+02	0.172E+02	0.1266E+03	0.195E+01	0.519E+02	5.3

Subgroup: Prov D

Summary of 10 sample N= 17 species

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S	E	H`
1	D01	is empty							
2	D02	1.588	2.418	27.00	0.00	8.00	6	0.885	1.585
3	D03	0.8824	1.354	15.00	0.00	5.00	6	0.902	1.617
4	D04	0.1765	0.4435	3.000	0.00	2.00	2	0.918	0.637
5	D05	0.9412	1.555	16.00	0.00	5.00	4	0.989	1.371
6	D06	1.235	2.134	21.00	0.00	10.0	8	0.786	1.634
7	D07	5.118	9.299	87.00	0.00	46.0	12	0.704	1.750
8	D08	1.118	1.777	19.00	0.00	7.00	6	0.877	1.571
9	D09	2.765	3.501	47.00	0.00	12.0	9	0.887	1.950
10	D10	1.353	1.738	23.00	0.00	8.00	11	0.880	2.111
AVERAGES:		1.52	2.42	25.80	0.00	10.3	6.4	0.783	1.423

Number of cells in main matrix = 170
Percent of cells empty = 62.353
Matrix total = 2.5800E+02
Matrix mean = 1.5176E+00
Variance of totals of sample = 6.0902E+02

S = Richness = number of non-zero elements in row
E = Evenness = H / ln (Richness)
H = Diversity = - sum (Pi*ln(Pi))
where Pi = importance probability in element i (element i relativized by row total)

Summary of 17 species N= 10 sample

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S
1	Balamp	0.600E+00	0.190E+01	0.6000E+01	0.000E+00	0.600E+01	1
3	Chispp	0.190E+01	0.373E+01	0.1900E+02	0.000E+00	0.120E+02	4
5	Cyapol	0.250E+01	0.255E+01	0.2500E+02	0.000E+00	0.800E+01	8
8	Geudem	0.100E+00	0.316E+00	0.1000E+01	0.000E+00	0.100E+01	1
9	Hydrsp	0.200E+00	0.632E+00	0.2000E+01	0.000E+00	0.200E+01	1
10	Hypgra	0.120E+01	0.187E+01	0.1200E+02	0.000E+00	0.500E+01	4
11	Lepplu	0.200E+00	0.632E+00	0.2000E+01	0.000E+00	0.200E+01	1
12	Melnit	0.100E+00	0.316E+00	0.1000E+01	0.000E+00	0.100E+01	1
14	Mytleu	0.500E+00	0.127E+01	0.5000E+01	0.000E+00	0.400E+01	2
15	Nemesp	0.250E+01	0.321E+01	0.2500E+02	0.000E+00	0.800E+01	5
16	Neasuc	0.110E+01	0.202E+01	0.1100E+02	0.000E+00	0.600E+01	3
17	Notosp	0.100E+01	0.163E+01	0.1000E+02	0.000E+00	0.500E+01	4
18	Olispp	0.310E+01	0.318E+01	0.3100E+02	0.000E+00	0.100E+02	8
19	Rancun	0.640E+01	0.141E+02	0.6400E+02	0.000E+00	0.460E+02	7
20	Rhihar	0.800E+00	0.155E+01	0.8000E+01	0.000E+00	0.500E+01	4
21	Scovir	0.350E+01	0.334E+01	0.3500E+02	0.000E+00	0.100E+02	9
24	Synlae	0.100E+00	0.316E+00	0.1000E+01	0.000E+00	0.100E+01	1

AVERAGES:	0.152E+01	0.250E+01	0.1518E+02	0.000E+00	0.776E+01	3.8

Subgroup: Prov E

Summary of 10 sample N= 21 species

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S	E	H`
1	E01	4.952	7.856	104.0	0.00	30.0	9	0.881	1.935
2	E02	4.571	13.52	96.00	0.00	68.0	10	0.516	1.187
3	E03	4.143	9.664	87.00	0.00	48.0	12	0.655	1.628
4	E04	4.714	5.927	99.00	0.00	22.0	13	0.885	2.270
5	E05	9.095	12.88	191.0	0.00	56.0	14	0.833	2.198
6	E06	7.667	8.732	161.0	0.00	32.0	16	0.874	2.423
7	E07	10.19	24.49	214.0	0.00	123.	15	0.608	1.645
8	E08	5.714	10.52	120.0	0.00	52.0	14	0.766	2.021
9	E09	7.857	19.58	165.0	0.00	92.0	8	0.637	1.326
10	E10	5.429	6.834	114.0	0.00	25.0	12	0.903	2.244
AVERAGES:		6.43	12.0	135.1	0.00	54.8	12.3	0.756	1.888

Number of cells in main matrix = 210
Percent of cells empty = 41.429
Matrix total = 1.3510E+03
Matrix mean = 6.4333E+00
Variance of totals of sample = 1.9668E+03

S = Richness = number of non-zero elements in row
E = Evenness = H / ln (Richness)
H = Diversity = - sum (Pi*ln(Pi))
where Pi = importance probability in element i (element i relativized by row total)

Summary of 21 species N= 10 sample

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S
1	Balamp	0.450E+01	0.550E+01	0.4500E+02	0.000E+00	0.170E+02	6
2	Boclig	0.120E+01	0.346E+01	0.1200E+02	0.000E+00	0.110E+02	2
3	Chispp	0.480E+01	0.492E+01	0.4800E+02	0.000E+00	0.160E+02	8
4	Corosp	0.150E+01	0.280E+01	0.1500E+02	0.000E+00	0.800E+01	3
5	Cyapol	0.900E+00	0.994E+00	0.9000E+01	0.000E+00	0.300E+01	6
6	Edotri	0.200E+00	0.632E+00	0.2000E+01	0.000E+00	0.200E+01	1
7	Gamdai	0.200E+00	0.632E+00	0.2000E+01	0.000E+00	0.200E+01	1
8	Geudem	0.170E+01	0.250E+01	0.1700E+02	0.000E+00	0.700E+01	4
9	Hydrsp	0.700E+00	0.134E+01	0.7000E+01	0.000E+00	0.400E+01	3
10	Hypgra	0.151E+02	0.165E+02	0.1510E+03	0.300E+01	0.560E+02	10
11	Lepplu	0.246E+02	0.447E+02	0.2460E+03	0.000E+00	0.123E+03	5
12	Melnit	0.500E+01	0.432E+01	0.5000E+02	0.000E+00	0.100E+02	7
13	Monosp	0.700E+00	0.106E+01	0.7000E+01	0.000E+00	0.300E+01	4
14	Mytleu	0.910E+01	0.610E+01	0.9100E+02	0.200E+01	0.220E+02	10
15	Nemesp	0.890E+01	0.441E+01	0.8900E+02	0.400E+01	0.170E+02	10
16	Neasuc	0.640E+01	0.707E+01	0.6400E+02	0.000E+00	0.220E+02	9
17	Notosp	0.600E+00	0.158E+01	0.6000E+01	0.000E+00	0.500E+01	2
18	Olispp	0.780E+01	0.985E+01	0.7800E+02	0.000E+00	0.270E+02	8
19	Rancun	0.338E+02	0.173E+02	0.3380E+03	0.160E+02	0.680E+02	10
20	Rhihar	0.120E+01	0.169E+01	0.1200E+02	0.000E+00	0.500E+01	5
21	Scovir	0.620E+01	0.627E+01	0.6200E+02	0.000E+00	0.180E+02	9
AVERAGES:		0.643E+01	0.684E+01	0.6433E+02	0.119E+01	0.212E+02	5.9

Subgroup: Prov F

Summary of 2 sample N= 16 species

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S	E	H`
1	F01	5.500	7.763	88.00	0.00	28.0	13	0.722	1.852
2	F02	10.06	20.29	161.0	0.00	91.0	10	0.531	1.222
AVERAGES:		7.78	14.0	124.5	0.00	59.5	11.5	0.626	1.537

Number of cells in main matrix = 32
Percent of cells empty = 28.125
Matrix total = 2.4900E+02

```
Matrix mean  =   7.7812E+00
Variance of totals of sample   =   2.6645E+03
---------------------------------------------
S = Richness  = number of non-zero elements in row
E = Evenness  = H / ln (Richness)
H = Diversity = - sum (Pi*ln(Pi))
        where Pi = importance probability in element i (element i
                   relativized by row total)
```

Summary of 16 species N= 2 sample

No.	Name	Mean	Stand.Dev.	Sum	Minimum	Maximum	S
1	Balamp	0.500E+00	0.707E+00	0.1000E+01	0.000E+00	0.100E+01	1
2	Boclig	0.200E+01	0.000E+00	0.4000E+01	0.200E+01	0.200E+01	2
3	Chispp	0.350E+01	0.212E+01	0.7000E+01	0.200E+01	0.500E+01	2
4	Corosp	0.500E+00	0.707E+00	0.1000E+01	0.000E+00	0.100E+01	1
7	Gamdai	0.500E+00	0.707E+00	0.1000E+01	0.000E+00	0.100E+01	1
8	Geudem	0.500E+00	0.707E+00	0.1000E+01	0.000E+00	0.100E+01	1
10	Hypgra	0.465E+02	0.629E+02	0.9300E+02	0.200E+01	0.910E+02	2
11	Lepplu	0.100E+01	0.141E+01	0.2000E+01	0.000E+00	0.200E+01	1
12	Melnit	0.150E+01	0.212E+01	0.3000E+01	0.000E+00	0.300E+01	1
14	Mytleu	0.115E+02	0.778E+01	0.2300E+02	0.600E+01	0.170E+02	2
15	Nemesp	0.100E+01	0.141E+01	0.2000E+01	0.000E+00	0.200E+01	1
16	Neasuc	0.115E+02	0.163E+02	0.2300E+02	0.000E+00	0.230E+02	1
18	Olispp	0.175E+02	0.148E+02	0.3500E+02	0.700E+01	0.280E+02	2
19	Rancun	0.250E+02	0.311E+02	0.5000E+02	0.300E+01	0.470E+02	2
20	Rhihar	0.500E+00	0.707E+00	0.1000E+01	0.000E+00	0.100E+01	1
21	Scovir	0.100E+01	0.000E+00	0.2000E+01	0.100E+01	0.100E+01	2
AVERAGES:		0.778E+01	0.897E+01	0.1556E+02	0.144E+01	0.141E+02	1.4

26 Mar 2015, 15:10:05

************************* End of Data Summarization *************************