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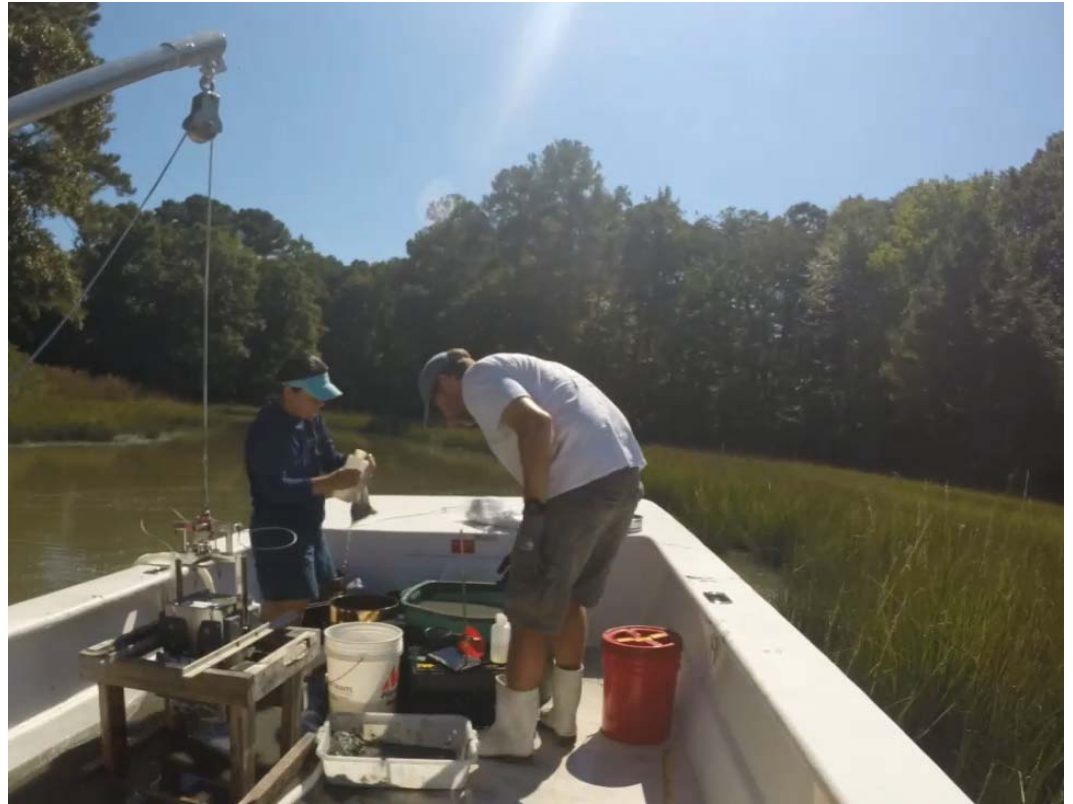
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ASSESSMENT OF BENTHIC MACROFAUNA COMMUNITY WITHIN INTERTIDAL MUDFLATS



5/17/2019

Hurds Cove, Lynnhaven River, Virginia

A final report to:
Waterway Surveys and Engineering Ltd.

Prepared by:
M. Lisa Kellogg and Jennifer C. Dreyer

Assessment of benthic macrofauna community within intertidal mudflats

HURDS COVE, LYNNHAVEN RIVER, VIRGINIA

Award Information

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Award Period: October 08, 2018 – June 1, 2019

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Project Summary

A total of 30 samples were collected from eight locations in Hurds Cove, Lynnhaven River, VA. All samples were rinsed over a 500- μ m mesh sieve and all material retained on the sieve was analyzed to determine benthic macrofaunal community identity, abundance and biomass. With the exception of one sample with relatively high biomass (50.68 g AFDW m^{-2}) attributable to a single (*Rangia cuneata*), biomass across all locations was low, ranging from 0.16-0.67 g AFDW m^{-2} . At five of the eight locations, all measurable biomass was contributed by polychaete worms. At the other three locations, polychaetes accounted for 45-57% of total biomass. At two locations, isopods contributed >25% biomass and, at one location, decapod crustaceans accounted for 13.7% of the total biomass. Polychaetes and/or ostracods were the most abundant organisms in all locations. However, despite being abundant, ostracod biomass was below detection limits (<0.0001 g m^{-2}) for most locations.

Project Goal

The goal of this project was to collect the data needed to formulate a VIMS recommendation for appropriate mitigation for the Hurds Cove SSD Dredging Project in Lynnhaven River, VA.

Approach

The methods described below were selected based upon a combination of the logistic constraints of sampling in Hurds Cove and the desire to compare the data collected from these samples to data from the Chesapeake Bay Program's Benthic Monitoring Program (CBP-BMP). Towards this end, the area sampled by the gear described below is the same as that sampled by the CBP-BMP as part of the probabilistic sampling program they conduct each summer. Also following the CBP-BMP protocols, we collected data on the identity, abundance and biomass of macrofaunal organisms retained on a 500-micron mesh. This approach allowed the samples from Hurds Cove to be evaluated in the context of previous data collected in the region.

Sample collection

Based upon findings of the initial rapid assessment by Dr. Mark Luckenbach and his subsequent recommendations, we selected 30 sampling points in intertidal soft-sediment habitats (hereafter "mudflats") for additional sampling. Because the areal extent of the mudflats varies between creeks within Hurds Cove, samples were allocated based on the size of the area recommended for additional sampling, the desire to collect data from across potential gradients within each creek, and the desire to have a minimum of three samples from each creek. For the smallest creek areas, three points were randomly selected. For larger creek areas, the area will be divided into upstream, downstream and midstream sections and a minimum one sampling point was be allocated per creek section.

Due to the shallow depths of the sampling sites, all samples were collected at high tide from a Carolina Skiff equipped with a davit and an Ekman grab (KC Denmark). An Ekman grab was selected for use because it can be easily operated from a small, shallow-draft boat and because it collects sediments from an area (0.04 m²), which is identical to the area of samples collected by the Chesapeake Bay Program's Benthic Monitoring Program. Preliminary sampling on October 1, 2018 demonstrated that this gear combination was effective at reaching all sampling sites and was capable of collecting samples to a depth of >7cm within all creeks in need of additional sampling.

Approximate locations of all sampling sites are shown in Figure 1 and shown in the context of the surrounding landscape in Figures 2.1 – 2.7. In most cases, the mapped location is the location where the sample was taken. However, in some instances, submerged objects (e.g. tree trunks) precluded sampling at the selected location or the presence of vegetation required selection of a different point that was in the correct habitat type. In these instances, samples were collected as close as possible to the selected sites. In most cases, samples were collected within 3m of the originally selected location. Using this approach, we successfully collected samples from all 30 designated sampling locations.

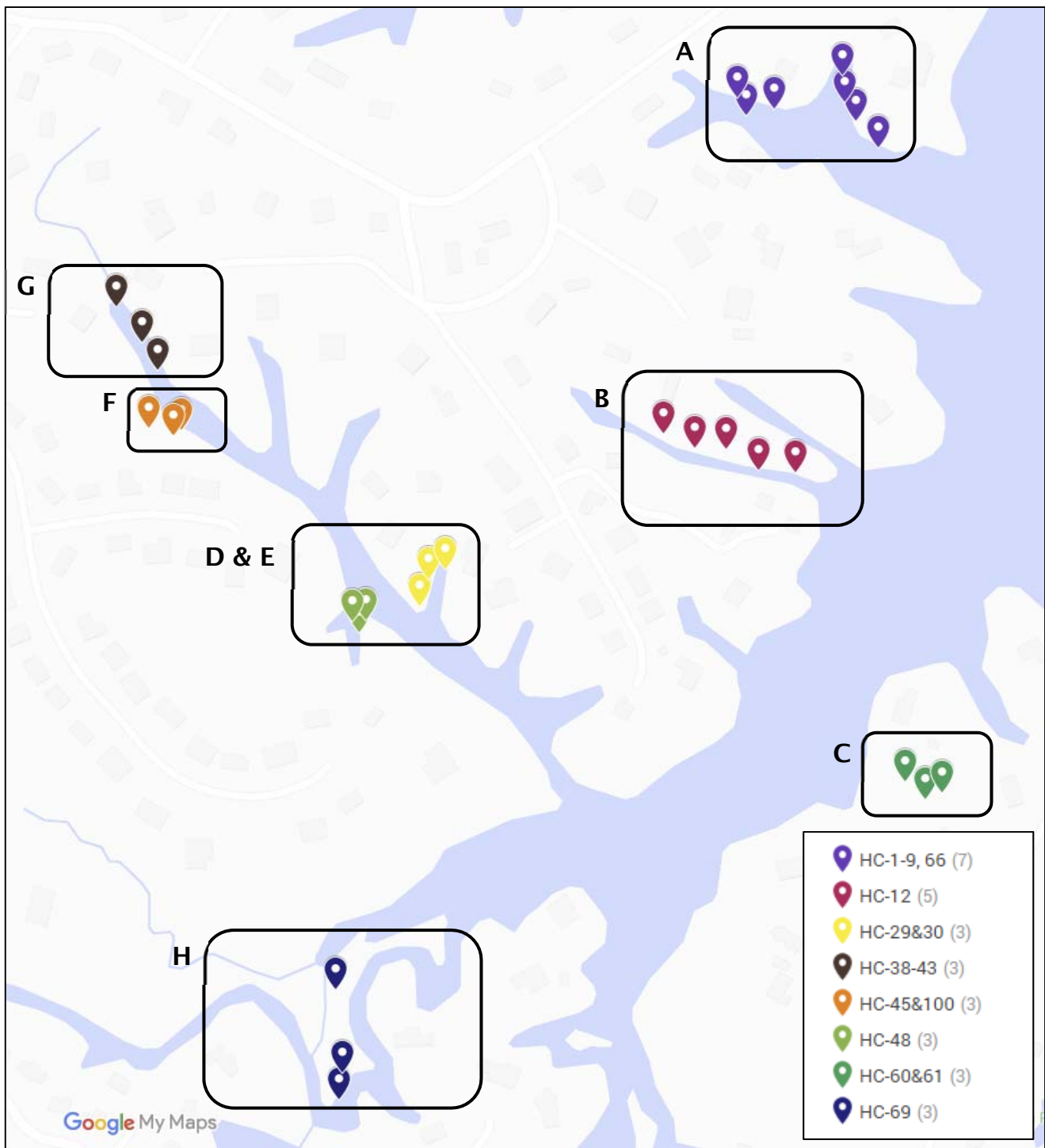
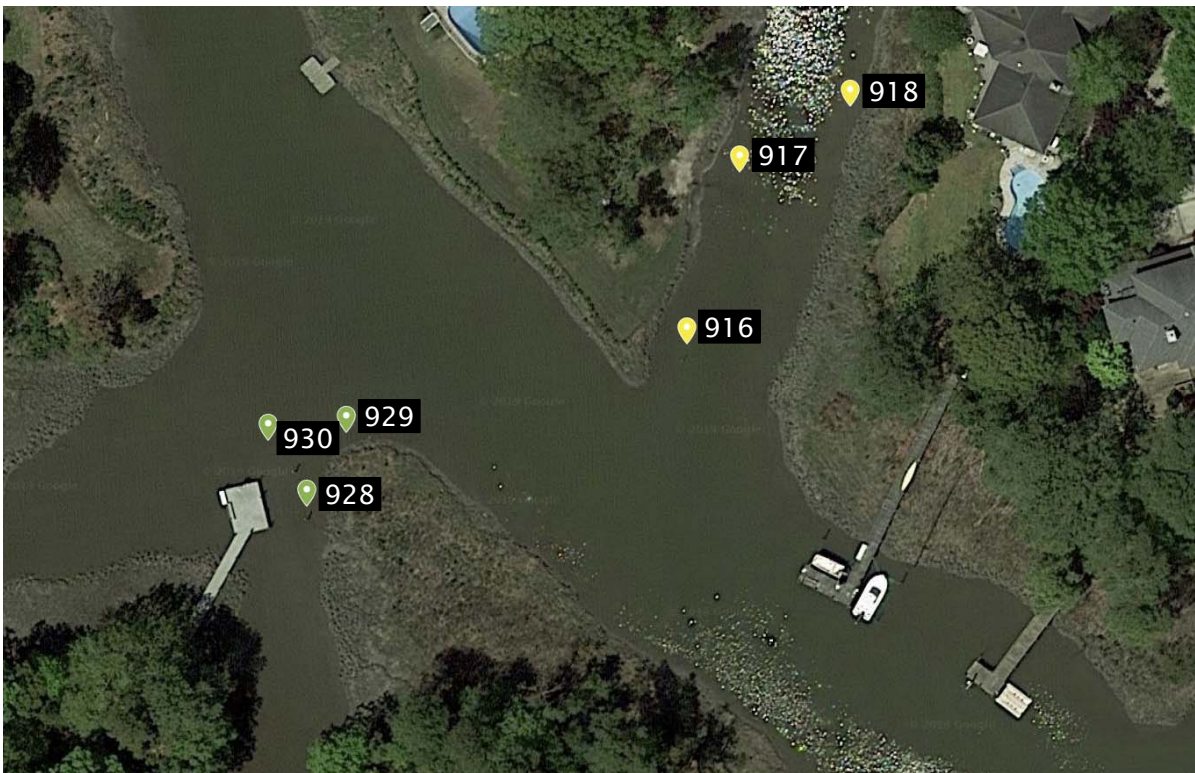


Figure 1. Map of all sampling locations within Hurds Cove, Lynnhaven River, VA. Labels in legend correspond to adjacent land parcel numbers. Each lettered sampling area is shown in greater detail within its landscape context in Figure 2.



Figures 2.1 & 2.2. Aerial photographs of sampling areas A (top) and B (bottom) showing assigned sample numbers and their location within their landscape context. All images from Google Earth accessed May 11, 2019.



Figures 2.3 & 2.4. Aerial photographs of sampling areas C (top) and D&E (bottom) showing assigned sample numbers and their location within their landscape context. All images from Google Earth accessed May 11, 2019.



Figures 2.5 & 2.6. Aerial photographs of sampling areas F (top) and G (bottom) showing assigned sample numbers and their location within their landscape context. All images from Google Earth accessed May 11, 2019.



Figure 2.7. Aerial photographs of sampling areas H showing assigned sample numbers and their location within their landscape context. All images from Google Earth accessed May 11, 2019.

Field processing

Once sediment samples were collected, the depth to which the Eckman penetrated the sediments was calculated by measuring the distance from the surface of the sample while it was still in the grab and subtracting that from the known height of the grab. The depth of all grabs was greater than the required depth of 7cm (Table 1). Any water retained in the grab was then siphoned off onto a 500- μ m mesh screen. The sample was then released from the grab into a tray and, in most cases, a photo of the sample was taken. The sample was then gently rinsed within a 500- μ m mesh bag. All material retained in the bag was fixed in Normalin in the field and returned to the laboratory. After remaining in Normalin for a minimum of 48 hours, samples were transferred to 70% ethanol to await further analyses.

Table 1. Sampling point information including location with respect to closed parcel number, designated sample number that corresponds to locations given in Fig. 2.1-2.7, approximate latitude and longitude, and the depth below the sediment surface to which the sample was collected.

Location	Sample #	Latitude	Longitude	Depth of Sample Recovered (cm)
HC-60&61	901	36.85947	-76.07286	11.43
HC-60&61	902	36.85933	-76.07266	14.61
HC-60&61	903	36.85938	-76.07250	12.70
HC-1-9,66	904	36.86436	-76.07311	15.24
HC-1-9,66	905	36.86457	-76.07333	12.70
HC-1-9,66	906	36.86471	-76.07343	15.88
HC-1-9,66	907	36.86492	-76.07346	11.43
HC-1-9,66	908	36.86466	-76.07411	17.78
HC-1-9,66	909	36.86461	-76.07438	19.05
HC-1-9,66	910	36.86475	-76.07446	13.97
HC-12	911	36.86215	-76.07517	12.70
HC-12	912	36.86204	-76.07487	8.89
HC-12	913	36.86203	-76.07457	16.51
HC-12	914	36.86187	-76.07426	10.16
HC-12	915	36.86185	-76.07391	10.16
HC-12	916	36.86082	-76.07751	12.70
HC-29&30	917	36.86103	-76.07743	14.61
HC-29&30	918	36.86111	-76.07726	14.61
HC-69	919	36.85701	-76.07828	17.15
HC-69	920	36.85722	-76.07825	17.78
HC-69	921	36.85786	-76.07832	17.78
HC-45&100	922	36.86218	-76.07980	16.51
HC-45&100	923	36.86214	-76.07987	15.24
HC-45&100	924	36.86220	-76.08011	16.51
HC-38-43	925	36.86264	-76.08002	13.34
HC-38-43	926	36.86286	-76.08017	13.97
HC-38-43	927	36.86313	-76.08042	11.43
HC-48	928	36.86062	-76.07809	14.61
HC-48	929	36.86071	-76.07803	14.61
HC-48	930	36.86070	-76.07815	13.97

Laboratory analyses

As expected, almost all samples contained large amounts of plant detritus, consistent with the proximity of surrounding vegetation and the low energy hydrodynamic regime of the sampling locations. Analysis of 100% of the material collected would have delayed completion of this project beyond its scheduled timeline. Although we had proposed to separate the samples into >1-mm and 500 μ m – 1 mm size fractions, this approach proved impractical because of the nature of the detritus contained in the samples (most stands of plant detritus >50mm in length). To provide data within the time constraints of the project, we instead analyzed 100% of the material contained within 15 of the samples and 25% of the material contained in the remaining 15 samples.

All material used for analyses was examined with the aid of a dissecting scope. All organisms found were identified to the lowest practical taxon and counted. Biomass was determined for all organisms for which the sample contained sufficient biomass to be detectable (>0.0001g). Notes were made when biomass was present but below detection limit (BDL). Wherever possible, biomass was determined as both dry weight and ash-free dry weight to the nearest 0.0001g.

Results

Polychaetes and/or ostracods were the most abundant organisms in all locations (Tables 2&3, Fig. 3). However, despite being abundant, ostracod biomass was below detection limits (<0.0001 g m⁻²) for most locations. Isopods and decapods were found at three locations, bivalves were found at two locations, and all other organisms were found at only one location. Total organism abundance ranged from 450 to 1,355 individuals m⁻².

With the exception of one sample with relatively high biomass (50.68 g AFDW m⁻²) due to the presence of a single clam (*Rangia cuneata*), biomass across all locations was low, ranging from 0.16-0.67 g AFDW m⁻² (Tables 4&5, Figs. 4&5). At five of the eight locations, all measurable biomass was contributed by polychaete worms. At the other three locations, polychaetes accounted for 45-57% of total biomass. At two locations, isopods contributed >25% biomass and, at one location, decapod crustaceans accounted for 13.7% of the total biomass.

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Table 2. Mean abundance of organisms per unit area in each sampling area. Letters correspond to sampling areas shown in Figure 1.

Location	Abundance (ind. m ⁻²)								
	Annelid	Arthropod				Mollusc		Total	
	Polychaete	Arachnid	Decapod	Isopod	Ostracod	Bivalve	Gastropod		
A	HC-1-9,66	227	0	25	31	1,046	25	0	1,355
B	HC-12	286	0	25	25	663	100	0	1,098
C	HC-60&61	456	0	0	50	163	0	25	694
D	HC-29&30	567	100	0	0	300	0	0	967
E	HC-48	350	0	0	0	100	0	0	450
F	HC-45&100	367	0	0	0	250	0	0	617
G	HC-38-43	300	0	100	0	0	0	0	400
H	HC-69	400	0	0	0	350	0	0	750

Table 3. Relative abundance of organisms as a percentage of total organisms. Letters correspond to sampling areas shown in Figure 1.

Location	Abundance (% of Total)							
	Annelid	Arthropod				Mollusc		Total
	Polychaete	Arachnid	Decapod	Isopod	Ostracod	Bivalve	Gastropod	
A	HC-1-9,66	17%	0%	2%	2%	77%	2%	0%
B	HC-12	26%	0%	2%	2%	60%	9%	0%
C	HC-60&61	66%	0%	0%	7%	23%	0%	4%
D	HC-29&30	59%	10%	0%	0%	31%	0%	0%
E	HC-48	78%	0%	0%	0%	22%	0%	0%
F	HC-45&100	59%	0%	0%	0%	41%	0%	0%
G	HC-38-43	75%	0%	25%	0%	0%	0%	0%
H	HC-69	53%	0%	0%	0%	47%	0%	0%

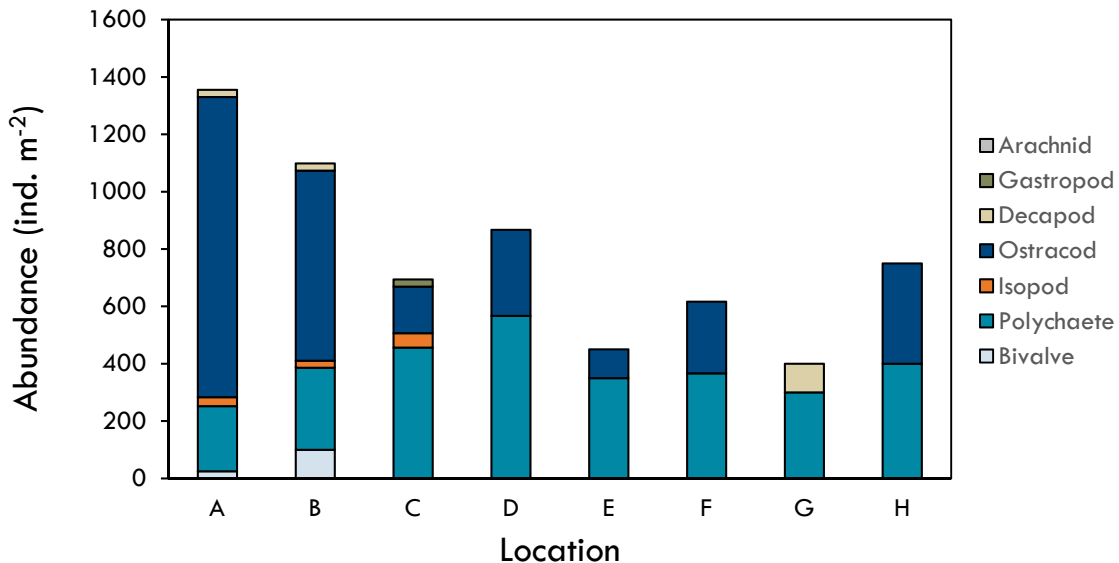


Figure 3. Mean abundance of organisms per unit area. Letters designating locations correspond to sampling areas shown in Figure 1.

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Table 4. Mean biomass of organisms per unit area in each sampling area. Letters correspond to sampling areas shown in Figure 1. BDL = below detection limit.

Location	Biomass (g AFDW m ⁻²)									
	Annelid		Arthropod				Mollusc		Total	
	Oligochaete	Polychaete	Arachnid	Decapod	Isopod	Ostracod	Bivalve	Gastropod		
A	HC-1-9,66	0.0000	0.1133	0.0000	0.0275	0.0519	0.0075	BDL	0.0000	0.2001
B	HC-12	0.0000	0.1271	0.0000	BDL	0.0950	0.0350	50.6800	0.0000	50.9371
C	HC-60&61	0.0000	0.1275	0.0000	0.0000	0.1550	BDL	0.0000	BDL	0.2825
D	HC-29&30	0.0000	0.2900	BDL	0.0000	0.0000	BDL	0.0000	0.0000	0.2900
E	HC-48	0.0000	0.6650	0.0000	0.0000	0.0000	BDL	0.0000	0.0000	0.6650
F	HC-45&100	0.0000	0.4133	0.0000	0.0000	0.0000	BDL	0.0000	0.0000	0.4133
G	HC-38-43	BDL	0.2250	0.0000	BDL	0.0000	0.0000	0.0000	0.0000	0.2250
H	HC-69	0.0000	0.1550	0.0000	0.0000	0.0000	BDL	0.0000	0.0000	0.1550

Table 5. Relative biomass of organisms as a percentage of total organisms. Letters correspond to sampling areas shown in Figure 1.

Location	Biomass (% of Total)								
	Annelid		Arthropod				Mollusc		Total
	Oligochaete	Polychaete	Arachnid	Decapod	Isopod	Ostracod	Bivalve	Gastropod	
A	HC-1-9,66	0.0%	56.6%	0.0%	13.7%	25.9%	3.7%	BDL	0.0%
B	HC-12	0.0%	0.2%	0.0%	BDL	0.2%	0.1%	99.5%	0.0%
C	HC-60&61	0.0%	45.1%	0.0%	0.0%	54.9%	BDL	0.0%	BDL
D	HC-29&30	0.0%	100.0%	BDL	0.0%	0.0%	BDL	0.0%	0.0%
E	HC-48	0.0%	100.0%	0.0%	0.0%	0.0%	BDL	0.0%	0.0%
F	HC-45&100	0.0%	100.0%	0.0%	0.0%	0.0%	BDL	0.0%	0.0%
G	HC-38-43	BDL	100.0%	0.0%	BDL	0.0%	0.0%	0.0%	0.0%
H	HC-69	0.0%	100.0%	0.0%	0.0%	0.0%	BDL	0.0%	0.0%

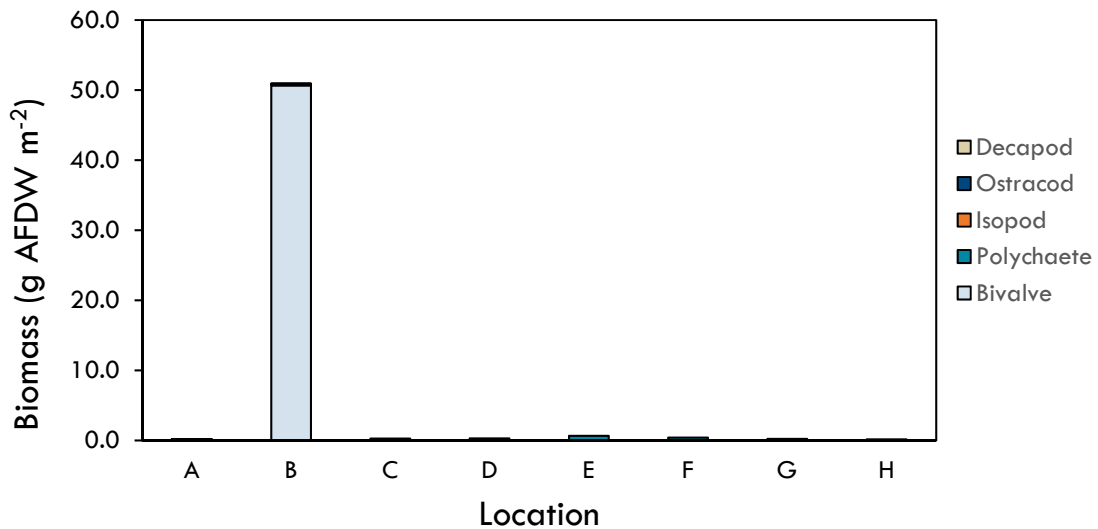


Figure 4. Mean biomass of organisms per unit area. Letters designating locations correspond to sampling areas shown in Figure 1.

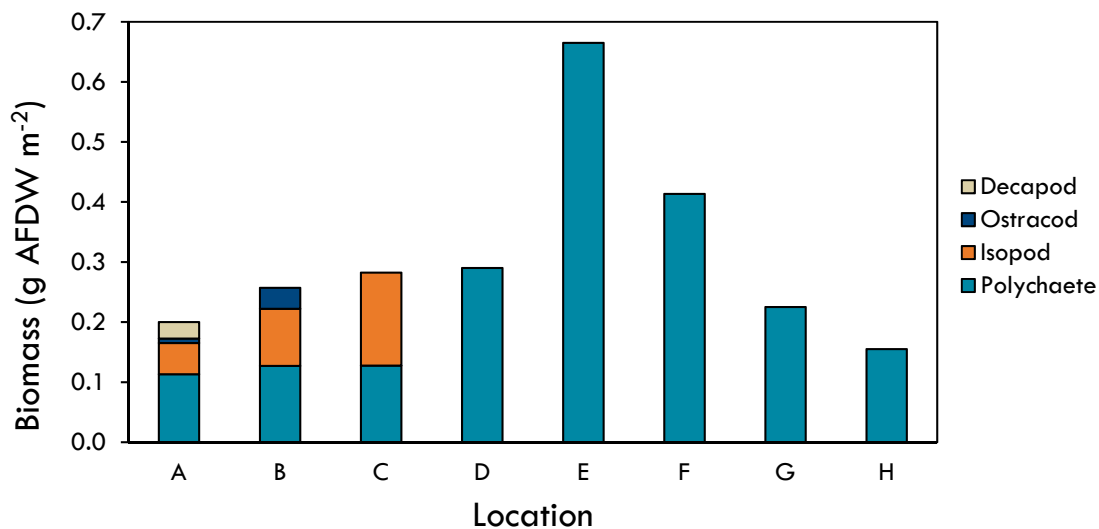


Figure 5. Mean biomass of organisms per unit area after excluding biomass of single *Rangia cuneata* found in sample #915. Letters designating locations correspond to sampling areas shown in Figure 1.

Appendix

Table 6. Abundance data for all samples.

Sample #	Abundance (ind. m ⁻²)											
	Annelid					Arthropod				Mollusc		
	Polychaete					Arachnid	Decapod	Isopod	Ostracod	Bivalve		Gastropod
	<i>Alitta succinea</i>	<i>Heteromastus filiformis</i>	<i>Hobsonia florida</i>	<i>Laeonereis culveri</i>	<i>Leitoscoloplos sp.</i>	Mite	<i>Callinectes sapidus</i>	<i>Cyathura polita</i>	Ostracod A	<i>Arcuatula papyria</i>	<i>Gemma gemma</i>	<i>Rangia cuneata</i>
901	0	0	0	325	0	0	0	0	0	0	0	0
902	0	0	0	750	0	0	0	0	275	0	0	0
903	25	0	0	725	0	0	0	50	50	0	0	25
904	0	0	0	0	0	0	0	0	2,625	0	25	0
905	25	0	0	600	0	0	25	25	875	0	0	0
906	0	0	0	200	0	0	0	25	1,050	25	25	0
907	0	0	0	450	0	0	0	50	300	0	0	0
908	25	50	0	450	0	0	0	0	650	0	0	0
909	0	0	0	25	0	0	0	0	1,600	0	0	0
910	0	25	0	625	25	0	0	25	225	0	0	0
911	25	0	0	625	0	0	25	0	250	0	0	0
912	50	0	0	325	0	0	0	0	950	0	0	0
913	25	0	0	525	0	0	0	25	50	0	0	0
914	0	0	0	425	0	0	0	25	375	0	0	0
915	0	0	0	0	0	0	0	0	2,300	0	0	100
916	0	0	0	0	0	0	0	0	50	0	0	0
917	100	0	0	400	0	100	0	0	300	0	0	0
918	0	0	0	1,200	0	0	0	0	300	0	0	0
919	0	0	0	300	0	0	0	0	0	0	0	0
920	0	0	0	0	0	0	0	0	500	0	0	0
921	0	0	0	500	0	0	0	0	200	0	0	0
922	0	0	0	200	0	0	0	0	300	0	0	0
923	0	0	0	300	0	0	0	0	0	0	0	0
924	0	0	0	600	0	0	0	0	200	0	0	0
925	0	0	0	400	0	0	0	0	0	0	0	0
926	0	0	0	200	0	0	100	0	0	0	0	0
927	0	0	0	0	0	0	0	0	0	0	0	0
928	0	0	0	400	0	0	0	0	100	0	0	0
929	0	0	0	300	0	0	0	0	0	0	0	0
930	0	0	0	0	0	0	0	0	0	0	0	0

Table 7. Biomass data for all samples.

Sample #	Biomass (g AFDW m ⁻²)														
	Oligochaete	Annelid						Arthropod				Mollusc			
		Polychaete						Arachnid	Decapod	Isopod	Ostracod	Bivalve			Gastropod
		Oligochaete fragment	<i>Alitta succinea</i>	<i>Heteromastus filiformis</i>	<i>Hobsonia florida</i>	<i>Laeonereis culveri</i>	<i>Leitoscoloplos sp.</i>					Polychaete fragment	Mite	<i>Callinectes sapidus</i>	
901	0	0	0	0	0.0700	0	0	0	0	0	0	0	0	0	0
902	0	0	0	0	0.2000	0	0	0	0	0	BDL	0	0	0	0
903	0	0.1025	0	0	0.1375	0	0	0	0	0.1550	BDL	0	0	0	BDL
904	0	0	0	0	0	0	0	0	0	0	0.0150	0	BDL	0	0
905	0	0.0900	0	0	0.1475	0	0	0	0.0275	0.0175	BDL	0	0	0	0
906	0	0	0	0	0.0225	0	0	0	0	0.0475	BDL	BDL	BDL	0	0
907	0	0	0	0	0.1225	0	0	0	0	0.0050	BDL	0	0	0	0
908	0	0.1900	0.0025	0	0.2700	0	0	0	0	0	BDL	0	0	0	0
909	0	0	0	0	BDL	0	0	0	0	0	0.0075	0	0	0	0
910	0	0	0.0025	0	0.2650	0.0200	0	0	0	0.1375	BDL	0	0	0	0
911	0	0.1225	0	0	0.3000	0	0	0	BDL	0	BDL	0	0	0	0
912	0	0	0	0	0.0325	0	0	0	0	0	0.0100	0	0	0	0
913	0	0.0550	0	0	0.1250	0	0	0	0	0.0925	BDL	0	0	0	0
914	0	0	0	0	0.1275	0	0	0	0	0.0975	BDL	0	0	0	0
915	0	0	0	0	0	0	0	0	0	0	0.0600	0	0	50.6800	0
916	0	0	0	0	0	0	0	0	0	0	BDL	0	0	0	0
917	0	0.3200	0	0	0.1700	0	0	BDL	0	0	BDL	0	0	0	0
918	0	0	0	0	0.3800	0	0	0	0	0	BDL	0	0	0	0
919	0	0	0	0	0.1000	0	0	0	0	0	0	0	0	0	0
920	0	0	0	0	BDL	0	0	0	0	0	BDL	0	0	0	0
921	0	0	0	0	0.2100	0	0	0	0	0	BDL	0	0	0	0
922	0	0	0	0	0.1900	0	BDL	0	0	0	BDL	0	0	0	0
923	0	0	0	0	0.3100	0	0	0	0	0	0	0	0	0	0
924	0	0	0	0	0.7400	0	0	0	0	0	BDL	0	0	0	0
925	0	0	0	0	0.2500	0	0	0	0	0	0	0	0	0	0
926	BDL	0	0	0	0.2000	0	0	0	BDL	0	0	0	0	0	0
927	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
928	0	0	0	0	1.0100	0	0	0	0	0	BDL	0	0	0	0
929	0	0	0	0	0.3200	0	0	0	0	0	0	0	0	0	0
930	0	0	0	BDL	0	0	0	0	0	0	0	0	0	0	0