

Role of habitat and predators in maintaining functional diversity of estuarine bivalves

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Table S1. Results of multiple comparisons for bivalve diversity in different habitats. Bonferroni-adjusted p values from bootstrap hypothesis tests are given for Gini-Simpson diversity index and functional diversity (Gini-Simpson index of functional groups) in different habitats in lower Chesapeake Bay. Only contrasts significant at $\alpha = 0.05$ are shown.

Contrast	Diversity		Functional Diversity	
	Cohen's d	p	Cohen's d	p
<i>Seagrass v. Detrital Mud</i>	0.11	0.01	0.16	0.0005
<i>Seagrass v. Shell Hash</i>	0.10	0.001	0.11	0.0005
<i>Seagrass v. Oyster Shell</i>	0.07	0.04	0.10	0.006

Table S2. Gini-Simpson diversity index generalized linear model results. Model was fit with family = Gaussian, link = identity. Model based on 180 observations. McFadden's pseudo $R^2 = 0.28$. Null deviance 12.52 on 179 df. Residual deviance 8.99 on 157 df. Significant variables at $\alpha = 0.05$ are bolded.

	Estimate	Std. Error	t value	p
<i>Intercept</i>	0.163	0.107	1.515	0.132
<i>Year 2013</i>	-0.079	0.042	-1.860	0.065
<i>Season Spring</i>	0.076	0.058	1.321	0.188
<i>Season Summer</i>	-0.016	0.061	-0.257	0.797
<i>Subestuary Mobjack</i>	-0.046	0.107	-0.430	0.668
<i>Subestuary York</i>	-0.117	0.111	-1.056	0.292
<i>Coarse sand</i>	0.046	0.098	0.471	0.638
<i>Oyster shell</i>	0.094	0.084	1.115	0.267
<i>Seagrass</i>	0.372	0.091	4.073	< 0.001
<i>Shell hash</i>	0.079	0.076	1.040	0.300
<i>Habitat volume (L)</i>	0.033	0.024	1.349	0.180
<i>Fish density (m⁻²)</i>	0.090	0.068	1.326	0.187
<i>Crab density (m⁻²)</i>	-0.005	0.082	-0.065	0.948
<i>Ray pit density (m⁻²)</i>	0.768	0.294	2.615	0.010
<i>Lynnhaven Site 1</i>	0.037	0.101	0.369	0.712
<i>Lynnhaven Site 2</i>	0.105	0.098	1.070	0.286
<i>Lynnhaven Site 3</i>	-0.065	0.093	-0.695	0.488
<i>Mobjack Site 1</i>	-0.006	0.091	-0.067	0.946
<i>Mobjack Site 2</i>	-0.061	0.091	-0.669	0.504
<i>Mobjack Site 3</i>	-0.076	0.088	-0.867	0.387
<i>York Site 1</i>	-0.104	0.116	-0.897	0.371
<i>York Site 2</i>	0.186	0.107	1.737	0.084
<i>York Site 3</i>	0.294	0.111	2.660	0.009

Table S3. Functional diversity generalized linear model results. Model was fit with family = Gaussian, link = identity. Model based on 180 observations. McFadden's pseudo R² = 0.27. Null deviance 10.31 on 179 df. Residual deviance 7.55 on 157 df. Significant variables at $\alpha = 0.05$ are bolded.

	<i>Estimate</i>	<i>Std. Error</i>	<i>t value</i>	<i>p</i>
<i>Intercept</i>	0.154	0.098	1.559	0.121
<i>Year 2013</i>	-0.018	0.039	-0.469	0.640
<i>Season Spring</i>	0.014	0.053	0.258	0.797
<i>Season Summer</i>	-0.086	0.056	-1.537	0.126
<i>Subestuary Mobjack</i>	-0.029	0.098	-0.296	0.768
<i>Subestuary York</i>	-0.096	0.102	-0.942	0.347
<i>Coarse sand</i>	0.046	0.090	0.515	0.608
<i>Oyster shell</i>	0.019	0.077	0.246	0.806
<i>Seagrass</i>	0.341	0.084	4.071	< 0.001
<i>Shell hash</i>	0.055	0.070	0.785	0.434
<i>Habitat volume (L)</i>	0.017	0.022	0.744	0.458
<i>Fish density (m⁻²)</i>	0.085	0.062	1.373	0.172
<i>Crab density (m⁻²)</i>	0.015	0.075	0.194	0.847
<i>Ray pit density (m⁻²)</i>	0.842	0.269	3.130	0.002
<i>Lynnhaven Site 1</i>	0.089	0.092	0.965	0.336
<i>Lynnhaven Site 2</i>	0.108	0.090	1.210	0.228
<i>Lynnhaven Site 3</i>	-0.032	0.085	-0.377	0.707
<i>Mobjack Site 1</i>	-0.013	0.083	-0.150	0.881
<i>Mobjack Site 2</i>	-0.081	0.083	-0.971	0.333
<i>Mobjack Site 3</i>	-0.081	0.081	-1.000	0.319
<i>York Site 1</i>	-0.038	0.106	-0.353	0.725
<i>York Site 2</i>	0.095	0.098	0.970	0.334
<i>York Site 3</i>	0.165	0.101	1.628	0.106

Table S4. Rarefied species richness generalized linear model results. Model was fit with family = Gaussian, link = identity. Model based on 180 observations. McFadden's pseudo R² = 0.24. Null deviance 2847.7 on 179 df. Residual deviance 2151.4 on 157 df. Significant variables at $\alpha = 0.05$ are bolded.

	<i>Estimate</i>	<i>Std. Error</i>	<i>t value</i>	<i>p</i>
<i>Intercept</i>	3.315	1.662	1.995	0.048
<i>Year 2013</i>	0.404	0.655	0.617	0.538
<i>Season Spring</i>	1.522	0.889	1.711	0.089
<i>Season Summer</i>	0.586	0.940	0.623	0.534
<i>Subestuary Mobjack</i>	-2.213	1.647	-1.343	0.181
<i>Subestuary York</i>	-2.137	1.713	-1.247	0.214
<i>Coarse sand</i>	2.921	1.512	1.932	0.055
<i>Oyster shell</i>	4.288	1.306	3.283	0.001
<i>Seagrass</i>	6.883	1.413	4.870	< 0.001
<i>Shell hash</i>	3.570	1.180	3.026	0.003
<i>Habitat volume (L)</i>	0.765	0.375	2.042	0.043
<i>Fish density (m⁻²)</i>	0.962	1.047	0.919	0.359
<i>Crab density (m⁻²)</i>	-1.870	1.265	-1.479	0.141
<i>Ray pit density (m⁻²)</i>	-3.944	4.543	-0.868	0.387
<i>Lynnhaven Site 1</i>	-0.436	1.555	-0.280	0.780
<i>Lynnhaven Site 2</i>	-1.725	1.512	-1.141	0.256
<i>Lynnhaven Site 3</i>	0.529	1.442	0.367	0.715
<i>Mobjack Site 1</i>	0.362	1.405	0.257	0.797
<i>Mobjack Site 2</i>	-0.116	1.404	-0.082	0.935
<i>Mobjack Site 3</i>	0.313	1.361	0.230	0.818
<i>York Site 1</i>	1.695	1.794	0.945	0.346
<i>York Site 2</i>	6.148	1.657	3.710	< 0.001
<i>York Site 3</i>	5.426	1.712	3.169	0.002

Table S5. Functional richness generalized linear model results. Model was fit with family = Gaussian, link = identity. Model based on 180 observations. McFadden's pseudo $R^2 = 0.21$. Null deviance 190.20 on 179 df. Residual deviance 149.58 on 157 df. Significant variables at $\alpha = 0.05$ are bolded.

	<i>Estimate</i>	<i>Std. Error</i>	<i>t value</i>	<i>p</i>
Intercept	1.165	0.438	2.658	0.009
<i>Year 2013</i>	0.083	0.173	0.482	0.631
<i>Season Spring</i>	0.397	0.234	1.695	0.092
<i>Season Summer</i>	0.059	0.248	0.241	0.810
<i>Subestuary Mobjack</i>	-0.368	0.434	-0.846	0.399
<i>Subestuary York</i>	-0.540	0.452	-1.194	0.234
<i>Coarse sand</i>	0.285	0.399	0.715	0.476
<i>Oyster shell</i>	0.228	0.344	0.661	0.510
<i>Seagrass</i>	1.469	0.373	3.943	< 0.001
<i>Shell hash</i>	0.387	0.311	1.242	0.216
Habitat volume (L)	0.213	0.099	2.151	0.033
<i>Fish density (m⁻²)</i>	0.105	0.276	0.382	0.703
<i>Crab density (m⁻²)</i>	-0.199	0.333	-0.598	0.551
<i>Ray pit density (m⁻²)</i>	1.455	1.198	1.215	0.227
<i>Lynnhaven Site 1</i>	0.238	0.410	0.580	0.562
<i>Lynnhaven Site 2</i>	0.096	0.399	0.240	0.810
<i>Lynnhaven Site 3</i>	0.014	0.380	0.037	0.971
<i>Mobjack Site 1</i>	-0.016	0.371	-0.044	0.965
<i>Mobjack Site 2</i>	-0.289	0.370	-0.781	0.436
<i>Mobjack Site 3</i>	-0.187	0.359	-0.520	0.604
<i>York Site 1</i>	-0.076	0.473	-0.160	0.873
<i>York Site 2</i>	0.790	0.437	1.809	0.072
<i>York Site 3</i>	1.238	0.451	2.742	0.007

Table S6. Deposit-feeding (DF) bivalve abundance generalized linear model results. Model was fit with family = Quasi-Poisson, link = log. Model based on 180 observations. McFadden's pseudo $R^2 = 0.79$. Null deviance 5093.3 on 179 df. Residual deviance 1068.3 on 157 df. Significant variables at $\alpha = 0.05$ are bolded. Samples were collected in a 0.11 m² area.

	<i>Estimate</i>	<i>Std. Error</i>	<i>t value</i>	<i>p</i>
<i>Intercept</i>	-0.513	1.107	-0.464	0.644
Year 2013	0.741	0.241	3.079	0.002
Season Spring	1.223	0.444	2.755	0.007
<i>Season Summer</i>	0.247	0.510	0.484	0.629
<i>Subestuary Mobjack</i>	-0.731	1.497	-0.488	0.626
<i>Subestuary York</i>	-1.112	1.559	-0.713	0.477
<i>Coarse sand</i>	-0.759	0.436	-1.741	0.084
Oyster shell	-1.032	0.399	-2.586	0.011
<i>Seagrass</i>	1.024	1.011	1.012	0.313
<i>Shell hash</i>	-0.306	0.309	-0.989	0.324
<i>Habitat volume (L)</i>	-0.199	0.146	-1.364	0.175
<i>Fish density (m⁻²)</i>	0.428	0.306	1.396	0.165
Crab density (m⁻²)	-2.090	0.604	-3.463	0.001
Ray pit density (m⁻²)	-5.019	2.008	-2.500	0.013
<i>Lynnhaven Site 1</i>	1.662	1.192	1.395	0.165
<i>Lynnhaven Site 2</i>	0.392	1.233	0.318	0.751
<i>Lynnhaven Site 3</i>	1.083	1.130	0.959	0.339
<i>Mobjack Site 1</i>	0.292	0.924	0.316	0.752
<i>Mobjack Site 2</i>	0.644	0.810	0.975	0.428
<i>Mobjack Site 3</i>	0.248	0.890	0.279	0.781
York Site 1	5.299	1.211	4.374	< 0.001
York Site 2	4.592	1.205	3.810	< 0.001
York Site 3	3.971	1.214	3.271	0.001

Table S7. Deep-burrowing and suspension-feeding (DBSF) bivalve abundance generalized linear model results. Model was fit with family = Quasi-Poisson, link = log. Model based on 180 observations. McFadden's pseudo $R^2 = 0.19$. Null deviance 909.23 on 179 df. Residual deviance 734.06 on 157 df. Significant variables at $\alpha = 0.05$ are bolded. Samples were collected in a 0.11 m^2 area.

	<i>Estimate</i>	<i>Std. Error</i>	<i>t value</i>	<i>p</i>
<i>Intercept</i>	0.588	0.622	0.945	0.346
<i>Year 2013</i>	-0.184	0.242	-0.758	0.449
<i>Season Spring</i>	0.227	0.315	0.721	0.472
<i>Season Summer</i>	-0.096	0.358	-0.267	0.790
<i>Subestuary Mobjack</i>	-0.410	0.579	-0.709	0.479
<i>Subestuary York</i>	0.285	0.537	0.530	0.597
<i>Coarse sand</i>	0.190	0.613	0.309	0.757
<i>Oyster shell</i>	0.341	0.540	0.631	0.529
<i>Seagrass</i>	0.834	0.570	1.463	0.146
<i>Shell hash</i>	0.931	0.473	1.968	0.051
<i>Habitat volume (L)</i>	0.282	0.125	2.260	0.025
<i>Fish density (m^{-2})</i>	-0.083	0.387	-0.215	0.830
<i>Crab density (m^{-2})</i>	-0.583	0.545	-1.069	0.287
<i>Ray pit density (m^{-2})</i>	-0.962	1.863	-0.516	0.606
<i>Lynnhaven Site 1</i>	-0.170	0.541	-0.314	0.754
<i>Lynnhaven Site 2</i>	0.141	0.471	0.300	0.764
<i>Lynnhaven Site 3</i>	-0.437	0.536	-0.814	0.417
<i>Mobjack Site 1</i>	0.153	0.509	0.301	0.764
<i>Mobjack Site 2</i>	-0.265	0.562	-0.472	0.638
<i>Mobjack Site 3</i>	-0.298	0.548	-0.542	0.588
<i>York Site 1</i>	-1.559	0.728	-2.143	0.034
<i>York Site 2</i>	-0.072	0.510	-0.141	0.888
<i>York Site 3</i>	-1.491	0.752	-1.983	0.049

Table S8. Thin-shelled and surface-dwelling (TSSD) bivalve abundance generalized linear model results. Model was fit with family = Quasi-Poisson, link = log. Model based on 180 observations. McFadden's pseudo $R^2 = 0.47$. Null deviance 1735.26 on 179 df. Residual deviance 914.26 on 157 df. Significant variables at $\alpha = 0.05$ are bolded. Samples were collected in a 0.11 m^2 area.

	<i>Estimate</i>	<i>Std. Error</i>	<i>t value</i>	<i>p</i>
<i>Intercept</i>	1.319	0.972	1.357	0.177
<i>Year 2013</i>	0.130	0.339	0.384	0.702
<i>Season Spring</i>	0.023	0.494	0.047	0.963
<i>Season Summer</i>	1.192	0.583	2.046	0.042
<i>Subestuary Mobjack</i>	-1.536	0.827	-1.857	0.065
<i>Subestuary York</i>	-2.014	0.981	-2.052	0.042
<i>Coarse sand</i>	0.348	0.946	0.367	0.714
<i>Oyster shell</i>	0.653	0.853	0.766	0.445
<i>Seagrass</i>	0.678	0.822	0.825	0.411
<i>Shell hash</i>	0.183	0.794	0.230	0.818
<i>Habitat volume (L)</i>	0.435	0.221	1.966	0.051
<i>Fish density (m^{-2})</i>	-1.021	0.696	-1.467	0.145
<i>Crab density (m^{-2})</i>	-1.898	1.022	-1.857	0.065
<i>Ray pit density (m^{-2})</i>	-5.002	3.098	-1.614	0.108
<i>Lynnhaven Site 1</i>	-2.561	0.984	-2.602	0.010
<i>Lynnhaven Site 2</i>	-2.733	0.986	-2.771	0.006
<i>Lynnhaven Site 3</i>	-0.229	0.629	-0.364	0.717
<i>Mobjack Site 1</i>	1.189	0.646	1.840	0.068
<i>Mobjack Site 2</i>	1.194	0.613	1.947	0.053
<i>Mobjack Site 3</i>	1.459	0.544	2.684	0.008
<i>York Site 1</i>	-1.192	1.597	-0.747	0.456
<i>York Site 2</i>	-2.941	3.139	-0.937	0.350
<i>York Site 3</i>	-0.419	1.320	-0.317	0.752

Table S9. Armored (ARM) bivalve abundance generalized linear model results. Model was fit with family = Quasi-Poisson, link = log. Model based on 180 observations. McFadden's pseudo R² = 0.36. Null deviance 447.09 on 179 df. Residual deviance 286.85 on 157 df. Significant variables at $\alpha = 0.05$ are bolded. Samples were collected in a 0.11 m² area.

	<i>Estimate</i>	<i>Std. Error</i>	<i>t value</i>	<i>p</i>
Intercept	-2.345	0.951	-2.467	0.015
Year 2013	0.860	0.308	2.798	0.006
<i>Season Spring</i>	-0.561	0.385	-1.457	0.147
<i>Season Summer</i>	-0.772	0.424	-1.823	0.070
<i>Subestuary Mobjack</i>	0.766	0.845	0.907	0.366
<i>Subestuary York</i>	1.005	0.855	1.175	0.242
<i>Coarse sand</i>	0.698	0.835	0.835	0.405
Oyster shell	1.988	0.650	3.059	0.003
Seagrass	1.569	0.753	2.085	0.039
<i>Shell hash</i>	1.034	0.644	1.605	0.111
Habitat volume (L)	0.400	0.153	2.613	0.010
<i>Fish density (m⁻²)</i>	0.593	0.413	1.436	0.153
<i>Crab density (m⁻²)</i>	0.102	0.504	0.203	0.840
<i>Ray pit density (m⁻²)</i>	3.424	2.170	1.578	0.117
<i>Lynnhaven Site 1</i>	0.170	0.794	0.213	0.831
<i>Lynnhaven Site 2</i>	-0.401	0.920	-0.436	0.663
<i>Lynnhaven Site 3</i>	0.438	0.761	0.576	0.566
<i>Mobjack Site 1</i>	-0.342	0.598	-0.571	0.569
<i>Mobjack Site 2</i>	-1.513	0.870	-1.739	0.084
<i>Mobjack Site 3</i>	0.378	0.521	0.726	0.469
York Site 1	-2.986	1.202	-2.484	0.014
<i>York Site 2</i>	0.641	0.628	1.020	0.309
<i>York Site 3</i>	-0.311	0.805	-0.386	0.700

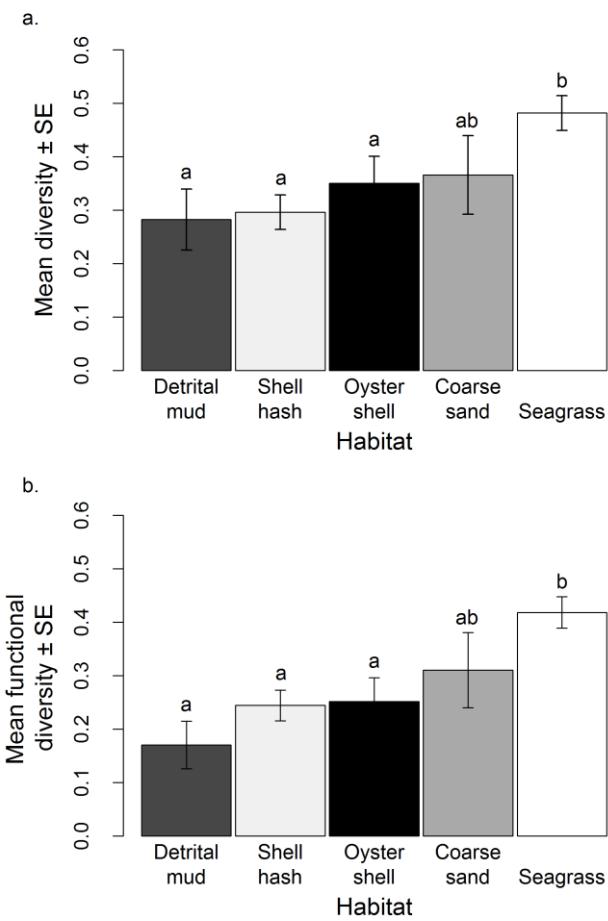


Figure S1. Bivalve diversity in different habitats. Means \pm 1 standard error (SE) for a) Gini-Simpson diversity index and b) functional diversity (Gini-Simpson diversity index of functional groups) in different habitat types in lower Chesapeake Bay. Samples were collected in detrital mud ($n = 21$), shell hash ($n = 61$), oyster shell ($n = 30$), coarse sand ($n = 13$), and seagrass ($n = 55$). Letters denote significant differences at $\alpha = 0.05$.