Data Final

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Introduction

Oysters are an important member of their ecosystems, but their population has been in major decline. Oyster reefs are sites that provide habitats for many organisms, where important nutrient cycles are managed, and many more beneficial processes occur.

Sadly, a catastrophic decline in New Hampshire oyster population has been recorded, with only 10% of the population being what it was in the 1980's. Decline has been attributed to major diseases, human harvest and anthropogenic impacts, decline in oyster shell substrate for larval settling, and low recruitment.

There have been restorative efforts in the local Great Bay Estuary (GBE) of New Hampshire. Oyster spat has been distributed in restoration sites in the GBE, with different sites having varying degrees of success. Restorative success depends on recruitment in wild populations of oysters, which can depend on many factors. The ocean absorbs CO_2 from the air. When air CO_2 concentrations increase, it causes the pH of the ocean to go down into a more acidic environment called ocean acidification which can affect shell growth in early larval stages.

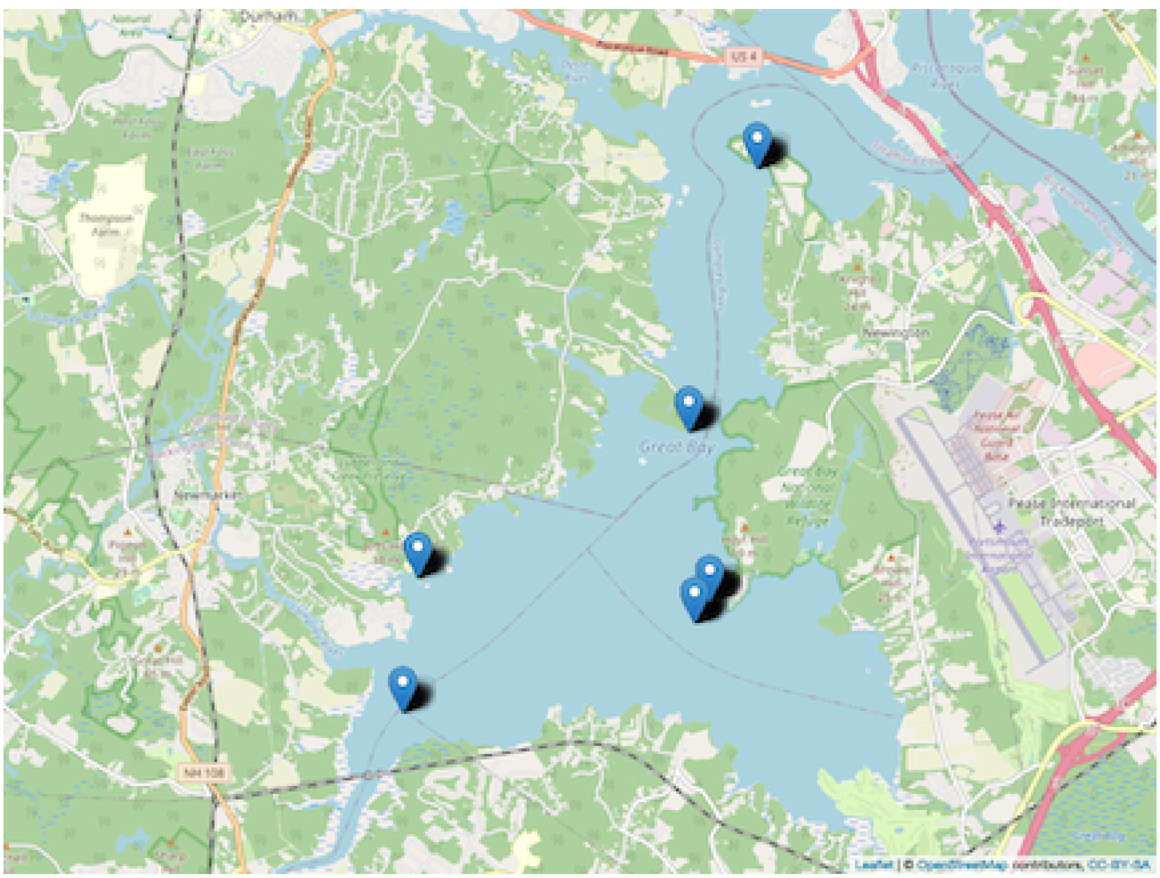

Figure 1: Six sites marked with blue markers in the Great Bay Estuary where oyster data was collected. For a more detailed description of data collection, see *Stasse et al.*

Salinity stuff, temperature stuff.

By finding where oyster larvae are most abundant throughout the GBE, this study aims to find the best environmental conditions for oyster reproduction. This data will aid future restoration efforts by showing what factors to focus on for optimal restoration results.

Methods

All data was collected at the Great Bay Estuary in New Hampshire. Six sites in total were used in the study. Woodman's Point (WP), Nannie Island (NI), the Lamprey River (LR), and Squamscott River (SR) were collected in the 2018 and 2019 seasons. In the 2020 season WP and NI were used again, while Adams Point (AP) and an oyster farm (OF) were added. Collection of samples from the GBE and counting of D-hinge and Veliger larvae was completed by *Stasse et al.* (All techniques can be found in *insert here*). Physiochemical data was collected by the Oceanic and Atmospheric Administration's (NOAA) National Estuarine Research Reserve System (NERRS) data buoy for each sampling day.

An analysis of variance (ANOVA) test was performed to test for differences of D-hinge and veliger counts among years. A Tukey's honnestly significant difference (HSD) was performed *post-hoc* among sampling years for D-hinge annd veliger counts. Regression models were performed for pH, temperature, and salinity as independent variables, and D-hinge and veliger counts as dependent variables using log(count) adjusted data to meet normalcy standards. Stats were all performed using R *stuff here*.

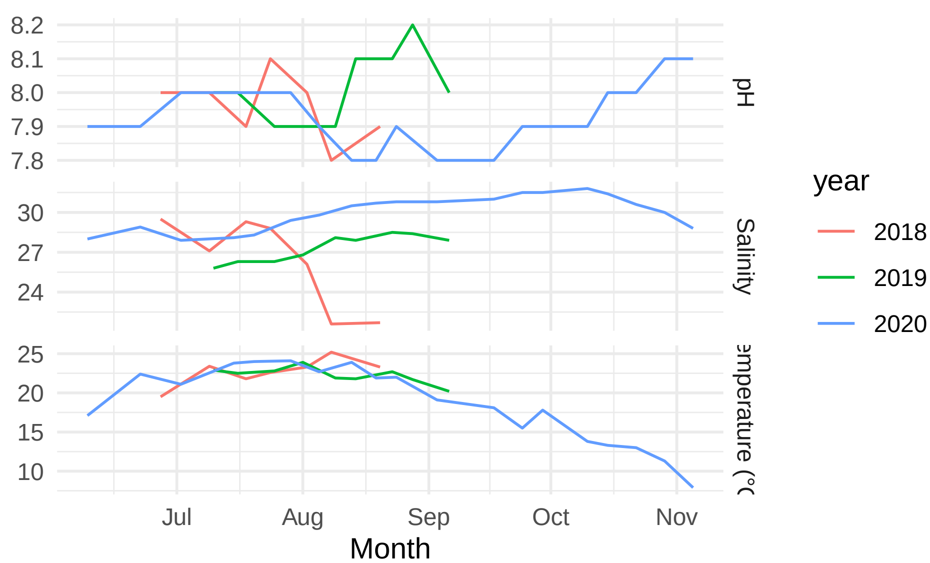

Figure 2: Physiochemical data from 2018, 2019, and 2020. pH (Top), salinity (Middle), and Temperature (Bottom) are included.

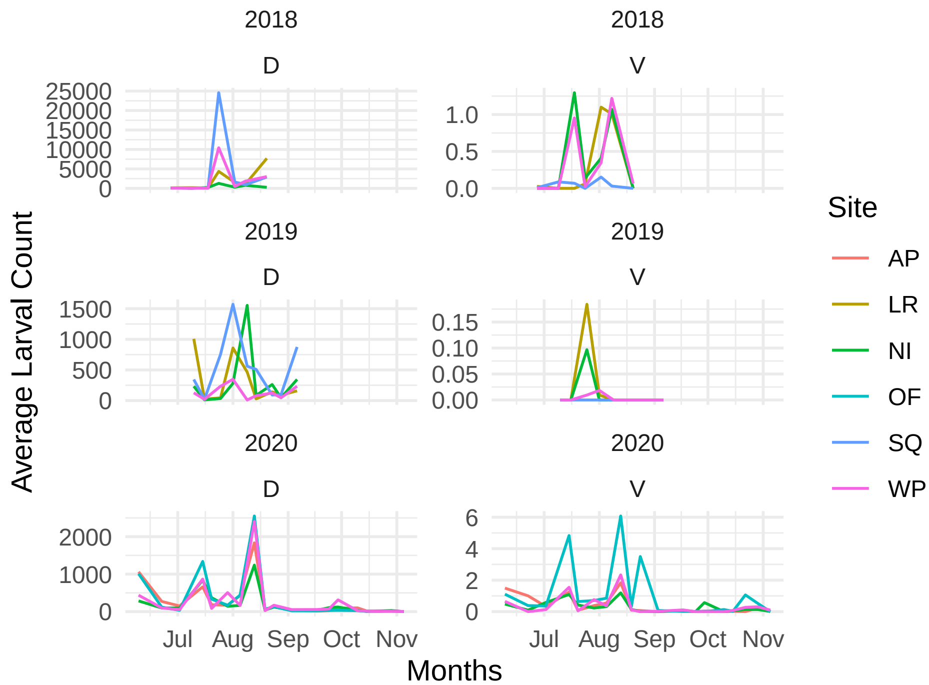

Figure 3: D-hinge and veliger oyster larval counts by site. 2018 (Top), 2019 (Middle), 2020 (Bottom) are included.

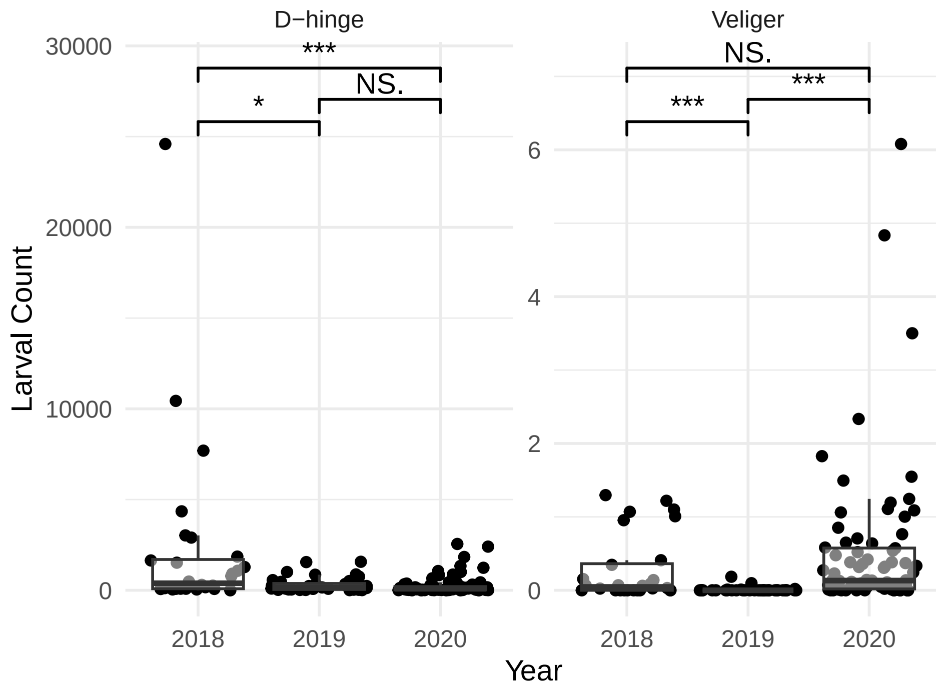

Figure 4: GBE larval counts of D-hinge (Left) and veliger (Right) collected in 2018, 2019, and 2020. Black dots are counts during individual collection days. Midlines within each boxplot represent median values, and the boxes represent the first (Bottom) and third (Top) quartile ranges (25th and 75th percentiles)

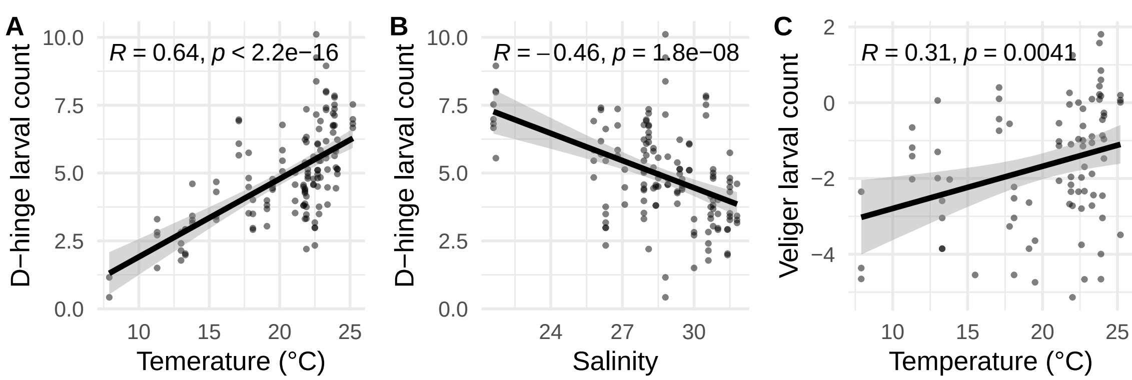

Figure 5: (A) Regression model of D-hinge oyster larvae and temperature (°C), (B) D-hinge oyster larvae and salinity, and (C) veliger oyster larvae and temperature with corresponding trendlines and 95% confdence intervals shown in gray

Results

In 2018, mean abundance was 2293 (SE = 945) D-hinge larvae m^{-3}, and 0.29 (SE = 0.085) veliger larvae m^{-3}. In 2019, mean abundance was 325 (SE = 68) D-hinge larvae m^{-3}, and 0.0088 (SE = 0.0057) veliger larvae m^{-3}. In 2020, mean abundance was 273 (SE = 58) D-hinge larvae m^{-3}, and 0.53 (SE = 0.12, Fig. 3) veliger larvae m^{-3}. Analysis of variance showed significant differences in the count of both D-hinge and veliger larvae between years ($F = 8$, $p < 0.001$, Fig. 4). It was found that temperature was positively associated with D-hinge larval counts ($p < 0.001$, adj. $R^2 = 0.4$, Fig. 5_A).

It was found that salinity was negatively associated ($p < 0.001$, adj. $R^2 = 0.2$, Fig. 5_V) with D-hinge larval counts.

It was found that temperature was positively associated ($p = 0.0041$, adj. $R^2 = 0.084$, Fig. 5_C) with veliger larval counts.

Discussion

The purpose of studying this data was to find factors that could effect oyster larval levels within the GBE. Out of the physiochemical factors that were recorded and analyzed, only temperature effected both D-hinge and veliger larval levels,

larvalType	Site	2018	2019	2020
D-hinge				
D-hinge	LR	2144	313	NA
D-hinge	NI	419	316	200
D-hinge	SQ	4319	535	NA
D-hinge	WP	2291	135	283
D-hinge	AP	NA	NA	277
D-hinge	OF	NA	NA	334
Veliger				
Veliger	LR	0.31	0.022	NA
Veliger	NI	0.42	0.011	0.29
Veliger	SQ	0.05	0	NA
Veliger	WP	0.37	0.0031	0.36
Veliger	AP	NA	NA	0.39
Veliger	OF	NA	NA	1.1

ANOVA stuff

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
year	2	44974095	22487048	7.99983	<0.001	***

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
year	2	68.28091	34.14045	13.06356	<0.001	***

term	contrast	null.value	estimate	conf.low	conf.high	adj.p.value
year	2019-2018	0	-1.2901058	-2.265538	-0.3146732	0.0059565
year	2020-2018	0	-1.8560980	-2.717534	-0.9946619	0.0000033
year	2020-2019	0	-0.5659922	-1.344547	0.2125629	0.2003965

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
year	2	18.2834	9.141701	3.519239	0.034	*

term	contrast	null.value	estimate	conf.low	conf.high	adj.p.value
year	2019-2018	0	-1.7198362	-3.6646811	0.2250087	0.0938719
year	2020-2018	0	0.2585154	-0.7715272	1.2885581	0.8209916
year	2020-2019	0	1.9783516	0.1898108	3.7668925	0.0265306

	Estimate	CI (lower)	CI (upper)	Std. Error	t value	Pr(>|t|)	
(Intercept)	-0.9608414	-2.1904714	0.2687886	0.6217499	-1.545383	0.125	
Temp	0.2873778	0.2284754	0.3462802	0.0297834	9.648924	<0.001	***

	Estimate	CI (lower)	CI (upper)	Std. Error	t value	Pr(>|t|)	
(Intercept)	14.487593	11.3220159	17.6531708	1.6006421	9.051114	<0.001	***
Sal	-0.334339	-0.4447297	-0.2239483	0.0558179	-5.989814	<0.001	***

	Estimate	CI (lower)	CI (upper)	Std. Error	t value	Pr(>|t|)	
(Intercept)	22.074191	-1.682120	45.8305018	12.012137	1.837657	0.068	.
pH	-2.154769	-5.140972	0.8314329	1.509943	-1.427054	0.156	

	Estimate	CI (lower)	CI (upper)	Std. Error	t value	Pr(>|t|)	
(Intercept)	-3.9043737	-5.4557835	-2.3529640	0.7800106	-5.005539	<0.001	***
Temp	0.1113013	0.0362334	0.1863691	0.0377423	2.948982	0.004	**

	Estimate	CI (lower)	CI (upper)	Std. Error	t value	Pr(>|t|)	
(Intercept)	0.9261270	-3.4627274	5.3149815	2.2066080	0.4197062	0.676	
Sal	-0.0897185	-0.2414179	0.0619809	0.0762707	-1.1763163	0.243	

	Estimate	CI (lower)	CI (upper)	Std. Error	t value	Pr(>|t|)
(Intercept)	13.403288	-16.659660	43.46624	15.11491	0.8867594	0.378
pH	-1.897819	-5.684939	1.88930	1.90407	-0.9967171	0.322

	year	larvalType	mean	sd	n	se
1	2018	D-hinge	2293	5002	28	945
2	2018	Veliger	0.29	0.45	28	0.085
3	2019	D-hinge	325	405	36	68
4	2019	Veliger	0.0088	0.034	36	0.0057
5	2020	D-hinge	273	505	76	58
6	2020	Veliger	0.53	1	76	0.12

```
## # A tibble: 6 x 6
## # Groups:   year [3]
##   year  larvalType mean   sd         n se
##   <fct> <fct>      <chr>  <chr>   <int> <chr>
## 1 2018  D-hinge    2293   "5002"     28 "945"
## 2 2018  Veliger    0.29   "0.45"     28 "0.085"
## 3 2019  D-hinge    325    "405"      36 " 68"
## 4 2019  Veliger    0.0088 "0.034"    36 "0.0057"
## 5 2020  D-hinge    273    "505"      76 " 58"
## 6 2020  Veliger    0.53   "  1"      76 "0.12"
```