

Addition of juvenile oysters fails to enhance oyster reef development in Pamlico Sound

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Supplement. The statistical models used for analysis and summaries of statistical results are provided in the supplement.

Table S1. *Crassostrea virginica*. Number of oysters per shell fit to mixed effect-generalized linear models. Models are listed from the simplest to the most complex for each model family. Best model (lowest Akaike's information criterion, AIC) is bolded, and NA indicated model would not run because of lack of replication

Model	Family	df	AIC
# oysters=treatment, random=mound	Poisson	5	12757.96
# oysters=treatment*site, random=mound	Poisson	13	12724.48
# oysters=treatment+site+year, random=mound	Poisson	8	12605.14
# oysters=treatment*site*year, random=mound	Poisson	NA	NA
# oysters=treatment+site+year+treatment:site+treatment:year+site:year, random=mound	Poisson	19	11688.92
# oysters=treatment, random=mound	negative binomial	6	9646.92
# oysters=treatment*site, random=mound	negative binomial	14	9613.64
# oysters=treatment+site+year, random=mound	negative binomial	9	9586.02
# oysters=treatment*site*year, random=mound	negative binomial	NA	NA
# oysters=treatment+site+year+treatment:site+treatment:year+site:year, random=mound	negative binomial	20	9264.5

Table S2. *Crassostrea virginica*. Results for the number of oysters per shell fit to a negative-binomial mixed effect model. Factors included were treatment, site, year sampled, and the 2-way interactions. The intercept estimate is the estimated mean, and estimates for all of the factor levels are changes relative to the intercept estimate. The pr is the estimated probability that the listed factor level or interaction is significantly different from the factor level that is the control (not listed). Pair-wise comparisons are significant if the standard errors relative to the respective means do not overlap

	Estimate	SE	z	Pr(> z)
(Intercept)	2.8438	0.154	18.47	<2E-16
Treatment-Early small	-0.0733	0.2172	-0.34	0.7358
Treatment-Late small	-1.5322	0.222	-6.9	5.20E-12
Treatment-Late large	-0.5349	0.2194	-2.44	0.0148
Site-Gibbs Shoal	-1.6461	0.2219	-7.42	1.20E-13
Site-Clam Shoal	-1.93	0.2246	-8.59	<2E-16
Sampling-Fall 2011	-0.0509	0.1089	-0.47	0.6403
Early small seed:Gibbs Shoal	0.5157	0.3097	1.67	0.0959
Late small seed:Gibbs Shoal	1.6711	0.3136	5.33	9.90E-08
Late large seed:Gibbs Shoal	1.4598	0.3143	4.64	3.40E-06
Early small seed:Clam Shoal	1.0103	0.3102	3.26	0.0011
Late small seed:Clam Shoal	0.5394	0.3228	1.67	0.0947
Late large seed:Clam Shoal	1.2972	0.312	4.16	3.20E-05
Early small seed: Sampling-fall 2011	-0.3834	0.128	-2.99	0.0027
Late small seed: Sampling-fall 2011	0.8649	0.1488	5.81	6.10E-09
Late large seed: Sampling-fall 2011	-0.0647	0.1391	-0.47	0.6417
Gibbs Shoal: Sampling-fall 2011	0.5969	0.1344	4.44	9.00E-06
Clam Shoal: Sampling-fall 2011	-1.3622	0.1106	-12.32	<2E-16

Table S3. *Crassostrea virginica*. Results for the number of oysters per shell fit to a negative-binomial mixed effect model. Analyses were run with data from fall 2011 for each site separately, with treatment (fixed) and mound (random) as independent factors. The late large seed treatment is missing for Gibbs Shoal because only 1 shell was found on the 2 mounds

Crab Hole	Estimate	SE	z	Pr(> z)
(Intercept)	2.554	0.166	15.350	<0.001
Treatment-Early small seed	-0.230	0.232	-0.990	0.320
Treatment-Late small seed	-0.355	0.286	-1.240	0.210
Treatment-Late large seed	-0.279	0.229	-1.220	0.220

Gibbs Shoal	Estimate	SE	z	Pr(> z)
(Intercept)	1.774	0.159	11.150	<0.001
Treatment-Early small seed	0.465	0.237	1.960	0.050
Treatment-Late small seed	0.403	0.234	1.720	0.086

Clam Shoal	Estimate	SE	z	Pr(> z)
(Intercept)	-0.084	0.261	-0.320	0.750
Treatment-Early small seed	-0.069	0.351	-0.200	0.840
Treatment-Late small seed	-0.325	0.353	-0.920	0.360
Treatment-Late large seed	-0.116	0.358	-0.320	0.750

Table S4. *Crassostrea virginica*. Size of oysters on deployed shell fit to mixed effect-general linear models. Models are listed from the simplest to the most complex for each model family. Best model (lowest Akaike's information criterion, AIC) is bolded, and NA indicated model would not run because of lack of replication

Model	df	AIC
oyster size=treatment, random=mound	6	10462.84
oyster size=treatment+site, random = mound	8	10438.37
oyster size=treatment+year, random = mound	7	10421.75
oyster size=treatment*site, random = mound	14	10419.52
oyster size=treatment*year, random = mound	NA	NA
oyster size=treatment*year*site, random = mound	NA	NA

Table S5. *Crassostrea virginica*. Results for the size of oysters on deployed shell fit to a negative-binomial mixed effect model. Factors included were treatment, site, and the 2-way interactions

	Value	SE	df	<i>t</i>	p
(Intercept)	25.278493	1.416065	1457	17.851226	0
Treatment-Early small seed	1.289854	1.989079	12	0.648468	0.5289
Treatment-Late small seed	-7.455579	2.040513	12	-3.65E+00	0.0033
Treatment-Late large seed	-5.490506	1.979502	12	-2.77E+00	0.0168
Site-Gibbs Shoal	7.943172	2.035137	12	3.90E+00	0.0021
Site-Clam Shoal	-0.825575	2.05927	12	-4.01E-01	0.6955
Early small seed:Gibbs Shoal	-3.721463	2.868715	12	-1.297258	0.2189
Late small seed:Gibbs Shoal	-0.521924	2.900534	12	-0.179941	0.8602
Late large seed:Gibbs Shoal	-5.296975	2.877028	12	-1.841128	0.0904
Early small seed:Clam Shoal	-3.882938	2.867001	12	-1.354355	0.2006
Late small seed:Clam Shoal	3.33342	2.967718	12	1.123227	0.2833
Late large seed:Clam Shoal	-2.210245	2.8818	12	-0.766967	0.4579

Table S6. *Crassostrea virginica*. Number of oysters on marl fit to mixed effect-generalized linear models. Models are listed from the simplest to the most complex for each model family. Best model (lowest Akaike's information criterion, AIC) is bolded

Model	Family	df	AIC
# oysters=site, random=mound	Poisson	4	624110
# oysters=treatment*site, random=mound	Poisson	16	624108
# oysters=treatment+site+sampling, random=mound	Poisson	8	11035.98
# oysters=site*depth*sampling, random=mound	Poisson	19	208554
# oysters=treatment+site+sampling+treatment:site+treatment:sampling+site:sampling, random=mound	Poisson	19	10555.72
# oysters=treatment, random=mound	negative binomial	7	6409.10
# oysters=treatment*site, random=mound	negative binomial	17	6369.04
# oysters=treatment+site+depth+sampling, random=mound	negative binomial	12	6347.46

# oysters=site*depth*sampling, random= mound	negative binomial	20	6187.98
# oysters=site+depth+sampling+site:depth+site:sampling+depth:sampling, random=mound	negative binomial	16	6190.06
# oysters=treatment+site+sampling+treatment:site+treatment:sampling+site:sampling, random=mound	negative binomial	31	6271.02

Table S7. *Crassostrea virginica*. Results for the number of oysters on marl fit to a negative-binomial mixed effect model. Factors included were site, depth, and sampling

	Estimate	SE	z	Pr(> z)
(Intercept)	6.985	0.1328	52.61	< 2e-16
Site-Gibbs Shoal	0.1557	0.1872	0.83	0.40569
Site-Clam Shoal	1.7991	0.1869	9.62	< 2e-16
Depth-Bottom	1.0079	0.1769	5.7	1.20E-08
Sampling-2	-0.1239	0.1783	-0.69	0.48718
Sampling-3	0.65	0.1765	3.68	0.00023
Gibbs Shoal:Bottom	-0.5064	0.249	-2.03	0.04196
Clam Shoal:Bottom	-0.8484	0.2487	-3.41	0.00065
Gibbs Shoal:Sampling-2	-0.0732	0.2507	-0.29	0.77039
Clam Shoal:Sampling-2	-0.1216	0.2502	-0.49	0.62708
Gibbs Shoal:Sampling-3	0.6608	0.2487	2.66	0.00788
Clam Shoal:Sampling-3	-1.6619	0.2486	-6.69	2.30E-11
Bottom:Sampling-2	0.0691	0.2619	0.26	0.79192
Bottom:Sampling-3	-0.9774	0.2496	-3.92	9.00E-05
Gibbs Shoal:Bottom:Sampling-2	0.4411	0.3608	1.22	0.22158
Clam Shoal:Bottom:Sampling-2	-0.2241	0.3621	-0.62	0.53594
Gibbs Shoal:Bottom:Sampling-3	0.3859	0.3514	1.1	0.27221
Clam Shoal:Bottom:Sampling-3	0.6344	0.3516	1.8	0.07119

Table S8. *Crassostrea virginica*. Results for the density of oysters on marl fit to a negative-binomial mixed effect model. Analyses were run with data from fall 2011 for each site separately, with treatment (fixed) and mound (random) as independent factors

Crab Hole	Estimate	SE	z	Pr(> z)
(Intercept)	8.035	0.201	40.05	<0.001
Treatment-Early shell	-0.462	0.284	-1.63	0.1035
Treatment-Early small seed	-0.418	0.284	-1.47	0.1412
Treatment-Late small seed	-0.282	0.284	-0.99	0.3206
Treatment-Late large seed	-0.768	0.284	-2.71	0.0068
Gibbs Shoal	Estimate	SE	z	Pr(> z)
(Intercept)	8.273	0.1556	53.19	<0.001
Treatment-Early shell	0.3258	0.22	1.48	0.14
Treatment-Early small seed	0.1861	0.22	0.85	0.4
Treatment-Late small seed	0.1453	0.22	0.66	0.51
Treatment-Late large seed	-0.0284	0.22	-0.13	0.9
Clam Shoal	Estimate	SE	z	Pr(> z)
(Intercept)	7.783	0.139	55.83	<0.001
Treatment-Early shell	-0.286	0.197	-1.45	0.147
Treatment-Early small seed	-0.207	0.197	-1.05	0.293
Treatment-Late small seed	0.247	0.197	1.25	0.21
Treatment-Late large seed	-0.38	0.197	-1.93	0.054

Table S9. *Crassostrea virginica*. Number of oysters on marl from sites seeded and sampled by NCDMF fit to mixed effect-generalized linear models. Models are listed from the simplest to the most complex for each model family. Best model (lowest Akaike's information criterion, AIC) is bolded, and NA indicated model would not run because of lack of replication

Model	Family	df	AIC
# oysters~seeded+(1 mound)	Poisson	3	125478.2
# oysters~seeded+(1 mound)	negative binomial	4	8924.94
# oysters~seeded*depth+(1 mound)	negative binomial	8	8926.42
# oysters~seeded*year created+(1 mound)	negative binomial	6	8919.94
# oysters~seeded*site+(1 Mound)	negative binomial	8	8921.02
# oysters~seeded*mound age+(1 mound)	negative binomial	6	8831.04
# oysters~seeded+mound age+year created+(1 mound)	negative binomial	6	8825.18
# oysters~seeded*mound age*year created+(1 mound)	negative binomial	10	8813.02
# oysters~seeded+mound age+year created+seeded:mound age+ seeded:year created+mound age:year created (1 mound)	negative binomial	9	8811.16
# oysters~seeded*mound age*site+(1 mound)	negative binomial	14	8723.9
# oysters~seeded+mound age+site+seeded:mound age+ seeded:site+mound age:site (1 mound)	negative binomial	10	8831.8
# oysters~seeded+mound age+site+year created+(1 mound)	negative binomial	8	8820.02
# oysters~seeded*mound age*site*year created+(1 mound)	negative binomial	NA	NA

Table S10. *Crassostrea virginica*. Results for the number of oysters on marl from sites seeded and sampled by NCDMF fit to a negative-binomial mixed effect model. Factors included were seeded, mound age, and site

	Estimate	SE	z	Pr(> z)
(Intercept)	1.23E+01	4.38E+01	-0.28	0.7792
Seeded-yes	1.64E+01	4.38E+01	-0.37	0.7089
Mound age	1.77E+01	4.65E+01	0.38	0.7033
Site-South River	2.96E+01	9.29E+01	0.32	0.7497
Site-West Bluff	1.83E+17	6.84E+16	2.68	0.0073
Seeded-yes:Mound age	1.47E+01	3.29E+01	-0.45	0.6538
Seeded-yes:South River	4.08E+01	1.16E+02	-0.35	0.7252
Seeded-yes:West Bluff	1.18E+18	3.16E+18	-0.37	0.7096
Mound age:South River	1.61E+01	4.62E+01	-0.35	0.7275
Mound age:West Bluff	9.17E+16	3.42E+16	-2.68	0.0073
Seeded-yes:Mound age:South River	1.40E+01	3.39E+01	0.41	0.6791
Seeded-yes:Mound age:West Bluff	5.88E+17	1.58E+18	0.37	0.7096