Temporal variation in dispersal modifies dispersal–diversity relationships in an experimental seagrass metacommunity

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Table S1. Presence/absence data for eighteen taxa sampled across three sampling dates, listed in order of averaged abundance. At each sampling date, organisms were collected from Bogue Sound, NC and mixed together to form a species pool. Samples were taken from the species pool and either preserved for identification or added as propagules to the mesocosm experiment. Filled cells indicate that the taxa was present in at least one preserved sample on sampling date. From Amphilochid down (ranks 14-18), ≤ 3 individuals were counted across all samples from all dates

Taxa (Ranked in order of abundance)	Presence in preserved sample 6/28	7/5	7/12	Dispersing life stage
Copepod (**1**)	▪	▪	▪	Pelagic larva/Juvenile/Adult
Corophium (**2**)	▪	▪	▪	Juvenile/Adult
Ampithoid (**3**)	▪	▪	▪	Juvenile/Adult
Dulichiella (**4**)	▪	▪	▪	Juvenile/Adult
Elasmopus (**5**)	▪	▪	▪	Juvenile/Adult
Bivalve (**6**)	▪	▪	▪	Larval
Caprellid (**7**)	▪	▪	▪	Juvenile/Adult
Stenothoe (**8**)	▪	▪	▪	Juvenile/Adult
Erichthonius (**9**)	▪		▪	Juvenile/Adult
Gastropod (**10**)	▪	▪	▪	Pelagic larva
Paracerceis (**11**)	▪	▪	▪	Juvenile/Adult
Polychaete (**12**)	▪	▪	▪	Pelagic larva
Jassa (**13**)	▪	▪	▪	Juvenile/Adult
Amphilochid (**14**)		▪		Juvenile/Adult
Paraphinotus seclusus (**15**)		▪	▪	Juvenile/Adult
Lembos (**16**)		▪	▪	Juvenile/Adult
Tanaid (**17**)		▪		Juvenile/Adult
Erichsonella attenuata (**18**)		▪		Juvenile/Adult

Figure S1. Plot of proportional abundance of taxa sampled across all three sampling dates vs. the overall rank of each taxa in the entire data set. Ranks correspond to the numbers listed next to each taxa on Table S1. Sampling dates are indicated by line type, color, and shape as follows: 6/28 (open circle, solid black line), 7/5 (black square, long-dashed green line), 7/12 (grey triangle, short-dashed blue line)
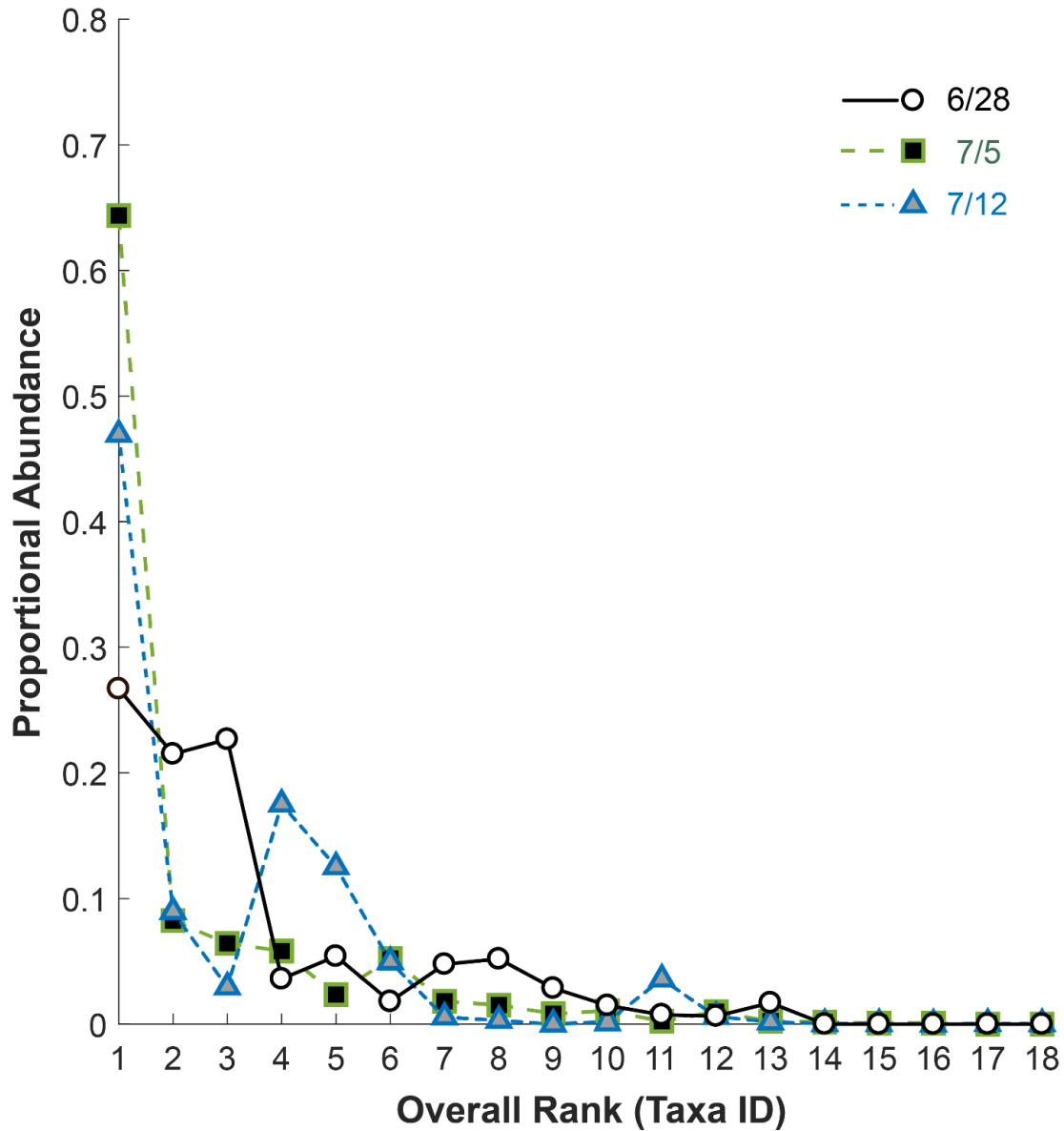
Text S1. Diversity Rarefaction

1. For all treatments we determined the minimum number of individuals in any replicate of that treatment, and then randomly subsampled that number of individuals in proportion to their abundance on the focal treatment.
2. For each treatment, we repeated this subsampling 1000 times. For each replicate, we computed measures of both species richness and beta diversity (the mean bootstrapped distance from each reef to the respective treatment centroid [i.e., distance between each reef's multivariate location and the multivariate location of the mean community composition per treatment]). Because our treatments had unequal sample sizes, we bias corrected the estimated distances to centroid in each of the contrasted groups using a sqrt(n/(n-1)) correction (analogous to the correction applied in the standard estimation procedure for sample standard deviations). This bias correction for beta diversity contrasts based on unequal sample sizes is novel, although the possibility of such bias is mentioned (and dismissed) by Anderson (2001) and this type of bias correction is discussed in more detail (in a different context) by O'Neill and Mathews (2000). An option for applying this bias correction automatically will be available in the betadisper function in an upcoming release of the vegan package for community analysis (J. Oksanen, personal communication).
3. Finally, we compared the estimated species richness and beta diversity distributions for each treatment group within a contrast using a two-tailed test.

Table S2. Effects of Temporal Variance in Dispersal on Beta Diversity
Pairwise comparisons of variance effects for each dispersal intensity treatment. All p-values corrected using Hochberg correction. Statistically significant effects ($p < 0.05$) are in bold.

Dispersal Intensity Treatment	F-Statistic	Jaccard	F-Statistic	Raup-Crick
Small Add	8.9504	**0.048**	9.4371	0.112
Med-Lo Add	2.1139	0.991	13.008	**0.004**
Med-High Add	1.0282	0.994	24.753	**0.004**
Lg Add	0.1428	0.995	14.696	**0.004**

Table S3. Pairwise Tukey HDS contrasts of individual dispersal treatments based on the Raup-Crick index of beta diversity. P-values

Contrast	difference	lower CI	upper CI	Tukey Adjusted P-value
LgHighVariance-LgLowVariance	-0.1104	-0.2338	0.013	0.1133
MedHighLowVariance-LgLowVariance	-0.1319	-0.2508	-0.013	0.0195
MedHighHighVariance-LgLowVariance	0.0306	-0.0928	0.154	0.9962
MedLoLowVariance-LgLowVariance	-0.196	-0.3195	-0.0726	1.00E-04
MedLoHighVariance-LgLowVariance	-0.1408	-0.2642	-0.0174	0.0146
None-LgLowVariance	-0.1883	-0.3072	-0.0693	2.00E-04
SmallLowVariance-LgLowVariance	-0.1698	-0.2888	-0.0509	8.00E-04
SmallHighVariance-LgLowVariance	-0.1169	-0.2359	0.002	0.0572
MedHighLowVariance-LgHighVariance	-0.0215	-0.1404	0.0974	0.9996
MedHighHighVariance-LgHighVariance	0.141	0.0176	0.2644	0.0144
MedLoLowVariance-LgHighVariance	-0.0857	-0.2091	0.0378	0.3903
MedLoHighVariance-LgHighVariance	-0.0304	-0.1538	0.093	0.9964
None-LgHighVariance	-0.0779	-0.1968	0.041	0.4693
SmallLowVariance-LgHighVariance	-0.0595	-0.1784	0.0595	0.7882
SmallHighVariance-LgHighVariance	-0.0066	-0.1255	0.1124	1
MedHighHighVariance-MedHighLowVariance	0.1625	0.0436	0.2814	0.0016
MedLoLowVariance-MedHighLowVariance	-0.0641	-0.1831	0.0548	0.7133
MedLoHighVariance-MedHighLowVariance	-0.0089	-0.1278	0.11	1
None-MedHighLowVariance	-0.0564	-0.1706	0.0579	0.8
SmallLowVariance-MedHighLowVariance	-0.0379	-0.1522	0.0763	0.9749
SmallHighVariance-MedHighLowVariance	0.015	-0.0993	0.1292	1
MedLoLowVariance-MedHighHighVariance	-0.2267	-0.3501	-0.1032	0
MedLoHighVariance-MedHighHighVariance	-0.1714	-0.2948	-0.048	0.0013
None-MedHighHighVariance	-0.2189	-0.3378	-0.0999	0
SmallLowVariance-MedHighHighVariance	-0.2005	-0.3194	-0.0815	1.00E-04
SmallHighVariance-MedHighHighVariance	-0.1476	-0.2665	-0.0286	0.0057
MedLoHighVariance-MedLoLowVariance	0.0552	-0.0682	0.1787	0.8714
None-MedLoLowVariance	0.0078	-0.1111	0.1267	1
SmallLowVariance-MedLoLowVariance	0.0262	-0.0927	0.1451	0.9983
SmallHighVariance-MedLoLowVariance	0.0791	-0.0398	0.198	0.4481
None-MedLoHighVariance	-0.0475	-0.1664	0.0715	0.9282
SmallLowVariance-MedLoHighVariance	-0.029	-0.148	0.0899	0.9966
SmallHighVariance-MedLoHighVariance	0.0239	-0.0951	0.1428	0.9992
SmallLowVariance-None	0.0184	-0.0958	0.1327	0.9998
SmallHighVariance-None	0.0713	-0.0429	0.1856	0.5342
SmallHighVariance-SmallLowVariance	0.0529	-0.0614	0.1672	0.8492

Table S4. Pairwise Tukey HDS contrasts of individual dispersal treatments based on the Jaccard's index of beta diversity

Contrast	difference	lower CI	upper CI	Tukey Adjusted P-value
LgHighVariance-LgLowVariance	0.0174	-0.1226	0.1574	1
MedHighLowVariance-LgLowVariance	-5.00E-04	-0.1354	0.1344	1
MedHighHighVariance-LgLowVariance	0.0525	-0.0875	0.1925	0.9489
MedLoLowVariance-LgLowVariance	-0.0273	-0.1673	0.1127	0.9993
MedLoHighVariance-LgLowVariance	0.0431	-0.0968	0.1831	0.9842
None-LgLowVariance	0.0108	-0.1241	0.1457	1
SmallLowVariance-LgLowVariance	-0.0044	-0.1393	0.1305	1
SmallHighVariance-LgLowVariance	0.072	-0.0629	0.2069	0.7243
MedHighLowVariance-LgHighVariance	-0.0179	-0.1528	0.117	1
MedHighHighVariance-LgHighVariance	0.0351	-0.1049	0.1751	0.9959
MedLoLowVariance-LgHighVariance	-0.0447	-0.1846	0.0953	0.9804
MedLoHighVariance-LgHighVariance	0.0258	-0.1142	0.1658	0.9995
None-LgHighVariance	-0.0066	-0.1415	0.1283	1
SmallLowVariance-LgHighVariance	-0.0218	-0.1567	0.1131	0.9998
SmallHighVariance-LgHighVariance	0.0546	-0.0803	0.1895	0.9223
MedHighHighVariance-MedHighLowVariance	0.0531	-0.0819	0.188	0.9336
MedLoLowVariance-MedHighLowVariance	-0.0267	-0.1616	0.1082	0.9992
MedLoHighVariance-MedHighLowVariance	0.0437	-0.0912	0.1786	0.9784
None-MedHighLowVariance	0.0113	-0.1183	0.1409	1
SmallLowVariance-MedHighLowVariance	-0.0038	-0.1334	0.1258	1
SmallHighVariance-MedHighLowVariance	0.0726	-0.057	0.2022	0.6714
MedLoLowVariance-MedHighHighVariance	-0.0798	-0.2198	0.0602	0.6506
MedLoHighVariance-MedHighHighVariance	-0.0094	-0.1494	0.1306	1
None-MedHighHighVariance	-0.0417	-0.1766	0.0932	0.9838
SmallLowVariance-MedHighHighVariance	-0.0569	-0.1918	0.078	0.9043
SmallHighVariance-MedHighHighVariance	0.0195	-0.1154	0.1544	0.9999
MedLoHighVariance-MedLoLowVariance	0.0704	-0.0696	0.2104	0.7828
None-MedLoLowVariance	0.038	-0.0969	0.1729	0.9911
SmallLowVariance-MedLoLowVariance	0.0229	-0.112	0.1578	0.9998
SmallHighVariance-MedLoLowVariance	0.0993	-0.0356	0.2342	0.3135
None-MedLoHighVariance	-0.0324	-0.1673	0.1025	0.997
SmallLowVariance-MedLoHighVariance	-0.0475	-0.1824	0.0874	0.9643
SmallHighVariance-MedLoHighVariance	0.0289	-0.106	0.1638	0.9987
SmallLowVariance-None	-0.0152	-0.1448	0.1145	1
SmallHighVariance-None	0.0612	-0.0684	0.1909	0.8344
SmallHighVariance-SmallLowVariance	0.0764	-0.0532	0.206	0.6089

Figure S2. Nonmetric multidimensional scaling (NMDS) plots based on Jaccard's index of dissimilarity based on species incidence in 8 different dispersal treatments. Increased overlap in hulls indicates that replicate mesocosms in different treatments were similar in mean community composition; the area of hulls can loosely be interpreted as a measure of beta diversity. The two variability treatments were a high variability, pulse treatment (open triangles, green), and a low variability, press treatment of propagules (closed circles, red).