Beyond a single patch: local and regional processes explain diversity patterns in a seagrass epifaunal metacommunity

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Appendix S1: Supporting Information

Table S1. Summary of evidence used to answer questions about metacommunity processes

Question	Analyses	Figure number
(1) Is the metacommunity characterized by dispersal limitation, intermediate dispersal, or high dispersal?	Dispersal limitation: Distance-decay of community similarity from HMSC joint species distribution models with and without accounting for environmental similarity	Fig. 1b
	Intermediate versus high dispersal: Biodiversity patterns across sites for signatures of high dispersal (compositional homogenization); HMSC model results indicating structured co-occurrence patterns and variation in composition explained by environmental	Fig. 3a, 3b
(2) Do species distribution patterns suggest environmental niche filtering, and if so along which environmental axis?	Variation partitioning of modelled site and region-level fixed and random effects of environmental covariates and calculating predictive power (proportion of deviance) of the fixed effects model	Fig. 2
(3) Do species co-variance patterns suggest possible biotic interactions influencing community assembly?	Correlation matrix of pairwise species co-occurences, after controlling for the effect of space and environment	Fig. 3a, 3b

Table S2. Species names, taxonomic groupings, and proportion of deviance (predictive power). Numbers correspond to those in Figure 2. The top twenty species with highest predicted abundances according to the HMSC model are bolded.

Number	Species name	Broad taxonomic group	Adjusted deviance explained for the HMSC model (D^2_{adj})
1	*Alia carinata*	Gastropod (snail)	0.15
2	***Alvania compacta***	**Gastropod (snail)**	**0.4**
3	*Amphissa columbiana*	Gastropod (snail)	0
4	*Crepidula* sp.	Gastropod (snail)	0.64
5	*Euspira lewisii*	Gastropod (snail)	0.46
6	*Harmothoe imbricata*	Gastropod (snail)	0
7	***Lacuna* spp. *(L. variegata and L. vincta)***	**Gastropod (snail)**	**0.45**
8	*Lirularia parcipincta*	Gastropod (snail)	0.46
9	*Lirularia* sp.	Gastropod (snail)	0
10	*Littorina* sp.	Gastropod (snail)	0.5
11	*Margarites pupillus*	Gastropod (snail)	0.45
12	*Lottia pelta*	Gastropod (limpet)	0.53
13	***Clinocardium nuttallii***	**Bivalve**	**0**
14	***Mytilus* sp.**	**Bivalve**	**0.28**
15	*Saxidomus gigantea*	Bivalve	0
16	*Unknown clam 1*	Bivalve	0.68
17	*Unknown clam 2*	Bivalve	0.35
18	*Dorvillea longicornis*	Polychaete	0.52
19	*Exogone sp.*	Polychaete	0.25
20	*Glycinde armigera*	Polychaete	0.05
21	*Lepidonotus squamatus*	Polychaete	0.55
22	*Neoamphitrite robusta*	Polychaete	0.22
23	*Unknown polychaete (Family Oenoidae)*	Polychaete	0.15
24	*Unknown polychaete (Family Opheliidae)*	Polychaete	0.36
25	***Spirorbis* sp.**	**Polychaete**	**0**
26	***Nereis* sp.**	**Polychaete**	**0.55**
27	***Ampithoe dalli***	**Gammarid amphipod**	**0.47**
28	*Ampithoe lacertosa*	Gammarid amphipod	0.34
29	***Ampithoe valida***	**Gammarid amphipod**	**0**
30	***Aoroides* spp.**	**Gammarid amphipod**	**0**
31	*Ceradocus spinicauda*	Gammarid amphipod	0
32	*Grandidierella japonica*	Gammarid amphipod	0
33	*Ischyocerus anguipes*	Gammarid amphipod	0.33
34	*Jassa marmorata*	Gammarid amphipod	0

35	***Monocorophium insidiosum***	**Gammarid amphipod**	**0.23**
36	*Orchomenella recondita*	Gammarid amphipod	0.73
37	***Photis brevipes***	**Gammarid amphipod**	**0**
38	***Pontogeneia rostrata***	**Gammarid amphipod**	**0.65**
39	*Unknown gammarid (Family Hyalidae)*	Gammarid amphipod	0.12
40	*Unknown gammarid (Family Isaeidae)*	Gammarid amphipod	0.10
41	*Unknown gammarid (Family Ischyoceridae)*	Gammarid amphipod	0.24
42	***Caprella californica***	**Caprellid amphipod**	**0.36**
43	***Caprella laeviuscula***	**Caprellid amphipod**	**0.06**
44	***Caprella natalensis***	**Caprellid amphipod**	**0.82**
45	*Cumella vulgaris*	Cumacean	0.36
46	***Leptochelia sp.***	**Tanaid**	**0.49**
47	*Nebalia gerkinae*	Leptostracan	0.39
48	***Porcellidium sp.***	**Copepod**	**0.33**
49	***Harpacticoid 1***	**Copepod**	**0**
50	***Harpacticoid 2***	**Copepod**	**0**
51	*Harpacticoid 3*	Copepod	0.50
52	*Anoplodactylus viridintestinalis*	Pycnogonid	0.01
53	*Idotea montereyensis*	Isopod	0.73
54	***Idotea resecata***	**Isopod**	**0.36**
55	*Munna sp.*	Isopod	0.20
56	*Pugettia producta*	Brachyuran crab	0.36
57	*Pugettia richii*	Brachyuran crab	0.34
58	*Hippolyte californiensis*	Caridean shrimp	0.45

Table S3. Summary of traditional biodiversity metrics for each site

Site abbrev	Region	Species richness	Raw abundance	Effective diversity (Hill number)
DC	Barkley Sound	21	1168	11.8
RP	Barkley Sound	17	1590	8.8
SA	Barkley Sound	17	924	6.8
DK	Clayoquot Sound	21	1168	11.8
EB	Clayoquot Sound	21	4812	8.5
IN	Clayoquot Sound	16	1803	7.5
CB	Gulf Islands	18	2112	5.0
GB	Gulf Islands	11	2239	4.3
JB	Gulf Islands	22	3522	7.1
LH	Gulf Islands	15	2259	6.6
SS	Gulf Islands	10	740	6.6
HL	Haida Gwaii	9	16743	1.3
RA	Haida Gwaii	14	934	8.6

Equation S1. Equations for D^2_{adj} calculations

Explained deviance or D^2 (Guisan and Zimmerman 2000) was calculated by the equation:

$$D^2 = 1 - \text{Residual deviance} / \text{Null deviance}$$

Where the residual deviance refers to the deviance in predicted species occurrences, and the null deviance refers to deviance in observed species occurrences.

Adjusted D^2 (Guisan and Zimmerman 2000) was calculated by the equation:

$$D^2_{adj} = 1-(((n-1)/(n-p-1)*(D^2-1))$$

Where n is the number of sites (13) in our study, and p is the number of parameters the model estimated (4, Ovaskainen et al. 2017, Supporting Information). Negative D^2_{adj} values (those which had greater residual deviance than null deviance) were set to 0.

Equation S2. Calculations for type III variation partitioning on the HMSC model (Borcard et al. 1992)

We estimated three versions of the HMSC model: 1) environmental variables only with the random effects (*m2*), and 2) spatial distances only with random effects, and 3) the original global model which included environmental and spatial variables, site- and region-level random effects (*m1*).

m1 = the fraction of variation explained by all environmental variables in the HMSC model estimated with only environmental variables;
m2 = the fraction of variation by spatial distances in the version of the HMSC model estimated with only spatial distances;
m3 = the global model including both;

From each model, we extracted the total variation explained by environment and space, the variation explained by environment, and the variation explained by space. To determine the shared fraction of variation between environment and space, we multiplied each whole fraction by the calculated community-level D^2_{adj} to reflect the model deviance in our variance partitioning estimates, and followed the equations to calculate fractions *a, b, c,* and *d.*

Fraction *ab* (pure environment + shared fraction) = $D^2_{adj}\ m1$
Fraction *bc* (pure space + shared fraction) = $D^2_{adj}\ m2$
Fraction *abc* (pure environment + shared fraction + pure space) = $D^2_{adj}\ m3$

Fraction *a* (pure environment) = *abc* - *bc*
Fraction *c* (pure space) = *abc* - *ab*
Fraction *b* (shared fraction) = *ab* + *bc* - *abc*
Fraction *d* (residuals) = 1 - *abc*

Fractions *a* ("Environmental conditions"), *c* ("Spatial distance"), *b* (shared fraction), and *d* ("Residuals") are shown in the Venn diagram in Fig. S3.

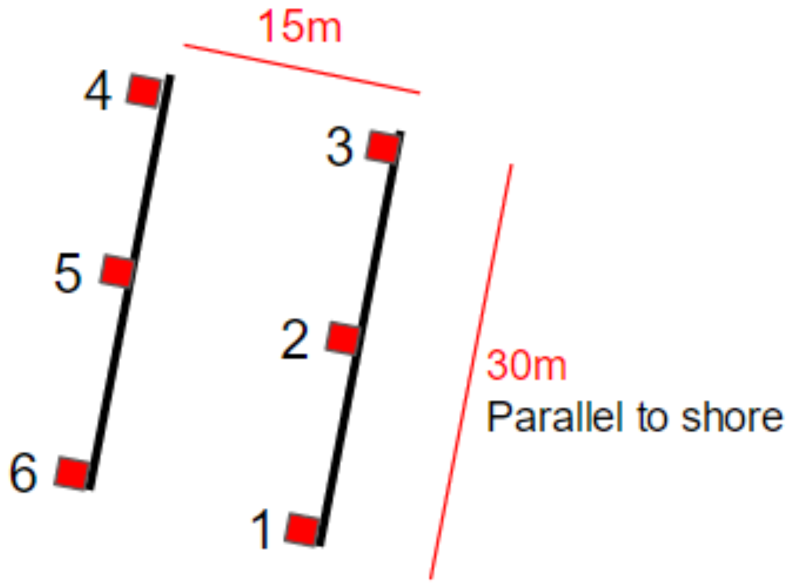

Figure S1. Schematic diagram field sampling regime. Black lines represent transect lines, and red boxes represent 0.25 x 0.25 m quadrats.

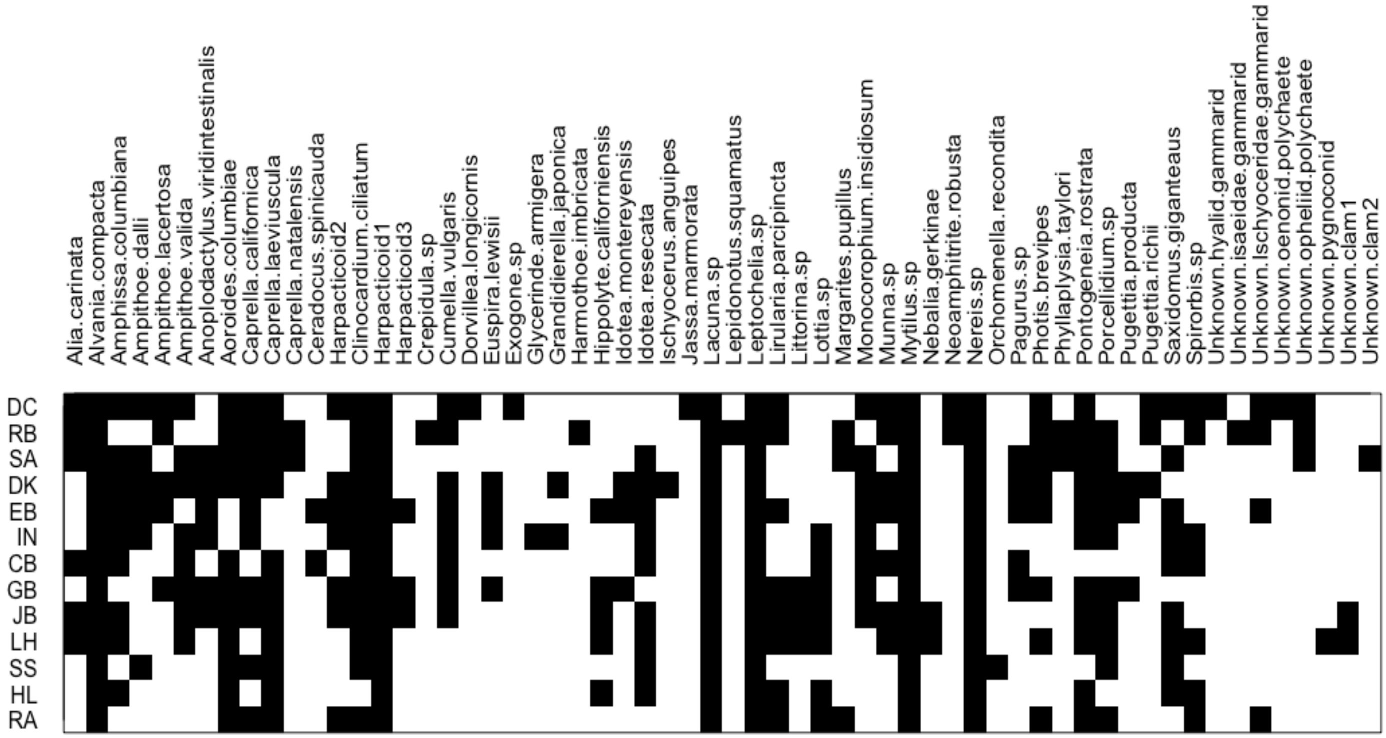

Figure S2. Site-by-species presence-absence matrix of all 58 invertebrate species in the study listed in alphabetical order. Black cells indicate species presences.

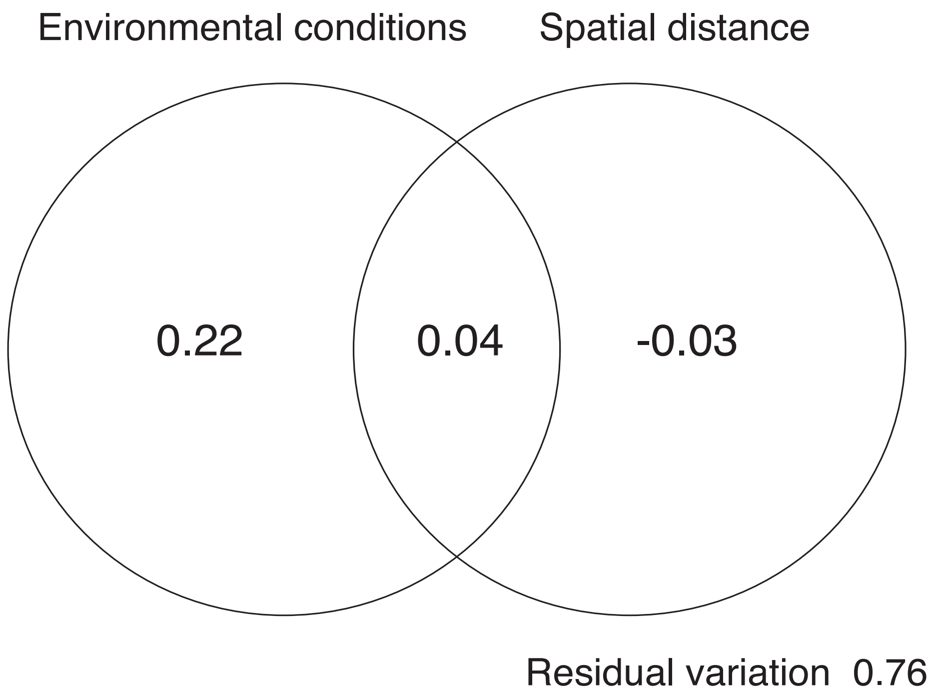

Figure S3. Venn diagram summarizing the fractions of variation explained by environmental covariates only (nine water quality and five biotic variables), spatial distance only, and the shared fraction explained by environment and space.

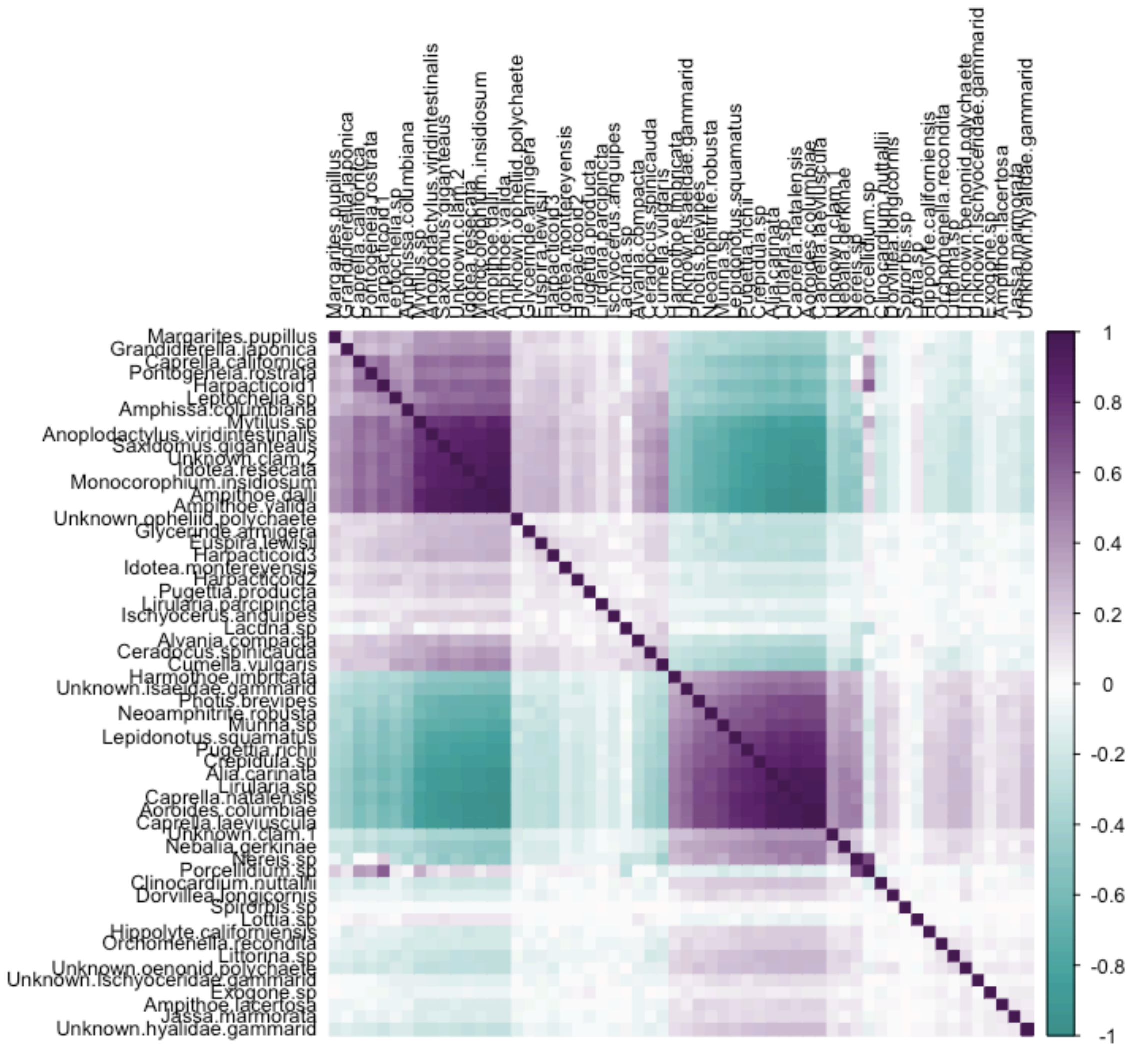

Figure S4. A correlation plot showing modelled site-level co-occurrence of species pairs across all species. Purple cells represent positively co-occurring species pairs, and turquoise cells represent negatively co-occurring species pairs. Species names along both axes are ordered according to the output of hierarchical clustering with Ward's criterion (Ward 1963) on pairwise co-occurrence values. This figure is a supplement to Fig. 4a in the main text.

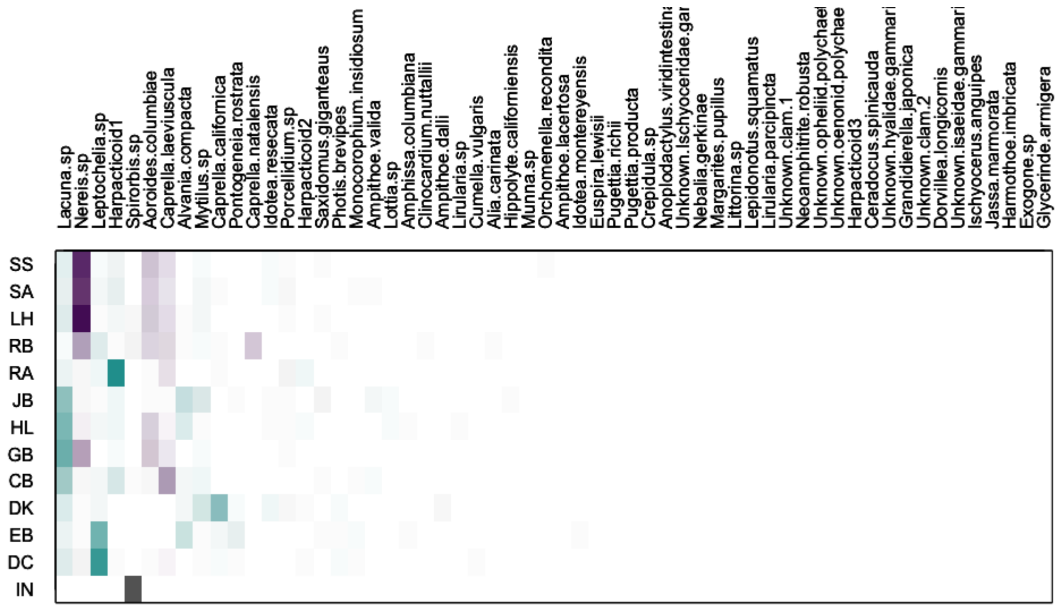

Figure S5. Heat map depicting abundance patterns in all 58 species in the study. Species names are ordered from highest to lowest predicted mean proportional abundance. Cell colours correspond to the co-occurrence groups in Fig. 3a, with purple cells representing members of the *Nereis* assemblage, and turquoise cells indicating members of the *C. californica* assemblage, and grey cells indicating species that did not significantly co-occur negatively or positively with other species. Cell shade strength represents proportional abundance at a given site (darker means higher abundance). Most species outside the top twenty most abundant had extremely low predicted proportional abundances owing to their low raw abundances. This figure is a supplement to Fig. 3b in the main text.

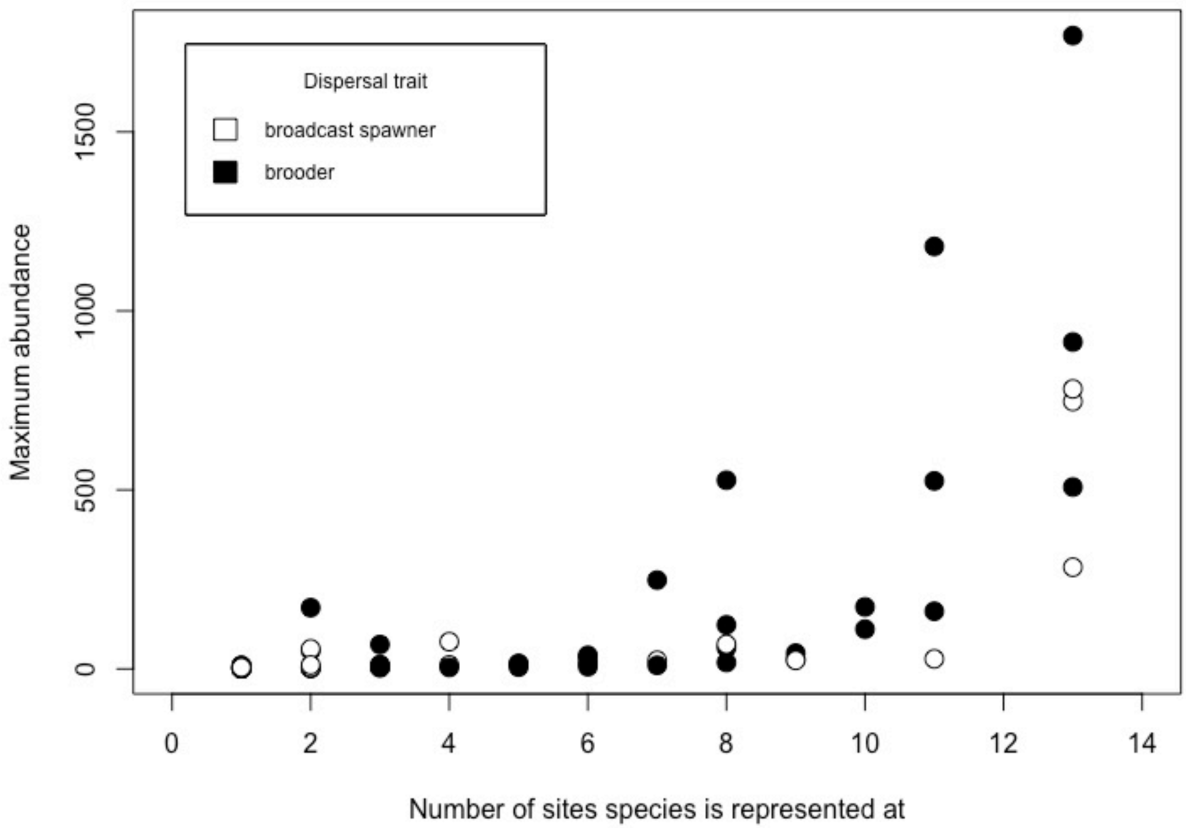

Figure S6. Plot showing relationship between maximum site-level abundance and site occupancy for all species. Black points represent broadcast spawners and white points represent brooders. Spirorbid polychaetes were excluded from this figure due to their unusually high maximum abundance (approximately 16 300 at one site). A two-tailed t-test showed that there was no significant difference in the number of sites colonized between brooders and broadcast spawners ($t = 0.052$, $df = 42.5$, $p = 0.96$).

Literature Cited

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