The following supplement accompanies the article

Consumers mediate natural variation between prey richness and resource use in a benthic marine community

Robin Elahi[1,2,*], Kenneth P. Sebens[1,2,3]

[1]**Friday Harbor Laboratories, University of Washington, Friday Harbor, Washington 98250, USA**
[2]**Department of Biology, University of Washington, Seattle, Washington 98195, USA**
[3]**School of Aquatic and Fisheries Sciences, University of Washington, Seattle, Washington 98195**

*Email: elahi@uw.edu

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Supplement. Additional material from the field survey and experiment, as well as the results of statistical models.

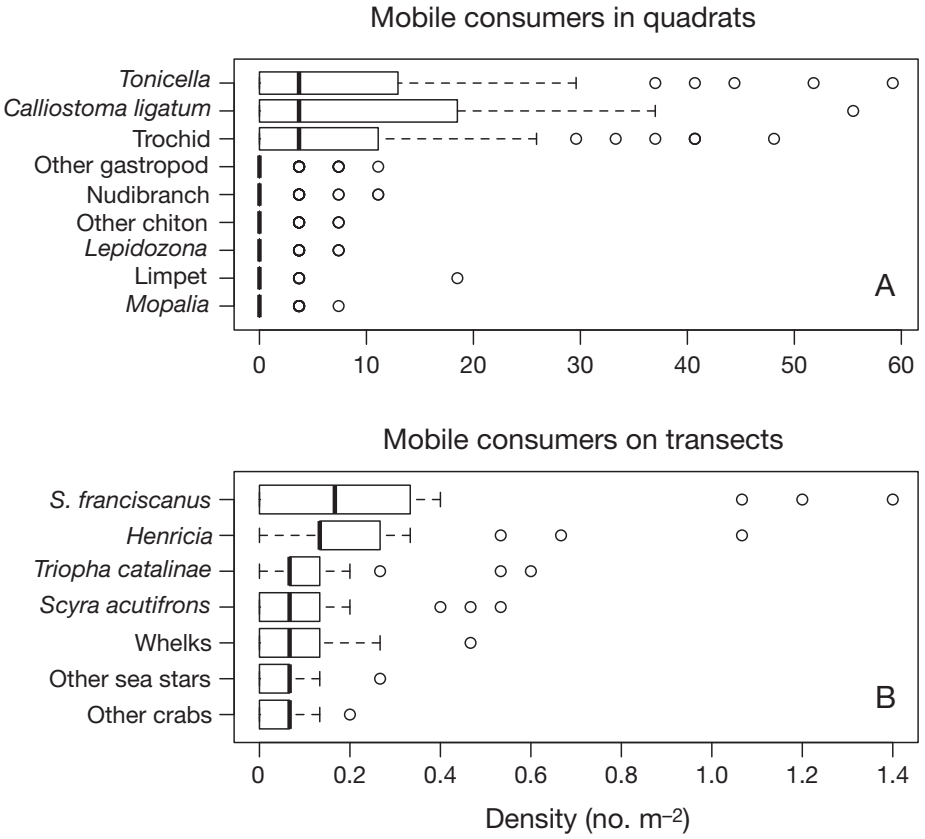

Fig. S1. The density of mobile consumers in (A) quadrats and (B) transects. Boxplots display the median and interquartile range (IQR) of data, with outliers plotted as circles beyond whiskers when the values are 1.5 times the IQR from the first or third quartile. *Tonicella*, *Lepidozona* and *Mopalia* are chitons. *Strongylocentrotus franciscanus*, *Henricia*, *Triopha catalinae* and *Scyra acutifrons* are urchins, sea stars, sea slugs and crabs, respectively

Table S1. We used a linear mixed-effects model to assess the strength and direction of the relationship between available space and consumer density in the 2008 surveys. Percent cover of space (logit-transformed) was the response, and the independent predictors were the abundance (log[x + 1]-transformed) of *Tonicella* spp., *Calliostoma ligatum*, trochid snails, *Strongylocentrotus franciscanus*, *Henricia* spp., *Triopha catalinae* and *Scyra acutifrons*. Transect was nested within site; both were treated as random effects. We used a Monte Carlo Markov chain (MCMC) resampling procedure (n = 5000) to assess the significance of the predictors in linear mixed-effects models; when the 95% confidence intervals of the estimate did not include zero, we considered the estimate to be significant. The density of *Tonicella* spp. and *S. franciscanus* was positively correlated with available space, suggesting that these consumers play a role in the provision of space. However, the density of *C. ligatum* correlated negatively with space, suggesting that this snail associates with sessile invertebrates and/or macroalgae, the space occupiers in this community

Taxon	Estimate	SE	*t*	MCMC lower limit	MCMC upper limit	Significance
Tonicella spp.	0.545	0.104	5.250	0.343	0.760	*
Calliostoma ligatum	–0.328	0.100	–3.279	–0.513	–0.106	*
Trochid snails	0.118	0.110	1.071	–0.076	0.368	ns
S. franciscanus	1.597	0.566	2.820	0.363	2.590	*
Henricia spp.	0.209	0.772	0.270	–1.152	1.899	ns
Triopha catalinae	–0.371	1.095	–0.339	–2.499	1.756	ns
Scyra acutifrons	0.638	1.263	0.505	–2.068	3.339	ns

Table S2. Density (±1 SD, n = 6 time points) of red urchins *Strongylocentrotus franciscanus* on experimental and control transects during the course of the 2009 experiment. Urchins were added to each transect at O'Neal, Pt. George and Shady Cove at approximately 2-weekly intervals to achieve a target density of 20 urchins per transect (4 urchins m^{-2}). Estimates of density on urchin addition transects do not include urchin counts concurrent with manipulations and thus can be considered conservative. Transects are ordered by ascending numerical density, and categorical densities correspond to those in Fig. 3

Site	Treatment	Transect	Density (urchins m^{-2})	Categorical density
Shady Cove	Control	SC_C_1	0	Low
Shady Cove	Control	SC_C_2	0	Low
Shady Cove	Control	SC_C_3	0	Low
O'Neal	Control	ON_C_1	0.07 ± 0.52	Low
Pt. George	Control	PG_C_1	0.20 ± 0.89	Low
Pt. George	Control	PG_C_2	0.20 ± 1.26	Low
O'Neal	Addition	ON_A_1	0.27 ± 1.75	Medium
O'Neal	Control	ON_C_3	0.27 ± 0.52	Medium
O'Neal	Addition	ON_A_3	0.47 ± 1.86	Medium
Pt. George	Control	PG_C_3	0.76 ± 1.72	Medium
O'Neal	Control	ON_C_2	0.90 ± 3.39	Medium
O'Neal	Addition	ON_A_2	1.13 ± 4.68	Medium
Pt. George	Addition	PG_A_2	1.27 ± 3.78	High
Pt. George	Addition	PG_A_1	2.60 ± 3.03	High
Pt. George	Addition	PG_A_3	2.83 ± 5.85	High
Shady Cove	Addition	SC_A_2	3.63 ± 1.47	High
Shady Cove	Addition	SC_A_3	3.9 ± 0.55	High
Shady Cove	Addition	SC_A_1	4.33 ± 1.86	High

Table S3. Quantile regression models estimating relationships between available space (percent cover) and 4 predictors (untransformed) in surveys of permanent quadrats in 2008 (n = 72), and at the end of the experiment in September 2009 (n = 108). Because of the increased sample size in 2009, we estimated slightly more extreme quantiles to better illustrate the limits to the relationship between available space and prey richness. We also estimated median regressions between the percent cover of macroalgae and clonal ascidians as a function of prey richness for quadrats in the urchin treatment before and after the experimental addition of urchins. Significant ($p < 0.05$) regressions are indicated in bold

	n	Intercept (SE)	Slope (SE)	p
Survey (2008)				
Space vs. prey richness				
85th quantile	72	93.38 (14.85)	–4.11 (0.96)	**<0.001**
50th quantile	72	39.85 (10.77)	–1.70 (0.67)	**0.013**
15th quantile	72	8.28 (5.33)	–0.18 (0.37)	0.622
Space vs. consumer richness				
85th quantile	72	12.51 (7.99)	18.62 (5.22)	**<0.001**
50th quantile	72	5.98 (2.60)	7.40 (2.13)	**<0.001**
15th quantile	72	1.26 (1.42)	3.76 (1.46)	**0.013**
Space vs. chiton density				
85th quantile	72	24.29 (5.21)	1.48 (0.47)	**0.002**
50th quantile	72	10.57 (1.60)	0.91 (0.26)	**<0.001**
15th quantile	72	2.93 (1.28)	0.85 (0.13)	**<0.001**
Space vs. urchin density				
85th quantile	72	26.28 (6.31)	46.09 (14.92)	**0.003**
50th quantile	72	8.93 (1.52)	26.80 (6.89)	**<0.001**
15th quantile	72	2.96 (1.19)	15.90 (3.96)	**0.002**
Experiment (2009)				
Space vs. prey richness				
Low urchin density, 50th quantile	36	21.31 (7.21)	–0.19 (0.40)	0.637
Intermediate urchin density, 50th quantile	36	52.15 (5.97)	–1.63 (0.48)	**0.002**
High urchin density, 50th quantile	36	92.12 (3.65)	–2.73 (0.24)	**<0.001**
All urchin densities, 90th quantile	108	96.11 (5.73)	–2.67 (0.40)	**<0.001**
All urchin densities, 10th quantile	108	20.21 (5.68)	–0.57 (0.33)	0.080
Macroalgae vs. prey richness				
Urchin treatment, before addition; 50th quantile	54	10.15 (5.70)	0.32 (0.41)	0.446
Urchin treatment, after addition; 50th quantile	54	–1.12 (2.77)	0.25 (0.19)	0.209
Clonal ascidians vs. prey richness				
Urchin treatment, before addition; 50th quantile	54	23.17 (7.95)	–0.30 (0.52)	0.573
Urchin treatment, after addition; 50th quantile	54	–0.04 (3.53)	1.12 (0.26)	**<0.001**

Table S4. Results of linear mixed-effects models testing the fixed effect of treatment on transect-scale change in dependent variables over the course of the 3 mo experiment. Site was treated as a random effect. A Monte Carlo Markov chain (MCMC) resampling procedure (n = 5000) assessed the significance of treatment; when the 95% confidence intervals of the parameter estimate did not include zero, the estimate was considered to be significant

Dependent variable	Estimate	SE	*t*	MCMC lower limit	MCMC upper limit	Significance
Non-calcified algal crusts	14.945	2.856	5.232	9.057	20.975	*
Calcified algal crusts	6.293	1.605	3.920	2.850	9.446	*
Bare rock	2.055	0.685	3.001	0.604	3.610	*
Solitary invertebrates	2.971	0.985	3.018	0.131	5.549	*
Bryozoans	–1.074	2.007	–0.535	–5.147	2.877	ns
Sponges	0.950	0.745	1.276	–0.570	2.455	ns
Other clonal invertebrates	–2.057	2.725	–0.755	–7.848	3.618	ns
Hydroids	–4.682	1.814	–2.581	–8.497	–0.672	*
Clonal ascidians	–10.052	3.072	–3.273	–16.417	–3.739	*
Macroalgae	–8.104	3.290	–2.463	–15.157	–1.320	*
Prey richness	–1.852	1.047	–1.769	–3.889	0.344	ns
Prey evenness	0.096	0.028	3.455	0.036	0.159	*
Consumer richness	1.185	0.494	2.398	0.171	2.228	*
Chiton density	11.100	4.506	2.464	1.915	20.496	*

Table S5. Results of a linear mixed-effects model testing the effects of urchin density and prey richness on available space (logit transformed) in quadrats at the end of the experiment in 2009. Transect was nested within site; both were treated as random effects. A Monte Carlo Markov chain (MCMC) resampling procedure (n = 5000) assessed the significance of the predictors; when the 95% confidence intervals of the parameter estimate did not include zero, the estimate was considered to be significant

	Estimate	SE	*t*	MCMC lower limit	MCMC upper limit	Significance
Urchin density (UD)	1.014	0.175	5.804	0.654	1.336	*
Prey richness (PR)	–0.024	0.025	–0.947	–0.078	0.022	ns
UD × PR	–0.033	0.009	–3.482	–0.051	–0.013	*

Table S6. R script for the structural equation models representing four alternative hypotheses among log (x + 1) transformed urchin density (urchin.ln), log (x + 1) transformed chiton density (chiton.ln), logit transformed available space (space.logit), and prey richness (prey.rich).

```
# A. Urchin facilitation, chiton grazing (saturated model)
mod.A <- '
# regressions
space.logit ~ urchin.ln
prey.rich ~ urchin.ln
space.logit ~ chiton.ln
prey.rich ~ chiton.ln
chiton.ln ~ urchin.ln
# covariances
space.logit ~~ prey.rich
' # end model

# B. No facilitation, chiton grazing
mod.B <- '
# regressions
space.logit ~ urchin.ln
prey.rich ~ urchin.ln
space.logit ~ chiton.ln
prey.rich ~ chiton.ln
chiton.ln ~ 0*urchin.ln
# covariances
space.logit ~~ prey.rich
' # end model

# C. Urchin facilitation, no chiton grazing
mod.C <- '
# regressions
space.logit ~ urchin.ln
prey.rich ~ urchin.ln
space.logit ~ 0*chiton.ln
prey.rich ~ 0*chiton.ln
chiton.ln ~ urchin.ln
# covariances
space.logit ~~ prey.rich
' # end model

# D. No facilitation, no chiton grazing
mod.D <- '
# regressions
space.logit ~ urchin.ln
prey.rich ~ urchin.ln
space.logit ~ 0*chiton.ln
prey.rich ~ 0*chiton.ln
chiton.ln ~ 0*urchin.ln
# covariances
space.logit ~~ prey.rich
' # end model
```

Table S7. Covariance matrices, means, and observations for the survey, experimental, and multi-group StEM analyses. Variables include log(x + 1)-transformed urchin density (urchin.ln), log(x + 1)-transformed chiton density (chiton.ln), logit-transformed available space (space.logit), and prey richness (prey.rich)

Survey
72 observations

	space.logit	prey.rich	chiton.ln	urchin.ln	mean
space.logit	1.780	–1.855	1.254	0.567	–1.544
prey.rich	–1.855	12.784	–1.488	–1.091	12.222
chiton.ln	1.254	–1.488	2.032	0.521	1.368
urchin.ln	0.567	–1.091	0.521	0.639	–1.133

Experiment
108 observations

	space.logit	prey.rich	chiton.ln	urchin.ln	mean
space.logit	1.059	–2.072	0.435	0.796	–0.810
prey.rich	–2.072	19.691	–0.821	–0.671	14.648
chiton.ln	0.435	–0.821	0.455	0.328	2.987
urchin.ln	0.796	–0.671	0.328	1.150	–0.154

Multi–group analysis
180 observations

	Survey					**Experiment**				
	space.logit	prey.rich	chiton.ln	urchin.ln	mean	space.logit	prey.rich	chiton.ln	urchin.ln	mean
space.logit	1.650	–1.575	1.020	0.458	–1.544	1.072	–2.141	0.446	0.825	–0.810
prey.rich	–1.575	12.327	–1.386	–0.572	12.222	–2.141	19.797	–0.580	–1.031	14.648
chiton.ln	1.020	–1.386	1.829	0.206	1.368	0.446	–0.580	0.483	0.371	2.987
urchin.ln	0.458	–0.572	0.206	0.639	–1.133	0.825	–1.031	0.371	1.150	–0.154