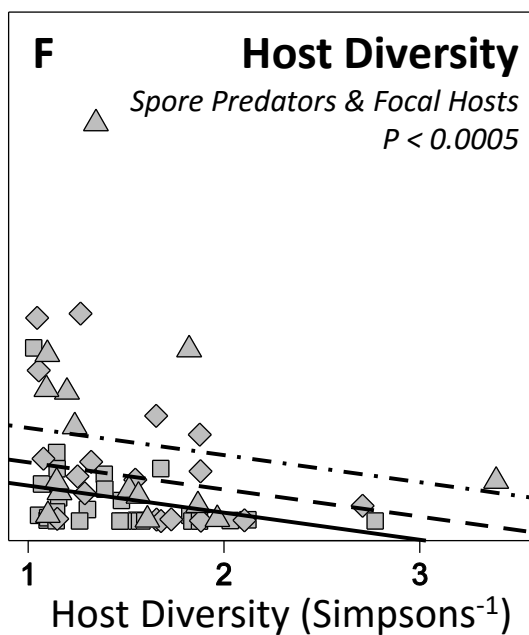
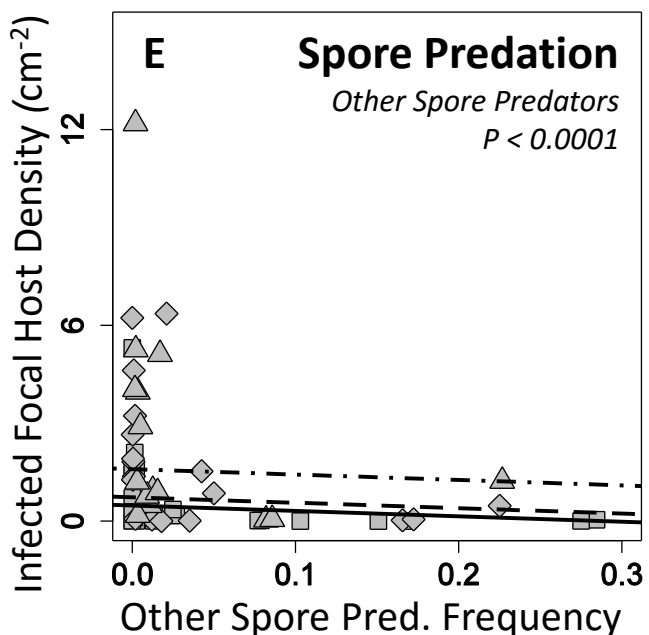
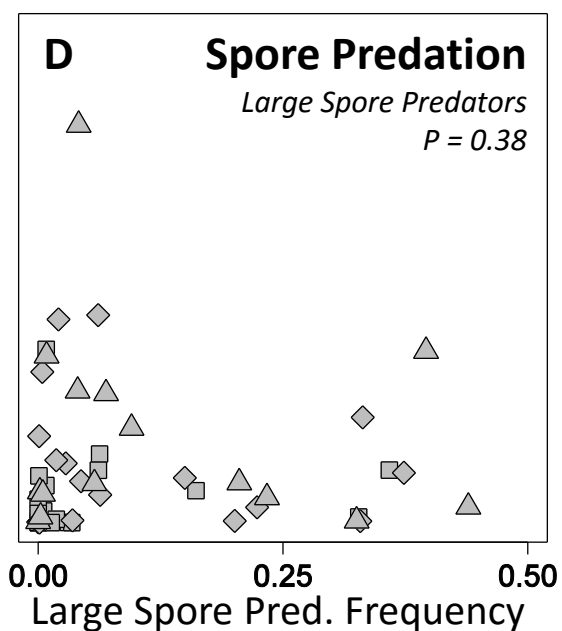
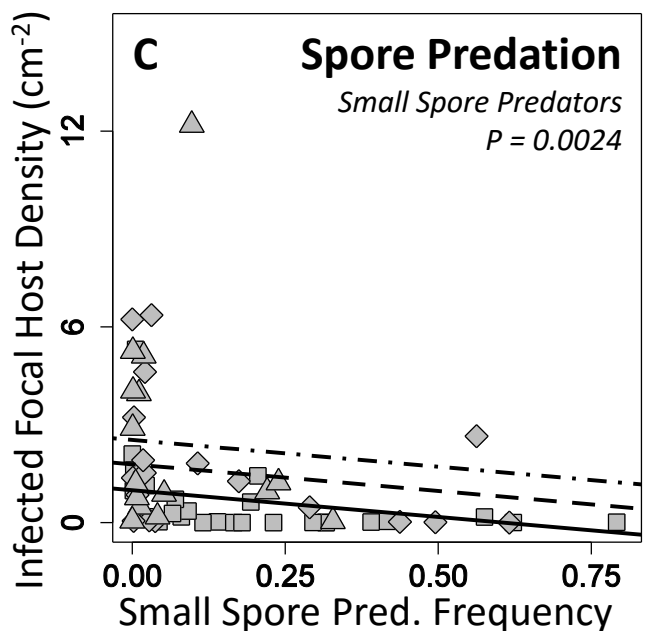
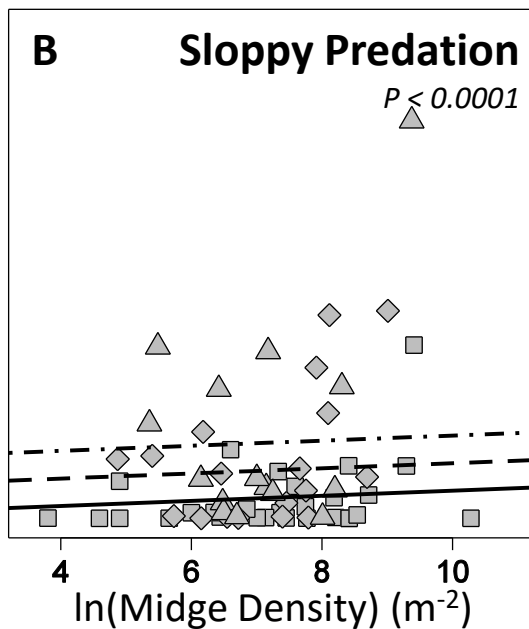
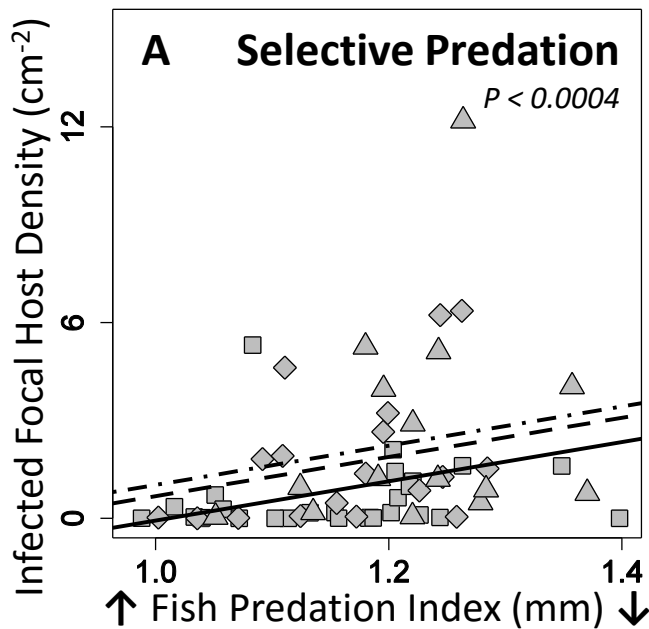





## SUPPORTING INFORMATION

### Appendix S1

In this Appendix, we first show correlations between three modes of predation and density of infected focal hosts (*Daphnia dentifera*).

Then, we provide additional details of our path models. First we summarize the test statistic criteria used to judge each model (Table S1). Then, we report all parameters of the path model predicting infection prevalence including host diversity (path model 1; Fig. 6; Table S2), the model predicting density of infected hosts (path model 2; Fig. 7 A; Table S3), and its analogue predicting infection prevalence without host diversity (path model 3; Fig. 7 B; Table S4).



**Legend:** 2009  2010  2014 

**Figure S1.** Three modes of predation (Table 1) are correlated with density of infected focal hosts (*Daphnia dentifera*). Infected host density is mean number of infected focal hosts per square centimeter during an epidemic season. Each point is a lake population in a given year.

**A)** Selective predation: fish predation is indexed by body size of adult focal hosts (mm). Smaller size = more fish predation (↑); larger size = less (↓). More fish predation (left on x-axis) correlated with lower density of infected hosts. **B)** Sloppy predation: more midge predators (*Chaoborus*) correlated with density of infected hosts. **C-E)** Spore predation: density of infected hosts dropped with **C)** higher frequencies small spore predators (*Ceriodaphnia*), but **D)** did not change with frequency of large spore predators (*D. pulicaria*). **E)** It also dropped with higher frequencies of other spore predators. **F)** Host diversity: higher cladoceran diversity also correlated with lower density of infected focal hosts, consistent with a dilution effect.

Regression models were fit with random “lake” effects, fixed “year” effects, and flexible variance functions to account for heteroscedasticity in the data.

**Table S1.** Test statistics, cutoff criteria for determining good model fit, and statistics of all three path models (Figs. 6-7). Test statistics exceeding the desired cutoff criteria confirm that the hypothesized model is a relatively good fit for the observed data (Hu and Bentler 1999). All results use a robust Satorra-Bentler chi square (Satorra and Bentler 2001).

<b>Test Statistic</b>	<b>Desired Cutoff</b>	<b>Model 1 (Fig. 5)</b>	<b>Model 2 (Fig. 7A)</b>	<b>Model 3 (Fig. 7B)</b>
Satorra-Bentler Chi Square	$P$ value > 0.05	$P = 0.903$	$P = 0.317$	$P = 0.404$
	<sup>1</sup>	$df = 9$	$df = 6$	$df = 6$
Comparative Fit Index (CFI)	CFI > 0.95	1.000	0.985	0.997
Tucker Lewis Index (TLI)	TLI > 0.95	1.152	0.948	0.990
Root Mean Square Error of Approx. (RMSEA)	RMSEA < 0.06	0.000	0.053	0.022
	<sup>2</sup>	(0.000-0.066)	(0.000-0.180)	(0.000-0.163)
Standardized Root Mean Square Residual (SRMR)	SRMR < 0.08	0.044	0.070	0.066

<sup>1</sup> Key to abbreviations:  $df$  = degrees of freedom. <sup>2</sup> 90% confidence interval

**Table S2.** Parameters for the path model predicting infection prevalence in focal hosts, including host diversity as a driver (path model 1; Fig. 6). Bold lines indicate significant or trending relationships.

Dep. Var. <sup>1</sup>		Par. <sup>1</sup>	SE <sup>1</sup>	Z-value	<i>P</i> <sup>1</sup>	Stand.
/ Model	Explanatory Variable	Est.		(Wald		Par.
Component				Statistic)		Est. <sup>1</sup>
Infection	<b>Small Spore Predators</b>	<b>-0.094</b>	<b>0.047</b>	<b>-1.981</b>	<b>0.048</b>	<b>-0.231</b>
Prevalence ~	Fish Predation Index	0.082	0.113	0.720	0.471	0.098
	<b>Midge Density</b>	<b>0.017</b>	<b>0.008</b>	<b>2.231</b>	<b>0.026</b>	<b>0.294</b>
	Other Spore Predators	-0.359	0.220	-1.633	0.103	-0.332
	Host Diversity	0.011	0.040	0.271	0.786	0.063
Host	<b>Other Spore Predators</b>	<b>4.212</b>	<b>0.873</b>	<b>4.824</b>	<b>0.000</b>	<b>0.664</b>
Diversity ~	<b>Small Spore Predators</b>	<b>0.868</b>	<b>0.269</b>	<b>3.230</b>	<b>0.001</b>	<b>0.365</b>
	<b>Large Spore Predators</b>	<b>1.754</b>	<b>0.149</b>	<b>11.787</b>	<b>0.000</b>	<b>0.479</b>
Small Spore	<b>Fish Predation Index</b>	<b>-0.718</b>	<b>0.232</b>	<b>-3.099</b>	<b>0.002</b>	<b>-0.351</b>
Predators~	<b>Refuge Size</b>	<b>-0.038</b>	<b>0.015</b>	<b>-2.621</b>	<b>0.009</b>	<b>-0.251</b>
	Midge Density	-0.006	0.018	-0.322	0.747	-0.039
Large Spore	<b>Fish Predation Index</b>	<b>0.337</b>	<b>0.109</b>	<b>3.093</b>	<b>0.002</b>	<b>0.254</b>
Predators~	<b>Refuge Size</b>	<b>0.059</b>	<b>0.013</b>	<b>4.405</b>	<b>0.000</b>	<b>0.600</b>
	Midge Density	-0.007	0.007	-1.038	0.299	-0.075
Fish Predation	<b>Refuge Size</b>	<b>0.022</b>	<b>0.008</b>	<b>2.853</b>	<b>0.004</b>	<b>0.297</b>
Index~						

Modeled	Sp. Pred. 1 ~~ Sp. Pred. 2	-0.001	0.001	-0.986	0.324	-0.085
Covariances:	Sp. Pred. 2 ~~ Other Sp. Pred.	0.001	0.001	1.211	0.226	0.108
	Sp. Pred. 1 ~~ Other Sp. Pred.	0.003	0.002	1.334	0.182	0.216
	<b>Fish Pred. ~~ Midge Density</b>	<b>0.033</b>	<b>0.017</b>	<b>1.942</b>	<b>0.052</b>	<b>0.281</b>
Intercepts:	Infection Prevalence	-0.140	0.128	-1.089	0.276	-1.801
	Host Diversity	1.077	0.063	16.985	0.000	2.369
	Small Spore Predators	1.087	0.241	4.511	0.000	5.680
	Large Spore Predators	-0.342	0.111	-3.078	0.002	-2.757
	Fish Predation Index	1.146	0.018	62.048	0.000	12.240
	Midge Density	7.162	0.233	30.677	0.000	5.474
	Other Spore Predators	0.040	0.014	2.852	0.004	0.564
	Refuge Size	1.317	0.210	6.266	0.000	1.050
Variances:	Infection Prevalence	0.004	0.001			0.696
	Host Diversity	0.038	0.013			0.185
	Small Spore Predators	0.028	0.007			0.752
	Large Spore Predators	0.008	0.002			0.490
	Fish Predation Index	0.008	0.002			0.912
	Midge Density	1.711	0.350			1.000
	Other Spore Predators	0.005	0.002			1.000
	Refuge Size	1.575	0.364			1.000

<sup>1</sup> Key to abbreviations: Dep. Var. = dependent variable; Par. Est. = parameter estimate; SE: =

Standard error;  $P$  =  $P$ -value of parameter estimate; Stand. = standardized

**Table S3.** Parameters for the path model predicting density of infected focal hosts (path model 2; Fig. 7 A). Bold lines indicate significant or trending relationships.

Dep. Var. <sup>1</sup> / Model Component	Explanatory Variable	Par. <sup>1</sup> Est.	SE <sup>1</sup>	Z-value (Wald Statistic)	<i>P</i> <sup>1</sup>	Stand. Par. Est. <sup>1</sup>
Density of Infected Focal Hosts~	Small Spore Predators	-0.131	0.093	-1.414	0.157	-0.116
	Fish Predation Index	0.124	0.295	0.419	0.675	0.054
	Midge Density	0.031	0.024	1.319	0.187	0.190
	<b>Focal Host Density</b>	<b>0.854</b>	<b>0.267</b>	<b>3.199</b>	<b>0.001</b>	<b>0.500</b>
Small Spore Predators~	<b>Fish Predation Index</b>	<b>-0.723</b>	<b>0.276</b>	<b>-2.617</b>	<b>0.009</b>	<b>-0.358</b>
	<b>Refuge Size</b>	<b>-0.032</b>	<b>0.015</b>	<b>-2.091</b>	<b>0.037</b>	<b>-0.211</b>
	Midge Density	-0.002	0.017	-0.136	0.892	-0.016
Large Spore Predators~	<b>Fish Predation Index</b>	<b>0.312</b>	<b>0.105</b>	<b>2.965</b>	<b>0.003</b>	<b>0.236</b>
	<b>Refuge Size</b>	<b>0.060</b>	<b>0.013</b>	<b>4.477</b>	<b>0.000</b>	<b>0.608</b>
	Midge Density	-0.007	0.007	-0.934	0.350	-0.070
Fish Pred. Index~	<b>Refuge Size</b>	<b>0.022</b>	<b>0.008</b>	<b>2.853</b>	<b>0.004</b>	<b>0.297</b>
Modeled Covariances:	Sp. Pred. 1 ~~ Sp. Pred. 2	-0.002	0.001	-1.316	0.188	-0.120
	<b>Sp. Pred. 1 ~~ Focal Host Dens.</b>	<b>-0.005</b>	<b>0.003</b>	<b>-1.810</b>	<b>0.070</b>	<b>-0.240</b>
	<b>Fish Pred. In. ~~ Midge Dens.</b>	<b>0.033</b>	<b>0.017</b>	<b>1.942</b>	<b>0.052</b>	<b>0.281</b>
	Sp. Pred. 2 ~~ Focal Host Dens.	0.000	0.002	-0.255	0.799	-0.032

Intercepts:	Density of Infected Focal Hosts	-0.358	0.372	-0.962	0.336	-1.672
	Small Spore Predators	1.060	0.286	3.710	0.000	5.606
	Large Spore Predators	-0.317	0.108	-2.948	0.003	-2.567
	Fish Predation Index	1.146	0.018	62.048	0.000	12.240
	Midge Density	7.162	0.233	30.677	0.000	5.474
	Focal Host Density	0.182	0.017	10.836	0.000	1.456
	Refuge Size	1.317	0.210	6.266	0.000	1.050
Variances:	Density of Infected Focal Hosts	0.030	0.011			0.658
	Small Spore Predators	0.028	0.007			0.779
	Large Spore Predators	0.008	0.002			0.493
	Fish Predation Index	0.008	0.002			0.912
	Midge Density	1.711	0.350			1.000
	Focal Host Density	0.016	0.003			1.000
	Refuge Size	1.575	0.364			1.000

<sup>1</sup> Key to abbreviations: Dep. Var. = dependent variable; Par. Est. = parameter estimate; SE: =

Standard error;  $P$  =  $P$ -value of parameter estimate; Stand. = standardized



**Table S4.** Parameters for the path model predicting infection prevalence without host diversity as a driver (path model 3; Fig. 7 B). Bold lines indicate significant or trending relationships.

Dep. Var. <sup>1</sup> / Model Component	Explanatory Variable	Par. <sup>1</sup> Est.	SE <sup>1</sup>	Z-value (Wald Statistic)	P <sup>1</sup>	Stand. Par. Est. <sup>1</sup>
Infection	<b>Small Spore Predators</b>	<b>-0.104</b>	<b>0.053</b>	<b>-1.975</b>	<b>0.048</b>	<b>-0.253</b>
Prevalence ~	Fish Predation Index	0.115	0.135	0.853	0.394	0.139
	<b>Midge Density</b>	<b>0.016</b>	<b>0.008</b>	<b>1.999</b>	<b>0.046</b>	<b>0.268</b>
	Focal Host Density	0.039	0.054	0.710	0.478	0.062
Small Spore	<b>Fish Predation Index</b>	<b>-0.723</b>	<b>0.276</b>	<b>-2.617</b>	<b>0.009</b>	<b>-0.358</b>
Predators~	<b>Refuge Size</b>	<b>-0.032</b>	<b>0.015</b>	<b>-2.091</b>	<b>0.037</b>	<b>-0.211</b>
	Midge Density	-0.002	0.017	-0.136	0.892	-0.016
Large Spore	<b>Fish Predation Index</b>	<b>0.311</b>	<b>0.105</b>	<b>2.951</b>	<b>0.003</b>	<b>0.235</b>
Predators~	<b>Refuge Size</b>	<b>0.060</b>	<b>0.013</b>	<b>4.548</b>	<b>0.000</b>	<b>0.609</b>
	Midge Density	-0.007	0.007	-0.933	0.351	-0.070
Fish Pred. Index~	<b>Refuge Size</b>	<b>0.022</b>	<b>0.008</b>	<b>2.853</b>	<b>0.004</b>	<b>0.297</b>
Modeled	Sp. Pred. 1 ~~ Sp. Pred. 2	-0.002	0.001	-1.309	0.191	-0.119
Covariances:	<b>Sp. Pred. 1 ~~ Focal Host Dens.</b>	<b>-0.005</b>	<b>0.003</b>	<b>-1.809</b>	<b>0.070</b>	<b>-0.240</b>
	<b>Fish Pred. In. ~~ Midge Dens.</b>	<b>0.033</b>	<b>0.017</b>	<b>1.942</b>	<b>0.052</b>	<b>0.281</b>
	Sp. Pred. 2 ~~ Focal Host Dens.	0.000	0.001	0.105	0.916	0.019

Intercepts:	Infection Prevalence	-0.172	0.159	-1.084	0.278	-2.217
	Small Spore Predators	1.060	0.286	3.710	0.000	5.606
	Large Spore Predators	-0.317	0.108	-2.934	0.003	-2.560
	Fish Predation Index	1.146	0.018	62.048	0.000	12.240
	Midge Density	7.162	0.233	30.677	0.000	5.474
	Focal Host Density	0.182	0.017	10.836	0.000	1.456
	Refuge Size	1.317	0.210	6.266	0.000	1.050
Variances:	Infection Prevalence	0.005	0.001			0.769
	Small Spore Predators	0.028	0.007			0.779
	Large Spore Predators	0.008	0.002			0.492
	Fish Predation Index	0.008	0.002			0.912
	Midge Density	1.711	0.350			1.000
	Focal Host Density	0.016	0.003			1.000
	Refuge Size	1.575	0.364			1.000

<sup>1</sup> Key to abbreviations: Dep. Var. = dependent variable; Par. Est. = parameter estimate; SE: = Standard error;  $P$  =  $P$ -value of parameter estimate; Stand. = standardized

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