

Supplementary Material

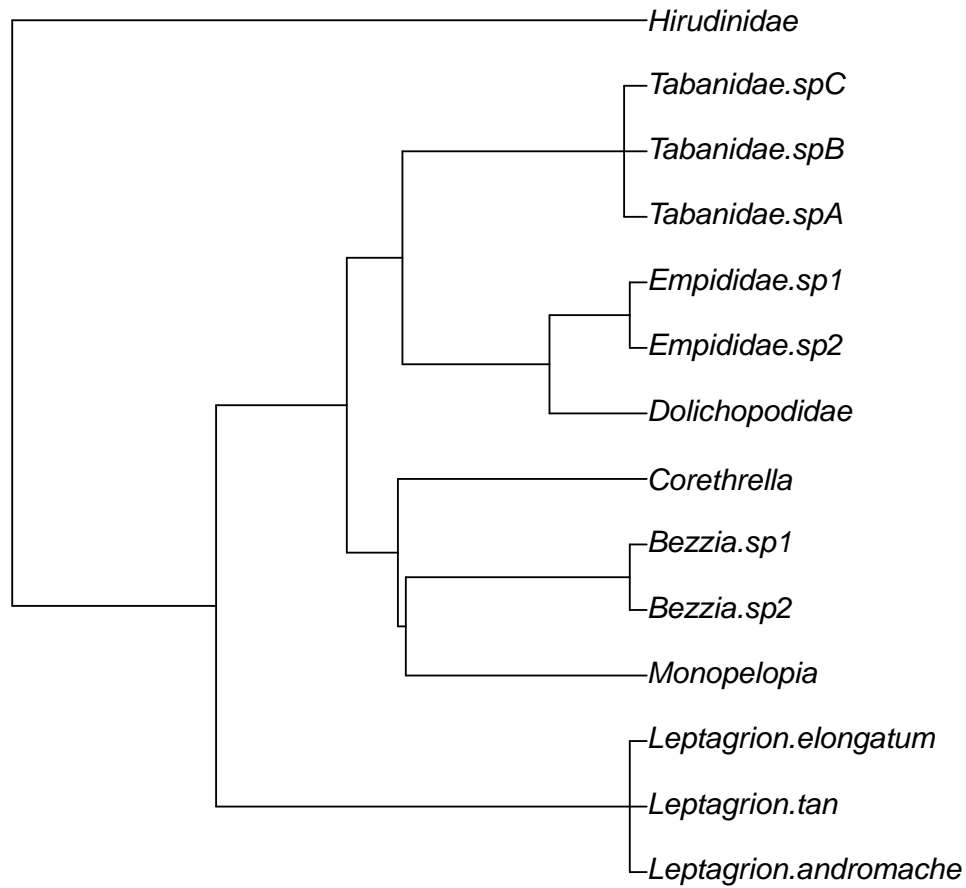
A. Andrew M. MacDonald; Diane S. Srivastava; Gustavo Q. Romero

Predator phylogeny

We used information from timetree.org to add node ages to our tree. This web service provides age estimates from the literature for all available pairs of taxa from the same groups as the searched taxa. Thus deeper nodes are estimated from more taxa and studies than shallower nodes.

Table S1 Studies used to date nodes on our predator phylogeny. When more than one study was available, we used the median value. Papers reporting phylogenetic time estimates include (Foley et al. 1998; Aris-Brosou and Yang 2002; Gaunt and Miles 2002; Otsuka and Sugaya 2003; Wiegmann et al. 2003; Peterson et al. 2004; Blair and Hedges 2005; Blair et al. 2005; Regier et al. 2005; Peterson et al. 2008).

Study taxon 1	Study taxon 2	Taxon.A	Taxon.B	Time	Reference
Ceratopogonidae	Chironomidae	Ceratopogonidae	Chironomidae	213	Bertone et al. 2008
Culicidae	Chironomidae	Chaoborinae	Chironomoidea	220	Bertone et al. 2008
Dolichopodidae	Tabanidae	Nemestrinoidea	Pelecorhynchidae	216	Wiegmann et al. 2003
Dolichopodidae	Empididae	Gloma	Liancalus	86	Wiegmann et al. 2003
Insecta	Hirudinea	Anophelinae	Capitellidae	610	Peterson et al. 2008
Insecta	Hirudinea	Arthropoda	Chaetopteridae	561	Foto et al. 2005
Insecta	Hirudinea	Arthropoda	Annelida	560	Peterson et al. 2004
Insecta	Hirudinea	Crustacea	Annelida	700	Otsuka et al. 2003
Insecta	Hirudinea	Culicidae	Lumbricidae	543	Aris-Brosou et al. 2002
Odonata	Tabanidae	Coenagrionidae	Anophelinae	385	Peterson et al. 2008
Odonata	Tabanidae	Hexagenia	Forficulidae	151	Regier et al. 2005
Odonata	Tabanidae	Enallagma	gambiae species complex	543	Blair et al. 2005
Odonata	Tabanidae	Hexagenia	Forficulidae	376.5	Regier et al. 2004
Tabanidae	Culicidae	Trichoceroidea	Oestroidea	196	Bertone et al. 2008
Tabanidae	Culicidae	Anopheles	Drosophila	280	Peterson et al. 2008
Tabanidae	Culicidae	Anopheles gambiae	Drosophila melanogaster	419	Blair et al. 2005
Tabanidae	Culicidae	Anopheles	Drosophila	474	Blair et al. 2005
Tabanidae	Culicidae	Aedes	Drosophila	184	Aris-Brosou et al. 2002
Tabanidae	Culicidae	Anopheles	Ceratitidini	265.2	Gaunt et al. 2002
Tabanidae	Culicidae	Culicini	Drosophila	106.2	Foley et al. 1998



11

12 **Figure S1** Predator phylogeny, with dated nodes derived from data in Table 1. When multiple time
 13 estimates were available for the same internal node, we used the median estimate.

14 Diet similarity

15 **Table S2** Proportion of predation in feeding trials. Each cell of the graph represents a predator-prey pair;
 16 note that some pairs are represented more than others (not shown). Composition of these trials was limited
 17 by the abundance of organisms in the field.

	L.elong	L.tan	L.andro	leech	Stibasoma sp.	Monopelopia	Tab.B	Tab.C
Tipulid	0.60	1.00	1.00	1.00	1.00	0.40	0.50	1.00
Culex	0.80	0.57	1.00	0.17		0.00		
Polypedilum.1	1.00	1.00	1.00		0.50	0.60		
Scirtes.A	0.82	0.75	0.80	0.67	0.20			
Chironomus.detriticula	1.00	1.00	1.00		0.80			
Psychodid	1.00		0.80	0.50	0.25			
Hirudinidae	0.17	0.00		0.00				
Ostracoda	0.27	0.62				0.00		
Phylloicus.bromeliarum	0.00	0.12				0.00		
Polypedilum.2	1.00		1.00		0.80			
Scirtes.B	0.57	0.57		0.67				
Monopelopia	1.00	0.75						

Predator diversity experiment

Prey community composition

We estimated the densities of these common prey species based on their abundances in our 2008 observational dataset. We estimated how many of each taxa would be found in a bromeliad of the same size as those we used in our experiment, and adjusted our estimates slightly to account for interannual variation in invertebrate abundance.

Table S4 Densities of prey species used in the 2010 predator diversity experiment.

Species	density
<i>Chironomus detriticula</i>	10
<i>Polypedium marcondesi</i>	4
<i>Polypedium kaingang</i>	2
Psychodid sp. 1	1
<i>Scyrtes</i> sp. A	5
<i>Culex</i> spp.	4
<i>Trentepholia</i> sp.	1

Experimental responses

We calculated means and standard error for every experimental treatment and response variable.

Table S3: Means and standard errors for all response variables for each predator treatment in our manipulative experiment. n = 5 for every pair of numbers, with only two exceptions due to missing values: **elong + leech x growth**, and **leech x decomp**.

treatment	decomp	fine	growth	N	total.surv
andro	0.37 ± 0.028	0.26 ± 0.041	4 ± 0.45	45 ± 6.2	5.8 ± 1.9
control	0.33 ± 0.023	0.38 ± 0.081	4.7 ± 1.2	53 ± 2.9	14 ± 2.7
elong	0.36 ± 0.0077	0.19 ± 0.054	2.9 ± 1.3	45 ± 6	7.8 ± 1.7
elong + andro	0.33 ± 0.024	0.58 ± 0.14	3.3 ± 1.2	52 ± 4.8	5.2 ± 1.4
elong + leech	0.32 ± 0.0083	0.32 ± 0.044	5.4 ± 0.62	43 ± 7.5	9 ± 1.1
elong + tab	0.37 ± 0.024	0.36 ± 0.25	4 ± 0.98	54 ± 7.8	10 ± 1.5
leech	0.35 ± 0.019	0.29 ± 0.092	2.6 ± 1.6	36 ± 5.2	5.2 ± 0.58
tabanid	0.31 ± 0.027	0.24 ± 0.12	5.1 ± 0.95	56 ± 7	5.8 ± 1.4

Differences among treatments

Number of predator species

3

We divided our experimental design into three separate hypothesis tests.

3. **Predator phylogenetic diversity:** We contrast our two predator species treatments to see how increasing PD of the predator assemblage effects our response variables.

Because the first and third hypotheses suggest a ranking of the independent variables (increasing species number and phylogenetic diversity) we used ordinal contrasts in the corresponding linear models.

Table S4: Number of predator species in each experimental treatment.

Nspp	treatment
none	control
one	andro
one	tabanid
one	leech
one	elong
two	elong + andro
two	elong + leech
two	elong + tab

Table S5: The effect of predator species number on all 5 response variables. We used ordinal contrasts to investigate how an increasing number of predator species influenced the response. Treatment order was none < one < two species. (See Table S6). For each non-control treatment, replicates were the mean of all bromeliads with the same predator treatment. Control (no predator) bromeliads were used as independent replicates. Thus there are 5 replicates for the “none” factor level, four replicates of “one predator” and three of “two predators”. Note that we model prey survival using OLS, rather than poisson regression, because we are modeling the distribution of means.

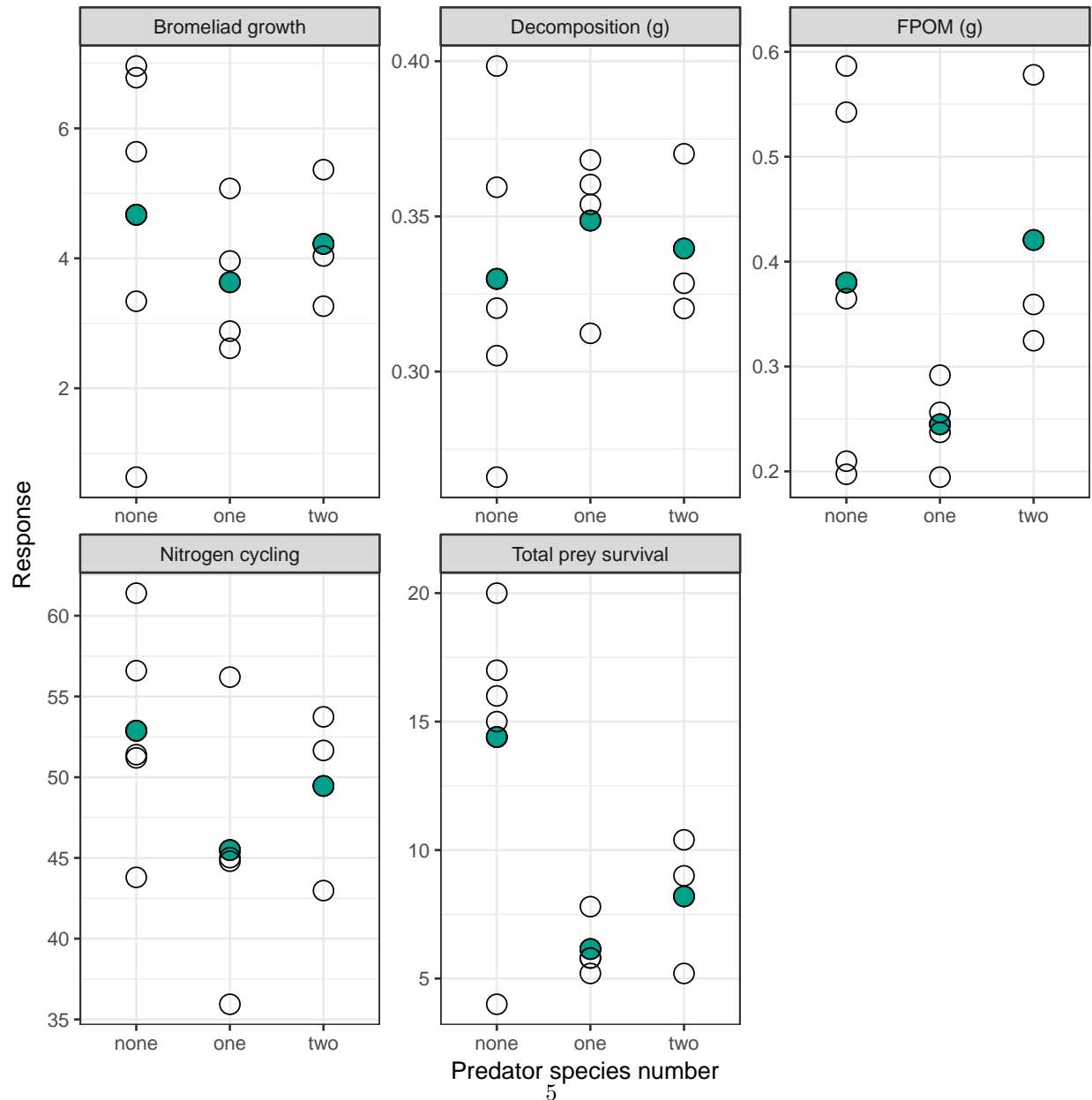
	<i>Dependent variable:</i>				
	Decomposition (g)	FPOM (g)	Bromeliad growth	Nitrogen cycling	Total prey survival
	(1)	(2)	(3)	(4)	(5)
Linear	0.007 (0.020)	0.029 (0.072)	−0.317 (1.015)	−2.418 (3.634)	−4.384* (2.228)
Quadratic	−0.011 (0.020)	0.127 (0.070)	0.664 (0.993)	4.638 (3.557)	4.205* (2.181)
Constant	0.339*** (0.011)	0.349*** (0.041)	4.175*** (0.580)	49.277*** (2.076)	9.583*** (1.273)
Observations	12	12	12	12	12
R ²	0.055	0.267	0.064	0.214	0.497
Adjusted R ²	−0.156	0.104	−0.143	0.039	0.385
Residual Std. Error (df = 9)	0.039	0.139	1.965	7.037	4.315
F Statistic (df = 2; 9)	0.260	1.636	0.310	1.226	4.450**

Note:

*p<0.1; **p<0.05; ***p<0.01

Table S6: Tukey post-hoc tests for the effects of predator species number on each response variable.

response	comparison	diff	lwr	upr	p.adj
Decomposition (g)	one-none	0.02	-0.05	0.09	0.76
Decomposition (g)	two-none	0.01	-0.07	0.09	0.94
Decomposition (g)	two-one	-0.01	-0.09	0.07	0.95
FPOM (g)	one-none	-0.14	-0.40	0.13	0.36
FPOM (g)	two-none	0.04	-0.24	0.32	0.92
FPOM (g)	two-one	0.18	-0.12	0.47	0.27
Bromeliad growth	one-none	-1.04	-4.72	2.64	0.72
Bromeliad growth	two-none	-0.45	-4.46	3.56	0.95
Bromeliad growth	two-one	0.59	-3.60	4.78	0.92
Nitrogen cycling	one-none	-7.39	-20.57	5.79	0.31
Nitrogen cycling	two-none	-3.42	-17.77	10.93	0.79
Nitrogen cycling	two-one	3.97	-11.04	18.98	0.75
Total prey survival	one-none	-8.25	-16.33	-0.17	0.05
Total prey survival	two-none	-6.20	-15.00	2.60	0.18
Total prey survival	two-one	2.05	-7.15	11.25	0.81



⁵⁵ **Figure S2:** The effect of predator species number on each of our response variables. Each dot represents
⁵⁶ the mean ($n = 5$) for different predator treatments. Green dots represent group (i.e. species number) means.

Differences among predator species

Within the single-predator treatments, we tested for difference in our response variables among different predator species.

Table S7 : Contrasting predator species effects. These linear models use treatment contrasts, which contrast all treatments with *L. andromache*. Coefficients (standard error) are given for *L. andromache*, and differences between coefficients (standard error of difference) for all other predators.

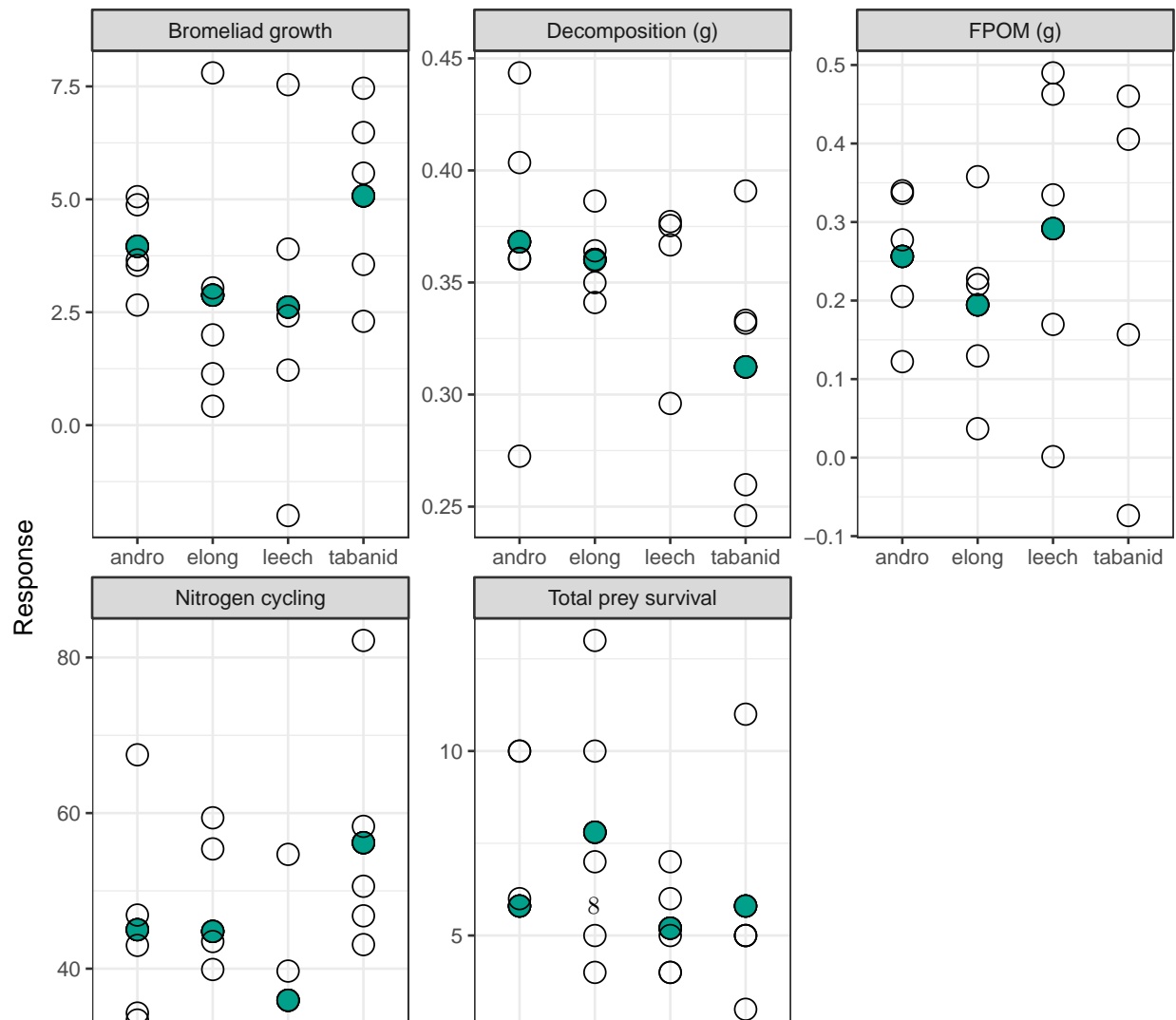
	<i>Dependent variable:</i>				
	Total prey survival	FPOM (g)	Decomposition (g)	Bromeliad growth	Nitrogen cycling
	(1)	(2)	(3)	(4)	(5)
<i>L. elongatum</i>	2.000 (2.069)	-0.062 (0.109)	-0.008 (0.031)	-1.080 (1.622)	-0.220 (8.656)
Hirudinidae	-0.600 (2.069)	0.035 (0.109)	-0.014 (0.033)	-1.344 (1.622)	-9.080 (8.656)
Tabanidae	-0.000 (2.069)	-0.019 (0.115)	-0.056* (0.031)	1.116 (1.622)	11.180 (8.656)
<i>L. andromache</i>	5.800*** (1.463)	0.256*** (0.077)	0.368*** (0.022)	3.960*** (1.147)	45.020*** (6.121)
Observations	20	19	19	20	20
R ²	0.102	0.052	0.205	0.153	0.256
Adjusted R ²	-0.067	-0.137	0.046	-0.006	0.117
Residual Std. Error	3.271 (df = 16)	0.172 (df = 15)	0.049 (df = 15)	2.564 (df = 16)	13.686 (df = 16)
F Statistic	0.603 (df = 3; 16)	0.277 (df = 3; 15)	1.289 (df = 3; 15)	0.961 (df = 3; 16)	1.838 (df = 3; 16)

Note:

*p<0.1; **p<0.05; ***p<0.01

Table S8: Post-hoc Tukey tests for differences between predator species in all 5 responses.

response	comparison	diff	lwr	upr	p.adj
FPOM (g)	elong-andro	-0.06	-0.37	0.25	0.94
FPOM (g)	leech-andro	0.04	-0.28	0.35	0.99
FPOM (g)	tabanid-andro	-0.02	-0.35	0.31	1.00
FPOM (g)	leech-elong	0.10	-0.22	0.41	0.81
FPOM (g)	tabanid-elong	0.04	-0.29	0.37	0.98
FPOM (g)	tabanid-leech	-0.05	-0.39	0.28	0.96
Decomposition (g)	elong-andro	-0.01	-0.10	0.08	0.99
Decomposition (g)	leech-andro	-0.01	-0.11	0.08	0.97
Decomposition (g)	tabanid-andro	-0.06	-0.15	0.03	0.31
Decomposition (g)	leech-elong	-0.01	-0.10	0.09	1.00
Decomposition (g)	tabanid-elong	-0.05	-0.14	0.04	0.44
Decomposition (g)	tabanid-leech	-0.04	-0.14	0.05	0.60
Bromeliad growth	elong-andro	-1.08	-5.72	3.56	0.91
Bromeliad growth	leech-andro	-1.34	-5.98	3.30	0.84
Bromeliad growth	tabanid-andro	1.12	-3.52	5.76	0.90
Bromeliad growth	leech-elong	-0.26	-4.90	4.38	1.00
Bromeliad growth	tabanid-elong	2.20	-2.44	6.84	0.54
Bromeliad growth	tabanid-leech	2.46	-2.18	7.10	0.45
Nitrogen cycling	elong-andro	-0.22	-24.98	24.54	1.00
Nitrogen cycling	leech-andro	-9.08	-33.84	15.68	0.72
Nitrogen cycling	tabanid-andro	11.18	-13.58	35.94	0.58
Nitrogen cycling	leech-elong	-8.86	-33.62	15.90	0.74
Nitrogen cycling	tabanid-elong	11.40	-13.36	36.16	0.57
Nitrogen cycling	tabanid-leech	20.26	-4.50	45.02	0.13



⁶⁶ **Figure S3:** The effect of predator species identity on each of our response variables. Each dot represents
⁶⁷ the observed value for a different predator treatment. Green dots represent group means.

Increasing predator phylogenetic diversity

Our two-species combinations represent a range of increasing phylogenetic distance. By examining differences between these three treatments, we can test how increasing PD *per se* influences our response variables.

Table S9: Effects of increasing phylogenetic diversity of the predator assemblage on 5 response variables. We used linear contrasts, ranking the independent variable by increasing predator PD (see Figure S4). Linear model coefficients (standard error) are shown for Linear, Quadratic and Constant contrasts.

	<i>Dependent variable:</i>				
	Decomposition (g)	FPOM (g)	Bromeliad growth	Nitrogen cycling	Total prey survival
	(1)	(2)	(3)	(4)	(5)
treatment.L	-0.006 (0.020)	-0.179 (0.167)	1.486 (1.027)	-6.138 (6.841)	2.687* (1.354)
treatment.Q	-0.037* (0.020)	0.075 (0.167)	0.227 (0.988)	-5.242 (6.841)	-2.694* (1.354)
Constant	0.340*** (0.012)	0.421*** (0.096)	4.222*** (0.582)	49.460*** (3.950)	8.200*** (0.782)
Observations	15	15	14	15	15
R ²	0.229	0.102	0.161	0.104	0.397
Adjusted R ²	0.101	-0.048	0.009	-0.045	0.296
Residual Std. Error	0.045 (df = 12)	0.372 (df = 12)	2.164 (df = 11)	15.297 (df = 12)	3.028 (df = 12)
F Statistic	1.787 (df = 2; 12)	0.681 (df = 2; 12)	1.056 (df = 2; 11)	0.696 (df = 2; 12)	3.949** (df = 2; 12)

Note:

*p<0.1; **p<0.05; ***p<0.01

Table S10: Tukey post-hoc tests for differences between predator phylogenetic diversity treatments on all response variables.

response	comparison	diff	lwr	upr	p.adj
Decomposition (g)	elong + tab-elong + andro	0.04	-0.03	0.12	0.34
Decomposition (g)	elong + leech-elong + andro	-0.01	-0.08	0.07	0.96
Decomposition (g)	elong + leech-elong + tab	-0.05	-0.13	0.03	0.22
FPOM (g)	elong + tab-elong + andro	-0.22	-0.85	0.41	0.63
FPOM (g)	elong + leech-elong + andro	-0.25	-0.88	0.37	0.55
FPOM (g)	elong + leech-elong + tab	-0.03	-0.66	0.59	0.99
Bromeliad growth	elong + tab-elong + andro	0.77	-2.92	4.47	0.84
Bromeliad growth	elong + leech-elong + andro	2.10	-1.82	6.02	0.35
Bromeliad growth	elong + leech-elong + tab	1.33	-2.59	5.25	0.64
Nitrogen cycling	elong + tab-elong + andro	2.08	-23.73	27.89	0.97
Nitrogen cycling	elong + leech-elong + andro	-8.68	-34.49	17.13	0.65
Nitrogen cycling	elong + leech-elong + tab	-10.76	-36.57	15.05	0.53
Total prey survival	elong + tab-elong + andro	5.20	0.09	10.31	0.05
Total prey survival	elong + leech-elong + andro	3.80	-1.31	8.91	0.16
Total prey survival	elong + leech-elong + tab	-1.40	-6.51	3.71	0.75

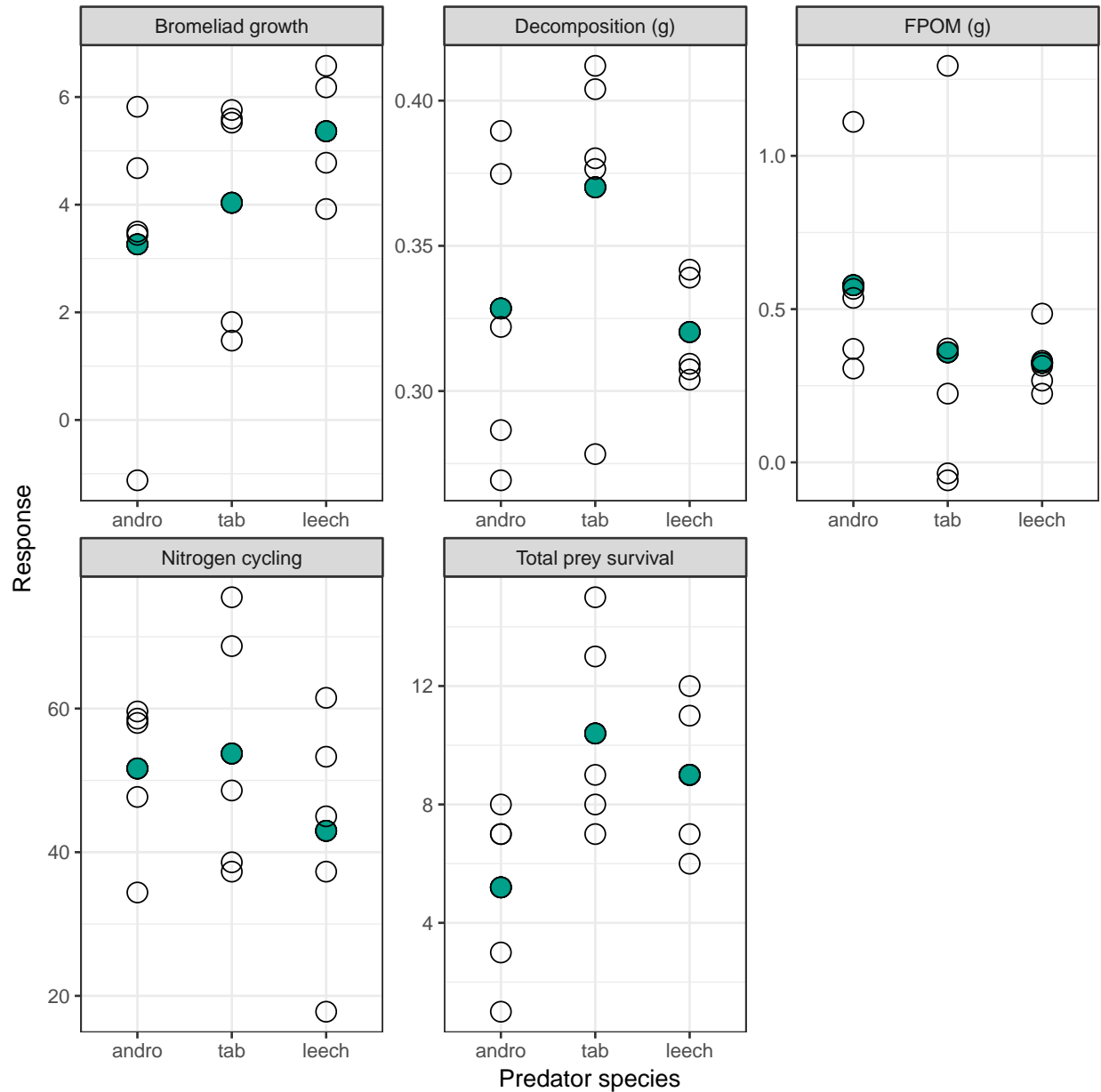


Figure S4: The effect of increasing phylogenetic signal on each of our response variables in our community experiment. In each treatment category, *Leptagrion elongatum* is paired with another predator; these treatments are ordered by increasing phylogenetic diversity. For clarity the axes are labelled with abbreviations for species names: andro = *Leptagrion andromache*, tab = Tabanidae, leech = Hirudinidae.

Correlation matrix

Table S11: Correlation matrix of all variables in our experiment. n = 30 for most of these values. Bold type indicates values of Pearson's product moment correlation with $p < 0.05$.

	decomp	fine	growth	N	total.surv
decomp		0.08	-0.33	0.13	0.15
fine	0.08		0.02	-0.12	-0.09
growth	-0.33	0.02		0.1	0.11
N	0.13	-0.12	0.1		0.2
total.surv	0.15	-0.09	0.11	0.2	

References

- Aris-Brosou, S., and Z. Yang. 2002. Effects of models of rate evolution on estimation of divergence dates with special reference to the metazoan 18S ribosomal RNA phylogeny. *Systematic Biology* 51:703–714.
- Blair, J. E., and S. B. Hedges. 2005. Molecular clocks do not support the Cambrian explosion. *Molecular Biology and Evolution* 22:387–390.
- Blair, J. E., P. Shah, and S. B. Hedges. 2005. Evolutionary sequence analysis of complete eukaryote genomes. *BMC bioinformatics* 6:53.
- Foley, D. H., J. H. Bryan, D. Yeates, and A. Saul. 1998. Evolution and systematics of Anopheles: Insights from a molecular phylogeny of Australasian mosquitoes. *Molecular Phylogenetics and Evolution* 9:262–275.
- Gaunt, M. W., and M. A. Miles. 2002. An Insect Molecular Clock Dates the Origin of the Insects and Accords with Palaeontological and Biogeographic Landmarks. *Molecular Biology and Evolution* 19:748–761.
- Otsuka, J., and N. Sugaya. 2003. Advanced formulation of base pair changes in the stem regions of ribosomal RNAs; its application to mitochondrial rRNAs for resolving the phylogeny of animals. *Journal of Theoretical Biology* 222:447–460.
- Peterson, K. J., J. A. Cotton, J. G. Gehling, and D. Pisani. 2008. The Ediacaran emergence of bilaterians: Congruence between the genetic and the geological fossil records. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences* 363:1435–1443.
- Peterson, K. J., J. B. Lyons, K. S. Nowak, C. M. Takacs, M. J. Wargo, and M. A. McPeck. 2004. Estimating metazoan divergence times with a molecular clock. *Proceedings of the National Academy of Sciences of the United States of America* 101:6536–6541.
- Regier, J. C., J. W. Shultz, and R. E. Kambic. 2005. Pancrustacean phylogeny: Hexapods are terrestrial crustaceans and maxillopods are not monophyletic. *Proceedings. Biological Sciences / The Royal Society* 272:395–401.
- Wiegmann, B. M., D. K. Yeates, J. L. Thorne, and H. Kishino. 2003. Time flies, a new molecular time-scale for brachyceran fly evolution without a clock. *Systematic Biology* 52:745–756.