

Supplementary Material

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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.

study taxa	Reference	Taxon.A	Taxon.B	Time	Year
Ceratopogonidae_Chironomidae	Bertone et al.	Ceratopogonidae	Chironomidae	213	2008
CulicidaetoChironomidae	Bertone et al.	Chaoborinae	Chironomoidea	220	2008
dolicho_tabanid	Wiegmann et al.	Nemestrinoidea	Pelecorhynchidae	216	2003
empididaeDolichopodidae	Wiegmann et al.	Gloma	Liancalus	86	2003
insects.to.leeches	Peterson et al.	Anophelinae	Capitellidae	610	2008
insects.to.leeches	Foto et al.	Arthropoda	Chaetopteridae	561	2005
insects.to.leeches	Peterson et al.	Arthropoda	Annelida	560	2004
insects.to.leeches	Otsuka et al.	Crustacea	Annelida	700	2003
insects.to.leeches	Aris-Brosou et al.	Culicidae	Lumbricidae	543	2002
odonata-Tabanidae	Peterson et al.	Coenagrionidae	Anophelinae	385	2008
odonata-Tabanidae	Regier et al.	Hexagenia	Forficulidae	151	2005
odonata-Tabanidae	Blair et al.	Enallagma	gambiae species complex	543	2005
odonata-Tabanidae	Regier et al.	Hexagenia	Forficulidae	376.5	2004
tabanidae_culidicae_ie_Diptera	Bertone et al.	Trichoceroidea	Oestroidea	196	2008
tabanidae_culidicae_ie_Diptera	Peterson et al.	Anopheles	Drosophila	280	2008
tabanidae_culidicae_ie_Diptera	Blair et al.	Anopheles gambiae	Drosophila melanogaster	419	2005
tabanidae_culidicae_ie_Diptera	Blair et al.	Anopheles	Drosophila	474	2005
tabanidae_culidicae_ie_Diptera	Aris-Brosou et al.	Aedes	Drosophila	184	2002
tabanidae_culidicae_ie_Diptera	Gaunt et al.	Anopheles	Ceratitidini	265.2	2002
tabanidae_culidicae_ie_Diptera	Foley et al.	Culicini	Drosophila	106.2	1998

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

Phylogenetic distance and similarity in distribution and diet: non-linear models

Both biological and statistical effects could cause a nonlinear relationship between similarity in distribution or diet and phylogenetic distance. Biological, because the fixed composition of the prey community limits dissimilarity between predators. Statistical, because Pianka's similarity index is bounded by 0 and 1 and therefore an OLS linear model could potentially predict impossible (i.e. < 0 or > 1) values. We fit several nonlinear equations to our data in order to describe how the amount of divergence in distribution or diet between predators changed over evolutionary time.

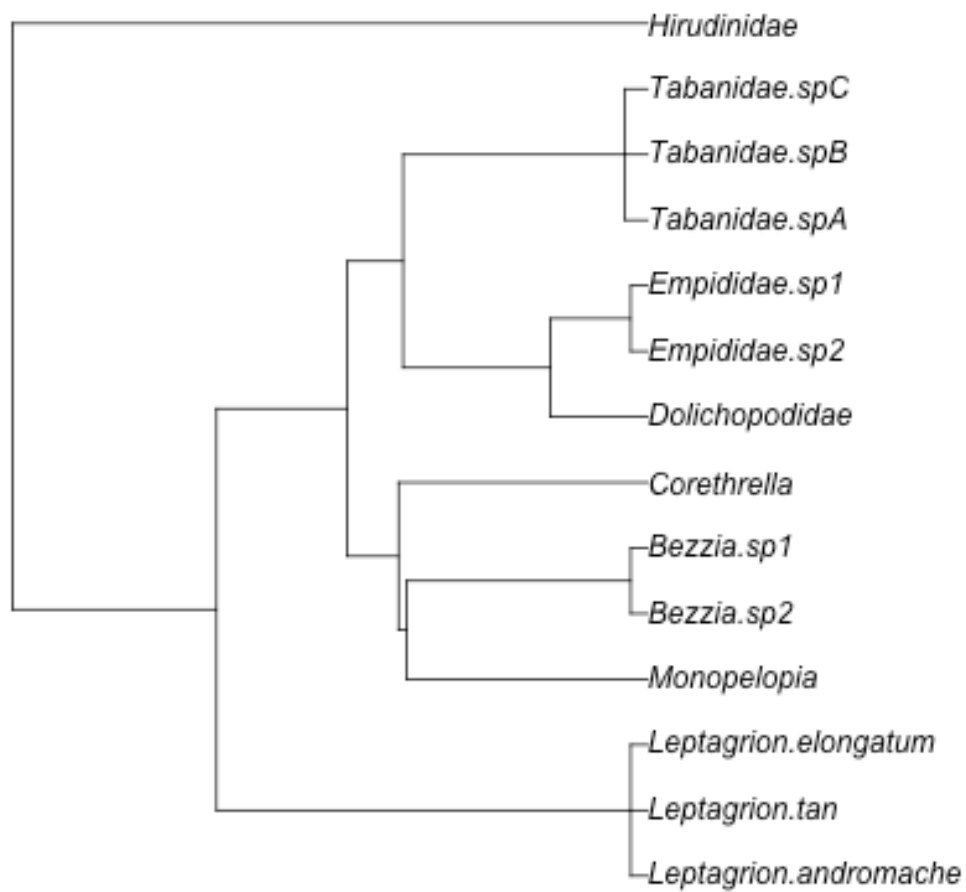


Figure 1: plot of chunk FIG_predatorphylo

Distributional similarity

Table S2 Linear, nonlinear and constant functions fit to the relationship of diet similarity and predator phylogenetic distance.

model	Equation	AIC
bellshaped	$a \times (PD)^2 + b \times PD + c$	20.77
quadratic	$a \times x + b$	21.51
linear	$\frac{c \times e^{(a \times PD)}}{(c \times e^{(a \times PD)} + (1 - c))}$	21.56
exponential	$b \times e^{(a \times PD)}$	21.92
constant	$peak \times e^{(-1 \times (PD)^2 / a)}$	21.97

Diet similarity

Table S3 Proportion of predation in feeding trials. Each cell of the graph represents a predator-prey pair; note that some pairs are represented more than others (not shown). Composition of these trials was limited 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.detrictula	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						

Table S3 Linear, nonlinear and constant functions fit to the relationship of diet similarity and predator phylogenetic distance. These models are weighted by the number of prey species tested, but do not correct for the phylogenetic non-independence of the predator taxa.

model	Equation	AIC
quadratic	$a \times x + b$	-638
exponential	$b \times e^{(a \times PD)}$	-634.9
linear	$\frac{c \times e^{(a \times PD)}}{(c \times e^{(a \times PD)} + (1 - c))}$	-634.7
bellshaped	$a \times (PD)^2 + b \times PD + c$	-630.5
constant	$peak \times e^{(-1 \times (PD)^2 / a)}$	-625.2

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 S5: 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

We divided our experimental design into three separate hypothesis tests.

- 1. Predator species number:** We compared the five control replicates with the means of the four single species treatments and the means of the three two-species treatments. This tests whether species number *per se* has an effect.
- 2. Predator species identity:** We compared the four different predator taxa to see if any of these differed in their effect on the community.

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 S6: 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 S7: 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 S8: Tukey post-hoc tests for the effects of predator species number on each response variable.

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

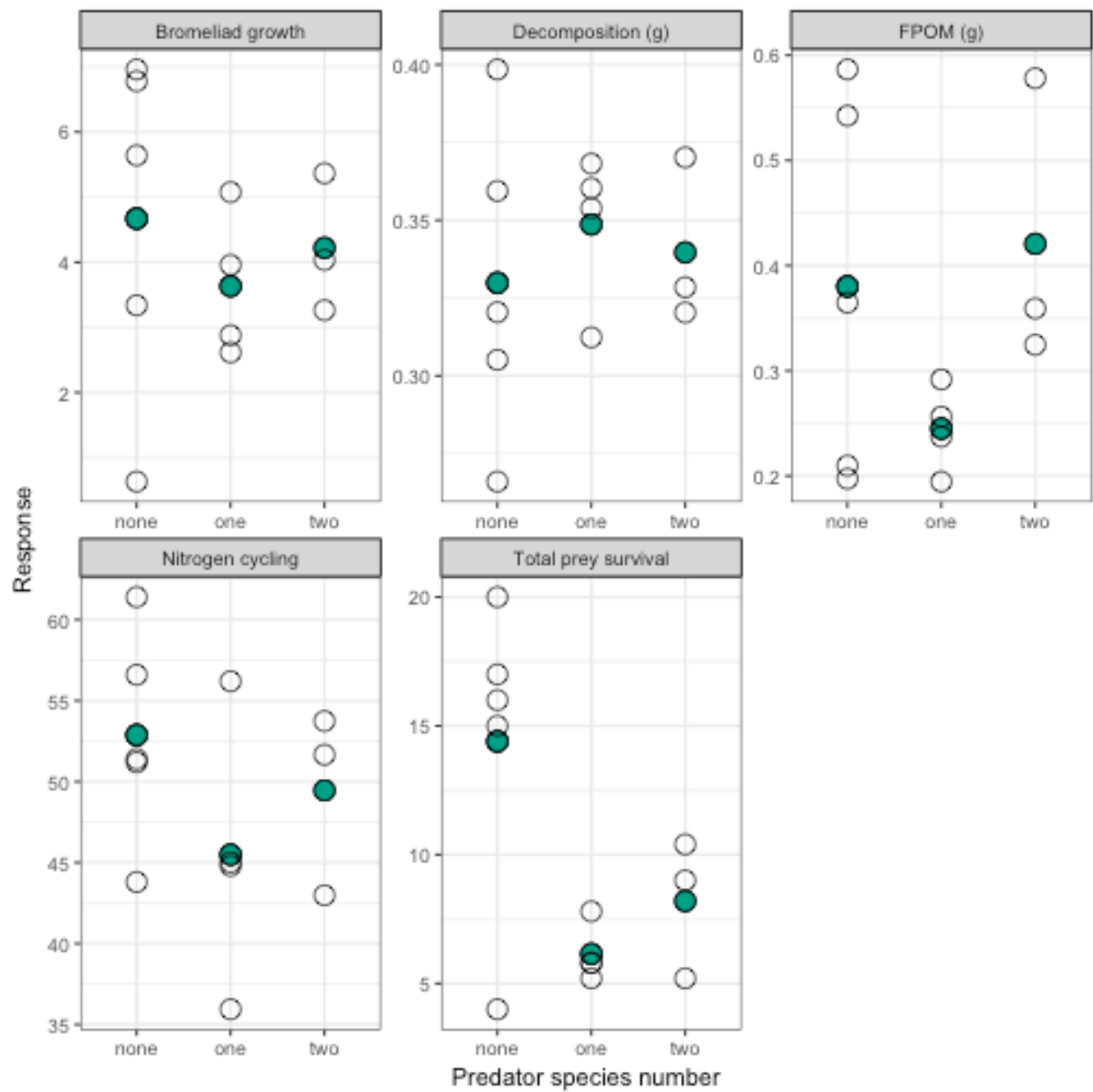


Figure 2: plot of chunk FIG_spp_number

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

Differences among predator species

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

Table S9 : 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.

	Dependent variable:				
	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 S10: Post-hoc Tukey tests for differences between predator species in all 5 responses.

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

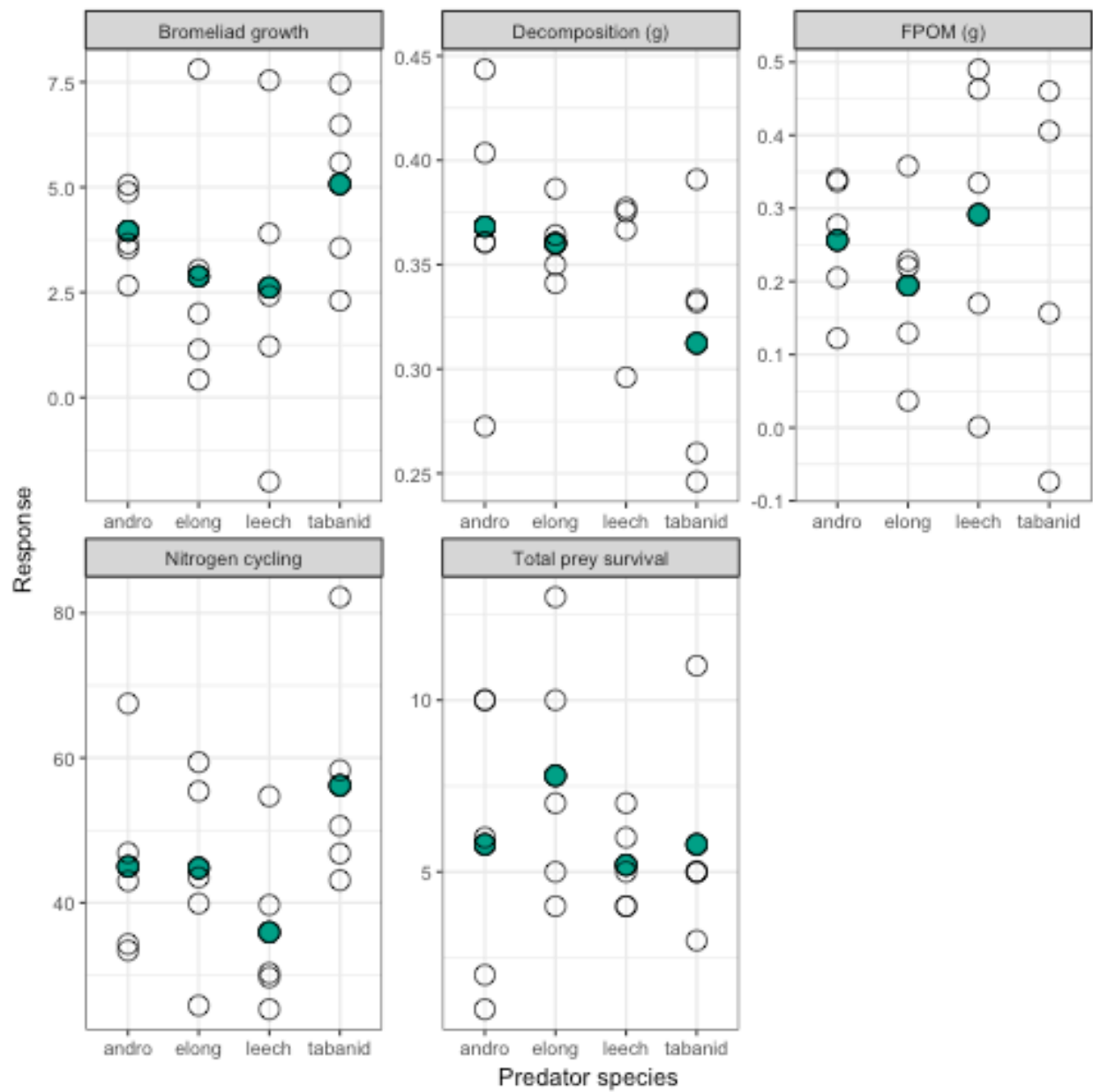


Figure 3: plot of chunk FIG_predsp

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

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 S11: 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.

	Dependent variable:				
	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 S12: 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 S13: 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	

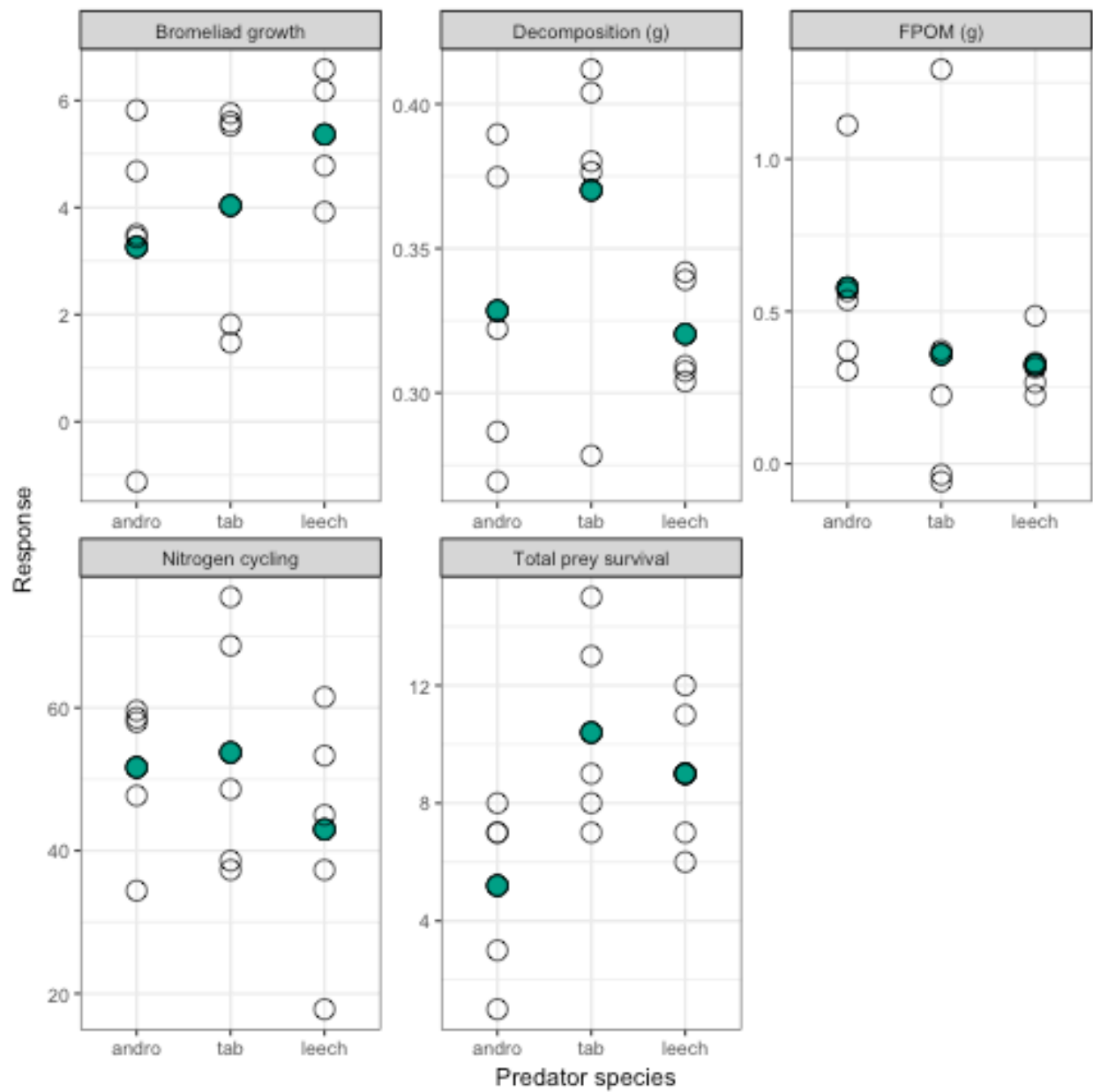


Figure 4: plot of chunk FIG_twopred