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

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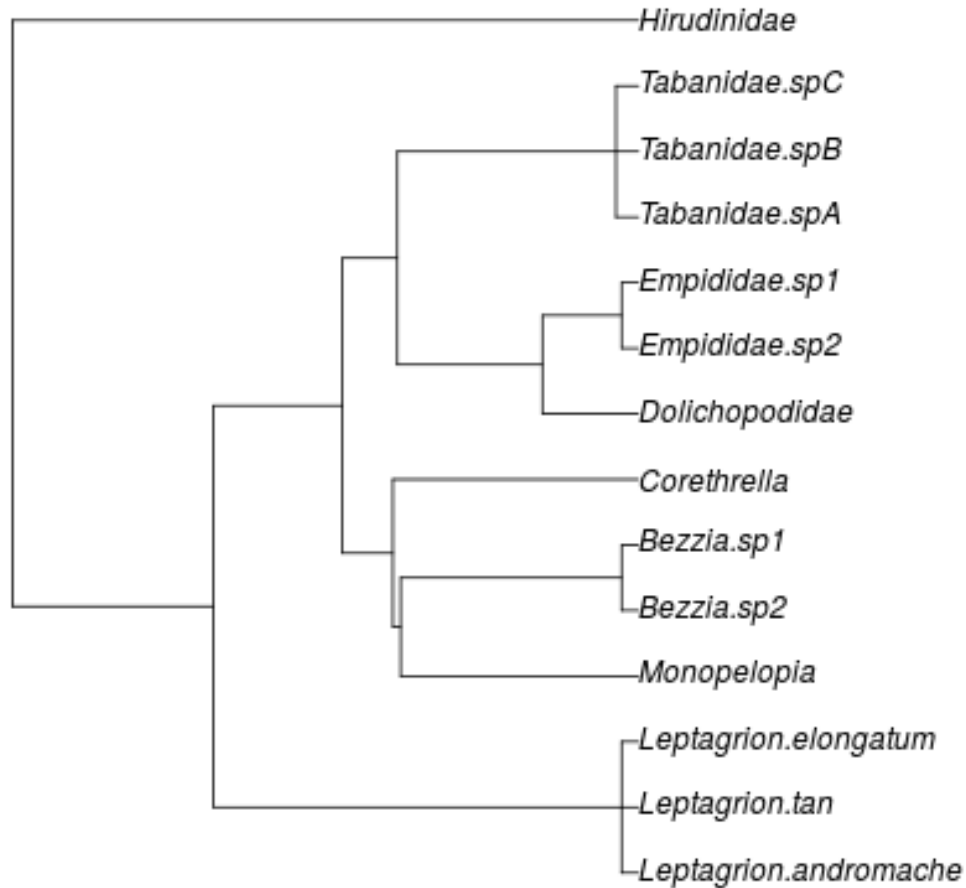
Figure S1 Predator phylogeny, with dated nodes derived from data in Table 1. When multiple time estimates were available for the same internal node, we used the median estimate.

Phylogenetic distance and similarity in distribution and diet: nonlinear models

Both biological and statistical effects could cause a nonlinear relationship between similarity in distribution or diet and phylogenetic distance. Biological, because the fixed compositon 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.

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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.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						

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
Chironomus detriticula	10
Polypedium marcondesi	4
Polypedium kaingang	2
Psychodid sp. 1	1
Scyrtes sp. A	5
Culex spp.	4
Trentepholia 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	total.surv	fine	decomp	growth	N
andro	5.8 ± 1.9	0.26 ± 0.041	0.37 ± 0.028	4 ± 0.45	45 ± 6.2
control	14 ± 2.7	0.38 ± 0.081	0.33 ± 0.023	4.7 ± 1.2	53 ± 2.9
elong	7.8 ± 1.7	0.19 ± 0.054	0.36 ± 0.0077	2.9 ± 1.3	45 ± 6
elong + andro	5.2 ± 1.4	0.58 ± 0.14	0.33 ± 0.024	3.3 ± 1.2	52 ± 4.8
elong + leech	9 ± 1.1	0.32 ± 0.044	0.32 ± 0.0083	5.4 ± 0.62	43 ± 7.5
elong + tab	10 ± 1.5	0.36 ± 0.25	0.37 ± 0.024	4 ± 0.98	54 ± 7.8
leech	5.2 ± 0.58	0.29 ± 0.092	0.35 ± 0.019	2.6 ± 1.6	36 ± 5.2
tabanid	5.8 ± 1.4	0.24 ± 0.12	0.31 ± 0.027	5.1 ± 0.95	56 ± 7

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.

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

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

56 **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

57 **Table S7**: The effect of predator species number on all 5 response variables. We used ordinal contrasts
58 to investigate how an increasing number of predator species influenced the response. Treatment order was
59 none < one < two species. (See Table S6). For each non-control treatment, replicates were the mean of all
60 bromeliads with the same predator treatment. Control (no predator) bromeliads were used as independent
61 replicates. Thus there are 5 replicates for the "none" factor level, four replicates of "one predator" and three
62 of "two predators". Note that we model prey survival using OLS, rather than poisson regression, because we
63 are modeling the distribution of means.

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

Note: *p<0.1; **p<0.05; ***p<0.01

65 **Table S8**: Tukey post-hoc tests for the effects of predator species number on each response variable.

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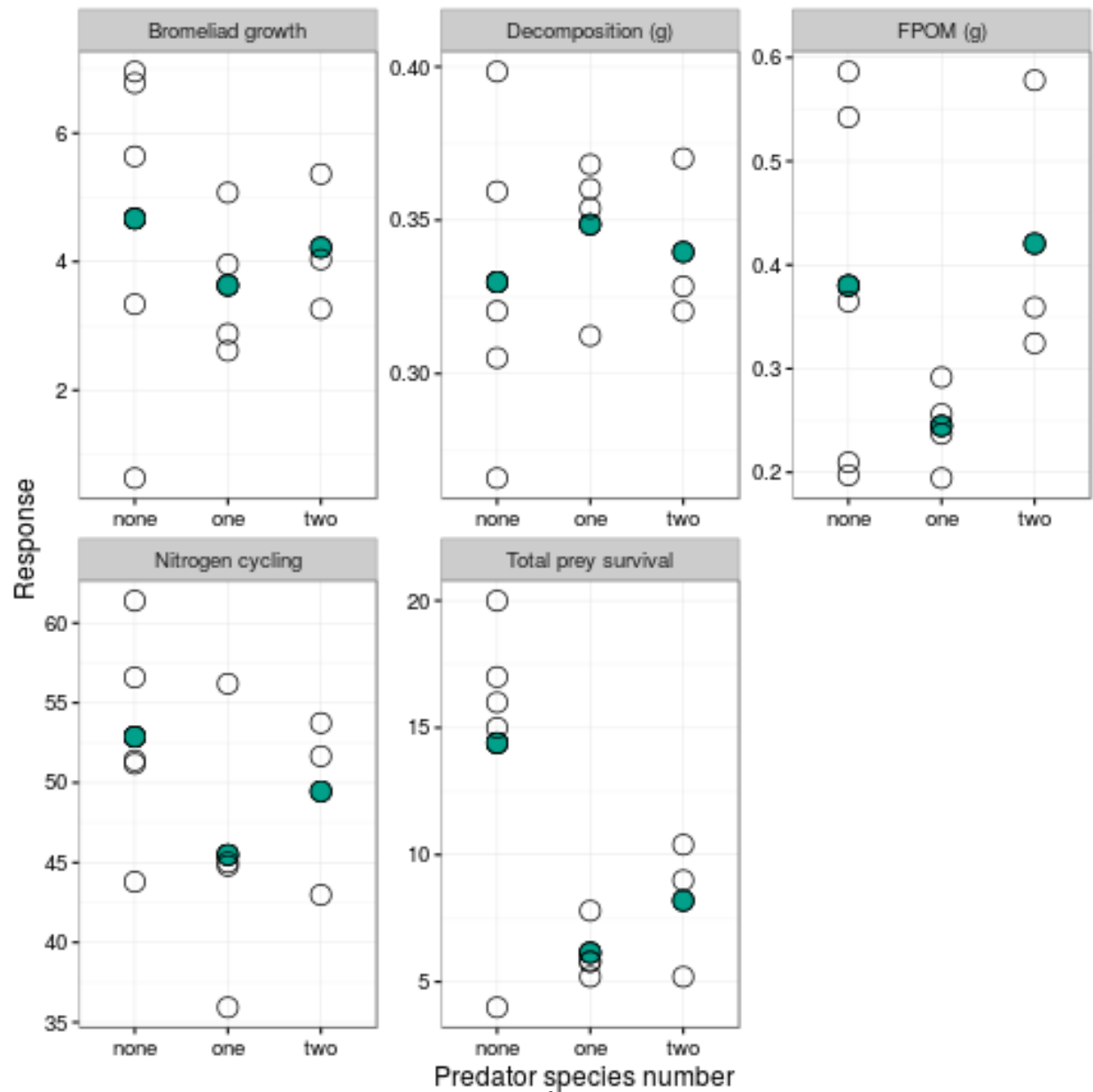
Figure S2: The effect of predator species number on each of our response variables. Each dot represents
the mean (n = 5) for different predator treatments. Green dots represent group (i.e. species number) means.

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*. Coefficents (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)
L. elongatum	2.000	−0.062	−0.008	−1.080	−0.220
	(2.069)	(0.109)	(0.031)	(1.622)	(8.656)
Hirudinidae	−0.600	0.035	−0.014	−1.344	−9.080
	(2.069)	(0.109)	(0.033)	(1.622)	(8.656)
Tabanidae	−0.000	−0.019	−0.056*	1.116	11.180
	(2.069)	(0.115)	(0.031)	(1.622)	(8.656)
L. andromache	5.800***	0.256***	0.368***	3.960***	45.020***
	(1.463)	(0.077)	(0.022)	(1.147)	(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.

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

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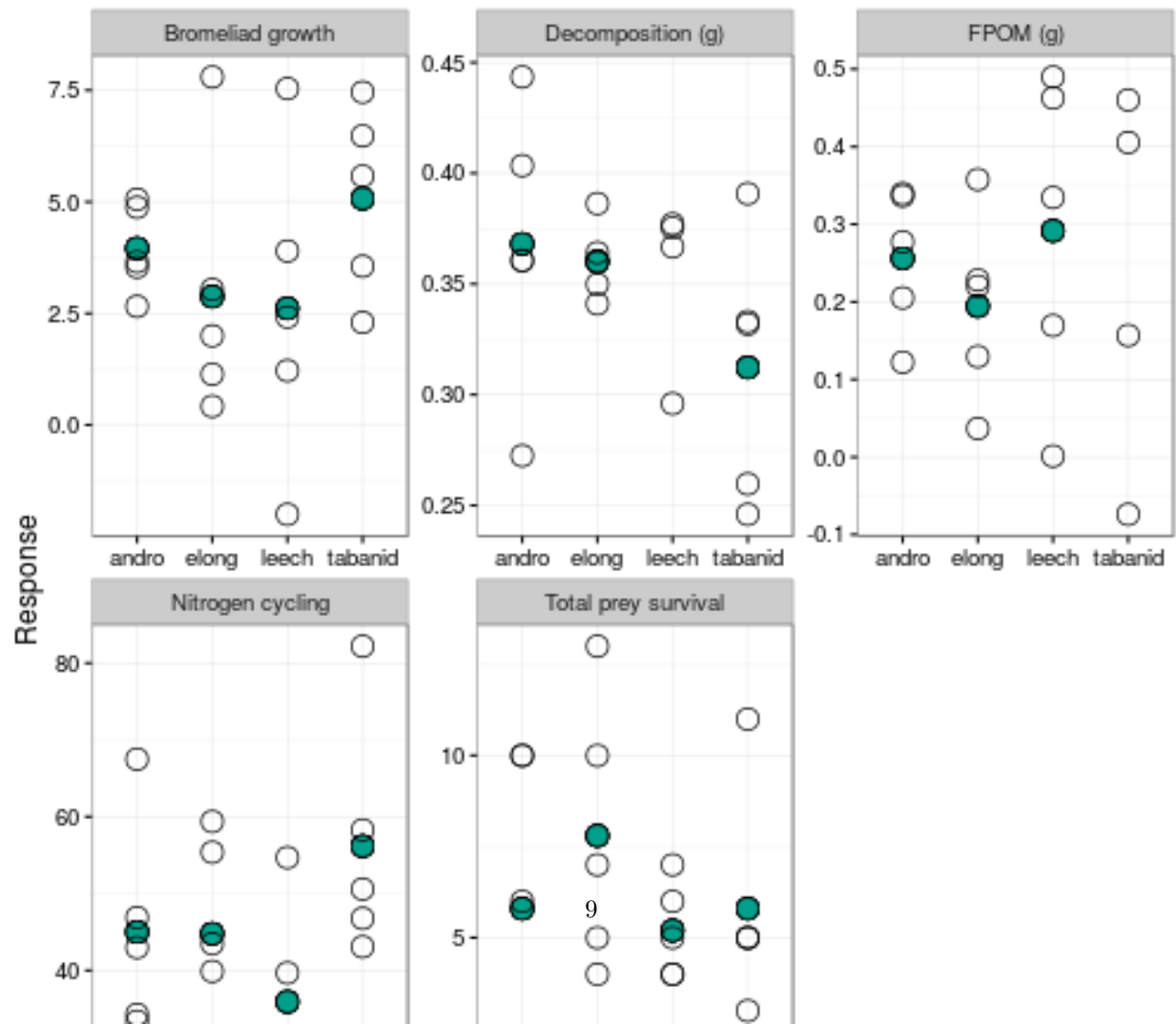
Figure S3: The effect of predator species identity on each of our response variables. Each dot represents
the observed value for a different predator treatment. Green dots represent group means.

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:				
	Total prey survival	FPOM (g)	Decomposition (g)	Bromeliad growth	Nitrogen cycling
	(1)	(2)	(3)	(4)	(5)
treatment.L	2.687*	−0.179	−0.006	1.486	−6.138
	(1.354)	(0.167)	(0.020)	(1.027)	(6.841)
treatment.Q	−2.694*	0.075	−0.037*	0.227	−5.242
	(1.354)	(0.167)	(0.020)	(0.988)	(6.841)
Constant	8.200***	0.421***	0.340***	4.222***	49.460***
	(0.782)	(0.096)	(0.012)	(0.582)	(3.950)
Observations	15	15	15	14	15
R^2	0.397	0.102	0.229	0.161	0.104
Adjusted R^2	0.296	−0.048	0.101	0.009	−0.045
Residual Std. Error	3.028 (df = 12)	0.372 (df = 12)	0.045 (df = 12)	2.164 (df = 11)	15.297 (df = 12)
F Statistic	3.949** (df = 2; 12)	0.681 (df = 2; 12)	1.787 (df = 2; 12)	1.056 (df = 2; 11)	0.696 (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
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
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
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
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
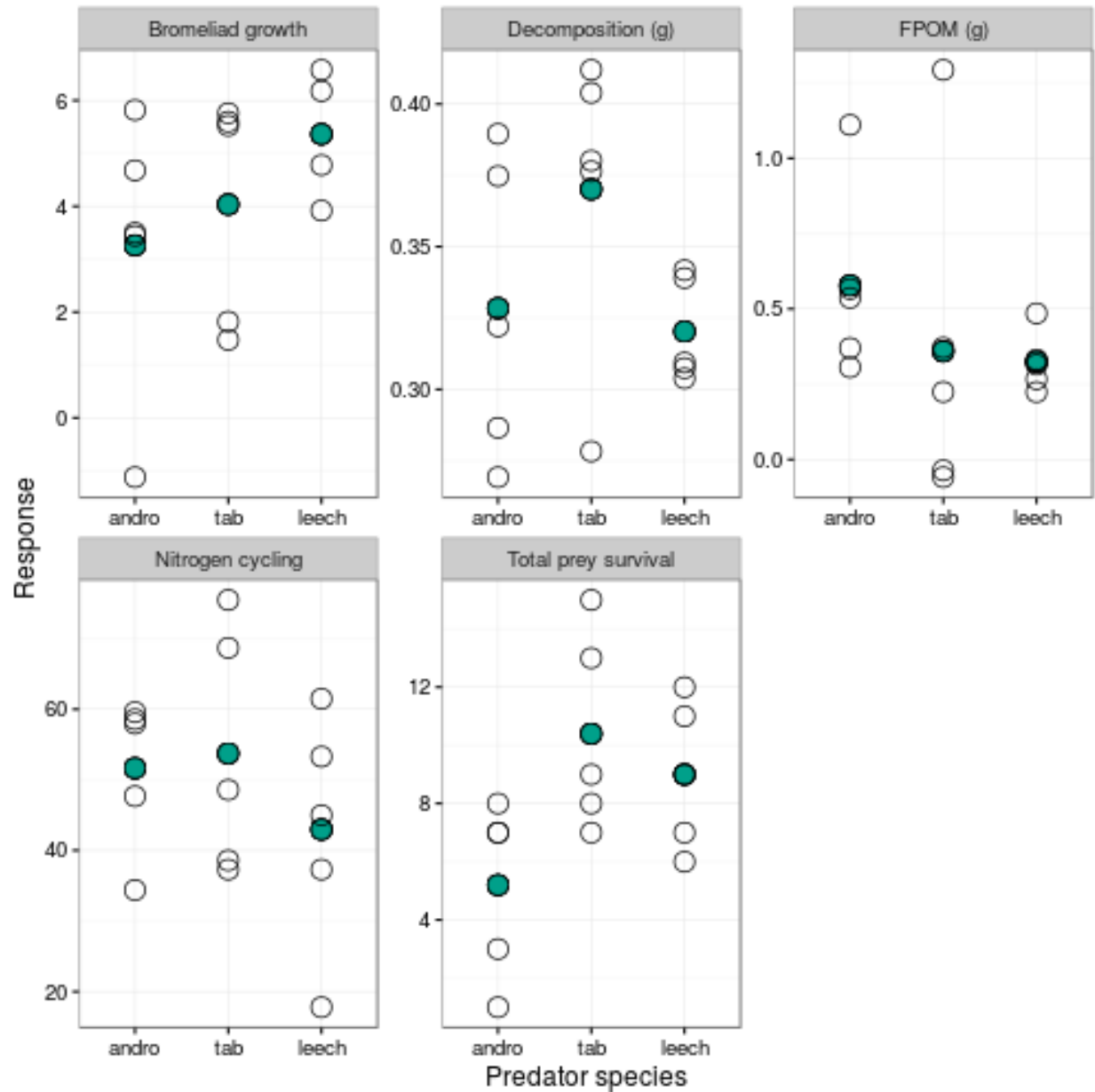
Figure S4: The effect of increasing phylogenetic signal on each of our response variables in our community experiment. In each treatment category, *Leptagrion elongatum* is paired with another predator; these treatments are ordered by increasing phylogenetic diversity. For clarity the axes are labelled 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	