Electronic Supplementary Material

Phylogeny vs. body size as determinants of food-web structure

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Table S1. Descriptions of the 13 studied food webs. S denotes the number of species.

Despite these webs being among the highest quality data available, in terms of taxonomic resolution, sampling effort, and the methods used to determine the trophic interactions, there are always concerns about biases induced by data quality. We can see two ways in which these data could be improved: 1) improving taxonomic resolution would probably result in a stronger phylogenetic signal, as the lumping of species often concerns taxa that have similar body sizes (e.g., phytoplankton). 2) Further increasing the sampling effort would tend to add rare interactions, thus progressively homogenizing trophic similarity across the network, and it would then be necessary to turn to quantitative descriptions of the strength of interactions; it is however unlikely that this would affect differently the contribution of body size or of phylogeny.

web	S	name	geographic location	habitat	specific habitat / main interaction type	reference
BS	29	Broadstone Stream	Broadstone Stream, Sussex, UK	freshwater	spring-fed acidic stream, 120 m elevation / predator-prey	Woodward et al. [1]
SL	37	Sierra Lakes	Sierra Nevada mountains, California, USA	freshwater	small subalpine and alpine lakes, less than 3 m deep / predator-prey	Harper-Smith et al. [2]
CS	57	Celtic Sea	Celtic Sea, Europe	marine	demersal food web / predator-prey	Pinnegar et al. [3]
S	58	Sheffield	Sheffield, UK	freshwater	laboratory study / predator-prey	Warren, unpublished
MR	62	Mulgrave River	Mulgrave River, Australia	freshwater	lowland coastal river / predator-prey	Rayner, unpublished
TL	66	Tuesday Lake	Tuesday Lake, Michigan, USA	freshwater	small, mildly acidic lake, 1984 data / predator-prey	Jonsson et al. [4]
SP	67	Skipwith Pond	Skipwith Common, North Yorkshire, UK	freshwater	acidic pond, up to 1 m deep, 0.25 ha / predator-prey	Warren [5]
MS	79	Mill Stream	River Frome, Dorset, UK	freshwater	lowland chalk stream / predator-prey	Ledger et al., unpublished
WS	452	Eastern Weddell Sea	Eastern Weddell Sea, Antarctica	marine	shelf sea / predator-prey	Jacob et al., unpublished
G	24	Goettingen	Goettingen, Germany	terrestrial	beech forest / host-parasitoid	Ulrich [6]
SPa	34	Silwood Park	Silwood Park, Berkshire, UK	terrestrial	abandoned field / host-parasitoid	Cohen et al. [7]
B	55	Broom	Silwood Park, Berkshire, UK	terrestrial	source web on broom, *Cytisus scoparius* / host-parasitoid and predator-prey	Memmott et al. [8]
Gr	57	Grassland	UK	terrestrial	grassland / host-parasitoid	Dawah et al. [9]

Table S2. Mantel tests of trophic, foraging and vulnerability similarity, phylogeny, and body size.

The initials in the first column refer to the food webs described in table S1. Trophic similarity (tro.) is a Jaccard index quantifying how alike are pairs of species based on all their feeding interactions, whereas foraging similarity (for.) considers only their resources, and vulnerability (vul.) considers only their consumers. For each of these three measures, we provide Pearson correlation coefficients, r, and the corresponding p-values from Mantel tests. P-values < 0.05 are indicated in bold.

	trophic						foraging						vulnerability					
web	phylo. vs. b.s.		phylo. vs. tro.		b.s. vs. tro.		phylo. vs. b.s.		phylo. vs. for.		b.s. vs. for.		phylo. vs. b.s.		phylo. vs. vul.		b.s. vs. vul.	
	r	p-value	r	p-value	r	p-value	r	p-value	r	p-value	r	p-value	r	p-value	r	p-value	r	p-value
BS	0.033	0.338	0.312	**0.001**	0.103	0.087	0.112	0.293	0.258	0.094	0.100	0.271	0.033	0.331	0.482	**<0.001**	0.161	**0.032**
SL	0.596	**<0.001**	0.347	**<0.001**	0.385	**<0.001**	0.743	**<0.001**	0.576	**<0.001**	0.309	**0.003**	0.569	**<0.001**	0.558	**<0.001**	0.479	**<0.001**
CS	0.173	**0.001**	0.158	**0.001**	0.460	**<0.001**	-0.020	0.561	0.119	0.062	0.232	**0.003**	0.199	**0.008**	0.192	**0.005**	0.196	**0.001**
S	0.266	**<0.001**	0.069	0.110	0.038	0.243	0.041	0.396	0.523	**0.006**	0.134	0.157	0.268	**0.001**	0.135	**0.015**	0.084	0.075
MR	0.579	**<0.001**	0.365	**<0.001**	0.323	**<0.001**	0.081	0.144	0.110	0.122	0.147	**0.016**	0.316	**0.002**	0.279	**0.006**	0.158	**0.063**
TL	0.322	**<0.001**	0.626	**<0.001**	0.430	**<0.001**	0.554	**<0.001**	0.780	**<0.001**	0.613	**<0.001**	0.322	**<0.001**	0.610	**<0.001**	0.420	**<0.001**
SP	0.448	**<0.001**	0.219	**<0.001**	0.164	**0.002**	0.304	**0.031**	0.097	0.183	0.172	**0.048**	0.478	**<0.001**	0.240	**0.001**	0.186	**0.002**
MS	0.657	**<0.001**	0.349	**<0.001**	0.535	**<0.001**	-0.047	0.745	-0.116	0.885	0.053	0.224	0.645	**<0.001**	0.453	**<0.001**	0.402	**<0.001**
WS	0.325	**<0.001**	0.174	**<0.001**	0.126	**<0.001**	0.232	**<0.001**	0.158	**<0.001**	0.103	**<0.001**	0.388	**<0.001**	0.330	**<0.001**	0.135	**<0.001**
G	0.178	**0.032**	0.409	**<0.001**	0.155	**0.005**	-0.140	0.766	0.162	0.110	0.153	0.073	0.161	**0.015**	0.483	**<0.001**	0.225	**0.019**
SPa	0.065	0.113	0.488	**<0.001**	0.118	**0.023**	0.697	**0.001**	-0.055	0.621	0.157	0.127	0.051	0.221	0.415	**<0.001**	0.209	**0.012**
B	0.622	**<0.001**	0.091	**0.045**	0.012	0.446	0.607	**<0.001**	0.140	**0.021**	0.071	0.198	0.152	0.071	0.437	**<0.001**	0.286	**0.003**
Gr	0.165	**0.025**	-0.015	0.665	-0.016	0.668	0.201	**0.025**	-0.113	1.000	-0.036	0.814	-0.084	0.802	-0.011	0.544	0.006	0.449

Table S3a. Path analysis for trophic similarity.

For each food web we provide the values of the path coefficient representing the effect that a change in one factor would have on the others. The final pair of columns represents a comparison of the two paths of influence of phylogeny, taking the direct effect of phylogeny on trophic structure and subtracting the indirect effect of phylogeny acting via body size. The p-values are from permutation tests to assess whether the value is significantly different from random expectations. P-values < 0.05 are indicated in bold. In a) we show the results for trophic similarity, in b) for foraging similarity, and in c) for vulnerability similarity.

Food web	phylo → body size		phylo → web		body size → web		phylo → web direct – indirect path	
	value	p-value	value	p-value	value	p-value	value	p-value
Broadstone Stream	0.033	0.341	0.326	**0.002**	0.098	0.086	0.323	**0.002**
Sierra Lakes	0.743	**<0.001**	0.200	**<0.001**	0.244	**<0.001**	0.019	0.640
Celtic Sea	0.175	**0.014**	0.092	**0.030**	0.497	**<0.001**	0.004	0.913
Sheffield	0.276	**0.002**	0.063	0.123	0.021	0.349	0.058	0.272
Mulgrave River	0.711	**<0.001**	0.290	**<0.001**	0.149	**<0.001**	0.184	**<0.001**
Tuesday Lake	0.340	**<0.001**	0.734	**<0.001**	0.326	**<0.001**	0.624	**<0.001**
Skipwith Pond	0.501	**<0.001**	0.187	**0.002**	0.076	0.088	0.149	**0.007**
Mill Stream	0.872	**<0.001**	-0.006	0.448	0.481	**<0.001**	-0.413	**<0.001**
Eastern Weddell Sea	0.343	**<0.001**	0.151	**<0.001**	0.075	**0.001**	0.125	**<0.001**
Goettingen	0.180	**0.032**	0.433	**<0.001**	0.093	0.098	0.416	**<0.001**
Silwood Park	0.066	0.114	0.556	**<0.001**	0.099	**0.045**	0.549	**<0.001**
Broom	0.794	**<0.001**	0.137	**0.006**	-0.057	0.179	0.091	0.060
Grassland	0.167	**0.026**	-0.013	0.353	-0.013	0.359	0.011	0.709

Table S3b. Path analysis for foraging similarity.

Food web	phylo → body size		phylo → web		body size → web		phylo → web direct – indirect path	
	value	p-value	value	p-value	value	p-value	value	p-value
Broadstone Stream	0.113	0.282	0.259	0.102	0.075	0.314	0.251	0.151
Sierra Lakes	1.111	**<0.001**	0.971	**<0.001**	-0.223	**0.001**	0.723	**<0.001**
Celtic Sea	-0.020	0.437	0.128	**0.045**	0.243	**0.003**	0.123	0.063
Sheffield	0.041	0.400	0.614	**0.006**	0.134	0.165	0.608	**0.006**
Mulgrave River	0.081	0.140	0.101	0.146	0.140	**0.019**	0.089	0.330
Tuesday Lake	0.665	**<0.001**	1.084	**<0.001**	0.369	**0.002**	0.839	**<0.001**
Skipwith Pond	0.320	**0.033**	0.050	0.317	0.152	0.067	0.002	0.935
Mill Stream	-0.047	0.258	-0.115	0.119	0.048	0.246	0.113	0.247
Eastern Weddell Sea	0.239	**<0.001**	0.144	**<0.001**	0.070	**0.003**	0.127	**<0.001**
Goettingen	-0.141	0.238	0.193	0.089	0.183	**0.047**	0.167	0.090
Silwood Park	0.972	**0.002**	-0.332	**<0.001**	0.283	**0.028**	0.057	0.090
Broom	0.765	**<0.001**	0.155	**0.013**	-0.018	0.429	0.142	**0.019**
Grassland	0.205	**0.024**	-0.110	**<0.001**	-0.014	0.366	0.108	**0.004**

Table S3c. Path analysis for vulnerability similarity.

Food web	phylo → body size		phylo → web		body size → web		phylo → web direct – indirect path	
	value	p-value	value	p-value	value	p-value	value	p-value
Broadstone Stream	0.033	0.336	0.552	**<0.001**	0.168	**0.026**	0.546	**<0.001**
Sierra Lakes	0.692	**<0.001**	0.523	**<0.001**	0.244	**0.017**	0.354	**<0.001**
Celtic Sea	0.203	**0.009**	0.164	**0.015**	0.166	**0.004**	0.131	0.061
Sheffield	0.278	**<0.001**	0.123	**0.019**	0.050	0.178	0.109	**0.043**
Mulgrave River	0.333	**0.002**	0.265	**0.018**	0.077	0.221	0.240	**0.016**
Tuesday Lake	0.340	**<0.001**	0.699	**<0.001**	0.312	**<0.001**	0.593	**<0.001**
Skipwith Pond	0.544	**<0.001**	0.203	**0.002**	0.083	0.103	0.158	**0.013**
Mill Stream	0.843	**<0.001**	0.378	**<0.001**	0.163	**0.016**	0.240	**<0.001**
Eastern Weddell Sea	0.421	**<0.001**	0.347	**<0.001**	0.008	0.242	0.344	**<0.001**
Goettingen	0.163	**0.018**	0.532	**<0.001**	0.173	0.074	0.504	**<0.001**
Silwood Park	0.051	0.227	0.456	**<0.001**	0.211	**0.012**	0.445	**<0.001**
Broom	0.154	0.073	0.462	**<0.001**	0.254	**0.009**	0.423	**0.001**
Grassland	-0.084	0.200	-0.011	0.452	0.005	0.466	0.010	0.819

Derivation of the formulae for the path analysis - code in Mathematica [10] format

```
(* Causal Model Definition: *)

dP = e1;
(* The distances in phylogeny between all pairs of species,
dP, follow a random noise with unit variance e1. *)

dB = pBP dP + e2;
(* The distances in body size, dB are linearly related
  to the distances in phylogeny (with path coefficient pBP) plus a random unit noise e2. *)

dT = pTB dB + pTP dP + e3;
(* The distances in trophic behaviours, dT,
are linearly related to the distances in phylogeny (with path coefficient pTP) and to
 the distances in body size (with path coefficient pTB) plus a random unit noise e3 *)

(* The correlation coefficients between the phylogenetic distances,
body size distances and trophic behaviour distances (rBP, rTB and rTP) can be expressed
 as functions of the path coefficients in the definition of the causal model. *)
corr[a_, b_] := Plus @@ Coefficient[a b, {e1^2, e2^2, e3^2}] /
     (Plus @@ Coefficient[a^2, {e1^2, e2^2, e3^2}]) ^ (1/2) /
    (Plus @@ Coefficient[b^2, {e1^2, e2^2, e3^2}]) ^ (1/2);
rSys = {rBP == corr[dB, dP], rTB == corr[dT, dB], rTP == corr[dT, dP]}
```

$$\left\{rBP == \frac{pBP}{\sqrt{1+pBP^2}},\ rTB == \frac{pTB + pBP^2\ pTB + pBP\ pTP}{\sqrt{1+pBP^2}\ \sqrt{1+pTB^2+pBP^2\ pTB^2+2\ pBP\ pTB\ pTP+pTP^2}},\ rTP == \frac{pBP\ pTB + pTP}{\sqrt{1+pTB^2+pBP^2\ pTB^2+2\ pBP\ pTB\ pTP+pTP^2}}\right\}$$

```
(* The next 4 steps solve the previous equations, computing the path coefficients
 in the causal model as functions of the known correlation coefficients. *)

(*Step1: convert rSys into a Rule for later use: *)
rRule = Solve[rSys, {rBP, rTB, rTP}] // Last
```

$$\left\{rBP \to \frac{pBP}{\sqrt{1+pBP^2}},\ rTB \to \frac{pTB + pBP^2\ pTB + pBP\ pTP}{\sqrt{1+pBP^2}\ \sqrt{1+pTB^2+pBP^2\ pTB^2+2\ pBP\ pTB\ pTP+pTP^2}},\ rTP \to \frac{pBP\ pTB + pTP}{\sqrt{1+pTB^2+pBP^2\ pTB^2+2\ pBP\ pTB\ pTP+pTP^2}}\right\}$$

```
(*Step2: Solve for pBP: *)
p1Rule = Solve[rSys[[1]], pBP] // Last
```

$$\left\{pBP \to \frac{rBP}{\sqrt{1-rBP^2}}\right\}$$

```
(*Step3: Solve for pTP and pTB. We first
  transform the problem to get rid of most of the square roots: *)
p2Rule = Solve[{rBTorTP == (rBP / rTP /. rRule), rTTorTB == (rTP / rTB /. rRule)}, {pTP, pTB}] // First //
  FullSimplify
```

$$\Big\{pTP \to -\Big(\Big(\sqrt{1+pBP^2}\ rTTorTB + pBP\ (1+pBP^2)\ (-1+rTTorTB^2)\Big)\sqrt{\Big(1\Big/\Big(\sqrt{1+pBP^2}\Big)\ pBP^2\ \Big(\sqrt{1+pBP^2}\ rBTorTP^2\ rTTorTB^2 - 2\,pBP\,rBTorTP^2\ rTTorTB^3 - 2\,pBP^3\ (-1+rBTorTP^2)\ rTTorTB^3 - pBP^4\sqrt{1+pBP^2}\ (-1+rTTorTB^2)^2 + pBP^2\sqrt{1+pBP^2}\ (1+rTTorTB^2)\ (-1+rBTorTP^2\ rTTorTB^2)\Big)\Big)}\Big)\Big/\Big(\sqrt{\Big(pBP^4+pBP^6-2\,pBP^2\ (pBP^4+rBTorTP^2+pBP^2\ (-1+rBTorTP^2))\ rTTorTB^2 + (1+pBP^2)\ (pBP^2-rBTorTP^2)^2\ rTTorTB^4\Big)}\ (-1+pBP^2\ (-1+rTTorTB^2))\Big),$$

$$pTB \to \Big(\sqrt{\Big(1\Big/\Big(\sqrt{1+pBP^2}\Big)\ pBP^2\ \Big(\sqrt{1+pBP^2}\ rBTorTP^2\ rTTorTB^2 - 2\,pBP\,rBTorTP^2\ rTTorTB^3 - 2\,pBP^3\ (-1+rBTorTP^2)\ rTTorTB^3 - pBP^4\sqrt{1+pBP^2}\ (-1+rTTorTB^2)^2 + pBP^2\sqrt{1+pBP^2}\ (1+rTTorTB^2)\ (-1+rBTorTP^2\ rTTorTB^2)\Big)\Big)}\Big)\Big/\Big(\sqrt{\Big(pBP^4+pBP^6-2\,pBP^2\ (pBP^4+rBTorTP^2+pBP^2\ (-1+rBTorTP^2))\ rTTorTB^2 + (1+pBP^2)\ (pBP^2-rBTorTP^2)^2\ rTTorTB^4\Big)}\Big)\Big\}$$

```
(*Step4: Combine the results: *)
pRule = Join[p1Rule, p2Rule] /. rTTorTB → rTP / rTB /. rBTorTP → rBP / rTP // FullSimplify
```

$$\Big\{pBP \to \frac{rBP}{\sqrt{1-rBP^2}},\ pTP \to \Big(\Big(-pBP\ (1+pBP^2)\ rTB^2 + \sqrt{1+pBP^2}\ rTB\ rTP + (pBP+pBP^3)\ rTP^2\Big)\sqrt{\Big(1\Big/\Big(\sqrt{1+pBP^2}\ rTB^4\Big)\ pBP^2\ \Big(\sqrt{1+pBP^2}\ rBP^2\ rTB^2 - 2\,pBP\,rBP^2\ rTB\ rTP - pBP^4\sqrt{1+pBP^2}\ (rTB^2-rTP^2)^2 + 2\,pBP^3\ rTB\ rTP\ (-rBP^2+rTP^2) + pBP^2\sqrt{1+pBP^2}\ (rBP-rTB)\ (rBP+rTB)\ (rTB^2+rTP^2)\Big)\Big)}\Big)\Big/\Big(\Big((1+pBP^2)\ rTB^2 - pBP^2\ rTP^2\Big)\sqrt{\Big(1\Big/rTB^4\Big((1+pBP^2)\ (rBP^2-pBP^2\ rTB^2)^2 - 2\,pBP^2\ ((1+pBP^2)\ rBP^2 + pBP^2\ (-1+pBP^2)\ rTB^2)\ rTP^2 + pBP^4\ (1+pBP^2)\ rTP^4\Big)\Big)}\Big),$$

$$pTB \to \Big(\sqrt{\Big(\Big(pBP^2\ \Big(\sqrt{1+pBP^2}\ rBP^2\ rTB^2 - 2\,pBP\,rBP^2\ rTB\ rTP - pBP^4\sqrt{1+pBP^2}\ (rTB^2-rTP^2)^2 + 2\,pBP^3\ rTB\ rTP\ (-rBP^2+rTP^2) + pBP^2\sqrt{1+pBP^2}\ (rBP-rTB)\ (rBP+rTB)\ (rTB^2+rTP^2)\Big)\Big)\Big/\Big(\sqrt{1+pBP^2}\ rTB^4\Big)\Big)}\Big)\Big/\Big(\sqrt{\Big(1/rTB^4\Big((1+pBP^2)\ (rBP^2-pBP^2\ rTB^2)^2 - 2\,pBP^2\ ((1+pBP^2)\ rBP^2 + pBP^2\ (-1+pBP^2)\ rTB^2)\ rTP^2 + pBP^4\ (1+pBP^2)\ rTP^4\Big)\Big)}\Big)\Big\}$$

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