

Please cite the Published Version

Gutmann Roberts, C and Britton, JR (2018) Quantifying trophic interactions and niche sizes of juvenile fishes in an invaded riverine cyprinid fish community. *Ecology of Freshwater Fish*, 27 (4). pp. 976-987. ISSN 0906-6691

DOI: <https://doi.org/10.1111/eff.12408>

Publisher: Wiley

Version: Supplemental Material

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Table. 1. Sample size (n), standard length (LS) range (Min LS/ Max LS) and mean standard length (mm) (\pm 95% confidence intervals) for *Barbus barbuis*, *Squalius cephalus*, *Leuciscus leuciscus* and *Phoxinus phoxinus*.

Species	n	Min LS (mm)	Max LS (mm)	Mean LS (mm)
<i>B. barbuis</i>	427	12.3	36.8	21.7 \pm 0.49
<i>S. cephalus</i>	147	11.2	33.9	19.7 \pm 0.75
<i>L. leuciscus</i>	77	23.7	48.9	37.2 \pm 1.46
<i>P. phoxinus</i>	142	12.7	33.8	21.4 \pm 0.71

Table 2. Relative frequency (%) of prey items, vacuity index (% I_v) and mean standard length (mm) \pm CI for 0+ fishes in the samples collected from Sites 1,2, and 3: barbel *Barbus barbus* chub *Squalius cephalus*, , minnow *Phoxinus phoxinus* and dace *Leuciscus leuciscus*.

Prey items	<i>B. barbus</i>				<i>S. cephalus</i>				<i>P. phoxinus</i>				<i>L. leuciscus</i>
	1	2	3	Total	1	2	3	Total	1	2	3	Total	3
Chironomid larvae	80.4	75.7	90.1	83.3	32.3	20.6	59.5	43.5	64.0	31.0	65.4	57.7	51.8
Aufwuchs	3.8	13.7	4.6	5.9	15.6	3.9	19.3	15.4	29.5	54.4	27.2	33.7	10.3
Amphipods	0	0	0	0	0	0	0	0	0	0	0.2	0.1	0
Winged insects	1.5	1.0	0.9	1.1	22.8	40.2	7.4	18.2	4.2	10.2	1.8	4.4	6.8
Chalcid wasp	0	0	0	0	0	0.5	0.3	0.2	0	0	0	0	1.6
Copepod	2.3	2.0	1.8	2.0	2.3	2.0	5.2	3.7	0	0.4	0.4	0.2	0
Cladocera	11.1	6.0	1.8	6.5	5.3	0.5	3.4	3.6	0	0.4	0.4	0.3	0.8
Nymph	0.2	0.2	0.2	0.2	0.2	2.0	0	0.4	0	0.4	0.2	0.2	0.4
Water arachnids	0.2	0.4	0.3	0.3	7.9	2.5	0.3	3.3	2.2	0.9	0	1.0	0.3
Hemipteroid assemblage	0	0	0	0	10.9	13.7	1.2	6.7	0	0	0.2	0.1	24.3
Saucer bug	0	0	0	0	0	12.3	2.8	3.4	0	0	0	0	1.9
Caddisfly larva	0.5	0.8	0.3	0.4	2.3	2.0	0.3	1.3	0	1.8	0.2	0.5	0.4
Beetle	0	0	0	0	0	0	0	0	0	0.4	0	0.1	0
Beetle larvae	0.1	0.3	0.1	0.1	0.2	0	0	0.1	0	0	0	0	0.1
Springtail	0	0	0	0	0	0	0.3	0.2	0	0	0	0	0.5
Seed/spore/plant	0	0	0	0	0	0	0	0	0	0	4.2	1.8	0.3
Fish	0	0	0	0	0	0	0	0	0	0	0	0	0.1
% I_v	0	0	0.6	0.2	6.0	5.6	4.3	5.2	0	2.0	2.8	1.6	1.2
Mean L_S (mm) \pm CI	22.6 ± 0.9	20.9 ± 0.7	21.3 ± 0.9	21.6 ± 0.5	20.5 ± 1.5	17.6 ± 1.2	21.0 ± 0.8	19.8 ± 0.7	22.5 ± 1.2	23.1 ± 0.8	19.1 ± 0.9	21.5 ± 0.6	27.4 ± 1.4

Table 3. Output from multiple regression to determine significant explanatory variables of maximum prey size for each species (GH = gape height; L_S = standard length; GH: L_S interaction between gape height and standard length)

	df	Standardised β	F value	P
<i>Barbus barbuis</i>				
GH	1	-0.11	44.94	< 0.01
L _S	1	0.46	12.99	< 0.01
GH: L _S	1	-0.17	18.66	< 0.01
Residuals	513			
<i>Squalius cephalus</i>				
GH	1	0.02	2.05	0.15
L _S	1	-0.07	2.71	0.10
GH: L _S	1	-0.23	14.19	< 0.01
Residuals	183	0.21		
<i>Leuciscus leuciscus</i>				
GH	1	-0.57	0.92	0.34
L _S	1	0.72	7.33	< 0.01
GH: L _S	1	0.02	0.04	0.84
Residuals	104	-0.02		
<i>Phoxinus phoxinus</i>				
GH	1	-0.08	0.02	0.89
L _S	1	0.06	0.15	0.70
GH: L _S	1	0.03	0.23	0.63
Residuals	156	-0.03		

Table 4. Comparison of diet between the 0+ fishes, site and the interaction of site and species
(PERMANOVA)

Factor	Df	F	R ²	<i>P</i>
Species	3	80.75	0.24	< 0.01
Site	2	4.06	0.01	< 0.01
Species: site	4	6.56	0.03	< 0.01
Residuals	736		0.73	
Total	745		1.00	

Table 5. Sample sizes, mean standard length, 40% standard error ellipse area and pairwise comparisons and significance (PERMANOVA) testing in niche size differences between *Barbus barbuis* and the other fishes, as calculated in ‘vegan’ package v2.4 in R (R Core Team, 2016).

Site (S)/ species	n	Average LS (mm) ± 95% CL	Within group similarity	40% Ellipse area	R ²	P _{adj}
S1						
<i>B. barbuis</i>	140	22.6 ± 0.9	75%	0.28		
<i>S. cephalus</i>	43	20.7 ± 1.6	47%	1.29	0.21	0.04
<i>P. phoxinus</i>	47	22.6 ± 1.3	83%	0.18	0.08	0.04
S2						
<i>B. barbuis</i>	151	21.0 ± 0.7	76%	0.13		
<i>S. cephalus</i>	44	17.9 ± 1.2	34%	8.72	0.29	0.04
<i>P. phoxinus</i>	51	22.9 ± 0.6	51%	1.29	0.08	0.04
S3						
<i>B. barbuis</i>	136	21.5 ± 0.9	79%	0.18		
<i>S. cephalus</i>	54	21.0 ± 0.9	40%	1.76	0.24	0.04
<i>P. phoxinus</i>	42	22.0 ± 0.7	74%	0.41	0.10	0.04
<i>L. leuciscus</i>	33	30.9 ± 1.4	48%	1.35	0.25	0.04