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

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

Table 2. Relative frequency (%) of prey items, vacuity index ($\%I_v$) and mean standard length (mm) ± 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	*B. barbus*				*S. cephalus*				*P. phoxinus*				*L. leuciscus*
	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) ± 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
Barbus barbus				
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			
Squalius cephalus				
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		
Leuciscus leuciscus				
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		
Phoxinus phoxinus				
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	*P*
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 barbus* 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						
B. barbus	140	22.6 ± 0.9	75%	0.28		
S. cephalus	43	20.7 ± 1.6	47%	1.29	0.21	0.04
P. phoxinus	47	22.6 ± 1.3	83%	0.18	0.08	0.04
S2						
B. barbus	151	21.0 ± 0.7	76%	0.13		
S. cephalus	44	17.9 ± 1.2	34%	8.72	029	0.04
P. phoxinus	51	22.9 ± 0.6	51%	1.29	0.08	0.04
S3						
B. barbus	136	21.5 ± 0.9	79%	0.18		
S. cephalus	54	21.0 ± 0.9	40%	1.76	0.24	0.04
P. phoxinus	42	22.0 ± 0.7	74%	0.41	0.10	0.04
L. leuciscus	33	30.9 ± 1.4	48%	1.35	0.25	0.04