

Gillnet selectivity and its relationship with body shape for eight freshwater fish species

By J. Carol and E. García-Berthou

Institute of Aquatic Ecology, University of Girona, Girona, Spain

Summary

Knowledge of the size-selectivity of fishing gear types is crucial to fisheries management and ecology. The gillnet selectivity of most freshwater fish is poorly known. We caught 694 individuals of eight widely-distributed freshwater fish species (seven cyprinids and the pikeperch, *Sander lucioperca*) with multi-mesh gillnets in Spanish reservoirs. The SELECT method was applied to fit four different gillnet selectivity models (normal location, normal scale, lognormal, and gamma). The normal scale model (spread proportional to mesh size) had the best fit in four of the eight fish species. Predicted modal lengths for the best fit models are given to describe gillnet selectivity for the eight fish species. Significant variation in the selectivity parameters was explained by simple shape descriptors such as percent girth or percent depth, suggesting that these shape descriptors might be used as a preliminary tool to describe gillnet selectivity for other fish species.

Introduction

Knowledge of the size-selectivity of fishing gear types is crucial to fisheries management in order to maximize a sustainable yield (Millar and Holst, 1997; Huse et al., 2000). It is also essential for fish ecology in order to adjust the length distribution of the catches and to understand the population sampled. Gillnets are one of the most commonly used methods for sampling fish populations in reservoirs and lakes (Boy and Crivelli, 1988) and for commercial fisheries. The advantages of gillnets include ease of use, low cost, and possibility to be set at any depth and in areas with difficult bottom conditions (Hovgård and Lassen, 2000).

Gillnet selectivity studies are typically implemented by the simultaneous fishing of several gillnets of differing mesh sizes to guarantee no changes on the catchability of fishes when the fish size increases (Kurkilahti and Rask, 1996; Millar and Holst, 1997). In general, indirect estimates of gillnet selectivity are obtained by comparing the observed catch frequencies across several meshes (Millar and Holst, 1997). The size frequency distribution of the population and the selectivity parameters are thus estimated simultaneously (Hovgård and Lassen, 2000). Different approaches to indirect estimates have been used to obtain the selection curve using various manipulations of the selection equation. Holt's method (1963) is one of the most commonly used methods for estimating gillnets selectivity. However, it is restrictive due to the assumption of the normal location curve (the spread is constant for all mesh-sizes) as the selection model. Recently, other methods apply Baranov's principle of geometric similarity (selection is

described as a function of the fish length/mesh size ratio) to compare catches in the same length group taken by different gears, assuming that the fishing power is the same for all mesh sizes. One of these methods is the SELECT method, a rigorous statistical model that estimates gillnet selection curves from comparative gillnet catch and provides a cohesive approach to selectivity analyses (Millar and Holst, 1997; Millar and Fryer, 1999; Millar, 2000). Several studies of gillnet selectivity have been carried out for a variety of marine species using the SELECT method (Huse et al., 2000; Poulsen et al., 2000; Dos Santos et al., 2003; Fonseca et al., 2005). Gillnet selectivity studies of European freshwater fish are scarce and mostly restricted to a few species such as brown trout *Salmo trutta*, perch *Perca fluviatilis*, and roach *Rutilus rutilus* (Borgström, 1989; Jensen, 1995; Kurkilahti and Rask, 1996). As far as we know, the SELECT method has not been applied to European freshwater fish despite being usually sampled with gillnets and the importance of understanding gillnet selectivity.

The objectives of our paper are: (i) to model gillnet selectivity using the SELECT method for eight freshwater fish species widely distributed in Europe and introduced elsewhere; and (ii) to explore the relationship between selectivity curves and body shape for these freshwater fish.

Materials and methods

Field methods

We used multimesh gillnets of 50 × 1.5 m of size with ten panels each 5 m long of meshes ranging from 29 to 253 mm (stretched mesh) (See Table 2 for the ten meshes used). Mesh sizes were interspersed within the net to avoid confusion of the mesh size with environmental gradients and followed a geometric progression to optimize efficiency (Kurkilahti et al., 2002). Hanging ratio of the nets was 0.5 and nets were made of 0.1 mm monofilament twine.

We sampled thirteen reservoirs in Catalonia (NE Spain) from 19 February to 30 April 2003. Details on the limnology and fish assemblages of the reservoirs during this sampling period are provided in Carol et al. (2006). We used 3–7 gill nets in each reservoir depending on their capacity. The nets were placed overnight at 0–10 m depth. During the survey, 694 fishes of 8 different fish species were caught with the gillnets, sorted by mesh size, and total length was measured to the nearest millimetre.

Estimation of gillnet selectivity

The gillnet selectivity for each species was estimated by the SELECT method through S-PLUS 2000 code developed by Russell B. Millar, available at <http://www.stat.auckland.ac.nz/>

~millar/selectware/Splus. The SELECT method is a generalized linear model that estimates gillnet selection curves (i.e. retention probabilities) from comparative gillnet catch data (Millar and Holst, 1997; Millar and Fryer, 1999; Millar, 2000). In this method, the expected catch proportions are fitted to the observed catch using maximum likelihood, under the assumption that catches are Poisson random variables (Millar, 2000). When the catch data are Poisson distributed, then the estimators are known to be approximately unbiased and to have minimum variance. If the Poisson assumption is violated because the data have variance proportional to the expected value (rather than equal to), then SELECT retains these properties and can be viewed as quasi-likelihood (Millar, 2000).

Four models available as S-Plus 2000 code (normal location, normal scale, gamma and log-normal) were tested in the present study. The four models are unimodal and consist of

two parameters describing the location and dispersion of the curves. The normal location and normal scale models are based on the normal distribution, whereas the gamma and lognormal models are skewed curves with positive asymmetry. In addition to its statistical accuracy and the availability of several models (beyond the normal model, which is the traditional one), an additional advantage of the SELECT method is that data of all meshes are analyzed within a single model, increasing statistical precision and power.

The most widely used assumption of gillnet selectivity models is Baranov's principle of geometric similarity, which states that 'since all meshes are geometrically similar and all fish of the same species (within a reasonable size range) are also geometrically similar, the selectivity curves for different mesh sizes must be similar' (Hamley, 1975). Geometric similarity is observed in three of these models, with both the modal length and spread of the curves increasing proportion-

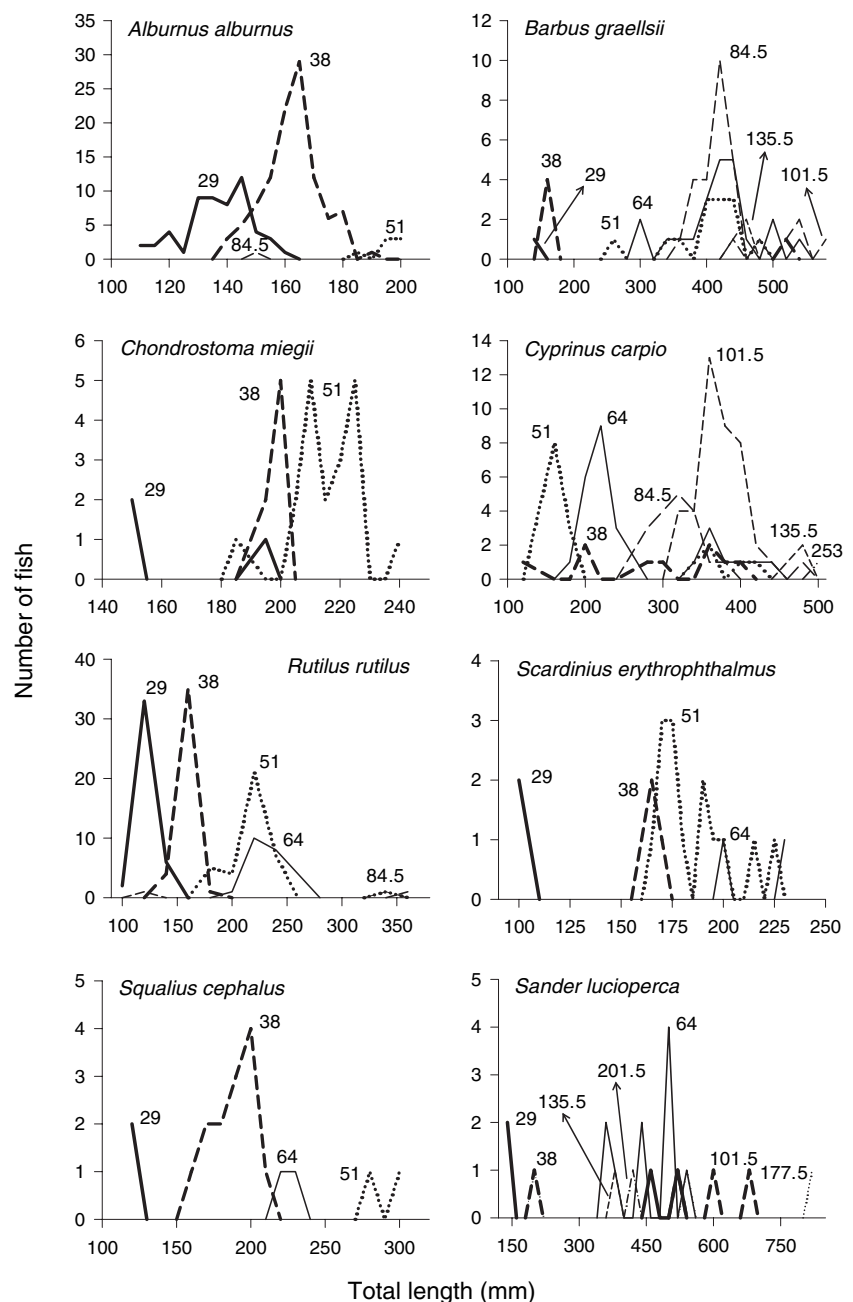


Fig. 1. Observed catch (number of fish per length class) of eight fish species in Catalan reservoirs for different gillnet mesh sizes (figures shown above lines = stretched mesh in mm)

ally to mesh size. The only exception is the normal location curve, where the modal length is also proportional to mesh size but the spread of the curve is fixed over mesh size (Millar and Fryer, 1999; Huse et al., 2000).

All models were fitted under the assumption of equal effort of mesh size. The bin width of the frequency distribution was optimized for each species, given the sample size and length range. The goodness of fit was evaluated by comparison of deviances, the lowest deviance value corresponding to the best fitting model (Dos Santos et al., 2003; Erzini et al., 2003), and the analysis of residual plots as in Millar and Holst (1997).

Comparison with fish morphometry

The estimates of selectivity parameters were compared with morphometrical descriptors of each fish species obtained from the literature and our own data. Depth (maximum height of the fish) and girth (maximum perimeter of the fish) were measured to the nearest millimetre for several individuals of each fish species and expressed as an average relative to TL (% girth and % depth, hereafter). Weight-length relationships (W-L relationships, hereafter) were obtained from Fishbase (Froese and Pauly, 2003). We used the median record of the W-L relationships reported in Fishbase, because we did not measure weight from the fish sampled. Although the W-L relationship varies among seasons and sites, the variation due to species-specific variation in shape is probably orders of magnitude larger; since our aim was to relate this species-

specific variation in shape with gillnet selectivity we are confident of our results. The intercepts of the W-L relationship were log-transformed following Froese and Pauly (2003), since they followed a decreasing power function with the slope. We also computed the weight for a fish of 150 mm (total length) (W_{150}), as $W_{150} = a \cdot 150^b$, where a and b are the W-L parameters ($W = a \cdot TL^b$). The relationship between selectivity and morphometric parameters was analyzed through linear correlation and multiple linear regression analyses with SPSS 12.

Results

Species-specific selectivity curves

Length-frequency distribution of the eight fish species caught by each gillnet mesh size is shown in Fig. 1. As expected, the mean length of captured fish increased with mesh size (Fig. 1), but there were a few fish in mesh sizes larger than expected (e.g. one 150 mm bleak in the 84.5 mm mesh) or smaller meshes than expected (e.g. several common carp in the 38 mm mesh size). Also quite apparent was the increased size variability of catches with increasing meshes (i.e. geometric similarity), particularly in bleak, roach and rudd (Fig. 1).

Fitting results of the SELECT method for all models are given in Table 1 and Fig. 2. The normal scale (proportional spread) model had the lowest deviance value (indicating a better fit) for bleak, chub, roach and rudd. For common carp and Iberian nase, the best fit model was the normal location (fixed spread) model; for the Ebro's barbel and pikeperch the

Table 1

Fitting results of different models of gillnet selectivity with the SELECT method for eight fish species in Catalan reservoirs. Parameters 1 and 2 are: k and σ for Normal location model; k_1 and k_2 for Normal scale model (spread proportional to mesh size); α and k for Gamma model; and μ_1 and σ for Lognormal model. Deviance statistic measures goodness of fit (lower deviance, in bold, indicates a better fit) and is distributed as a chi-square statistic. Significant results ($P < 0.05$, in bold) indicate lack of fit

Fish species	n	Model	Parameter 1	Parameter 2	Deviance	d.f.	P
<i>Alburnus alburnus</i>	168	Normal location	4.257	23.79	144.0	169	0.919
<i>Alburnus alburnus</i>	168	Normal scale	4.461	0.1979	51.70	169	1.000
<i>Alburnus alburnus</i>	168	Gamma	82.75	0.05391	73.21	169	1.000
<i>Alburnus alburnus</i>	168	Lognormal	4.858	0.1171	87.64	169	1.000
<i>Cyprinus carpio</i>	116	Normal location	3.755	93.40	204.2	160	0.010
<i>Cyprinus carpio</i>	116	Normal scale	4.875	2.603	271.9	160	<0.0005
<i>Cyprinus carpio</i>	116	Gamma	10.67	0.4427	224.8	160	0.001
<i>Cyprinus carpio</i>	116	Lognormal	4.858	0.3032	205.6	160	0.009
<i>Chondrostoma miegii</i>	29	Normal location	4.471	26.79	28.81	160	1.000
<i>Chondrostoma miegii</i>	29	Normal scale	4.715	0.2875	34.75	160	1.000
<i>Chondrostoma miegii</i>	29	Gamma	81.30	0.0580	31.72	160	1.000
<i>Chondrostoma miegii</i>	29	Lognormal	4.912	0.1102	30.54	160	1.000
<i>Barbus graellsii</i>	74	Normal location	5.500	110.8	98.63	205	1.000
<i>Barbus graellsii</i>	74	Normal scale	6.600	2.773	103.9	205	1.000
<i>Barbus graellsii</i>	74	Gamma	14.63	0.4482	90.56	205	1.000
<i>Barbus graellsii</i>	74	Lognormal	5.214	0.2707	87.53	205	1.000
<i>Rutilus rutilus</i>	145	Normal location	4.057	36.31	179.4	124	0.001
<i>Rutilus rutilus</i>	145	Normal scale	4.236	0.2899	79.25	124	0.999
<i>Rutilus rutilus</i>	145	Gamma	50.35	0.08452	102.0	124	0.926
<i>Rutilus rutilus</i>	145	Lognormal	4.812	0.1541	121.5	124	0.547
<i>Squalius cephalus</i>	19	Normal location	4.742	38.62	33.29	169	1.000
<i>Squalius cephalus</i>	19	Normal scale	4.927	0.3802	23.63	169	1.000
<i>Squalius cephalus</i>	19	Gamma	56.09	0.08795	24.71	169	1.000
<i>Squalius cephalus</i>	19	Lognormal	4.955	0.139	25.37	169	1.000
<i>Scardinius erythrophthalmus</i>	23	Normal location	3.667	24.70	14.86	241	1.000
<i>Scardinius erythrophthalmus</i>	23	Normal scale	3.832	0.1104	8.010	241	1.000
<i>Scardinius erythrophthalmus</i>	23	Gamma	119.1	0.03215	8.220	241	1.000
<i>Scardinius erythrophthalmus</i>	23	Lognormal	4.703	0.097	8.440	241	1.000
<i>Sander lucioperca</i>	23	Normal location	5.829	316.0	82.27	313	1.000
<i>Sander lucioperca</i>	23	Normal scale	9.899	17.78	85.83	313	1.000
<i>Sander lucioperca</i>	23	Gamma	4.442	2.369	81.23	313	1.000
<i>Sander lucioperca</i>	23	Lognormal	5.721	0.6030	80.91	313	1.000



Fig. 2. Fitted gillnet selectivity curves for eight fish species in Catalan reservoirs. Model shown with best fit for each species (see Table 1). The first curve is for 29 mm mesh (stretched), the second for 38 mm mesh, and so on consecutively (see Table 3 for mesh sizes) up to approx. maximum observed size of species

best fit model was the lognormal model. Goodness-of-fit tests indicated no deviation of the observed catch for the model predictions for all species ($P > 0.9$), except in common carp where all models presented a lack of fit ($P \leq 0.01$) and the normal location model for roach that was a worse fit than the rest of the models (Table 1). The gamma model was never the best fit model.

Model deviance (Table 1) significantly depended on fish species ($F_{7,16} = 55.8$, $P = 0.017$) but this was mostly an effect of sample size (correlation between deviance and n , $r = 0.598$, $P = 0.0001$), because species with larger sample sizes (e.g. common carp and roach) had much larger deviances than less-captured species (Fig. 3). There was also a significant model \times species interaction ($F_{7,16} = 4.31$, $P = 0.007$) because the fit of different models behaved the opposite in different species: when the normal location or lognormal

models were the best (lowest deviance), normal scale was the worst (e.g. common carp and Iberian nase); when the normal scale model was the best fit, normal location was the worst (roach, bleak, chub and rudd) (Fig. 3).

Most fishes were captured with the three smallest mesh sizes, in accordance with the observed range and the expected modal length of most fish species (Table 2).

Fish shape effects on gillnet selectivity

The % depth and % girth had significant positive correlation and both showed information about fish shape. Deeper fishes such as rudd or roach were more laterally compressed than spindle shaped fishes and thus had higher % girth (Matsushita and Ali, 1997). Rudd is the deepest fish species but has lower % girth because it is more laterally compressed. Roach and

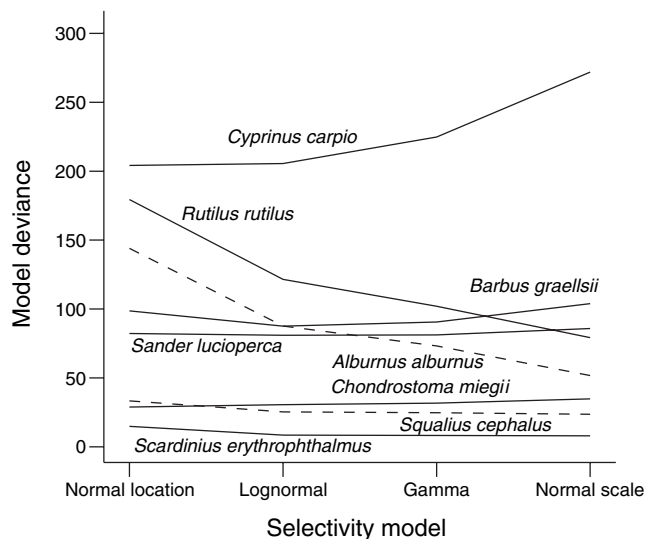


Fig. 3. Comparison of model deviances of four different selectivity models (normal location, lognormal, gamma and normal scale) and eight fish species in Catalan reservoirs

common carp had higher values of relative width than rudd, thus they show the highest values of girth. Both descriptors were also positively correlated with W_{150} , suggesting a relationship with condition factor of the fish, which is important in determining the shape of the selectivity curve for fish caught (Boy and Crivelli, 1988; Koutrakis and Tsikliras, 2003). The % depth was positively related to b (power parameter of the W-L relationship); thus, fish species with higher % depth such as rudd, roach and common carp had greater allometry and grew proportionately more in weight with ontogeny. In practice, this means that large fish have, on average, bigger depth and girth and this may affect the geometric similarity assumption (Kurkilahti et al., 2002).

The % depth was significantly and negatively related to $\log_{10} k_1$ (Fig. 4). K_1 is the parameter relating modal length (μ) and mesh (m_j), ($\mu = k_1 \cdot m_j$); thus, the deepest fish species (rudd, roach and common carp) had the smallest predicted modal lengths for a given mesh (Table 2) than more fusiform fish species (e.g. pikeperch and Ebro's barbel). The difference between modal lengths for a given mesh between deeper and fusiform species increased with mesh size (Table 2). Similarly, fish species with higher % girth showed a low value of $\log_{10} k_1$ (Fig. 5); i.e. for a given mesh size smaller individuals of species with higher % girth were captured. The negative correlation

between % girth and $\log_{10} k_1$ was not significant because of the small sample size (Table 3) but was actually higher than for % depth, and explained 52% of the variation.

Parameters k_1 (location) and k_2 (spread) of normal scale model were significantly related (Table 3), thus spread (k_2) increased when k_1 increased (regression function: $\log_{10} k_2 = -3.879 + 5.29 \log_{10} k_1$, $r^2 = 0.84$). Multiple linear regression did not improve the understanding of the relationships and only confirmed models with a single independent variable, probably because of the limited sample size (eight species).

Discussion

Species-specific selectivity curves

The normal scale model had the best fit in four of the eight fish species. The lognormal and the normal location models had the best fit for two fish species each and the gamma model for none. In general, gillnet selectivity curves may approach normal curves when most fish are wedged or gilled (Hamley, 1975). However, when many fish are entangled, catch data are skewed to the right, fitting better to gamma or lognormal models or multimodal models (Hamley, 1975; Pet et al., 1995; Kurkilahti et al., 1998; Dos Santos et al., 2003). In most studies, selectivity curves take unimodal form (Hamley, 1975); in Poulsen et al. (2000), the best fit was also achieved using a normal scale model. Recently, studies in several fish species have shown that bimodal curves (bi-normal) may yield better fit than unimodal models (Poulsen et al., 2000; Fujimori and Tokai, 2001; Dos Santos et al., 2003; Erzini et al., 2003). The bimodal model was not available in the S-PLUS scripts of SELECT but bimodality was not evident in our catch data (Fig. 1).

The fit of different models behaved the opposite in different species: when the normal location or lognormal models were the best (lowest deviance), normal scale was the worst. Residual analysis provided an explanation for this opposite behaviour. When the normal location model had lower fit (e.g. rudd), deviance residual plots (see Millar and Holst, 1997) showed for a given mesh that length residuals had positive asymmetry, which disappeared with models that incorporate positive asymmetry (e.g. normal scale model). For other species (e.g. common carp), the normal location model yielded more uniform and symmetric residuals, whereas models with positive asymmetry (e.g. normal scale model) produced larger residuals with negative asymmetry. Additionally, when the normal location model had the best fit (e.g. common carp and

Table 2

Predicted modal total length (mm) of eight fish species for different gillnet mesh sizes (stretched) in Catalan reservoirs. Selectivity model with best fit (see Table 1) used to estimate modal lengths (NS = normal scale; NL = normal location; LG = lognormal). Only modal lengths less than approx. known maximum length of species given. Mean and range of observed TL for each species also given

Fish species		Best fit model	Mesh size (mm)										Mean	
Scientific name	Common name		29	38	51	64	84.5	101.5	135.5	177.5	201.5	253	TL	range
<i>Alburnus alburnus</i>	bleak	NS	129.4	169.5	227.5								155.5	110–200
<i>Cyprinus carpio</i>	common carp	NL	108.9	142.7	191.5	240.3	317.3	381.2	508.9	666.6	756.7	950.1	317.1	110–500
<i>Chondrostoma miegii</i>	Iberian nase	NL	129.6	169.9	228.0	286.1							206.2	150–242
<i>Barbus graellsii</i>	Ebro's barbel	LG	151.2	198.1	265.9	333.7	440.6	529.2	706.5				405.6	134–581
<i>Rutilus rutilus</i>	roach	NS	122.8	161.0	216.0	271.1	357.9	430.0					177.8	107–369
<i>Squalius cephalus</i>	chub	NS	142.9	187.2	251.3	315.3	416.3	500.0					194.4	124–302
<i>Scardinius erythrophthalmus</i>	rudd	NS	111.1	145.6	195.4	245.2	323.8	388.9					133.7	101–231
<i>Sander lucioperca</i>	pikeperch	LG	166.2	217.8	292.3	366.9	484.4	581.8	776.7	1017.4	1155.0		441.6	143–811

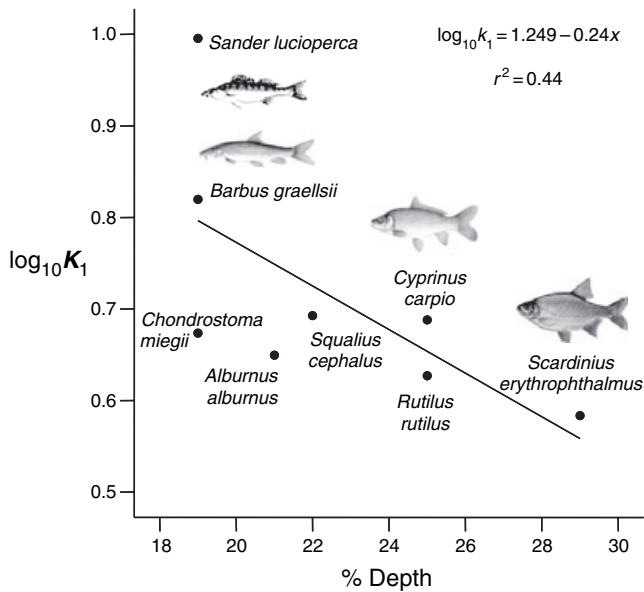


Fig. 4. Relationship between parameter k_1 (logarithmic scale) of normal scale model and % depth (percentage of depth with total length) for eight fish species in Catalan reservoirs. Linear regression function also shown

Iberian nose) the variability decreased with increasing mesh size. Just the opposite resulted when the normal scale model had the best fit (e.g. rudd, chub), because the variability increased with increasing mesh size (i.e. geometric similarity).

Parameters k_1 and k_2 of the normal scale model were significantly related; this fact is another evidence of geometric similarity and suggests that in general the normal location model should not be assumed unless shown by the data. Hamley (1975) indicated that the principle of geometrical similarity – assumed in the normal scale, gamma and lognormal models – is still a simplification, precisely because body shape of fish may change as they grow older, girths thus not being proportional to length.

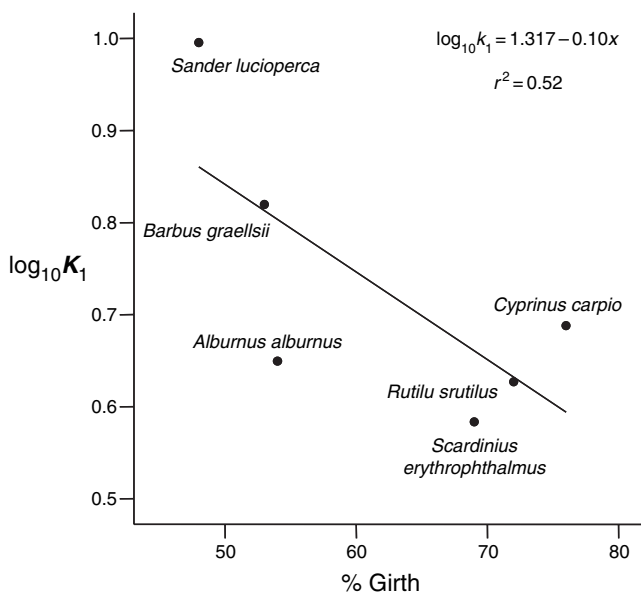


Fig. 5. Relationship between parameters k_1 (logarithmic scale) of normal scale model and % girth (percentage of girth with total length) for six fish species in Catalan reservoirs. Linear regression function also shown

Table 3

Correlation among selectivity parameters and morphometric descriptors for eight fish species in Catalan reservoirs. k_1 and k_2 are parameter estimates of Normal scale model; b and a are parameters of weight-length relationship; % girth is percentage of girth with total length; % depth is percentage of depth with total length; W_{150} is weight for a 150 mm (total length) fish. *, $P < 0.10$; **, $P < 0.05$; ***, $P < 0.01$. $n = 8$, except for % girth ($n = 6$)

	$\log_{10}k_1$	$\log_{10}k_2$	b	$\log_{10}a$	% girth	% depth
$\log_{10}k_2$	0.918***					
b	-0.212	-0.213				
$\log_{10}a$	0.128	0.339	-0.814**			
% girth	-0.723	-0.443	0.440	-0.005		
% depth	-0.661*	-0.489	0.683*	-0.417	0.845**	
W_{150}	-0.242	0.095	0.485	0.104	0.826**	0.629*

Fish shape effects on gillnet selectivity

The % depth and % girth had significant positive correlation and both showed information about fish shape. Both descriptors were negatively correlated with $\log_{10} k_1$, although % girth was more correlated than % depth (Figs 4 and 5). k_1 is the parameter relating modal lengths and mesh size and more than 40% of the variation of k_1 (log-transformed) was explained by fish shape. Furthermore, % depth and b of the W-L relationship were significantly correlated, so species with higher % depth had greater allometry (Fig. 4). Body shape and appendages are important in determining the particular way in which fish are caught in gillnets (Reis and Pawson, 1999). Girth is the main size factor determining the size of fish caught by different mesh sizes because girth at the point of capture has to be equal or slightly higher than the mesh perimeter. Although gear selectivity estimates are generally derived from length frequency distributions, girth distributions can be used as well (Reis and Pawson, 1999; Stergiou and Karpouzi, 2003). Measuring girth is more time-consuming than depth (easily measured from photographs), which could be used in selectivity studies. Furthermore, the probability of capture is determined by different girths, such as girth across the vertical eye

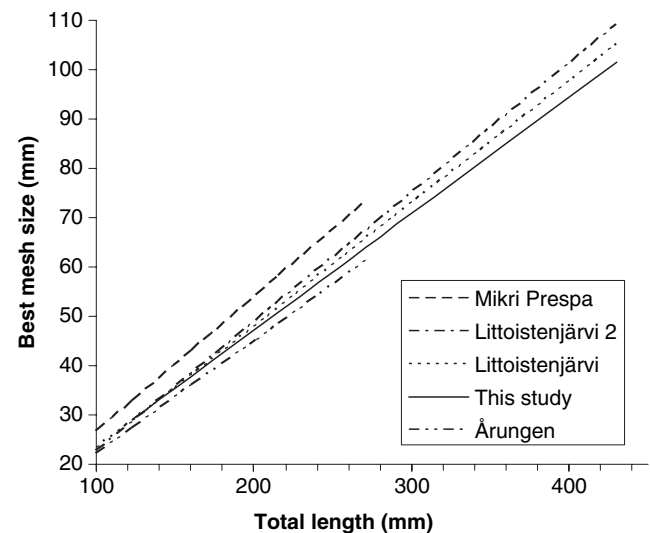


Fig. 6. Relationship between best mesh size (stretched) and total length of roach (*Rutilus rutilus*) in present and previous selectivity studies: Lake Mikri Prespa (Boy and Crivelli, 1988), Lake Littoistenjärvi (Kurkilahti and Rask, 1996) and Lake Årungen (Borgström, 1989). Mesh sizes of previous studies were doubled to convert them from bar size (knot to knot) to stretched size; for Lake Mikri Prespa, fork length converted to total length

diameter when fish are entangled, girth behind the gill-cover when fish are gilled, and girth in front of the dorsal fin when fish are wedged (Stergiou and Karpouzi, 2003). In addition, fish of the same length may have different girths. Hamley (1975) observed that neither length nor girth alone can accurately describe how fish size affects selectivity, so both measurements can be used to describe the selectivity of a particular net in relation to the capture of fish (Campos and Fonseca, 2003; Stergiou and Karpouzi, 2003).

The gillnet selectivity models and predicted modal lengths presented in this paper may be used for these widely distributed freshwater fishes, many of which are invasive species. Our selectivity estimates for roach (the only species previously well investigated) were intermediate to previous studies and very similar to some of them (Fig. 6), suggesting that despite the limited sample size (difficult to avoid for non-commercial and less abundant fish), the estimates were reliable. However, the variation among populations within a single species can be considerable (e.g. geographical differences in fish shape) and region- or site-specific should be preferably be developed.

The relationships between k_1 and k_2 , and between k_1 and simple shape descriptors such as % depth and % girth might be used as a preliminary tool to understand gillnet selectivity for fish species for which selectivity has never been studied. An additional advantage of the SELECT method with this regard is that mesh size is part of the model, and thus modal lengths for any mesh size can be predicted. However, further investigation is necessary to validate these relationships between body shape and gillnet selectivity, to increase the sample sizes and diversity of fish morphologies, to assess the effect of spatial and temporal variation in the weight-length relationship and hence to develop more comprehensive models. The SELECT method is a powerful framework to develop such models.

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Author's address: Emili García-Berthou, Institute of Aquatic Ecology, University of Girona, E-17071 Girona, Spain.
E-mail: emili.garcia@udg.es