Table S1. Description of the PCA used to summarize the 17 ecological / life history traits.

Seventeen traits related to feeding, habitat, reproduction and fish morphology were selected from the literature (we indicated whether the traits were categorical or numerical). We synthesize those 17 traits performing a PCA on a Gower distance matrix. The scores of the 28 fish species were taken from the first three axes to obtain three orthogonal estimates of aggregate functional trait values for each species ("Trait 1", "Trait 2" and "Trait 3" for the three axes respectively). The percentage of variance explained by each axis is indicated in brackets. We also indicated the strength of the relationship between each aggregate trait and the 17 traits. This relationship was expressed as the percentage of explained deviance (since some traits were categorical) and we bolded relationship for which the percentage of explained deviance was above 0.40 (i.e. 40 %).

Traits	Trait 1 (32.3%)	Trait 2 (23.9%)	Trait 3 (19.7%)	Trait category
Fecundity	0.004	0.001	**0.782**	numerical
Shape factor	0.273	0.022	0.032	numerical
Swimming factor	0.045	0.004	0.326	numerical
Body length	0.041	0.269	**0.463**	numerical
Relative fecundity	0.031	**0.544**	0.037	numerical
Spawning time	0.251	**0.486**	0.027	numerical
Life span	0.079	0.146	**0.504**	numerical
Female maturity	0.087	0.254	**0.452**	numerical
Larval length	0.146	**0.464**	0.035	numerical
Parental care	0.280	0.001	**0.449**	categorical
Tolerance to salinity	0.342	0.054	0.039	numerical
Incubation period	0.243	0.091	0.094	numerical
Feeding habitat	0.001	0.047	**0.403**	categorical
Habitat type	0.095	0.141	0.148	categorical
Feeding diet	**0.535**	0.028	0.167	categorical
Reproduction habitat	0.151	**0.428**	0.030	categorical
Migration status	**0.656**	0.065	0.184	categorical

Table S2: **Phylogenetic signal in ecological traits.**

Phylogenetic regression estimates of phylogenetic signal (d) in aggregated species functional traits. A principal component analysis was performed on 17 functional traits and the species scores across each of the first three PCA axes were taken as aggregated traits. Functional traits correlated to each axis are presented in *Table A1*. Values of $d>1$ indicate trait conservatism, while $d<1$ indicates less signal than expected based on Brownian motion evolution. For each trait, Akaike Information Criteria (AICs) have been calculated for both a "star" model (i.e. no phylogenetic signal) and a model including phylogeny; the lowest AIC value indicates the model that best fit the data.

Functional traits	Percentage of trait variation explained	Star models	Phylo models	d
Trait 1	32.30%	-0.727	-1.403	0.944
Trait 2	23.89%	-1.029	-1.214	0.417
Trait 3	19.70%	-1.222	-1.352	0.584