

Genetic erosion reduces biomass temporal stability in wild fish populations.

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Keywords : Eco-evolutionary dynamics; Genetic erosion; Intraspecific diversity, Biodiversity-Ecosystem function.

Supplementary Table 1. Detailed results from simplified causal models in chubs (a), gudgeons (b) and minnows (c).

In each species, there is a positive relationship between Intraspecific Genetic Diversity IGD and Mean Total Biomass Stability BSTA, though mostly expressed in upstream areas in the case of minnows (Supplementary Note 1). See Table 1 in main text for legend.

(a) Results in chubs:

Predictor → Response	Model A	Model B
	$\chi^2_{(9,20)} = 4.78$, p-value = 0.853 CFI = 1 SRMR = 0.086	$\chi^2_{(11,20)} = 8.44$, p-value = 0.750 CFI = 1 SRMR = 0.085
pcBIOM → BIOM	0.318 [-0.272; 0.909] / {1.057 0.291}	
	R ² = 0.102	
IGD → BSTA		0.273 [0.020; 0.526] / {2.115 0.034}
pcBSTA → BSTA		0.645 [0.353; 0.938] / {4.321 0}
EG → BSTA		-0.242 [-0.562; 0.077] / {-1.487 0.137}
	R ² = 0.509	
UDG → pcBIOM	-0.474 [-0.815; -0.133] / {-2.727 0.006}	
	R ² = 0.253	
UDG → pcBSTA		-0.242 [-0.503; 0.019] / {-1.816 0.069}
	R ² = 0.063	
UDG → IGD	0.389 [0.105; 0.673] / {2.683 0.007}	
BOT → IGD	-0.515 [-0.790; -0.240] / {-3.675 0}	
	R ² = 0.684	
UDG → BOT	-0.542 [-1.029; -0.055] / {-2.181 0.029}	
	R ² = 0.284	

(b) Results in gudgeons:

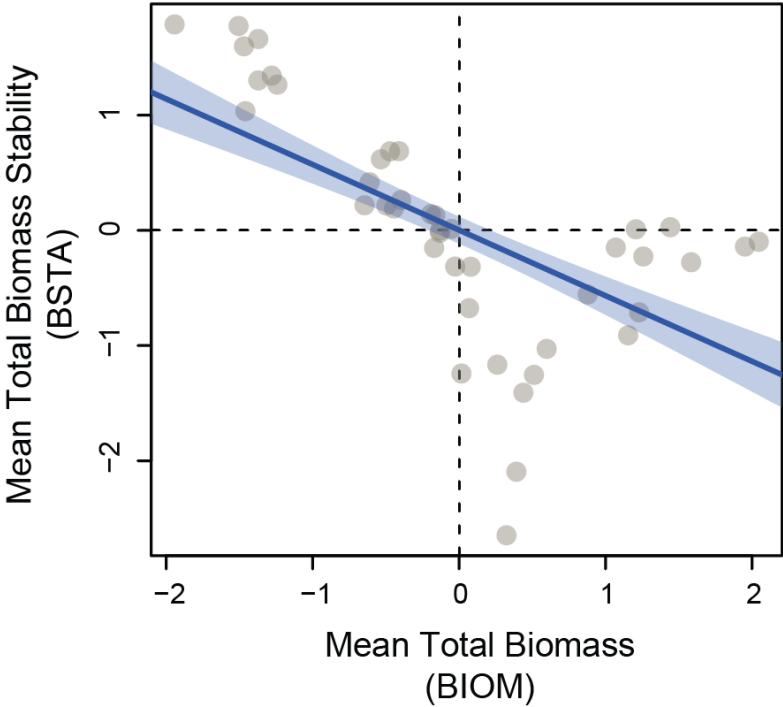
Predictor → Response	Model A	Model B
	$\chi^2_{(13,33)} = 10.49$, p-value = 0.653 CFI = 1 SRMR = 0.056	$\chi^2_{(10,33)} = 5.26$, p-value = 0.873 CFI = 1 SRMR = 0.063
UDG → BIOM	-0.697 [-0.877; -0.517] / {-7.581 0}	
EG → BIOM	0.122 [-0.466; 0.333] / {1.13 0.258}	
UDGxEG → BIOM	-0.289 [-0.272; -0.113] / {-3.215 0.001}	
	R ² = 0.515	
IGD → BSTA		0.463 [0.186; 0.740] / {3.278 0.001}
pcBSTA → BSTA		0.265 [-0.009; 0.538] / {1.898 0.058}
UDG → BSTA		-0.581 [-0.856; -0.306] / {-4.143 0}
	R ² = 0.475	
UDG → pcBIOM	-0.612 [-0.782; -0.443] / {-7.084 0}	
EG → pcBIOM	0.240 [-0.023; 0.503] / {1.790 0.073}	
	R ² = 0.512	
UDG → pcBSTA		-0.400 [-0.628; -0.172] / {-3.436 0.001}
	R ² = 0.200	
UDG → IGD		0.506 [0.295; 0.717] / {4.702 0}
EG → IGD		0.479 [0.272; 0.686] / {4.529 0}
BOT → IGD		-0.397 [-0.725; -0.069] / {-2.372 0.018}
	R ² = 0.563	
EG → BOT		0.166 [-0.182; 0.515] / {0.935 0.35}
	R ² = 0.028	

(c) Results in minnows:

	Model A	Model B
Predictor → Response	$\chi^2_{(13,31)} = 6.42$, p-value = 0.930	$\chi^2_{(15,31)} = 14.49$, p-value = 0.489
	CFI = 1	CFI = 1
	SRMR = 0.068	SRMR = 0.073
UDG → BIOM	-0.519 [-0.755; -0.284] / {-4.324 0}	
pcBIOM → BIOM	0.331 [0.157; 0.506] / {3.720 0}	
	R ² = 0.460	
pcBSTA → BSTA		0.256 [-0.084; 0.596] / {1.476 0.14}
UDG → BSTA		-0.445 [-0.929; 0.039] / {-1.803 0.071}
EG → BSTA		-0.339 [-0.647; -0.030] / {-2.151 0.031}
IGD → BSTA		0.160 [-0.218; 0.538] / {0.831 0.406}
UDGxIGD → BSTA		-0.367 [-0.685; -0.049] / {-2.265 0.044}
	R ² = 0.305	
UDG → pcBIOM	-0.369 [-0.753; 0.015] / {-1.883 0.06}	
EG → pcBIOM	0.307 [-0.042; 0.656] / {1.725 0.085}	
IGD → pcBIOM	0.340 [-0.030; 0.710] / {1.801 0.072}	
EGxIGD → pcBIOM	0.438 [0.060; 0.815] / {2.270 0.023}	
	R ² = 0.453	
UDG → pcBSTA		-0.028 [-0.337; 0.281] / {-0.178 0.859}
EG → pcBSTA		-0.010 [-0.431; 0.451] / {0.045 0.964}
UDGxEG → pcBSTA		0.428 [0.053; 0.803] / {2.235 0.025}
	R ² = 0.109	
UDG → IGD		0.421 [0.200; 0.641] / {3.740 0}
BOT → IGD		-0.230 [-0.535; 0.075] / {-1.477 0.140}
	R ² = 0.271	
EG → BOT		0.309 [-0.034; 0.652] / {1.767 0.077}
	R ² = 0.094	

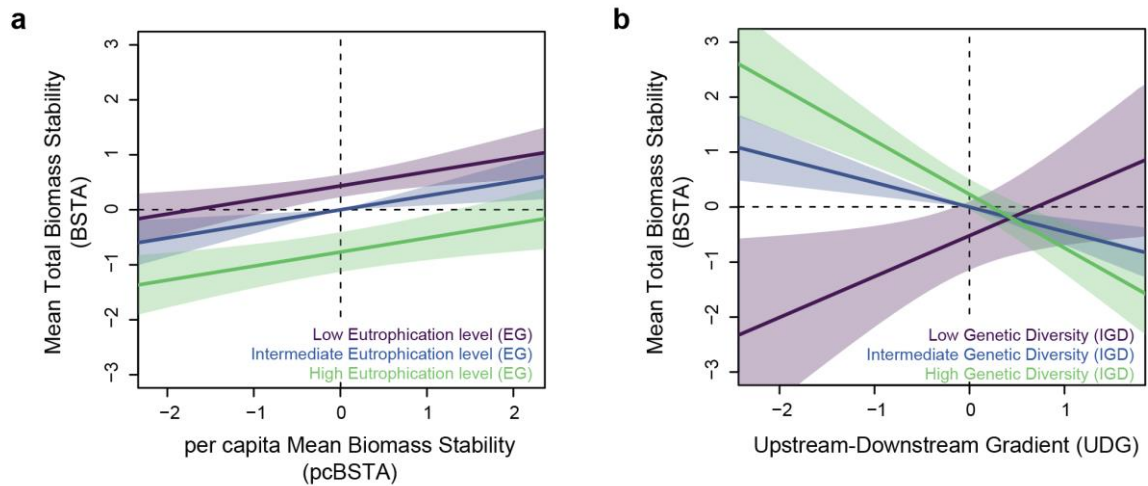
Supplementary Figure 1. Demographic and biomass data.

Predicted values of Mean Total Biomass Stability (BSTA) as a function of Mean Total Biomass (BIOM). Data are presented as predicted values (thick lines) +/- SD (colored envelopes). Overall, Mean Total Biomass Stability (BSTA) was negatively related to Mean Total Biomass (BIOM): the higher the Mean Total Biomass, the higher its fluctuations over the last decades. Source data are provided as a Source Data file.



Supplementary Figure 2. Drivers of Biomass Stability in minnows.

Predicted values of Biomass Stability BSTA in minnows given the retained links (per capita Biomass pcBSTA and Eutrophication Gradient EG in panel a; first-order interaction between Upstream-Downstream Gradient UDG and Intraspecific Genetic Diversity IGD in panel b) as indicated in Supplementary Table 1c. Data are presented as predicted values (thick lines) +/- SD (colored envelopes). The positive relationship between IGD and BSTA is here mostly expressed in upstream areas. Source data are provided as a Source Data file.



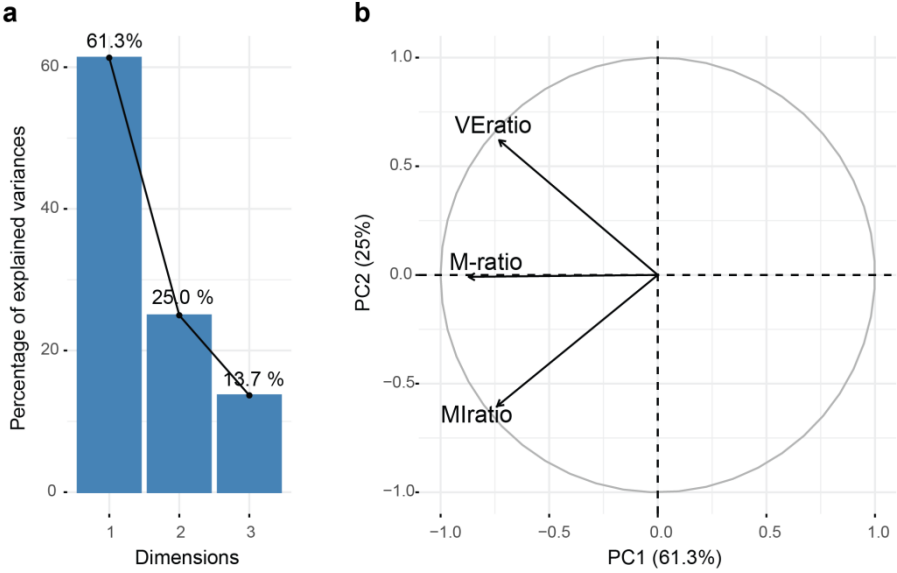
Supplementary Table 2. Raw metrics of bottleneck probability.

Minimal, maximal, mean and median values of raw metrics of bottleneck probability (out of 92 unique combinations of one species and one station), as well as their coordinates on the first PCA axis and their contribution expressed in percentage. Note that a simulation study by Paz-Vinas et al.¹ showed that, in rivers, demographic inferences based on microsatellites are more likely to detect false signals of population expansion than false signals of population decline: here, we only detected 7 (7.6% of datasets) and 6 (6.5% of datasets) signals of expansion ($\log\text{-ratio} > 0$) with the Mlratio and the VEratio, respectively.

	Min	Max	Mean	Median
M-ratio	0.427	0.880	0.697	0.705
Mlratio	-19.548	1.759	-5.501	-5.369
VEratio	-4.489	1.031	-1.694	-1.518

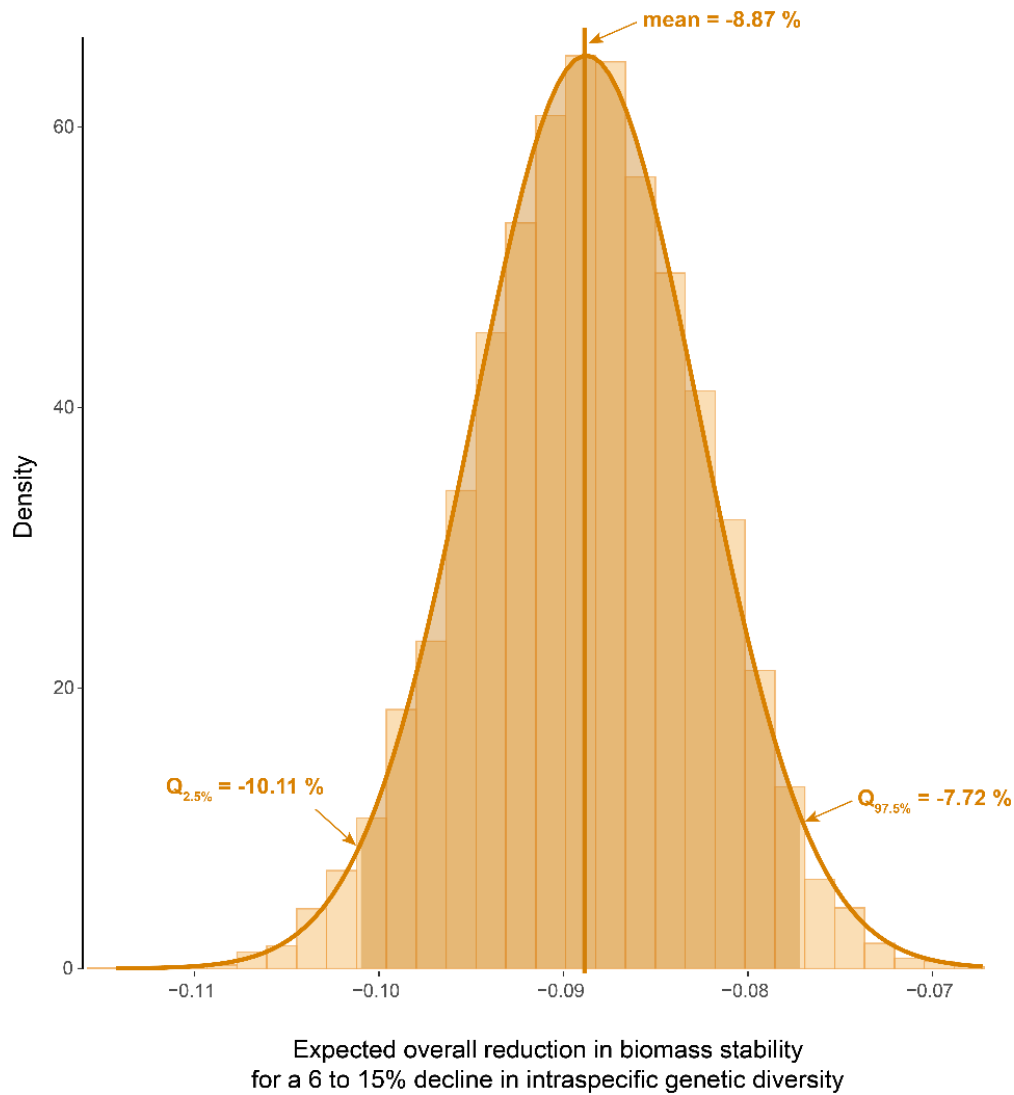
Supplementary Figure 3. Synthetic metric of bottleneck probability.

Visual representation of eigenvalues (corresponding to the amount of the variation explained by each PC; panel a) and of the two first principal components PC, with PC1 standing for bottleneck probability BOT (panel b). Source data are provided as a Source Data file.



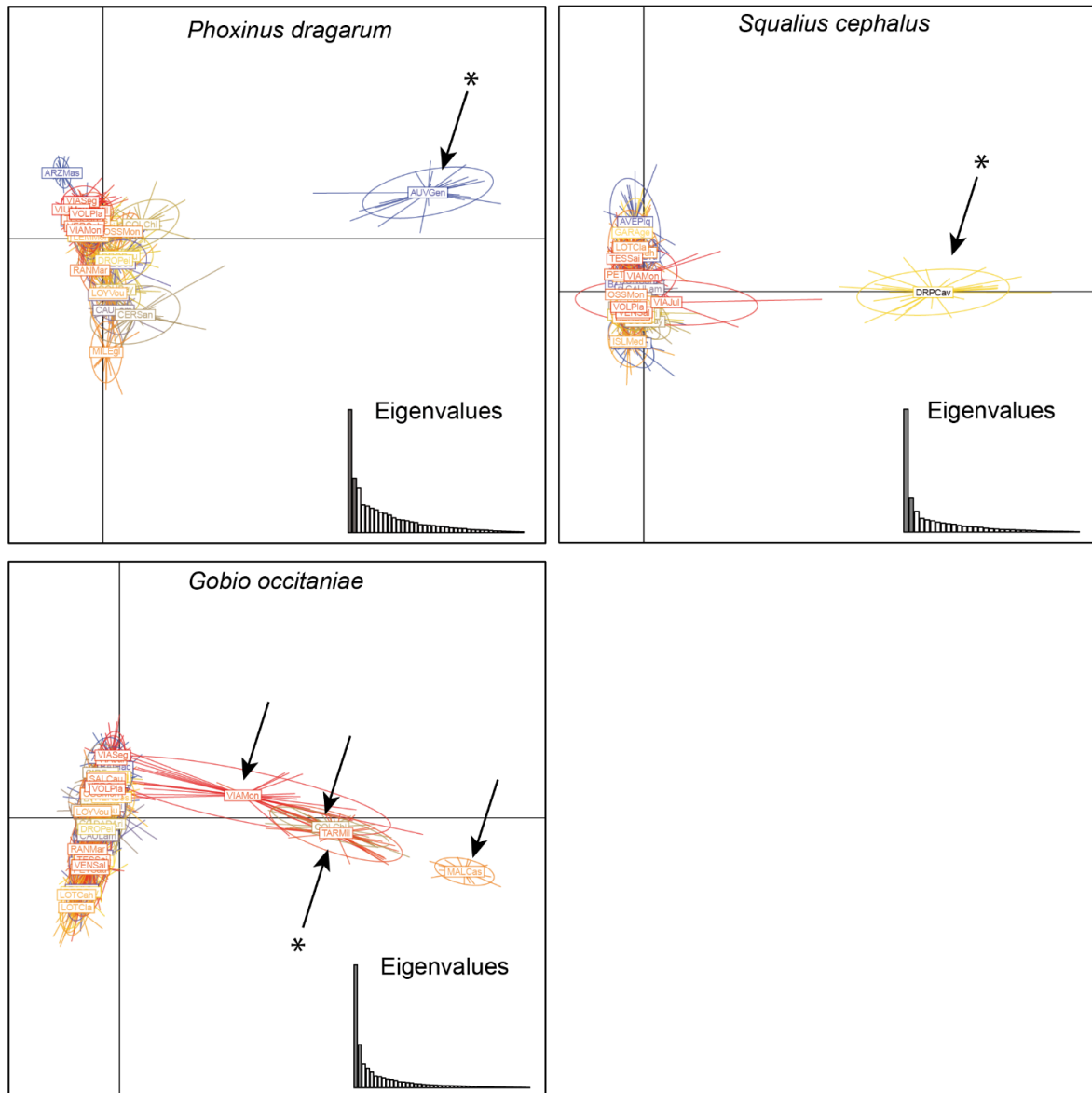
Supplementary Figure 4. Overall expected change in biomass stability given a 6 to 15% decline in intraspecific genetic diversity.

Distribution of \overline{D}_k , the predicted overall expected change in biomass stability given a 6 to 15% decline in IGD, along with the corresponding fitted normal curve (in orange), mean value and 95% confidence intervals. We found $\overline{D}_k = -8.87\%$ [-10.11; -7.72]. Source data are provided as a Source Data file.



Supplementary Figure 5. Outlier populations.

Discriminant analysis of principal components (dAPC) performed on each microsatellite dataset. Arrows indicate outlier populations, probably resulting from past stocking events. These populations were discarded from the final datasets. Asterisks indicate outlier populations used to design a draft reference genome in each species.

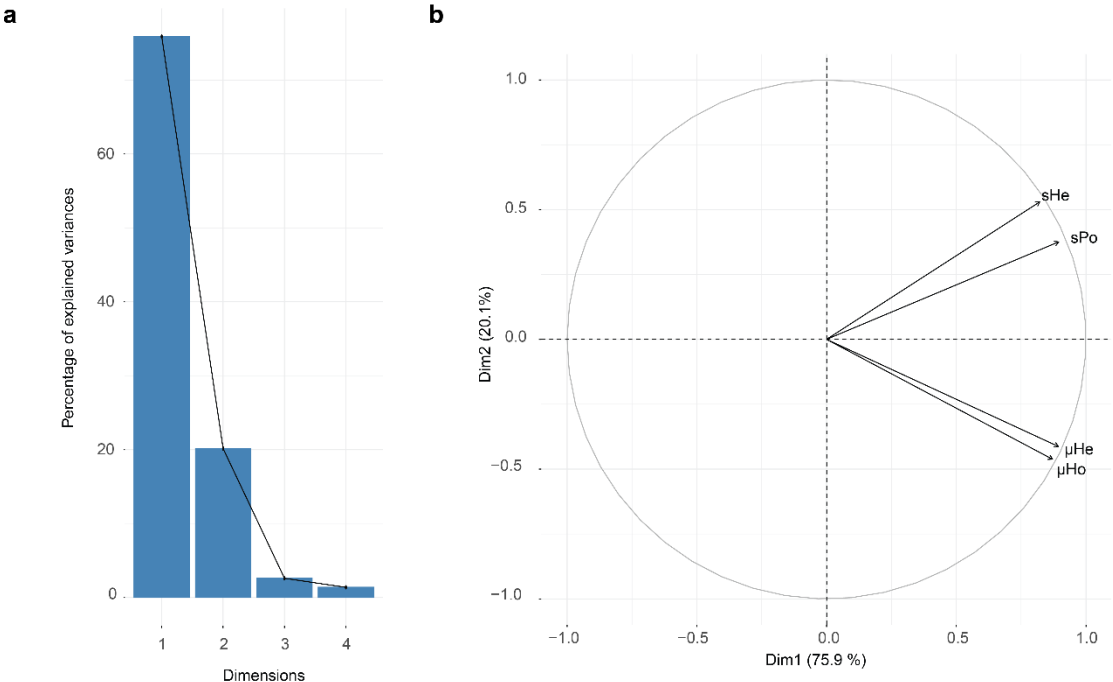


Supplementary Table 3. Main characteristics of final SNP datasets.

	<i>P. dragarum</i>	<i>G. occitaniae</i>	<i>S. cephalus</i>
Number of SNPs	1244	1892	1847
Number of populations	27	30	17
Mean coverage (\pm standard deviation)	99.2 \pm 41.9	77.5 \pm 34.8	51 \pm 13.1
Percentage of missing AF values (across SNPs and populations)	1.2	13.2	19.1

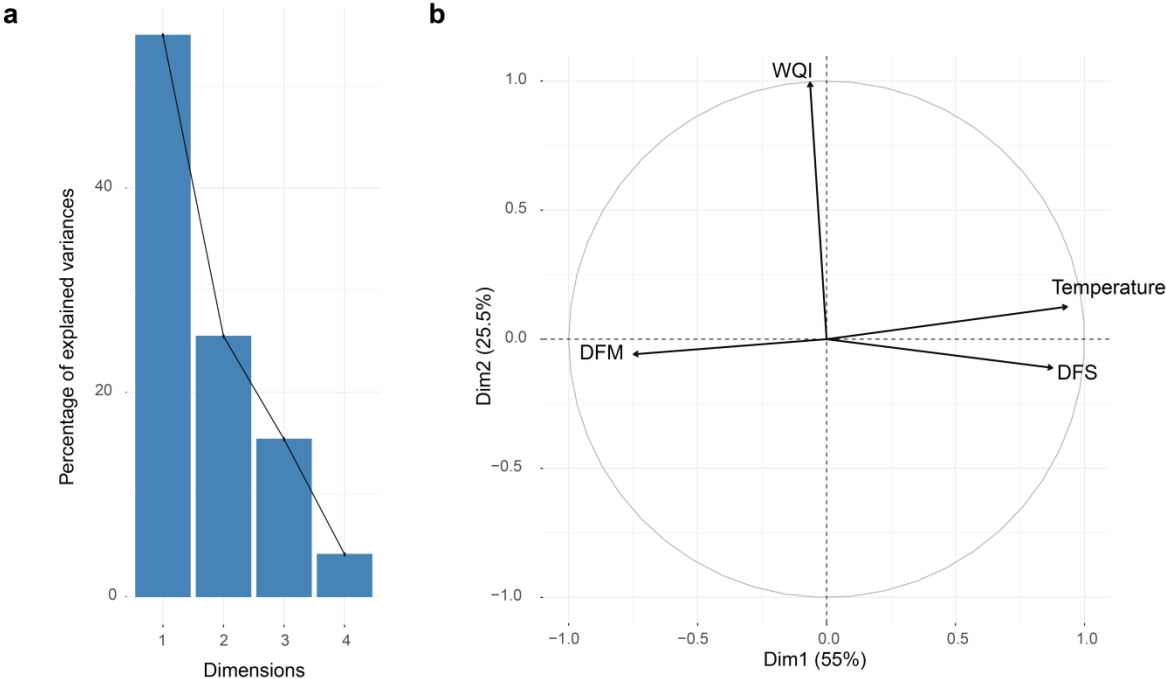
Supplementary Figure 6. Composite metric of Intraspecific Genetic Diversity.

Visual representation of eigenvalues (corresponding to the amount of the variation explained by each principal component PC; panel a) and of the two first PC, with PC1 standing for Intraspecific Genetic Diversity IGD (panel b). The percentage of variance explained by each component is also indicated. μ : microsatellites / s: SNPs; He: expected heterozygosity / Ho: observed heterozygosity / Po: Polymorphism (see main text for details). Source data are provided as a Source Data file.



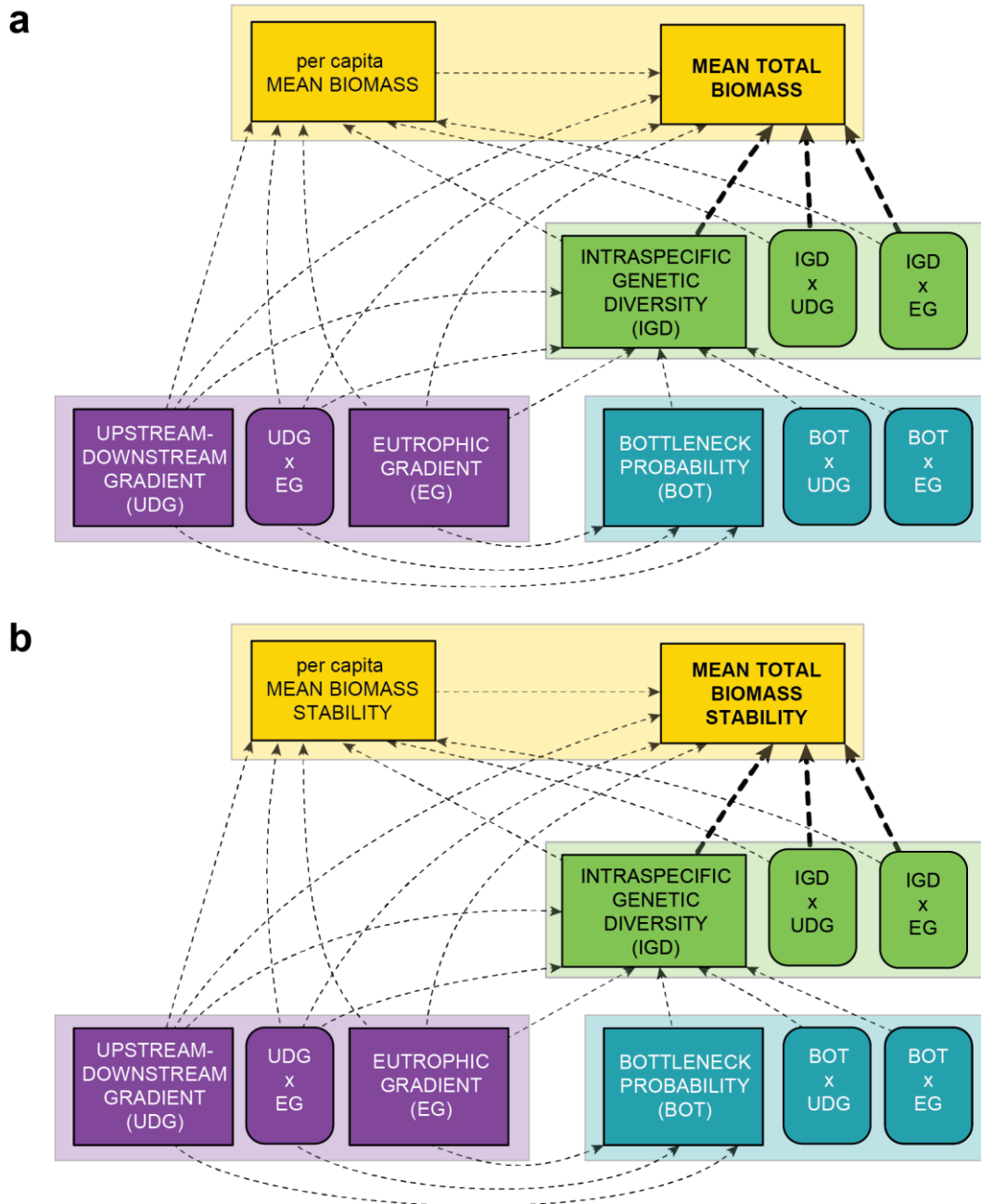
Supplementary Figure 8. Characteristics of the two first principal components (PC) based on environmental data.

Visual representation of eigenvalues (corresponding to the amount of the variation explained by each PC; panel a) and of the two first PC accounting for 80.5 % of the total variance in environmental variables, with PC1 standing for the upstream-downstream gradient (fresh upstream stations on the one hand (negative coordinates) and warmer downstream stations on the other hand) and PC2 standing for the eutrophic gradient (nutrient-impooverished river stations (very good ecological status) on the one hand (negative coordinates) and nutrient-rich stations (medium ecological status) on the other hand; panel b). The percentage of variance explained by each component is also indicated. DFM: Distance from the river mouth; DFS: Distance from the river source; WQI: Water Quality Index. Source data are provided as a Source Data file.



Supplementary Figure 9. Initial causal models.

Initial causal graphs depicting all the investigated links among environmental (purple), bottleneck (blue), genetic (light green), and biomass variables (per capita and total; yellow). Mean biomasses are investigated in a, biomass stability in b. Links of interest (between IGD variables and biomass variables) are in bold.



SUPPLEMENTARY REFERENCES

1. Paz-Vinas, I., Quéméré, E., Chikhi, L., Loot, G. & Blanchet, S. The demographic history of populations experiencing asymmetric gene flow: combining simulated and empirical data. *Mol. Ecol.* **22**, 3279–3291 (2013).