

Supplementary material

Table S1: List of the 143 supposedly neutral SNP markers from the brown trout genome

See file «List_markers.xlsx», sheet «SI.1»

This file contains, for each SNP, its identification (SNP_ID), the position of the SNP on the Rad tag (POStag_snp), the linkage group on the Brown trout linkage map (LG_Trutta), the position of the SNP on the brown trout linkage group (Pos_cM_Trutta), the recombination rate (recombination_rate_cM.Mb) and sequence of the tag (TAG_sequence).

Table S2: List of the 19 'candidate' SNP markers related to physiological functions of and/or tolerance or resistance to pathogens in brown trout

See file «List_markers.xlsx», sheet «SI.2»

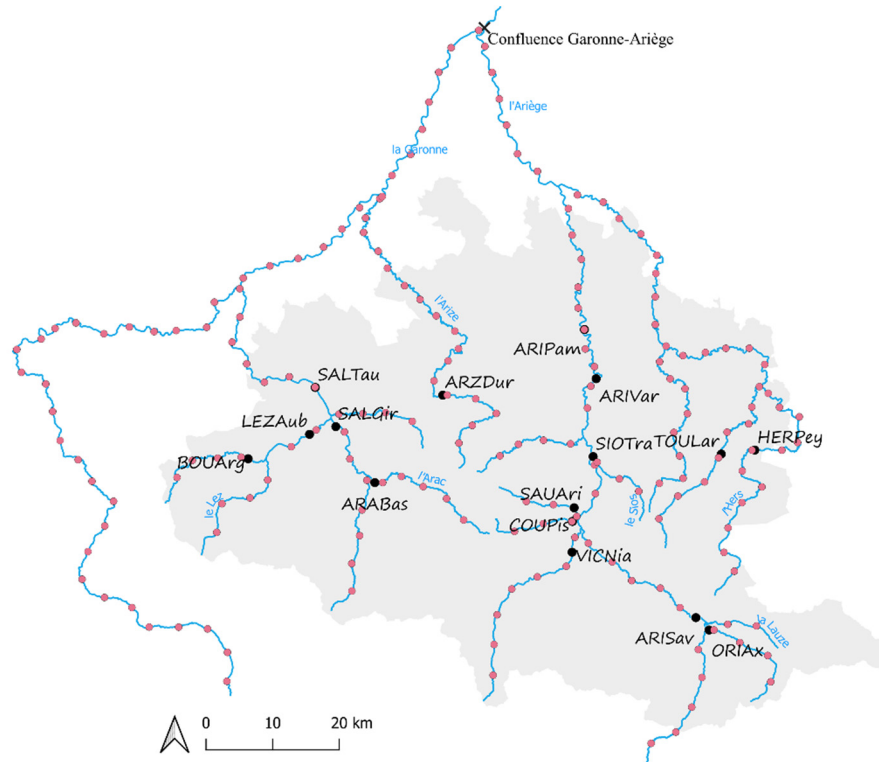
This file contains, for each SNP, its identification (SNP_ID), the related physiological functions (Trait; RPL: relative parasite load, Htc: haematocrit), the method used (Source; GWAS: genome-wide association studies; Random Forest: random forest classification), the position of the SNP on the Rad tag (POStag_snp), positions on the Atlantic salmon chromosome (POSsalar_snp), chromosome on Atlantic salmon (CHROMsalar) and sequence of the tag (TAG_sequence).

Table S3: Individual genotype in the MHC class II β gene (Satr-DAB)

See file «List_markers.xlsx», sheet «SI.3»

This file contains, for each individual, identification (ID), the associated cluster with the allele (1 or 2) of the MHC class II β gene (DAB_all1, DAB_all2), and the sequence of the associated cluster with the allele (SEQ_all1, SEQ_all2).

Figure S1: Map showing points added (in red light) to measure centrality. These points were added every 5km using the “Random points along line” option from the vector creation tools. We then generated distances between all these points using the “shortest path” option from the network analysis tools. Finally, we joined this attribute to our sites of interest via spatial location using the 'Join by location' option from the general vector tools, and counted the linear number that crossed each of our sites of interest. All these analyses were computed using Geographic Information System software (QGIS Development Team, 2008, V. 3.12).



Supporting Information S1: Null alleles and scoring errors

Potential null alleles were suggested at five populations for the MHC class II β gene: ARABas, HERPey, LEZAub, SALGir and SALTau, as is suggested by the general excess of homozygote for several allele size classes ($FIS > 0.05$). No evidence of scoring errors due to stuttering or large allele dropout was found in the whole dataset. We therefore concluded that neither potential null alleles nor scoring errors affected the outcome of the results.

Table S4: Mean pairwise F_{ST} values (calculated using GENEPOP v.4.7.5) between sites measured at SNPs, candidate SNPs and MHC class II β marker, hydrological distance (km) between sites and number of dams and/or weirs >3m between sites.

	Pop	ARABas	ARIPam	ARISav	ARIVar	ARZDur	BOUArg	COUPis	HERPey	LEZAub	ORIAx	SALGir	SALTau	SAUAri	SIOTra	TOULar	VICNia
SNPs	ARABas																
	ARIPam	0.0627															
	ARISav	0.1243	0.0836														
	ARIVar	0.0577	0.0288	0.0718													
	ARZDur	0.1168	0.1061	0.1981	0.1086												
	BOUArg	0.0544	0.0683	0.113	0.069	0.1351											
	COUPis	0.0504	0.0337	0.1007	0.0374	0.0963	0.0604										
	HERPey	0.1036	0.0804	0.1865	0.0953	0.1345	0.1004	0.0929									
	LEZAub	0.0326	0.0581	0.0946	0.0515	0.1047	0.0222	0.0625	0.092								
	ORIAx	0.1185	0.0892	-0.0007	0.0752	0.2015	0.1137	0.1121	0.1866	0.0929							
	SALGir	0.1262	0.0936	0.1796	0.1144	0.1758	0.1653	0.0915	0.1445	0.1425	0.1813						
	SALTau	0.0101	0.0453	0.1064	0.0667	0.093	0.0386	0.0486	0.1002	0.028	0.1079	0.129					
	SAUAri	0.0073	0.0513	0.1132	0.0488	0.0927	0.0313	0.0503	0.0857	0.0062	0.1189	0.1362	-0.001				
	SIOTra	0.062	0.0484	0.1108	0.0476	0.143	0.1042	0.055	0.1302	0.0791	0.0987	0.1277	0.0692	0.0721			
	TOULar	0.0371	0.0406	0.0906	0.0236	0.118	0.0646	0.0491	0.0878	0.0364	0.0863	0.1093	0.0444	0.028	0.0453		
	VICNia	0.0468	0.0535	0.1359	0.039	0.129	0.072	0.0551	0.1134	0.0566	0.1268	0.1421	0.0603	0.0515	0.0552	0.038	
	Mean	0.0674	0.0629	0.1139	0.0624	0.1302	0.0808	0.0664	0.1156	0.0640	0.1140	0.1373	0.0631	0.0595	0.0832	0.0599	0.0784
Candidate SNPs	ARABas																
	ARIPam	0.0484															
	ARISav	0.0763	0.0446														
	ARIVar	0.0357	0.0062	0.0111													
	ARZDur	0.1836	0.1808	0.1389	0.1215												
	BOUArg	0.0644	0.1075	0.0673	0.0561	0.0969											
	COUPis	0.1085	0.0408	0.0739	0.0504	0.1288	0.1066										
	HERPey	0.0473	0.0504	0.0121	0.0171	0.1489	0.0386	0.0816									
	LEZAub	0.0271	0.0593	0.0778	0.0178	0.1154	0.0059	0.0823	0.0392								
	ORIAx	0.0952	0.0547	-0.0139	0.0381	0.1224	0.0815	0.0643	0.0384	0.0982							
	SALGir	0.158	0.166	0.234	0.1432	0.1674	0.1926	0.1291	0.2303	0.1325	0.2137						
	SALTau	-0.0089	0.0128	0.0438	-0.0013	0.1387	0.0481	0.0659	0.0277	0.0107	0.0578	0.1193					
	SAUAri	0.0143	0.056	0.0459	-0.0045	0.0992	0.0188	0.0927	0.035	-0.0104	0.0717	0.1075	-0.0063				
	SIOTra	0.0846	0.0864	0.008	0.0451	0.1677	0.0887	0.1286	0.0335	0.0901	0.0343	0.2355	0.0655	0.0486			
	TOULar	0.0705	0.0692	0.0089	0.0193	0.0978	0.0568	0.0821	0.0402	0.0472	0.0217	0.1692	0.041	0.0154	0.0109		
	VICNia	0.0496	0.0595	0.066	0.0279	0.0735	0.055	0.0455	0.0695	0.0323	0.0705	0.0985	0.0188	0.0144	0.0994	0.0296	
	Mean	0.0703	0.0695	0.0596	0.0389	0.1321	0.0723	0.0854	0.0607	0.0550	0.0699	0.1665	0.0422	0.0399	0.0818	0.0520	0.0540
MHC class II β gene	ARABas																
	ARIPam	0.0487															
	ARISav	0.0694	0.0853														
	ARIVar	0.0406	0.0057	0.0649													
	ARZDur	0.1045	0.1182	0.1237	0.1192												
	BOUArg	0.1549	0.1914	0.1958	0.1932	0.2169											
	COUPis	0.0404	0.0293	0.0639	0.0385	0.0977	0.1723										
	HERPey	0.0696	0.0429	0.1106	0.06	0.1353	0.2115	0.0392									
	LEZAub	0.0284	0.0723	0.0857	0.0701	0.1018	0.0983	0.0596	0.0941								
	ORIAx	0.1232	0.1395	0.0165	0.1234	0.1807	0.2514	0.1271	0.1669	0.1418							
	SALGir	0.068	0.0788	0.0849	0.0815	0.1166	0.1868	0.0621	0.0781	0.0757	0.1422						
	SALTau	0.0062	0.0759	0.0828	0.0698	0.1033	0.1569	0.0569	0.095	0.0359	0.1395	0.0768					
	SAUAri	0.0438	0.1076	0.1094	0.1086	0.1302	0.122	0.0902	0.1266	-0.0029	0.1647	0.1052	0.0181				
	SIOTra	0.0099	0.0541	0.0943	0.049	0.1216	0.1842	0.0533	0.0753	0.0637	0.1419	0.0814	0.0429	0.1065			
	TOULar	0.0475	0.0565	0.0689	0.0606	0.1146	0.1893	0.0402	0.0781	0.0738	0.1285	0.0621	0.0536	0.0983	0.0457		

	VICNia	0.0456	0.0268	0.0698	0.0337	0.1046	0.1796	0.0426	0.0838	0.0648	0.1292	0.0696	0.0366	0.0841	0.0513	0.0329	
	<i>Mean</i>	0.0600	0.0755	0.0884	0.0746	0.1259	0.1803	0.0676	0.0978	0.0709	0.1411	0.0913	0.0700	0.0942	0.0783	0.0767	0.0703
Hydrological distances (km)	ARABas																
	ARIPam	181.15															
	ARISav	249.89	68.74														
	ARIVar	194.61	13.46	55.29													
	ARZDur	141.52	159.14	227.88	172.6												
	BOUArg	31.21	183.27	252.01	196.73	143.64											
	COUPis	223.61	42.46	28.4	29	201.59	225.72										
	HERPey	252.14	129.61	198.35	143.07	230.13	254.26	172.06									
	LEZAub	19.06	171.12	239.86	184.58	131.49	12.15	213.57	242.11								
	ORIAx	253.18	72.03	3.28	58.57	231.16	255.3	31.68	201.64	243.15							
	SALGir	13.02	168.13	236.87	181.59	128.5	18.19	210.58	239.12	6.04	240.16						
	SALTau	19.91	161.24	229.99	174.7	121.61	22.03	203.7	232.23	9.88	233.27	6.89					
	SAUAri	224.02	42.87	30.28	29.41	202	226.14	3.99	172.48	213.99	33.56	211	204.11				
	SIOTra	210.22	29.07	41.07	15.61	188.21	212.34	14.78	158.68	200.19	44.35	197.2	190.32	15.19			
	TOULar	245.56	123.03	191.77	136.49	223.55	247.68	165.48	45.84	235.53	195.06	232.54	225.65	165.9	152.1		
	VICNia	228.25	47.1	30.86	33.64	206.23	230.36	6.75	176.7	218.21	34.14	215.22	208.34	8.63	19.42	170.12	
Number of dams and/or weirs >3m	ARABas																
	ARIPam	0															
	ARISav	2	2														
	ARIVar	0	0	2													
	ARZDur	1	1	3	1												
	BOUArg	0	0	2	0	1											
	COUPis	1	1	1	1	2	1										
	HERPey	0	0	2	0	1	0	1									
	LEZAub	0	0	2	0	1	0	1	0								
	ORIAx	2	2	0	2	3	2	1	2	2							
	SALGir	0	0	2	0	1	0	1	0	0	2						
	SALTau	0	0	2	0	1	0	1	0	0	2	0					
	SAUAri	1	1	1	1	2	1	0	1	1	1	1	1				
	SIOTra	1	1	1	1	2	1	0	1	1	1	1	1	0			
	TOULar	0	0	2	0	1	0	1	0	0	2	0	0	1	1		
	VICNia	1	1	1	1	2	1	0	1	1	1	1	1	0	0	1	

Figure S2: Introgressive hybridization

For over a century, brown trout have been subject to fisheries management. Due to the release of domestic individuals for angling purposes, non-native alleles are introduced into the wild, leading to a potential introgressive hybridization between wild populations and captive-bred strains. Consequently, this may increase local diversity and reduce population differentiation. We therefore investigated whether the sampled brown trout populations were introgressed from domestic individuals and then estimated the genetic impact of hatchery releases. Specifically, we performed a genetic clustering algorithm implemented in the package ‘rmaverick’ (Verity and Nichols, 2016) of the R statistical software v.3.6.1 (R Development Core Team 2015). We conducted analyses using the admixture by adding four fish farm populations that are traditionally employed to our SNP datasets in order to quantify introgressive hybridization from captive-bred to wild populations (Saint-Pé et al., 2019). Log-likelihood plots were obtained using the thermodynamic integration procedure implemented in ‘rmaverick’ to determine the optimal genetic clusters K (i.e. the maximum number of sampled sites in our dataset). Ten iterations were performed for each value of K. Each iteration comprised a "Burnin" period of 10,000 steps, followed by a Monte Carlo Markov Chain (MCMC) of 200,000 steps. Individuals were assigned to the selected K groups with the greatest individual membership probabilities (Q-value).

Individuals were assigned to the cluster with the greatest Q-value, provided that value exceeded 0.7 based on a previous study (Saint-Pé et al., 2019). Individuals with intermediate Q-values (i.e., between 0.3 and 0.7) were considered genetically admixed. We used the probability of assignment (individual Q-value) to the cluster containing all individuals coming from hatcheries as an estimate of the individual introgression rate with the captive-bred population.

The Bayesian clustering method applied on the SNP genetic marker reveal an optimal number of groups, $K=3$, corresponding to three genetic groups. The four hatchery domestic populations are clustered in the purple group (PISBau, PISFag, PISSou and PISVou). The purple colour in other individuals hence indicates the presence of genetic introgression with domestic fish from these hatchery populations. The orange part corresponds to the wild brown trout from the Garonne and Ariège basin, while the yellow part corresponds to the upstream of the Ariège river.

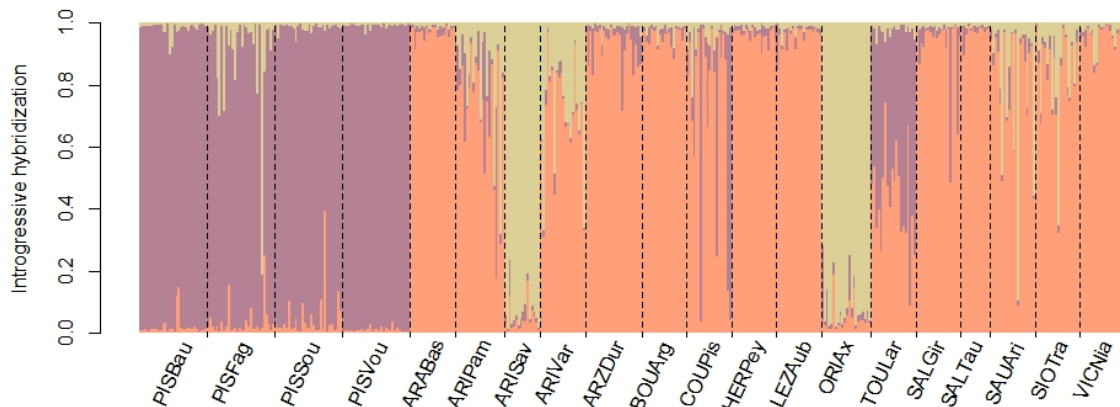


Table S5: Local diversity estimates based on expected heterozygosity (H_e)

We tested the relationships between local diversity (H_e), the distance from the confluence, the centrality and the type of genetic marker using a linear model. The model was written as follows:

$$H_e \sim \text{dist conf} * \text{markers} + \text{dist conf}^2 * \text{markers} + \text{centrality} * \text{markers} + \text{centrality}^2 * \text{markers}.$$

We then ran the corrected AICc to identify the best model. We then performed a model-averaging method on a set of best submodels ($\Delta\text{AICc} < 2$) using the *model.avg* function implemented in the R package *MuMIn* V 1.47.1 (Barton, 2019).

The distance from the confluence was the most important predictor explaining the local diversity, with higher diversity in populations farther away from the confluence.

Table S5a. Best submodels [Δ corrected Akaike's information criterion (AICc) < 2] explaining the variation in local diversity (H_e) along environmental gradients (distance from the confluence, centrality) considering the type of genetic markers (SNPs, candidate SNPs and MHC).

	<i>df</i>	Loglik.	AICc	Δ AICc	Weight
Genetic diversity (<i>Ar</i>)					
<i>d</i>	3	-61.271	129.1	0.00	0.406
<i>d + d</i> ²	4	-60.963	130.9	1.77	0.168

Loglik Log-likelihood, *d* distance from the confluence.

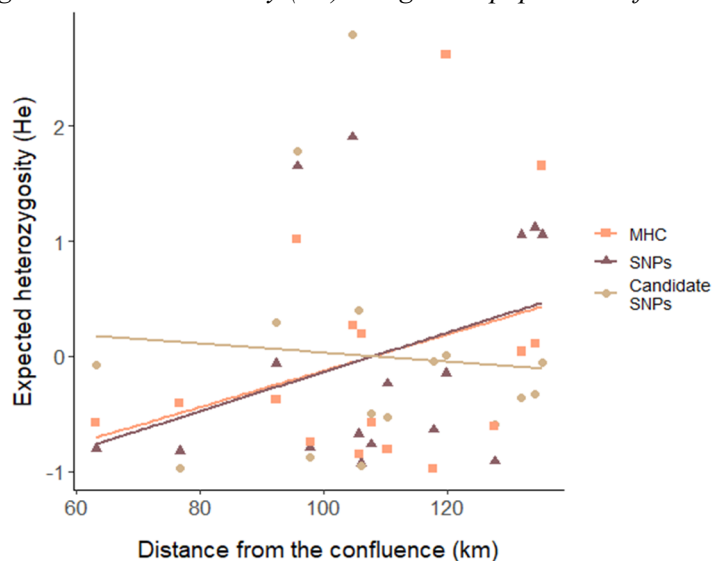
Table S5b. Model-averaged coefficients of best submodels (Δ AICc < 2) explaining the variation in genetic local diversity (H_e) along environmental gradients (distance from the confluence, centrality).

	Estimate \pm Se	CI	RI
Genetic diversity (<i>Ar</i>)			
<i>Distance from confluence</i>	-0.42 \pm 0.13	-0.69, -0.15	1
<i>Distance from confluence</i> ²	0.08 \pm 0.11	-0.13, 0.30	0.29

Parameter estimates are given \pm adjusted SE

CI-95 % Confidence interval, RI-relative importance of each parameter

Figure S3: Local diversity (H_e) is higher in populations farther away from the confluence.



Cited references:

Barton, K. 2019. MuMIn: Multi-Model Inference.

Saint-P , K., M. Leitwein, L. Tissot, N. Poulet, B. Guinand, P. Berrebi, G. Marselli, et al. 2019. Development of a large SNPs resource and a low-density SNP array for brown trout (*Salmo trutta*) population genetics. *BMC Genomics* 20: 582.

Verity, R., and R. A. Nichols. 2016. Estimating the Number of Subpopulations (K) in Structured Populations. *Genetics* 203: 1827–1839.