

Tracing the genetic impact of farmed turbot *Scophthalmus maximus* on wild populations

F. D. Prado, M. Vera, M. Hermida, A. Blanco, C. Bouza, G. E. Maes, F. A. M. Volckaert, AquaTrace Consortium, P. Martínez*

*Corresponding author: paulino.martinez@usc.es

Aquaculture Environment Interactions 10: 447–463 (2018)

Table S1. Sampling characteristics of all wild and farmed turbot (*S. maximus*). N= number of individuals, Lat: latitude, Long: longitude.

Sample location		ICES	Pop ID	Lat	Long	Sampling date	N
Baltic Sea	Baltic Sea - North	IIId	BAS-N	60.2	19.7	2013, 2014	40
	Baltic Sea - South	IIId	BAS-S	55.0	14.9	2001	50
Atlantic	Skagerrak – Transition area	IIIa	T	57.4	9.2	2013	42
	Norway Sea	IVa	NOR	62.0	4.0	2000	43
	North Sea - East	IVb	NS-E	56.4	6.1	2010, 2011	50
	North Sea - Central	IVb	NS-C	55.4	5.3	2011	48
	North Sea - South	IVc	NS-S	51.8	2.0	2010, 2011	32
	Iceland	Va	ICE	63.2	-21.1	2001	14
	Ireland- West	VIa, VIIb	IR-W	59.3	-4.5	2009 - 2013	49
	Ireland - East	VIIa	IR-E	53.5	-4.8	2000	47
	Ireland - Southwest	VIIg, VIIj	IR-SW	50.6	-6.0	2012	26
	Ireland - Southeast	VIIIf	IR-SE	50.4	-5.8	2013	33
	English channel	VIIId, VIIe	ECH	50.7	8.4	2009, 2010	29
	Biscay bay - France	VIIIa, VIIIb	BB-FR	46.2	-2.2	2009- 2011	41
	Biscay bay - Southeast	VIIIc	BB-SE	43.4	-3.8	2009, 2010, 2013	49
	Biscay bay - Southwest	VIIIc	BB-SW	43.7	-7.4	2009, 2010	43
	Spain coast – West	Ixa	SP-W.old	42.6	-8.9	2002	50
			SP-W.new			2010	48
Farmed						2014	174
TOTAL							908

Table S2. Pairwise F_{ST} matrix between all pure wild and farmed samples of turbot (*S. maximus*) based on 755 SNPs.

	BAS-N	BAS-S	T	NOR	NS-E	NS-C	NS-S	ICE	IR-W	IR-E	IR-SW	IR-SE	ECH	BB-FR	BB-SE	BB-SW	SP-W.old	F_ORI1	F_ORI2
BAS-N	-																		
BAS-S	0,003	-																	
T	0,007	0,000	-																
NOR	<u>0,025</u>	0,010	0,012	-															
NS-E	0,010	0,000	0,000	0,006	-														
NS-C	0,012	0,000	0,000	0,006	0,001	-													
NS-S	0,013	0,000	0,000	0,003	0,000	0,000	-												
ICE	0,017	0,000	0,007	0,000	0,000	0,000	0,000	-											
IR-W	<u>0,020</u>	0,000	0,000	0,000	0,002	0,000	0,000	0,000	-										
IR-E	<u>0,019</u>	0,005	0,000	0,000	0,000	0,000	0,000	0,000	0,000	-									
IR-SW	0,012	0,000	0,000	0,009	0,006	0,008	0,001	0,002	0,008	0,004	-								
IR-SE	0,012	0,000	0,000	0,004	0,000	0,002	0,001	0,000	0,003	0,000	0,007	-							
ECH	0,008	0,000	0,000	0,011	0,008	0,004	0,000	0,000	0,004	0,002	0,005	0,000	-						
BB-FR	0,014	0,000	0,000	0,012	0,000	0,000	0,000	0,000	0,000	0,000	0,005	0,002	-0,003	-					
BB-SE	0,013	0,003	0,000	0,012	0,000	0,003	0,000	0,000	0,000	0,000	0,007	0,003	0,003	0,000	-				
BB-SW	<u>0,026</u>	0,004	0,006	0,016	0,003	0,004	0,000	0,000	0,001	0,001	0,010	0,008	0,004	0,000	0,000	-			
SP-W.old	<u>0,018</u>	0,000	0,005	0,007	<u>0,012</u>	0,009	0,001	0,000	0,004	0,008	0,011	0,006	0,008	0,006	0,005	0,004	-		
F_ORI1	<u>0,079</u>	<u>0,080</u>	<u>0,059</u>	<u>0,065</u>	<u>0,056</u>	<u>0,054</u>	<u>0,061</u>	<u>0,036</u>	<u>0,057</u>	<u>0,056</u>	<u>0,076</u>	<u>0,062</u>	<u>0,060</u>	<u>0,047</u>	<u>0,059</u>	<u>0,060</u>	<u>0,067</u>	-	
F_ORI2	<u>0,048</u>	<u>0,046</u>	<u>0,022</u>	<u>0,046</u>	<u>0,034</u>	<u>0,038</u>	<u>0,036</u>	<u>0,031</u>	<u>0,038</u>	<u>0,030</u>	<u>0,037</u>	<u>0,031</u>	<u>0,029</u>	<u>0,032</u>	<u>0,037</u>	<u>0,040</u>	<u>0,048</u>	<u>0,049</u>	-

10.000 permutations; bold: $P < 0.05$; underlined and bold: significant values after sequential Bonferroni correction ($P < 0.0003$).

Figure S1. Graphical representation of tests applied for detecting signals of selection between W_{ATL} vs. F_{OR11} (a, b) and W_{ATL} vs. F_{OR12} (c, d) reference samples of turbot (*S. maximus*) (Table 3). For BAYESCAN (a, c), F_{ST} per locus is plotted against the logarithm of the probability of departure from neutrality ($\log(PO)$); continuous and dashed lines indicate $P = 0.95$ ($\text{Log}_{10}(\text{BF}) > 1.3$) and $P = 0.99$ ($\text{Log}_{10}(\text{BF}) > 2$) thresholds. For LOSITAN (b, d), F_{ST} is plotted against heterozygosity, dashed lines indicate 99% confidence thresholds.

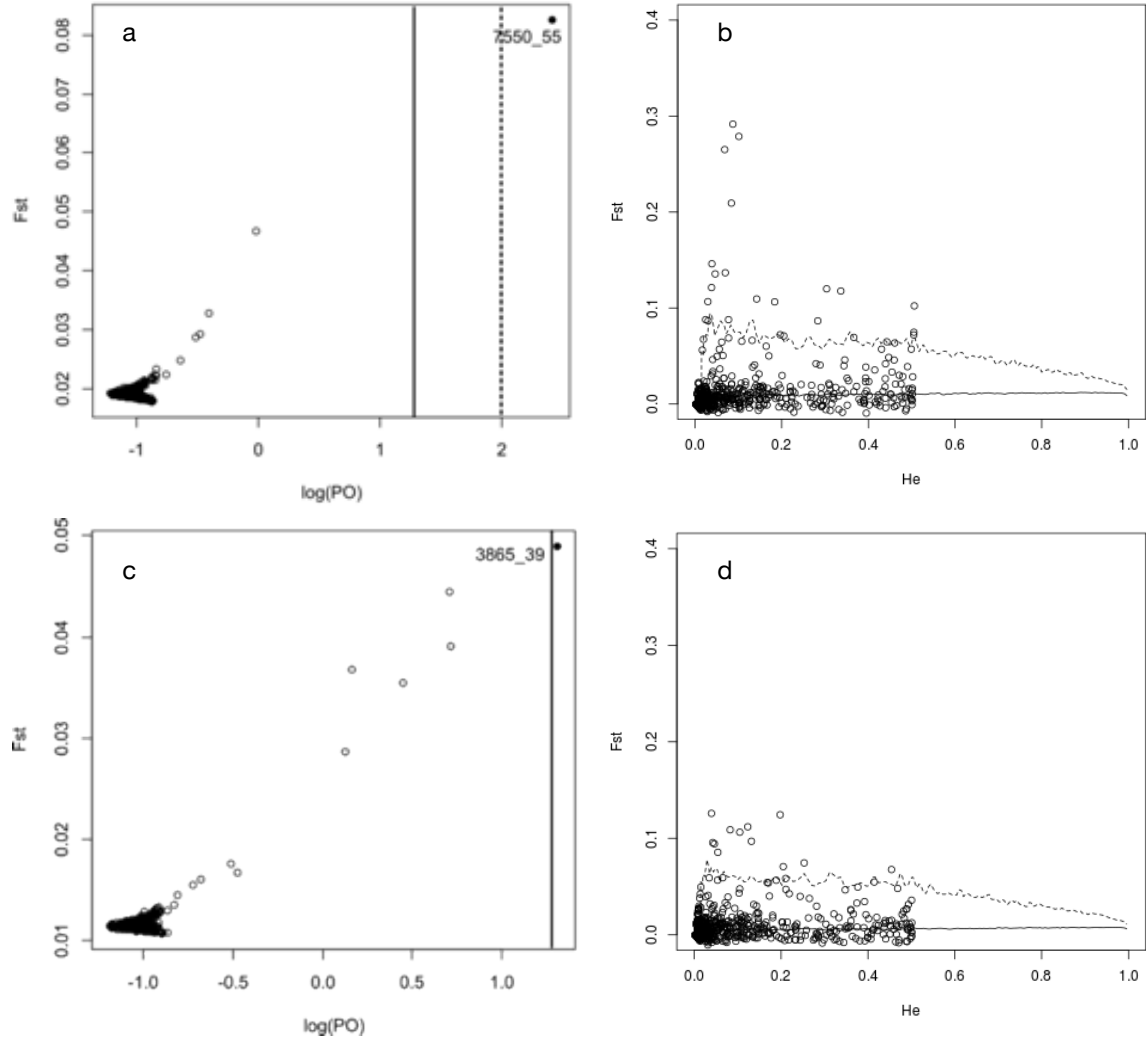


Figure S2. STRUCTURE results for the old and new samples of turbot (*S. maximus*) from the Spanish Coast genotyped for 755 SNPs (Table S4). Data shows K=3 to the reference samples (red: W_{ATL} cluster, yellow: F_{ORI1} cluster, blue: F_{ORI2} cluster).

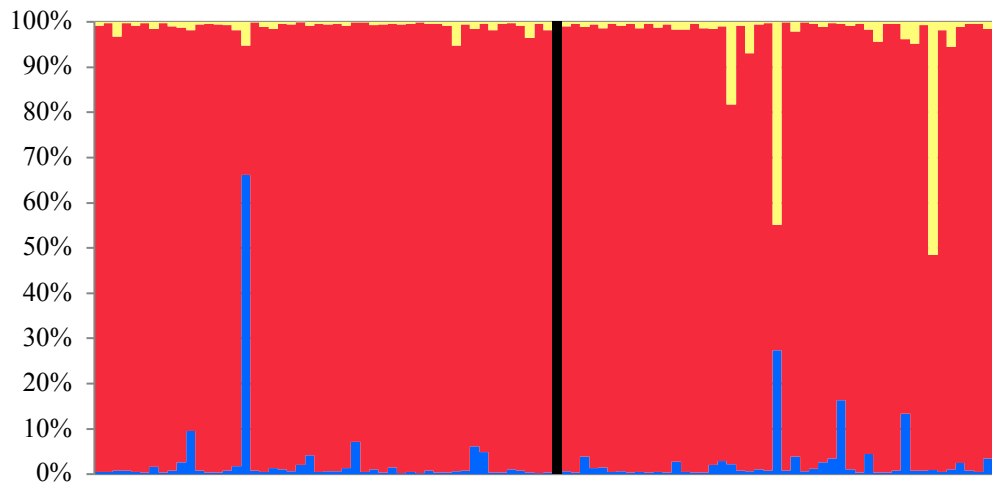


Figure S3. Venn diagram for the 100 most divergent SNPs from the three pairwise comparisons between reference populations of turbot (*S. maximus*), W_{ATL}, F_{ORI1} and F_{ORI2}.

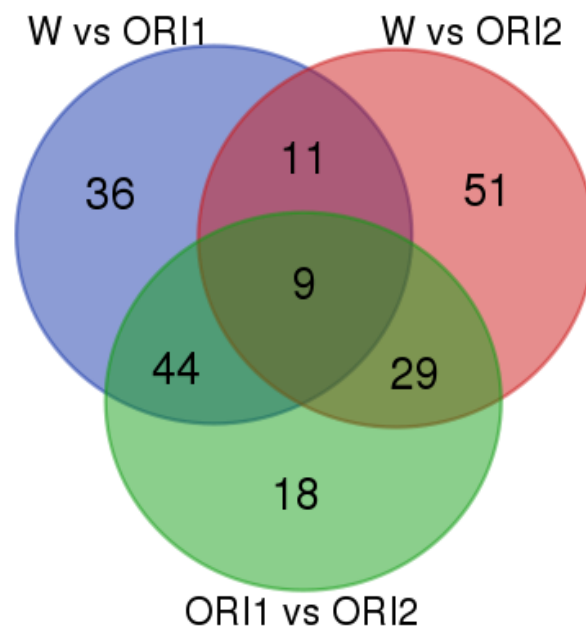


Figure S4. Frequency distribution of q_W of turbot individuals misclassified with A) the small SNP dataset vs the full dataset; and B) STRUCTURE vs GeneClass v2.0 with the small SNP dataset.

