

ELECTRONIC SUPPLEMENTS FOR

“Candidate gene variation reveals complex spatiotemporal patterns of selection between marine and lagoon habitats in the gilthead sea bream”

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**Supplementary Table S1:** *Sparus aurata*. List of forward (*F*) and reverse (*R*) primers for each microsatellite locus and long range (LR) amplicons used in this study.

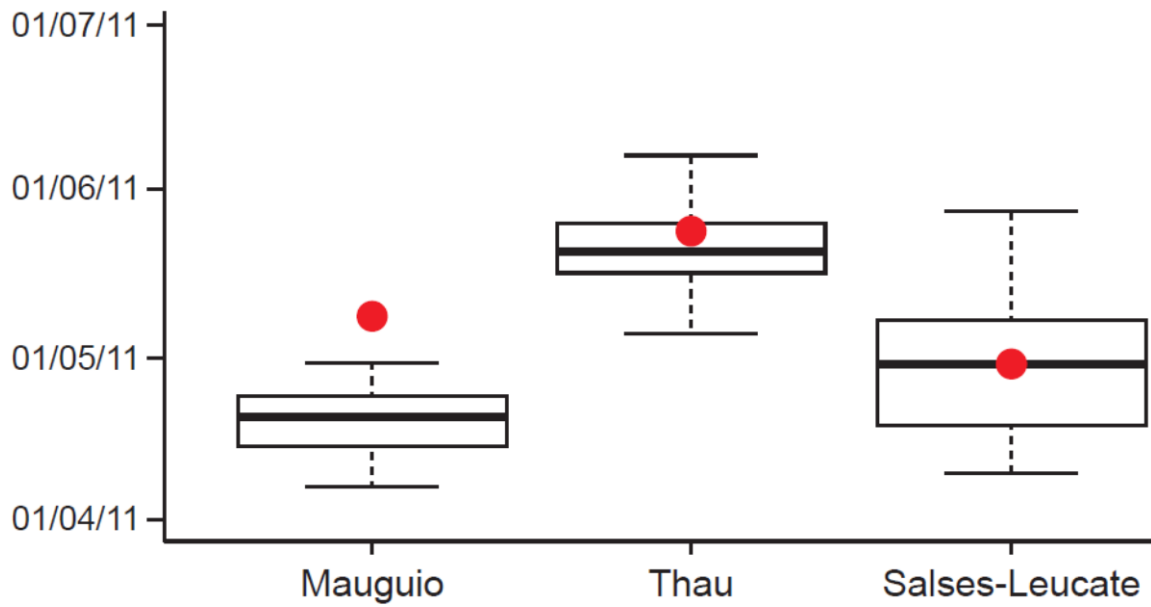
Locus	Primers (5' -> 3')	Primer source
<b>Microsatellites :</b>		
<i>Prl</i>	<i>F</i> GAAGAGTTTGCTTCCATTGG	Astola et al. 2003
	<i>R</i> CATCCATCCAATTAAGATGG	
<i>GH</i>	<i>F</i> CCTTAAATCAGTTCAGCCG	Almuly et al. 2005
	<i>R</i> GGTCAAGTTCTGGTACTAG	
<i>F7b</i>	<i>F</i> ATCGTTTTCTAGGGCGTGTG	Coscia et al. 2012
	<i>R</i> CGTTTCCTCACTGCTGGTG	
<i>B13b</i>	<i>F</i> CCTCCTGACCAGTCCTGCTTT	Coscia et al. 2012
	<i>R</i> ACCCCTGCATTCCAGCTTC	
<i>F6</i>	<i>F</i> CTGCTCACTGTTGACTGAATAC	Coscia et al. 2012
	<i>R</i> GATGACTGCCTCCCTCTTATC	
<i>Hd33F</i>	<i>F</i> TGAGTCTACAAAGCCAGAACCA	Coscia et al. 2012
	<i>R</i> AATAAAGCTCTGCCTGTGCC	
<i>Saimbb25</i>	<i>F</i> AAACAACCTCGGTCGTCAC	Coscia et al. 2012
	<i>R</i> CTGCACCTTATCCTCTTGACAC	
<i>SauE82</i>	<i>F</i> ATTGGGTGGCAGTTTAGTAGG	Coscia et al. 2012
	<i>R</i> CACTGCGATGAGTGACCC	
<i>Ad10F</i>	<i>F</i> TGGAGGAACAGTGACAGTCAG	Coscia et al. 2012
	<i>R</i> GGAATGGAAGTGCCTGATGT	
<i>Cld29T</i>	<i>F</i> GTCGGATTTTCGCATGTTGT	Coscia et al. 2012
	<i>R</i> CTGCAGGGAGGAAACAAGAC	
<i>Dd16T</i>	<i>F</i> CACATTTAGGGCACCATATCC	Franch et al. 2006
	<i>R</i> GGGAACTCTCTGTCTGTCTGG	
<i>Sau147</i>	<i>F</i> ACAGTACCCCACTGTCTCC	Franch et al. 2006
	<i>R</i> CCATATCATTACACTGTGGC	
<i>Dt23</i>	<i>F</i> CACACAACACACGATTACAGCA	Franch et al. 2006
	<i>R</i> CCAAAAACAGCGATTTGTCC	
<i>Bld04F</i>	<i>F</i> TCCGTGACTCTGTCTACCA	Franch et al. 2006
	<i>R</i> TCTTTGTCCGCATGTTTCAC	
<i>Fd92H</i>	<i>F</i> AGGCATTTTGTCAATGAGGG	Franch et al. 2006
	<i>R</i> CTGGGTTGGAGAGCTCAGAT	
<i>Cld35H</i>	<i>F</i> TGGGGTTTAGCTGTCAATCC	Franch et al. 2006
	<i>R</i> GCGGCTATGCCTACAACCTTC	

<i>C67b</i>	<i>F</i>	GCCCTGGTTATCATCTGTCGTT	Franch et al. 2006
	<i>R</i>	GCTCGTGTGTTGTTTGCTGTCT	
<i>Bld10T</i>	<i>F</i>	TCTCCACCACCTGCAGTTTT	Franch et al. 2006
	<i>R</i>	ACCGCCATCTTTGCTCTTTA	
<i>Ct27</i>	<i>F</i>	TTCAGATGAGAGTGGCATTAGG	Franch et al. 2006
	<i>R</i>	GGACGCTCTGGCTGTTCT	
<i>172EP</i>	<i>F</i>	GAGGGCATGTTGGAGGAAC	Franch et al. 2006
	<i>R</i>	GCACTCCATGTGGCTTCAG	
<i>P20</i>	<i>F</i>	AGAGCTCACTGTGACGATCAG	Franch et al. 2006
	<i>R</i>	CAGGATCCCATCCTTACACA	
<i>C77b</i>	<i>F</i>	CGATGGAACTACCCACCTC	Franch et al. 2006
	<i>R</i>	GCGACCATGAACCTGAAA	
<i>Bd14H</i>	<i>F</i>	TGCAGTGTCAAGGAAAACCA	Franch et al. 2006
	<i>R</i>	GCCATTATCAATCACTAACATGC	
<b>LR amplicons:</b>			
<i>GH</i> LR-PCR	<i>F</i>	CCAGAACCTGAACCAGACATGGACAG	This study
	<i>R</i>	GGCCTCTGGAGAGAGTCTACATTTTGC	
<i>Prl</i> LR-PCR	<i>F</i>	AGTCCTGCCGAATGAGTCCT	This study
	<i>R</i>	TGCTGCAGTTTGTCATCAGAC	

**Supplementary Table S2: *Sparus aurata*.** Summary of post filtering and post reference assembly steps for each of the 24 individuals used in haplotype reconstruction (MA: Manguio; TH: Thau).

Individuals	Total No. of filtered reads	No. of <i>GH</i> reads	No. of <i>Prl</i> reads	Total No. of reads assembled	Assembled reads (%)	Reads assembled to <i>GH</i> (%)	Reads assembled to <i>Prl</i> (%)
MA06	351,692	154,670	122,062	276,732	0.787	0.559	0.441
MA07	733,944	411,042	54,658	465,700	0.635	0.883	0.117
MA08	1,126,596	273,643	697,557	971,200	0.862	0.282	0.718
MA11	147,324	37,402	77,126	114,528	0.777	0.327	0.673
MA17	276,848	43,073	140,692	183,765	0.664	0.234	0.766
MA21	341,150	128,041	177,998	306,039	0.897	0.418	0.582
MA23	1,085,134	263,211	637,535	900,746	0.830	0.292	0.708
MA24	834,982	409,035	286,631	695,666	0.833	0.588	0.412
MA25	915,826	360,150	449,655	809,805	0.884	0.445	0.555
MA26	891,528	312,411	455,736	768,147	0.862	0.407	0.593
MA29	770,688	560,646	155,264	715,910	0.929	0.783	0.217
MA30	483,688	196,429	228,772	425,201	0.879	0.462	0.538
TH02	690,296	370,701	378,152	748,853	1.085	0.495	0.505
TH03	689,486	400,725	147,886	548,611	0.796	0.730	0.270
TH15	619,086	331,192	147,904	479,096	0.774	0.691	0.309
TH16	300,202	62,918	119,355	182,273	0.607	0.345	0.655
TH17	650,072	73,099	436,884	509,983	0.785	0.143	0.857
TH40	334,664	39,769	186,153	225,922	0.675	0.176	0.824
TH77	275,758	60,224	46,073	106,297	0.385	0.567	0.433
TH82	354,740	38,944	104,048	142,992	0.403	0.272	0.728
TH83	411,414	31,630	40,761	72,391	0.176	0.437	0.563
TH11	824,338	212,042	344,854	556,896	0.676	0.381	0.619
TH28	806,196	196,129	270,495	466,624	0.579	0.420	0.580
TH72	492,264	100,003	47,525	147,528	0.300	0.678	0.322
<b>Sum/Mean</b>	<b>14,407,916</b>	<b>5,067,129</b>	<b>5,753,776</b>	<b>10,820,905</b>	<b>0.712</b>	<b>0.459</b>	<b>0.541</b>

**Supplementary Figure S1:** *Sparus aurata*. Estimates of recruitment date of autumn (= migrating) individuals in each lagoon (box plots), together with sampling dates of spring (= entering) individuals (red circles). Estimates of recruitment events for autumn individuals were back-calculated from otolithometry data (Isnard et al. 2015). Adapted from Isnard et al. (2015).



**Supplementary Figure S2: *Sparus aurata*.** Results of Beaumont and Nichols' (1996) neutrality test using LOSITAN (Antao et al. 2008), based on comparisons among (A) entering (spring), and (B) migrating (autumn) samples, respectively. The test based on all samples is not provided because it reported a similar result as the one obtained for spring samples (see Fig. 2). Dots indicate markers, and only labels of outlier loci are reported. The grey area illustrates the 'neutral' envelop obtained with a null  $F_{ST}$  distribution generated with 100,000 simulated loci. Outlier loci falling in the red area were considered as candidate for diversifying selection. The locus falling in the yellow area (*Dd16T*) in panel B was not considered as a candidate for balancing selection due to the panmictic regime of the sea bream population studied (i.e. false positive). This locus exactly lies on the limit of the neutral envelop (p-value: 0.0503). He: expected heterozygosity.  $F_{ST}/He$ : " $F_{ST}$  conditional on heterozygosity", a feature of the Beaumont and Nichols (1996) model.

