Supplementary Online Material

Genetic biodiversity in the Baltic Sea: species-specific patterns challenge management

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Table S1 Summary statistics for each sample from each of the seven species of the present study. Information include geographic coordinates specifying where the sample was collected, number of scored loci, expected and observed heterozygosity, allelic richness, deviations from Hardy-Weinberg proportions as tested in GENEPOP (Raymond and Rousset 1997). Classification of the sample with respect to its diversity and divergence pattern in relation to the other samples from the same species within the Baltic Sea is indicated in the last column and this classification was performed using the methods described by Petit et al. (1998) implemented in the software MOLKIN 2.0 (Gutiérretz et al. 2005).

Sampling area	Coordinates (WGS84)		Number of individuals sampled	Number of loci	Expected hetero-zygosity	Observed hetero-zygosity	Allelic richness	Genotypes in agreement with Hardy-Weinberg proportions	Diversity-divergence pattern 1: higher diversity-higher divergence 2: higher diversity-lower divergence 3: lower diversity-higher divergence 4: lower diversity-lower divergence
	North	East							
Atlantic herring (*Clupea harengus*)									
Outside Baltic	57.32	10.54	47	9	0.83	0.83	13.71	No (heterozygote def.)	-
South Baltic	55.80	15.12	47	9	0.81	0.78	12.80	Yes	3
Baltic Proper West	57.32	16.90	47	9	0.82	0.82	13.46	Yes	3
Baltic Proper East	59.05	22.47	47	9	0.81	0.80	13.52	Yes	3
Gulf of Finland	60.50	27.76	47	9	0.80	0.80	13.13	Yes	3
Bothnian Sea	60.19	19.61	47	9	0.81	0.79	14.11	Yes	2
The Kvark	63.40	20.32	47	9	0.80	0.78	14.08	Yes	2
Bothnian Bay	65.62	24.87	47	9	0.80	0.79	13.68	Yes	1
Northern pike (*Esox lucius*)									
South Baltic	56.13	15.03	20	11	0.55	0.55	4.22	Yes	3
Baltic Proper West 1	57.79	19.01	20	11	0.60	0.57	4.44	Yes	3
Baltic Proper West 2	58.03	16.77	44	11	0.61	0.58	4.58	Yes	2
Baltic Proper West 3	59.52	18.56	42	11	0.60	0.56	4.43	Yes	4
Baltic Proper East	58.70	23.40	34	11	0.57	0.55	4.34	Yes	3
Gulf of Finland 1	60.22	25.20	30	11	0.63	0.65	4.75	Yes	2
Gulf of Finland 2	60.43	26.04	16	11	0.59	0.58	4.33	Yes	3
Bothnian Sea	60.27	20.10	41	11	0.62	0.63	4.74	Yes	2
The Kvark	62.90	21.30	41	11	0.60	0.59	4.37	Yes	4
Bothnian Bay	65.50	24.40	27	11	0.66	0.59	4.78	Yes	1

Table S1 cont.

Sampling area	Coordinates (WGS84)		Number of individuals sampled	Number of loci	Expected hetero-zygosity	Observed hetero-zygosity	Allelic richness	Genotypes in agreement with Hardy-Weinberg proportions	Diversity-divergence pattern 1: higher diversity-higher divergence 2: higher diversity-lower divergence 3: lower diversity-higher divergence 4: lower diversity-lower divergence
	North	East							
European Whitefish (*Coregonus lavaretus*)									
Outside Baltic	59.08	11.23	22	12	0.67	0.64	4.39	Yes	-
South Baltic	54.22	12.12	50	12	0.72	0.74	4.17	Yes	3
Baltic Proper West 1	57.47	16.70	47	12	0.77	0.74	5.06	Yes	1
Baltic Proper West 2	59.38	19.20	48	12	0.75	0.76	5.07	Yes	2
Baltic Proper East	58.36	21.90	43	12	0.71	0.70	4.86	Yes	3
Gulf of Finland	60.07	29.83	13	12	0.77	0.77	5.43	Yes	2
Bothnian Sea	61.09	21.29	48	12	0.72	0.74	4.93	Yes	2
The Kvark	63.73	20.79	34	12	0.72	0.70	4.63	Yes	3
Bothnian Bay 1	64.28	23.80	21	12	0.73	0.71	4.94	Yes	2
Bothnian Bay 2	65.11	24.69	20	12	0.73	0.73	4.98	Yes	2
Three-spined stickleback (*Gasterosteus aculeatus)*									
Outside Baltic	58.23	11.40	36	16	0.77	0.73	9.58	Yes	-
South Baltic	55.37	13.15	29	16	0.75	0.74	8.94	Yes	3
Baltic Proper West 1	57.00	18.20	36	16	0.76	0.76	9.32	Yes	2
Baltic proper West 2	58.65	17.00	34	16	0.75	0.73	9.26	Yes	1
Baltic Proper East	59.83	23.20	30	16	0.75	0.74	9.31	Yes	2
Gulf of Finland	60.35	28.62	31	16	0.73	0.72	8.70	Yes	3
Bothnian Sea 1	60.19	19.62	33	16	0.76	0.75	9.71	Yes	2
Bothnian Sea 2	61.72	17.11	36	16	0.74	0.74	8.88	Yes	4
The Kvark	62.51	17.72	36	16	0.76	0.75	9.30	Yes	1
Bothnian Bay	65.85	22.37	36	16	0.74	0.73	8.95	Yes	3

Table S1 cont.

Sampling area	Coordinates (WGS84)		Number of individuals sampled	Number of loci	Expected hetero-zygosity	Observed hetero-zygosity	Allelic richness	Genotypes in agreement with Hardy-Weinberg proportions	Diversity-divergence pattern 1: higher diversity-higher divergence 2: higher diversity-lower divergence 3: lower diversity-higher divergence 4: lower diversity-lower divergence
	North	East							
Nine-spined stickleback (*Pungitius pungitius*)									
Outside Baltic	58.23	11.40	40	19	0.51	0.47	4.96	No (heterozygote def.)	-
South Baltic	56.15	15.58	29	19	0.58	0.59	5.65	Yes	2
Baltic Proper West	58.65	17.10	15	19	0.59	0.59	5.37	Yes	1
Baltic Proper East	60.43	22.20	20	19	0.57	0.56	3.97	Yes	3
Gulf of Finland	60.45	26.25	38	19	0.60	0.58	5.63	Yes	2
Bothnian Sea	60.38	18.20	17	19	0.59	0.54	5.77	Yes	2
The Kvark	63.65	20.20	40	19	0.60	0.59	5.69	No (heterozygote def.)	2
Bothnian Bay	65.00	25.47	31	19	0.58	0.54	5.41	No (heterozygote def.)	2
Blue mussel (*Mytilus spp.*)									
Outside Baltic	56.11	12.47	30	10	0.07	0.07	1.40	Yes	-
South Baltic 1	53.98	14.46	30	10	0.30	0.26	2.00	Yes	2
South Baltic 2	54.60	18.60	30	10	0.24	0.21	2.00	Yes	2
South Baltic 3	54.74	12.18	30	10	0.31	0.24	1.98	Yes	1
Baltic Proper West 1	58.43	18.99	30	10	0.26	0.22	1.98	Yes	2
Baltic Proper West 2	58.82	17.65	30	10	0.18	0.18	1.79	Yes	3
Gulf of Finland	59.60	24.66	29	10	0.22	0.20	1.88	Yes	3
The Kvark	63.78	20.47	30	10	0.17	0.15	1.87	Yes	3
Bladderwrack (*Fucus vesiculosus*)									
Outside Baltic	57.55	11.83	42	7	0.72	0.68	4.71	Yes	-
South Baltic 1	55.51	12.90	25	7	0.69	0.71	4.29	Yes	1
South Baltic 2	55.57	12.89	24	7	0.67	0.64	4.39	Yes	2
Baltic Proper West	57.36	17.08	42	7	0.59	0.59	3.28	Yes	3
Baltic Proper East	58.28	22.77	22	7	0.55	0.52	3.33	Yes	4
Bothnian Sea 1	60.30	18.70	43	7	0.50	0.52	3.06	Yes	1
Bothnian Sea 2	62.38	17.68	29	7	0.55	0.52	2.84	Yes	3
The Kvark	63.34	21.48	12	6	0.51	0.76	2.58	No (Heterozygote exc.)	3

Table S2 a-g Pairwise F_{ST} values (below diagonal) and corresponding p-values (above diagonal). Significant values are marked in bold, and values significant after Bonferroni correction are underlined. Adjusted alpha levels after Bonferroni correction are based on the number of pairwise tests within each species. Sample numbers within regions denotes population number corresponding to Table S1.

Table S2a Atlantic herring (*Clupea harengus*), adjusted alpha=0.00179

	Outside Baltic	**South Baltic**	**Baltic Proper West**	**Baltic Proper East**	**Gulf of Finland**	**Bothnian Sea**	**The Kvark**	**Bothnian Bay**
Outside Baltic		**<u><0.001</u>**	**0.021**	**<u>0.004</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**
South Baltic	**<u>0.0089</u>**		0.480	0.585	0.383	0.656	0.248	0.535
Baltic Proper West	**0.0002**	-0.0005		0.720	0.639	0.517	0.245	0.059
Baltic Proper East	**<u>0.0041</u>**	-0.0006	-0.0012		0.156	0.789	0.119	0.391
Gulf of Finland	**<u>0.0104</u>**	0.0007	-0.0005	0.0034		0.571	0.651	0.413
Bothnian Sea	**<u>0.0100</u>**	0.0002	0.0013	0.0000	-0.0002		0.309	0.313
The Kvark	**<u>0.0101</u>**	0.0015	-0.0003	0.0038	-0.0028	0.0011		0.454
Bothnian Bay	**<u>0.0088</u>**	0.0002	0.0031	0.0039	0.0010	0.0016	0.0028	

Table S2b Northern pike (*Esox lucius*), adjusted alpha=0.00111

	South Baltic	**Baltic Proper West 1**	**Baltic Proper West 2**	**Baltic Proper West 3**	**Baltic Proper East**	**Gulf of Finland 2**	**Gulf of Finland 1**	**Bothnian Sea**	**The Kvark**	**Bothnian Bay**
South Baltic		**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**
Baltic Proper West 1	**<u>0.0321</u>**		**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**
Baltic Proper West 2	**<u>0.0345</u>**	**<u>0.0242</u>**		**0.006**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**
Baltic Proper West 3	**<u>0.0450</u>**	**<u>0.0397</u>**	**0.0123**		**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**
Baltic Proper East	**<u>0.0492</u>**	**<u>0.0416</u>**	**<u>0.0317</u>**	**<u>0.0480</u>**		**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**
Gulf of Finland 2	**<u>0.0151</u>**	**<u>0.0363</u>**	**<u>0.0239</u>**	**<u>0.0409</u>**	**<u>0.0600</u>**		**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**
Gulf of Finland 1	**<u>0.0380</u>**	**<u>0.0159</u>**	**<u>0.0222</u>**	**<u>0.0312</u>**	**<u>0.0423</u>**	**<u>0.0319</u>**		**<u><0.001</u>**	**<u><0.001</u>**	**<u><0.001</u>**
Bothnian Sea	**<u>0.0381</u>**	**<u>0.0408</u>**	**<u>0.0180</u>**	**<u>0.0145</u>**	**<u>0.0466</u>**	**<u>0.0391</u>**	**<u>0.0191</u>**		**<u><0.001</u>**	**<u><0.001</u>**
The Kvark	**<u>0.0185</u>**	**<u>0.0355</u>**	**<u>0.0275</u>**	**<u>0.0359</u>**	**<u>0.0458</u>**	**<u>0.0216</u>**	**<u>0.0158</u>**	**<u>0.0139</u>**		**<u><0.001</u>**
Bothnian Bay	**<u>0.0695</u>**	**<u>0.0738</u>**	**<u>0.0600</u>**	**<u>0.0749</u>**	**<u>0.0879</u>**	**<u>0.0701</u>**	**<u>0.0463</u>**	**<u>0.0487</u>**	**<u>0.0508</u>**	

Table S2c European whitefish (*Coregonus lavaretus*), adjusted alpha=0.00111

	Outside Baltic	South Baltic	Baltic Proper West 2	Baltic Proper West 1	Baltic Proper East	Gulf of Finland	Bothnian Sea	The Kvark	Bothnian Bay 2	Bothnian Bay 1
Outside Baltic		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
South Baltic	**0.1114**		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Baltic Proper West 2	**0.0761**	**0.0840**		**<0.001**	**<0.001**	**0.001**	**0.002**	**<0.001**	**<0.001**	**<0.001**
Baltic Proper West 1	**0.0698**	**0.0702**	**0.0094**		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Baltic Proper East	**0.0575**	**0.0780**	**0.0348**	**0.0300**		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Gulf of Finland	**0.0463**	**0.0640**	**0.0164**	**0.0086**	**0.0114**		0.106	**0.009**	**0.005**	0.485
Bothnian Sea	**0.0695**	**0.0770**	**0.0076**	**0.0166**	**0.0298**	0.0049		**<0.001**	**<0.001**	0.067
The Kvark	**0.0676**	**0.0754**	**0.0176**	**0.0166**	**0.0375**	**0.0047**	**0.0132**		0.086	0.107
Bothnian Bay 2	**0.0810**	**0.0752**	**0.0129**	**0.0218**	**0.0317**	**0.0078**	**0.0154**	-0.0015		0.455
Bothnian Bay 1	**0.0539**	**0.0743**	**0.0178**	**0.016**	**0.0224**	-0.0004	0.0083	-0.0021	-0.0018	

Table S2d Three-spined stickleback (*Gasterosteus aculeatus*), adjusted alpha=0.00111

	Outside Baltic	South Baltic	Baltic Proper West 1	Baltic Proper West 2	Baltic Proper East	Gulf of Finland	Bothnian Sea 2	Bothnian Sea 1	The Kvark	Bothnian Bay
Outside Baltic		**0.002**	**<0.001**	**<0.001**	**0.002**	**<0.001**	**<0.001**	**0.001**	**<0.001**	**<0.001**
South Baltic	**0.0109**		0.462	0.084	0.182	0.145	0.523	0.211	0.091	0.177
Baltic Proper West 1	**0.0099**	0.0021		0.121	0.211	**0.011**	0.644	0.565	0.565	0.124
Baltic Proper West 2	**0.0129**	0.0008	0.0014		0.573	0.799	0.335	0.261	0.065	0.198
Baltic Proper East	**0.0052**	0.0034	-0.0002	-0.0018		0.166	0.414	0.391	**0.038**	**<0.001**
Gulf of Finland	**0.0175**	0.0053	**0.0057**	-0.0036	0.0032		0.080	0.101	**0.003**	**0.023**
Bothnian Sea 2	**0.0095**	-0.0011	-0.0010	-0.0010	-0.0012	0.0049		0.324	0.565	0.227
Bothnian Sea 1	**0.0076**	0.0012	0.0011	-0.0020	-0.0022	0.0024	-0.0010		0.783	0.229
The Kvark	**0.0107**	0.0010	-0.0013	-0.0021	**0.0009**	**0.0057**	-0.0021	-0.0024		0.157
Bothnian Bay	**0.0159**	0.0009	0.0024	-0.0012	**0.0029**	**0.0029**	-0.0012	-0.0017	-0.0003	

Table S2e Nine-spined stickleback (*Pungitius pungitius*), adjusted alpha=0.00179

	Outside Baltic	South Baltic	Baltic Proper West	Baltic Proper East	Gulf of Finland	Bothnian Sea	The Kvark	Bothnian Bay
Outside Baltic		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
South Baltic	**0.1582**		0.555	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Baltic Proper West	**0.1777**	0.0021		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Baltic Proper East	**0.1957**	**0.0658**	**0.0585**		**<0.001**	**<0.001**	**<0.001**	**<0.001**
Gulf of Finland	**0.1513**	**0.0059**	**0.0077**	**0.0463**		**<0.001**	**0.003**	**<0.001**
Bothnian Sea	**0.1587**	**0.0181**	**0.0147**	**0.0569**	**0.0087**		**<0.001**	**<0.001**
The Kvark	**0.1485**	**0.0134**	**0.0159**	**0.0457**	**0.0039**	**0.0121**		**0.001**
Bothnian Bay	**0.1530**	**0.0196**	**0.0270**	**0.0688**	**0.0111**	**0.0114**	**0.0085**	

Table S2f Blue mussel (*Mytilus spp.*), adjusted alpha=0.00179

	Outside Baltic	South Baltic 3	South Baltic 2	South Baltic 1	Baltic Proper West 2	Baltic Proper West 1	Gulf of Finland	The Kvark
Outside Baltic		**<0.001**	**<0.001**	**<0.001**	**0.049**	**<0.001**	**<0.001**	**<0.001**
South Baltic 3	**0.1684**		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
South Baltic 2	**0.7860**	**0.5328**		0.515	**0.036**	0.902	0.710	**0.049**
South Baltic 1	**0.7251**	**0.4541**	0.0025		**<0.001**	0.122	**0.011**	**<0.001**
Baltic Proper West 2	**0.8292**	**0.5856**	**0.0141**	**0.0442**		0.059	**<0.001**	0.295
Baltic Proper West 1	**0.7692**	**0.5195**	-0.0033	0.0173	0.0262		0.897	**0.046**
Gulf of Finland	**0.7941**	**0.5383**	-0.0004	**0.0240**	**0.0168**	-0.0045		0.143
The Kvark	**0.8322**	**0.5851**	**0.0401**	**0.0514**	0.0297	**0.0363**	0.0181	

Table S2g Bladderwrack (*Fucus vesiculosus*), adjusted alpha=0.00179

	Outside Baltic	South Baltic 2	South Baltic 1	Baltic Proper West	Baltic Proper East	Bothnian Sea 2	Bothnian Sea 1	The Kvark
Outside Baltic		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
South Baltic 2	**0.0425**		**0.005**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
South Baltic 1	**0.0426**	**0.0293**		**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**
Baltic Proper West	**0.0917**	**0.1079**	**0.1185**		**<0.001**	**<0.001**	**<0.001**	**<0.001**
Baltic Proper East	**0.0888**	**0.1720**	**0.1288**	**0.1927**		**<0.001**	**<0.001**	**<0.001**
Bothnian Sea 2	**0.1139**	**0.1339**	**0.1556**	**0.1818**	**0.2489**		**<0.001**	**<0.001**
Bothnian Sea 1	**0.1553**	**0.1915**	**0.1330**	**0.2163**	**0.1462**	**0.1905**		**<0.001**
The Kvark	**0.1713**	**0.1894**	**0.1662**	**0.1877**	**0.1711**	**0.2761**	**0.1514**	

Genotyping methods

Atlantic herring *(Clupea harengus)*

DNA extraction and microsatellite analyses were performed at the University of Helsinki, Finland. DNA was extracted from ethanol-stored fin clips using a silica-based purification method (Ivanova 2006). Genetic variation was assessed using nine microsatellite markers: Cha1017, Cha1020, Cha1202 (McPherson et al. 2001), CPA101, CPA 111, CPA112, CPA113, CPA114, CPA1027 (Olsen et al. 2002). Markers were divided into two multiplexes, and 4 were run as single markers (See Table OS1). Each PCR was carried out in a 10 µl reaction consisting of ca. 2ng of DNA, 2pmol of each primer, and 1xPhusion® Flash High-Fidelity PCR Master Mix (Finnzymes). The cycling profile was: 98°C for 1 min, followed by 34 cycles of 98°C for 1 s, 58°C for 12 s, 72°C for 20 s, and a final extension at 72°C for 1 min. The PCR products were diluted to 1:100 and analysed using a MegaBace 1000 capillary sequencer and Fragment Profiler 1.2 software (GE Healthcare, Life Sciences).

Table S3 *Atlantic herring markers in electrophoresis panels and pcr-multiplexes.*

	Electrophoresis panel	PCR multiplex	Fluoro label	Primer conc.	Pooling amount
Cha1017	1	1	FAM	2µM	3µl
CPA112	1	1	TET	2µM	3µl
Cha1202	2	2	FAM	2µM	3µl
Cha1020	2	2	TET	2µM	3µl
CPA111	2	2	HEX	3µM	3µl
CPA101	3	3	TET	2µM	3µl
CPA113	4	4	TET	2µM	3µl
CPA114	5	5	FAM	2µM	3µl
CPA1027	6	6	HEX	3µM	3µl

European whitefish *(Coregonus lavaretus)*

DNA extraction and microsatellite analyses were performed at the Center of Evolutionary Applications, University of Turku, Finland. DNA was extracted from ethanol-stored fin clips or dried scales using a silica-based purification method modified from Elphistone et al (2003). Genetic variation was assessed at 12 markers *Cisco-90, C2-157* (Turgeon et al 1999), *Cla-Tet1, Cla-Tet3, Cla-Tet6* (Winkler and Weiss 2008), *Cocl-Lav4, Cocl-Lav8, Cocl-Lav18, Cocl-Lav61* (Rogers et al 2004), *BFRO-018* (Susnik et al 1999), *BWF2* (Patton et al 1997), and *SsBg26* (M. Säisä pers. comm.). Markers were divided in two separately analyzed panels (see tableA1). Each PCR multiplex was carried out in an 8µl reaction consisting of ca. 100 ng of DNA, 0.08 to 0.6 µM of each primer (one of which was fluorescently labeled) and 1X Qiagen multiplex PCR master mix (Qiagen Inc. Valencia, CA, USA). The PCR profile used was according to the manufacturer's standard protocol. Amplifications were performed on PTC-100 (MJ Research) and AB 2720 (Applied Biosystems) thermal cyclers. Microsatellite fragments were analyzed in two capillary electrophoresis runs with PCR products 0.9 to 4 µl of two of the four multiplexes pooled and diluted with 100 µl of sterile water. 2 µl of the pooled and diluted PCR product was combined with GS600LIZ size standard (Applied Biosystems) and HiDi-formamide (Applied Biosystems). Samples were denatured at 98 °C for three minutes and the size of the fragments was determined on an ABI Prism™ 3130*xl* genetic analysis instrument.

Table S4 *Whitefish markers in electrophoresis panels and pcr-multiplexes.*

	Electrophoresis Panel	PCR Multiplex	Flouro label	Primer conc.	Pooling amount
C2-157	1	1	ned	0.10	1.5
Cisco-90	1	1	fam	0.18	
Cla-Tet1	1	1	fam	0.10	
Cocl-Lav4	1	1	vic	0.15	
Cla-Tet3	1	2	vic	0.20	4.0
Cla-Tet6	1	2	ned	0.20	
Cocl-Lav61	1	2	fam	0.20	
Cocl-Lav8	2	3	pet	0.25	2.0
SsBg26	2	3	ned	0.60	
BFRO-018	2	4	fam	0.20	0.9
BWF2	2	4	pet	0.20	
Cocl-Lav18	2	4	fam	0.20	

Cocl-Lav8 showed signs of being subjected to slight diversifying selection.

Northern pike *(Esox lucius)*

DNA extraction and microsatellite analyses were performed at the Center of Evolutionary Applications, University of Turku, Finland. DNA was extracted from ethanol-stored fin-clips using a silica-based purification method from Elphistone et al (2003). Genetic variation was assessed at 11 microsatellite loci *Elu 19, Elu 51, Elu 64, Elu 76, Elu87*, *Elu 276* (Miller and Kapuscinski 1996), *EluB e INRA*, *EluB 38 INRA* (Launey et al. 2003), *Elu 10*, *Elu 12* (Hansen et al. 1999), and *EMAD4* (Sloss et al. 2008).

Amplification was carried out in three 8-µl reactions consisting of ca. 100 ng of DNA, 0.05 to 0.5 µM of each primer (one of which was fluorescently labeled) and 1X Qiagen multiplex PCR master mix (Qiagen Inc. Valencia, CA, USA). The PCR profile used was according to the manufacturer's standard protocol with the annealing temperatures of 60 °C for the multiplexes and and 58 °C for the single reaction. Amplifications were performed on PTC-100 (MJ Research) and AB 2720 (Applied Biosystems) thermal cyclers. For electrophoresis the PCR products were pooled (1.5 µl of MP1, 2 µl of MP2 and 1 µl of the single PCR) and diluted with 100 µl of sterile water. 2 µl of the pooled and diluted PCR product was combined with GS600LIZ size standard (Applied Biosystems) and HiDi-formamide (Applied Biosystems). Samples were denatured at 98 °C for three minutes and the size of the fragments was determined by capillary electrophoresis on an ABI Prism™ 3130*xl* genetic analysis instrument.

Table S5 *Northern pike markers in electrophoresis panels and pcr-multiplexes.*

	Electrophoresis Panel	PCR Multiplex	Flouro label	Primer conc.	Pooling amount
Esox-02	1	1	vic	0.05	1.5
Esox-03	1	1	vic	0.03	
Esox-04	1	1	fam	0.03	
Esox-11	1	1	fam	0.50	
Esox-14	1	1	ned	0.30	
Esox-15	1	1	fam	0.10	
Esox-19	1	1	ned	0.40	
Esox-01	1	2	ned	0.40	2.0
Esox-05	1	2	pet	0.30	
Esox-13	1	2	fam	0.20	
EMA D4	1	3	fam	0.20	1.0

Threespined stickleback *(Gasterosteus aculeatus)*
16 microsatellite markers were genotyped (Peichel et al. 2001); STN3, STN30, STN59, STN168; panel 2: STN38, STN79, STN110, STN204; panel 3: STN123, STN174, STN185, STN146; panel 4: STN23, STN42, STN195, STN132. Details of genotyping procedures can be found in DeFaveri et al. (2012).

Ninespined stickleback *(Pungitius pungitius)*
A total of 23 microsatellite loci were genotyped; Gac1125PBBE, Gac4174PBBE, Gac7033PBBE, GAest3, GAest7, GAest14, GAest35, GAest50, GAest66, GAest82, Stn49, Stn71, Stn89, Stn96, Stn100, Stn127, Stn130, Stn163, Stn173, Stn196, Stn198, Stn223 and Stn253 (Largiadèr et al. 1999; Peichel et al. 2001; Colosimo et al. 2004; Mäkinen et al. 2008; Shikano et al. 2010). Details of genotyping procedures can be found in DeFaveri et al. (2012).

GAest 7, GAest82, Stn89, Stn127, and Stn198 were removed from analyses because of large deviations from Hardy-Weinberg equilibrium in several populations.

Stn96 showed signs of diversifying selection and 1125P showed slight signs of balancing selection.

Blue mussel *(Mytilus spp.)*
DNA was isolated from mantle tissue using a modified CTAB method according to Hoarau et al. (2002) and suspended in sterile filtered distilled water. DNA extraction and SNP analyses were performed at Department of Genetics and Marine Biotechnology, Institute of Oceanology, Polish Academy of Sciences in Sopot.

EST sequences were obtained from a cDNA library of a single male collected from the Gulf of Gdańsk (Zbawicka et al. in review). Baltic EST sequences were aligned with appropriate GenBank EST sequences (mainly for *M. galloprovincialis* and *M. edulis*) using the ClustalX program version 1.83 (Thompson et al. 1997) with default settings. Multiple sequence alignments were used for SNP discovery using the Staden computer programs (Staden et al. 2001). Ten SNP were chosen for genotype (8 based on EST sequences and 2 already identified in Zbawicka et al. (2012): SNP2A and SNP3D, named respectively: BM202A and BM203D). SNPs were characterized by their type and location (Table 2).

SNP genotyping of 239 sampled individuals was performed using MassARRAY iPLEX Gold technology (Gabriel et al. 2009), following the protocol provided by Sequenom (www.sequenom.com). PCR and extension primers were designed using the Assay Design 3.1 program (Sequenom). Analysis and scoring were performed using Typer 3.4 software (Sequenom). Multiplex setup and SNP genotyping were performed at the Centre for Integrative Genetics (CIGENE), Department of Animal and Aquacultural Sciences, Norway. University of Life Sciences, Ås.

Table S6 *SNP genome location, reference, GenBank annotation and substitution (Zbawicka et al. in review).*

SNP	Allele	Location	Reference	GenBank annotation	Region
BM2G	G/T	UnKnown05	n.d.		noncoding
BM3B	A/C	UnKnown02	n.d.		coding
BM12A	C/T	Ribosomal protein L23a	AF526209		coding
BM22A	A/G	EP protein precursor	AY364453		coding
BM26B	A/T	UnKnown13	n.d.		noncoding
BM50B	A/G	CoA-binding protein	PF02629		coding
BM64A	C/T	Ribosomal protein L35	FJ429212		coding
BM92B	A/T	UnKnown06	n.d.		coding
BM202A*	A/C	*H3 histone* gene	AY267749.1	n.d.	noncoding

BM203D*	A/T	*H2A histone* gene	AY267757.1	n.d.	noncoding

Bladderwrack *(Fucus vesiculosus)*
DNA extraction and microsatellite analysis were performed at the Department of Biological and Environmental Sciences – Tjärnö, University of Gothenburg, Sweden. Dried samples stored in silica gel were pulverized in a milling instrument (Mixer Mill MM 301, Retsch GmbH, Haan, Germany) for 30 s at a frequency of 25 s^{-1}. DNA was extracted using Viogene's Plant Genomic DNA Extraction Miniprep System (Viogene, Sunnyvale, CA, USA). Genetic variation was assessed at nine microsatellite loci L20, L38, L58, L85, L94 (Engel et al. 2003) and Fsp1, Fsp2, Fsp3, Fsp4 (Perrin et al. 2007). PCR conditions and genotyping in capillary automated sequencer were as previously described (Johannesson et al. 2011).

Table S7 *Bladderwrack markers in electrophoresis panels and PCR-multiplexes.*

	Electrophoresis Panel	PCR Multiplex	Flouro label	Primer conc.	Pooling amount
L20	1	1	D2	0.5	4.5
L38	1	1	D3	0.5	2.0
L58	1	2	D3	0.5	2.0
L85	1	2	D2	0.5	4.5
L94	1	2	D4	0.5	1.2
Fsp1	1	3	D2	0.5	4.5
Fsp4	1	3	D4	0.5	1.7
Fsp2	1	4	D4	0.5	1.8
Fsp3	1	4	D2	0.5	4.5

L58 showed signs of slight diversifying selection.

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