

Supplementary material

Appendix 1. Information related to the primers used in the study.

Locus	Location	Alignment length (bp)	Primer sets	Ref.	Ann. temp.	Substitution Model
COI	mt	646	COIpasserF1 CCAACCACAAGACATCGGAACC COIpasserR1 GTAAACTTCTGGGTGACCAAAGAATC	Lohman et al. 2009	58°C	HKY + G
ACO1	Z	1014	ACO1-19F2 CTCCTCTCAGGATCCAGACTT ACO1-19R2 CAACTTTGTCTGGGGTCTTT	Kimball et al. 2009	61°C	HKY + G
132	26	365	132-F ATGGCTGTGATGTACATCAC 132-R CCATAGAAGTGGACAAAGGC	Backström et al. 2008	60°C	HKY + G
13336	10	568	13336F CAGTTAGCAGACAAACTACG 13336R GGTCATGGCATCTATTCC	Backström et al. 2008	60°C	HKY + I
15463	4	648	15463F TCTGGGAACAGATCTGTC 15463R AACTTCAGACTTACTGCC	Backström et al. 2008	60°C	HKY + G
16532	5	548	16532F GGCCCTGGTGGAGGTAG 16532R TTCAAGATCCCTCTGTTTGG	Backström et al. 2008	60°C	HKY + G
9663	9	364	9663F ATACAGGAAATCGACTTCG 9663R AGTATCCTCTTTGTGCAAG	Backström et al. 2008	58°C	TN93
RHO	12	689	RHO-1F CATCGAGGGCTTCTTTGCC RHO-1R TTTAGACACACAATTTCTATTTAACACCTGT	Primmer et al. 2002	61°C	HKY + G
TGFβ2	3	555	TGFβ2.5F GAAGCGTGCTCTAGATGCTG TGFβ2.6R AGGCAGCAATTATCCTGCAC	Primmer et al. 2002	65°C	HKY

Appendix 2. GenBank accession numbers of the different haplotypes for each marker.

Population	CO1	ACO1	132	13336	15483	16532	9663	RHO	TGFβ2
Iceland	KP772827	KP772823	KP772768	KP772782, KP772788-89, KP772792-93	KP772801, KP772805, KP772807	KP772812, KP772816, KP772819-20	KP772777-78	KP772846-47	KP772838
Faroe Islands	KP772827, KP772831	KP772822-23	KP772768, KP772773	KP772780-84	KP772800-02, KP772807	KP772809-13, KP772816	KP772777	KP772846-47	KP772838
Scotland	KP772827, KP772832-33	KP772822, KP772824-26	KP772768-69, KP772772	KP772794-99	KP772801-03, KP772805-06	KP772814, KP772816, KP772818		KP772846-47, KP772850-51, KP772853	KP772838, KP772840-41
S-Norway	KP772827, KP772834-35	KP772822-24	KP772768-72, KP772774-76	KP772785-87	KP772800-02, KP772804-06, KP772808	KP772809, KP772814, KP772816, KP772821		KP772846-47, KP772850-51	KP772838-39, KP772842-45
Denmark	KP772827-30	KP772822	KP772768-69		KP772800, KP772802-05	KP772811, KP772814-17	KP772777	KP772846-49	KP772838
Sweden	KP772827, KP772836-37	KP772824-25	KP772768, KP772772	KP772790-91	KP772800, KP772802-03, KP772805-06	KP772814, KP772816, KP772818	KP772777-79	KP772847, KP772850-52	KP772838-39

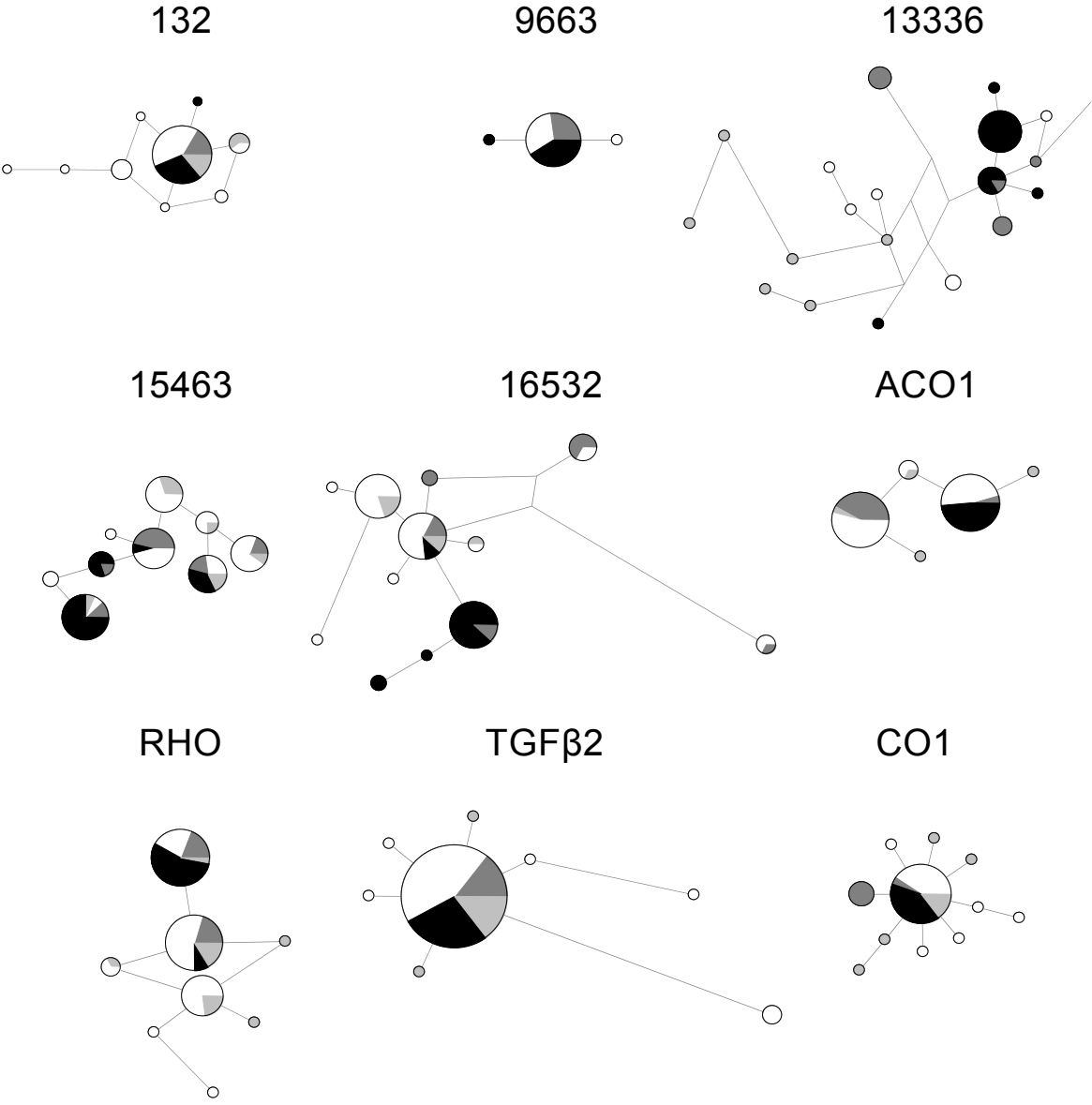
Appendix 3. Genetic variability indices obtained from the CO1 mitochondrial locus and 8 nuclear loci of Eurasian Wrens from populations in the Northeast Atlantic. *N*: sample size, *n*: number of sequences (for the nuclear loci, it displays the number of retained haploid sequences after phasing ($P=0.8$), #h: number of different haplotypes, S: number of polymorphic sites (indels included), π : nucleotide diversity, H: haplotype diversity, AR: allelic richness (corrected for rarefaction).

Loci	CO1	132	9663	13336	15463	16532	TGF β 2	ACO1	RHO		
Fragment size (bp)	646	365	364	568	648	548	555	1014	689		
Populations	<i>N</i>									Average	
<i>n</i>											
Iceland	11	11	11 (22)	7 (10)	11 (22)	10 (20)	11 (20)	11 (22)	10 (20)	11 (22)	10.25 (19.75)
Sweden	6	5	6 (12)	4 (6)	3 (2)	6 (10)	6 (8)	6 (12)	6 (12)	5 (10)	5.25 (9)
S-Norway	10	8	10 (20)	-	10 (4)	10 (12)	9 (14)	10 (18)	10 (18)	10 (16)	9.86 (14.57)
Faroe Islands	6	6	6 (12)	3 (6)	6 (10)	6 (12)	6 (12)	6 (12)	6 (12)	6 (12)	5.63 (11)
Denmark	6	5	5 (8)	1 (2)	2 (-)	6 (10)	5 (8)	6 (12)	5 (3)	5 (10)	4.37 (7.57)
Scotland	7	6	7 (14)	-	6 (6)	7 (8)	6 (6)	7 (14)	7 (4)	7 (10)	6.72 (8.86)
overall	46	41	45 (88)	15 (24)	37 (44)	45 (72)	43 (68)	46 (90)	44 (69)	44 (80)	39.88 (66.88)
#h											
Iceland	1	2	2	5	3	4	1	1	2	4	2.33
Sweden	3	2	2	2	5	3	2	2	2	4	2.78
S-Norway	3	8	-	3	7	4	6	3	4	4	4.75
Faroe Islands	2	1	1	5	4	6	1	2	2	2	2.67
Denmark	4	2	1	-	5	5	1	1	4	4	2.88
Scotland	3	3	-	6	5	3	3	4	5	5	4
overall (S)	11 (10)	9 (6)	3 (2)	20 (17)	9 (7)	13 (20)	8 (11)	5 (3)	8 (5)	8 (5)	9.56 (8.88)
π (x100)											
Iceland	0.000	0.025	0.056	0.175	0.286	0.153	0.000	0.000	0.025	0.025	0.102
Sweden	0.124	0.046	0.092	0.353	0.206	0.144	0.218	0.033	0.174	0.174	0.234
S-Norway	0.077	0.392	-	0.764	0.353	0.361	0.198	0.103	0.201	0.201	0.493
Faroe Islands	0.052	0.000	0.000	0.561	0.278	0.644	0.000	0.060	0.077	0.077	0.25
Denmark	0.217	0.235	0.000	-	0.600	0.743	0.000	0.158	0.239	0.239	0.251
Scotland	0.134	0.178	-	0.930	0.303	0.171	0.052	0.181	0.184	0.184	0.468
overall	0.116	0.167	0.046	0.658	0.358	0.517	0.079	0.100	0.187	0.187	0.511
H											
Iceland	0.000	0.091	0.200	0.563	0.590	0.437	0.000	0.000	0.173	0.173	0.228
Sweden	0.700	0.167	0.333	1.000	0.800	0.607	0.303	0.167	0.644	0.644	0.525
S-Norway	0.464	0.700	-	0.833	0.894	0.692	0.490	0.627	0.692	0.692	0.674
Faroe Islands	0.333	0.000	0.000	0.800	0.652	0.864	0.000	0.303	0.530	0.530	0.387
Denmark	0.900	0.429	0.000	-	0.844	0.857	0.000	0.000	0.711	0.711	0.468
Scotland	0.600	0.473	-	1.000	0.857	0.733	0.275	1.000	0.800	0.800	0.717
overall	0.560	0.345	0.163	0.877	0.859	0.832	0.190	0.545	0.687	0.687	0.562
AR ¹											
Iceland	0.000	0.364	0.200	0.563	1.796	1.705	0.000	0.000	0.714	0.714	0.594
Sweden	2.000	0.667	0.333	1.000	3.400	2.000	1.000	0.333	3.000	3.000	1.526
S-Norway	1.250	3.305	-	0.833	4.539	2.392	3.333	1.268	2.581	2.581	2.438
Faroe Islands	0.833	0.000	0.000	0.800	2.485	4.059	0.000	0.576	1.000	1.000	1.084
Denmark	3.000	1.000	0.000	-	3.578	4.000	0.000	0.000	3.000	3.000	1.822
Scotland	1.667	1.516	-	1.000	4.000	12.000	1.714	3.000	4.000	4.000	3.612
Fst	0.305***	0.090**	0	0.337***	0.160***	0.247***	0.055*	0.516***	0.264***	0.264***	0.219***
Φ st	0.343***	0.110**	0	0.732***	0.241***	0.368***	0.035	0.536***	0.335***	0.335***	0.299***
Φ st / Fst	1.12	1.22	-	2.17	1.50	1.49	0.64	1.04	1.27	1.27	1.37

¹: AR calculations under rarefaction correction

-: missing data

Appendix 4. Haplotype networks for the different markers. The sizes of the pies are proportional to the number of individuals for each haplotype.



■ *T. t. islandicus*

■ *T. t. borealis*

■ *T. t. indigenus*

□ *T. t. troglodytes*

Appendix 5. Deviation from neutrality in the four subspecies of Eurasian Wren estimated with the HKA test, Tajima's D and Fu & Li's D, with 1,000 iterations. *P*-values present number of simulations which gave a higher test statistic than the observed one. Significant values after bonferroni adjustment (corrected by number of tests within each test) are in bold.

		<i>T. t. troglodytes</i>	<i>T. t. indigenus</i>	<i>T. t. islandicus</i>	<i>T. t. borealis</i>	total					
	HKA-test <i>P</i>	0.161	0.546	0.070	0.080	0.066					
Tajima's D	132	-0.132	0.535	-0.957	0.747	-1.162	0.740	0.000	0.441	-0.936	0.802
	9663	-1.055	0.850	-	-	-1.112	0.723	0.000	0.456	-1.515	0.944
	13336	0.290	0.408	1.096	0.145	-1.232	0.916	1.204	0.142	-0.065	0.479
	15463	0.612	0.267	-0.503	0.643	0.564	0.316	0.466	0.359	1.402	0.066
	16532	-1.264	0.898	0.311	0.387	-0.440	0.628	-0.385	0.651	-1.234	0.907
	ACOI	2.041	0.018	1.090	0.187	0.000	0.459	-0.248	0.601	1.193	0.113
	RHO	0.664	0.228	0.700	0.233	-0.641	0.686	1.382	0.061	0.607	0.247
	TGFB2	-1.508	0.955	-1.481	0.922	0.000	0.480	0.000	0.466	-1.973	0.999
Fu and Li's I	132	-2.714	0.998	-0.007	0.535	-0.957	0.776	0.000	0.539	-6.155	1.000
	9663	-0.182	0.548	-	-	-0.339	0.590	0.000	0.479	-2.078	0.971
	13336	-0.687	0.686	-2.059	0.996	-1.015	0.810	0.456	0.388	-8.646	1.000
	15463	-0.650	0.708	-1.495	0.911	1.981	0.000	0.260	0.491	-0.658	0.739
	16532	-0.822	0.768	-0.304	0.606	-0.414	0.680	0.115	0.489	-1.915	0.954
	ACOI	1.723	0.000	-2.017	1.000	0.000	0.557	1.384	0.027	0.213	0.457
	RHO	-1.049	0.820	-1.671	0.930	-0.176	0.602	1.152	0.085	-1.368	0.882
	TGFB2	-1.811	0.939	-1.475	0.861	0.000	0.596	0.000	0.489	-5.977	1.000

Appendix 6. Extended Bayesian skyline plots. a) *T. t. borealis*, b) *T. t. islandicus*, c) *T. t. indigenus*, d) *T. t. troglodytes*. Note that the scale of the y-axis is shorter in panels a and b than c and d.

