

Widespread physical mixing of starry ray from differentiated populations and life histories in the North Atlantic

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Table S1. Microsatellite loci analysed in this study, including four problematic loci omitted from further analyses (marked with ** or ***). Multiplex arrangement, accession number, repeat motif, fluorophore (dye), and references are given.

Name	Accession number	Repeat Motif	Dye	Included in the study	Reference
Multiplex 1					
Ar-G4*	DR713467	(TA) ₁₂	VIC	+	Salomon et al., cited in Anderson et al. 2010
Ar-130*	EE991287	(GT) ₁₁	VIC	+	Salomon et al., cited in Anderson et al. 2010
Ar-G5*	DR713456	(GT) ₁₀	PET	+	Salomon et al., cited in Anderson et al. 2010
Ar-149*	EE992583	(TA) ₇	FAM	-**	Salomon et al., cited in Anderson et al. 2010
Multiplex 2					
Ar-20*	CV067262	(GCG) ₇	VIC	+	Salomon et al., cited in Anderson et al. 2010
Ar-132*	CV547492	(AT) ₁₀	FAM	-**	Salomon et al., cited in Anderson et al. 2010
Ar-151*	EE991874	(CT) ₇	NED	+	Salomon et al., cited in Anderson et al. 2010
LERI50	DR713467	(TA) ₁₁	PET	+	El Nagar et al. 2010
LERI63	CV221951	(TC) ₈	FAM	-***	El Nagar et al. 2010
Multiplex 3					
LERI44	EE991287	(GT) ₁₁	FAM	+	El Nagar et al. 2010
Ar-9m13*	GU017320	(CA) ₇ CG(CA) ₅	PET	-***	Salomon et al., cited in Anderson et al. 2010
LERI40	DR713467	(TA) ₁₁	VIC	+	El Nagar et al. 2010
LERI27	CV068389	(CT) ₁₅	FAM	+	El Nagar et al. 2010
LERI24	CV221951	(TC) ₈	NED	+	El Nagar et al. 2010

*Loci developed specifically for *A. radiata*.

** Not included in the study due to potential null alleles as identified by MicroChecker

***Inconsistent PCRs and difficult to genotype

Literature cited in Table S1

Anderson CM, Aparicio GJ, Atangana AR and others (2010) Permanent genetic resources added to Molecular Ecology Resources database 1 December 2009–31 January 2010. *Mol Ecol Resour* 10:576–579

El Nagar A, McHugh M, Rapp T, Sims DW, Genner MJ (2010) Characterisation of polymorphic microsatellite markers for skates (Elasmobranchii: Rajidae) from expressed sequence tags. *Conserv Genet* 11:1203–1206

Table S2. Number of samples (N), alleles (N_a), observed (H_o) and expected (H_e) heterozygosity and F_{IS} per sample and locus. Barents Sea east (BaE), Barents Sea west (BaW), Northeast Greenland (NEGr), Norwegian fjords (NF), North Sea (NS), Northwest Atlantic early maturing (NWe), Northwest Atlantic late maturing (NWl), Southeast Greenland (SEGr), Svalbard east (SvE), Svalbard west (SvW) and Southwest Greenland (SWGr).

Pop		Ar-G4	Ar-130	Ar-G5	Ar-20	Ar-151	LERI50	LERI-44	LERI-40	LERI-27	LERI-24
BaE	N	188	189	189	189	187	181	189	189	189	189
	Na	7	11	6	3	8	8	11	7	8	5
	Ho	0.707	0.593	0.481	0.063	0.738	0.757	0.556	0.735	0.825	0.206
	He	0.740	0.595	0.494	0.062	0.763	0.772	0.596	0.747	0.790	0.200
	F	0.043	0.003	0.026	-0.024	0.033	0.020	0.069	0.016	-0.044	-0.030
BaW	N	138	141	139	141	139	116	141	140	134	139
	Na	8	7	8	4	9	8	7	8	8	4
	Ho	0.688	0.681	0.518	0.028	0.669	0.767	0.631	0.736	0.791	0.165
	He	0.747	0.662	0.526	0.028	0.722	0.797	0.654	0.756	0.792	0.156
	F	0.079	-0.028	0.014	-0.010	0.073	0.038	0.036	0.026	0.002	-0.062
NEGr	N	4	4	4	5	5	5	5	5	5	5
	Na	4	5	3	2	2	4	5	5	5	2
	Ho	0.500	0.750	0.250	0.200	0.200	0.600	0.800	0.800	0.600	0.400
	He	0.563	0.688	0.406	0.180	0.420	0.580	0.740	0.680	0.720	0.320
	F	0.111	-0.091	0.385	-0.111	0.524	-0.034	-0.081	-0.176	0.167	-0.250
NF	N	45	45	45	45	45	44	45	45	44	45
	Na	7	8	4	3	7	8	8	7	6	4
	Ho	0.778	0.644	0.533	0.044	0.667	0.818	0.644	0.778	0.886	0.200
	He	0.750	0.628	0.561	0.044	0.771	0.765	0.615	0.755	0.791	0.186
	F	-0.037	-0.027	0.050	-0.017	0.135	-0.070	-0.047	-0.030	-0.120	-0.077
NS	N	23	23	23	23	22	20	23	23	22	23
	Na	6	8	6	2	7	7	8	7	6	4
	Ho	0.696	0.565	0.478	0.043	0.636	0.650	0.565	0.565	0.636	0.261
	He	0.628	0.615	0.437	0.043	0.743	0.686	0.615	0.647	0.752	0.237
	F	-0.108	0.081	-0.095	-0.022	0.143	0.053	0.081	0.127	0.154	-0.100
NWe	N	43	43	43	42	42	42	42	43	43	43
	Na	8	8	4	3	7	8	8	8	8	4
	Ho	0.837	0.744	0.512	0.048	0.571	0.857	0.714	0.860	0.767	0.233
	He	0.781	0.813	0.481	0.047	0.790	0.784	0.808	0.786	0.770	0.213
	F	-0.072	0.085	-0.064	-0.018	0.277	-0.093	0.115	-0.095	0.004	-0.093
NWl	N	27	28	28	28	28	25	28	28	28	28
	Na	8	6	5	2	6	8	6	8	7	3
	Ho	0.852	0.750	0.536	0.000	0.679	0.880	0.821	0.893	0.679	0.143
	He	0.763	0.766	0.435	0.069	0.755	0.751	0.767	0.766	0.751	0.135
	F	-0.116	0.021	-0.232	1.000	0.101	-0.171	-0.072	-0.166	0.097	-0.062
SEGr	N	21	21	21	21	21	21	21	21	21	21
	Na	9	6	4	3	7	9	6	9	7	4
	Ho	0.810	0.571	0.571	0.095	0.619	0.857	0.571	0.857	0.619	0.190
	He	0.718	0.568	0.448	0.092	0.726	0.759	0.568	0.730	0.745	0.178
	F	-0.128	-0.006	-0.276	-0.037	0.147	-0.130	-0.006	-0.174	0.169	-0.070
SvE	N	30	30	30	30	30	29	30	30	30	30
	Na	7	7	5	3	8	7	7	7	6	3
	Ho	0.633	0.667	0.533	0.100	0.833	0.690	0.633	0.633	0.967	0.167
	He	0.708	0.583	0.574	0.096	0.727	0.724	0.596	0.708	0.793	0.156
	F	0.106	-0.143	0.071	-0.040	-0.146	0.048	-0.063	0.106	-0.219	-0.068
SvW	N	69	69	69	69	69	67	69	68	68	69
	Na	8	7	5	1	7	8	7	8	8	4
	Ho	0.797	0.551	0.449	0.000	0.725	0.776	0.551	0.779	0.794	0.116
	He	0.746	0.561	0.495	0.000	0.736	0.753	0.561	0.752	0.808	0.124
	F	-0.068	0.018	0.093	#N/A	0.016	-0.030	0.019	-0.036	0.018	0.068
SWGr	N	62	62	62	62	62	62	62	62	62	62
	Na	7	8	5	1	8	7	8	7	8	4
	Ho	0.742	0.726	0.597	0.000	0.726	0.726	0.726	0.742	0.774	0.210
	He	0.793	0.662	0.496	0.000	0.762	0.799	0.662	0.793	0.760	0.194
	F	0.065	-0.097	-0.203	#N/A	0.047	0.092	-0.097	0.065	-0.018	-0.080

Value of BIC versus number of clusters

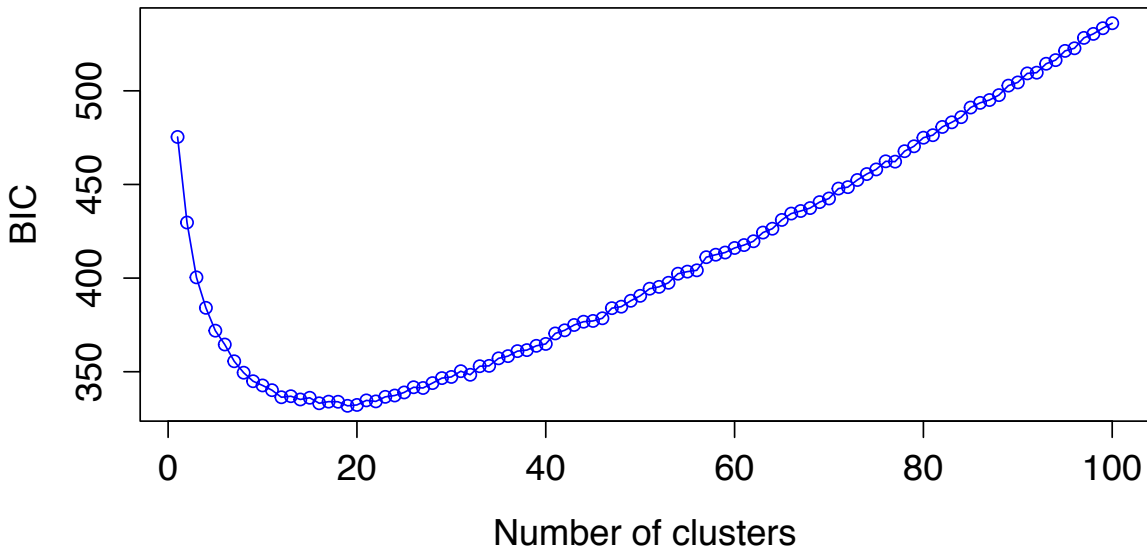


Fig. S1: Inference of the number of probable clusters based on the modified dataset (11 populations, 444 individuals). X-axis represents the number of clusters tested and y-axis represent corresponding BIC (Bayesian Information Criterion) values. The chosen number of clusters is the minimum number of clusters after which the BIC increases or decreases by a negligible amount. In our case, we assume K is ranges between 11-20.

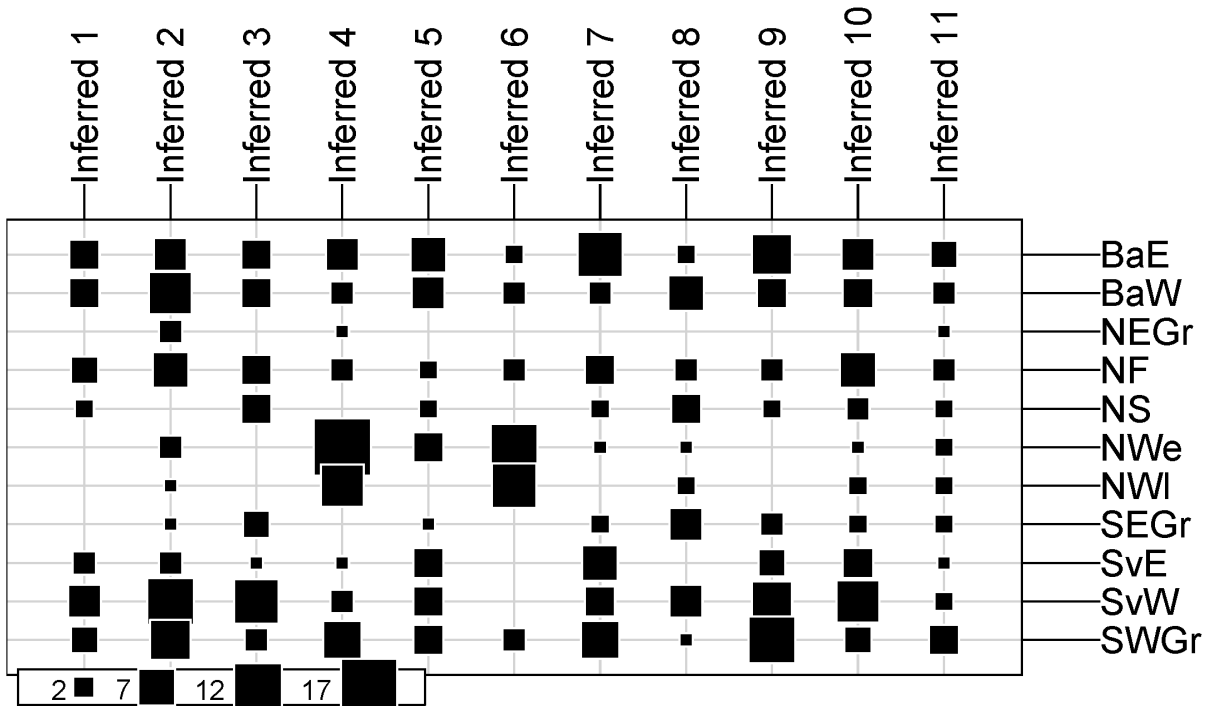


Fig. S2: Frequency plot describing the distribution of individuals from actual groups (i.e. sampling locations, sample codes as in Fig. 2) into 11 inferred groups. Rows represent the actual groups and columns represent the inferred groups. Size of the black squares represents the number of individuals from actual groups assigned into a particular inferred cluster.

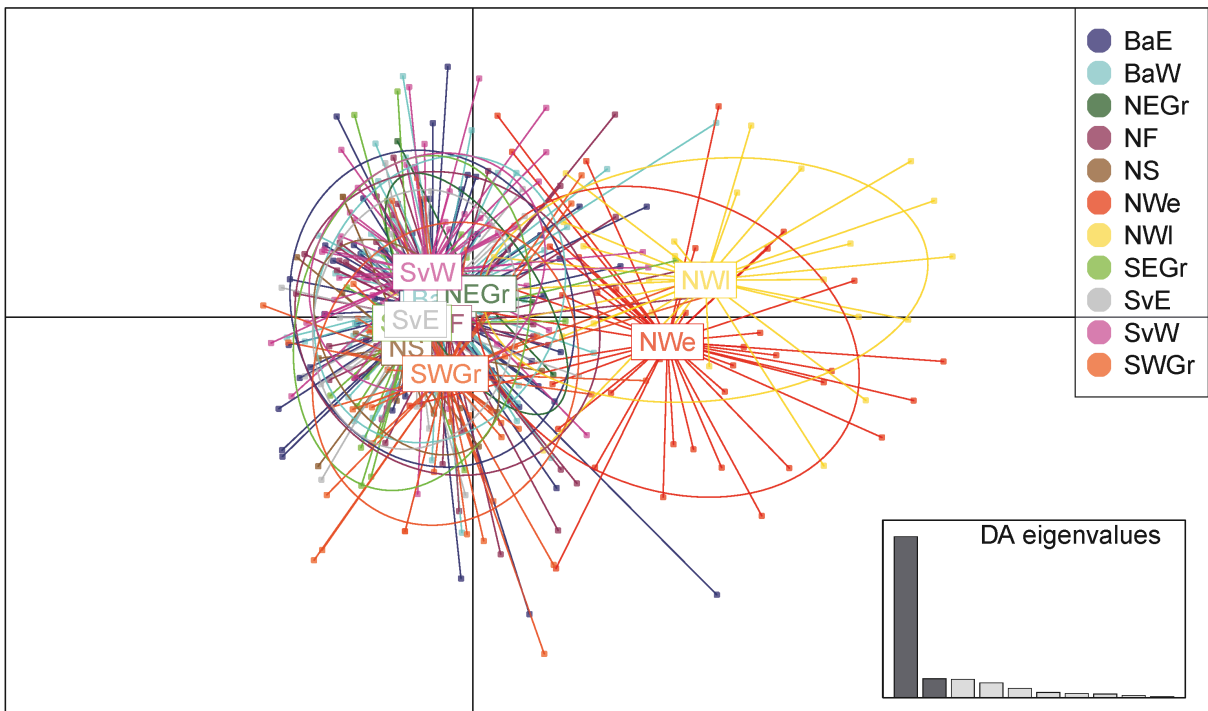


Fig. S3: Plot of the discriminant analysis of principal components (DAPC) analysing all sampling locations as prior groups. Sample codes as in Fig. 2. Labels are placed at the centre of dispersion for each group, further defined by inertia ellipses. Dots represent individuals. Eigen values used for analysis are displayed in inset.

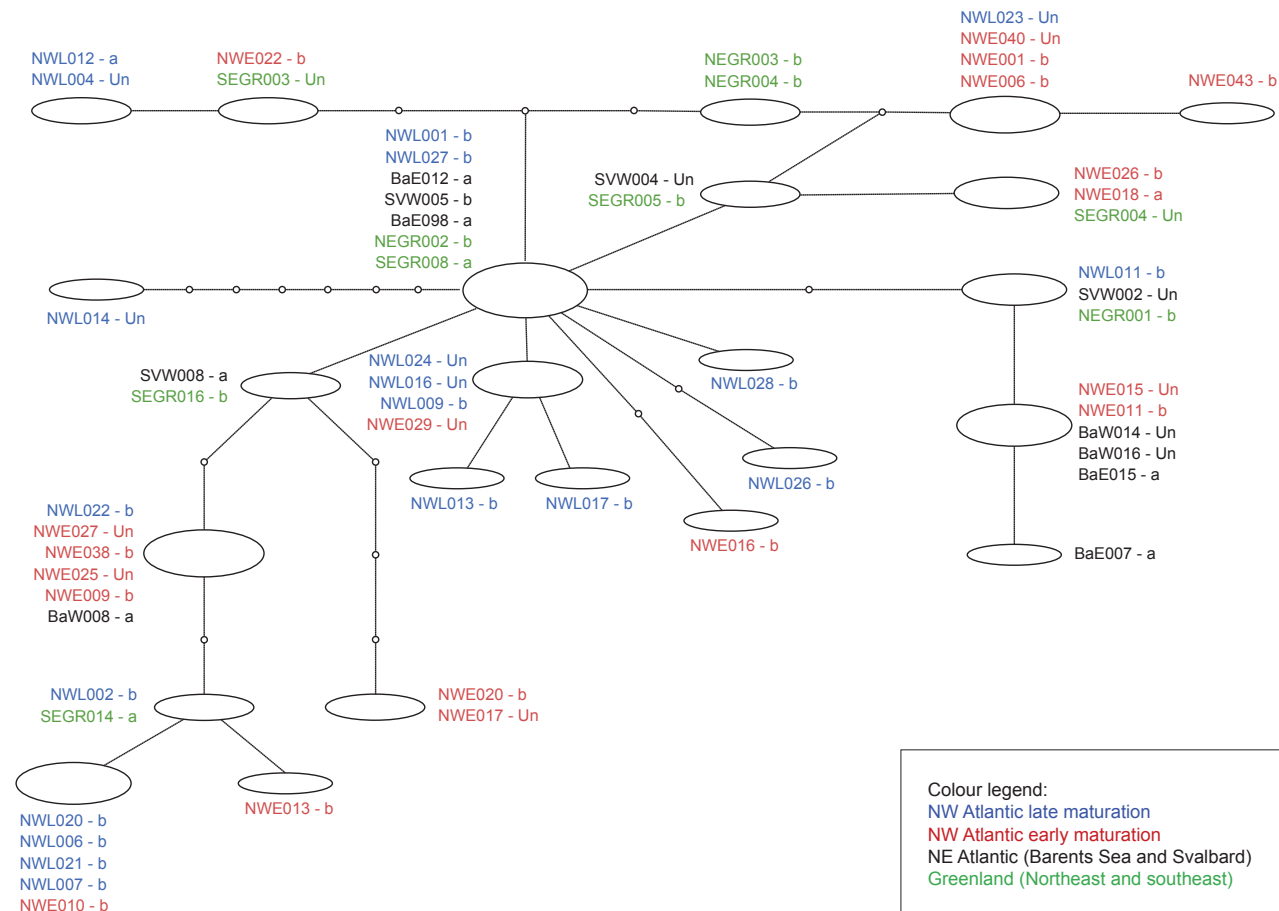


Fig. S4. Genotypes (nDNA) vs. haplotypes (mtDNA) from 60 individuals. The inferred cluster membership of each individual from the present paper (nDNA) is added to the haplotype network (mtDNA) from Lynghammar et al. (2014). The size of the ellipses is proportional to the number of individuals in each haplotype. Letters before the hyphen denotes the individuals' names, and the letters after the hyphen corresponds to the first round of STRUCTURE analysis in Fig. 3B and C in the present paper. a (n=10) and b (n=33) have an estimated membership fraction of more than 70% to R1a and R1b, respectively. Individuals not assigned to any of the two clusters are denoted Un (n=17, R1Un). The colours denotes the three major geographical regions (NW Atlantic, Greenland and NE Atlantic, as well as life history characteristics in NW Atlantic (early and late maturation)).