

Genetic variation in a newly established population of the Atlantic rock crab *Cancer irroratus* in Iceland

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Supplement. Detailed results of the various genetic comparison methods used in the present study

Table S1. *Cancer irroratus*. Comparison of genetic variability (number of alleles per locus, observed heterozygosity, gene diversity and variance) at 7 microsatellite loci in 6 samples. See Fig. 1 for location codes

Locus	Number of alleles per locus						Observed heterozygosity (H_o) Gene diversity (H_e)						Variance (s^2)					
	I	N	L	S	F	M	I	N	L	S	F	M	I	N	L	S	F	M
CPAG_5d8	8	11	9	9	11	11	0.782 0.788	0.763 0.834	0.840 0.855	0.610 0.808	0.829 0.834	0.769 0.834	55.573	77.992	60.483	123.220	134.163	71.479
CPAG-15	8	7	7	8	9	9	0.673 0.675	0.641 0.696	0.540 0.634	0.750 0.767	0.833 0.821	0.625 0.809	27.200	11.922	11.792	19.423	42.717	48.861
CPAG-4c1	5	6	5	8	9	7	0.564 0.591	0.641 0.695	0.680 0.721	0.725 0.752	0.750 0.813	0.700 0.790	1088.583	1490.398	1879.960	1859.923	1853.604	1815.663
CPAG-6c4A	2	2	3	2	3	3	0.291 0.323	0.256 0.264	0.180 0.167	0.250 0.258	0.229 0.208	0.175 0.281	23.251	18.989	11.501	18.592	14.340	18.975
CPAG-2d7	3	3	3	4	3	3	0.600 0.552	0.583 0.520	0.571 0.517	0.561 0.529	0.472 0.464	0.550 0.465	32.380	37.358	36.800	35.170	31.070	31.504
CPAG-4	16	18	20	19	20	18	0.927 0.902	0.825 0.933	0.920 0.920	0.875 0.918	0.944 0.941	0.875 0.913	246.043	266.987	215.523	199.572	265.852	286.519
CMA-1c8	12	14	11	9	12	14	0.722 0.785	0.692 0.812	0.714 0.682	0.750 0.759	0.833 0.797	0.900 0.858	1517.707	1377.236	458.247	1145.111	1151.887	1676.899

Table S2. *Cancer irroratus*. Deviation from the Hardy-Weinberg expectation, measured as inbreeding coefficient F_{IS} within 6 samples. Asterisks indicate significant values obtained with 1000 permutations, not adjusted for multiple tests: * $p < 0.05$; ** $p < 0.01$. All values were non-significant after Bonferroni adjustment (Sokal & Rohlf 1995). See Fig. 1 for location codes

Locus	F_{IS}					
	I	N	L	S	F	M
CPAG_5d8	0.008	0.085	0.018	0.246*	0.007	0.078
CPAG_15	0.003	0.079	0.149	0.023	-0.015	0.227*
CPAG_4c1	0.047	0.078	0.057	0.035	0.077	0.114
CPAG_6c4A	0.100	0.028	-0.078	0.032	-0.099	0.377*
CPAG_2d7	-0.087	-0.122	-0.105	-0.061*	-0.017	-0.183
CPAG_4	-0.029	0.116*	-0.0002	0.047	-0.004	0.041
CPAG_1c8	0.081	0.148**	-0.047	0.012	-0.045*	-0.049

Table S3. *Cancer irroratus*. M -ratio for microsatellite data in 6 samples. See Fig. 1 for location codes

Site	N	Microsatellite markers							Mean M
		CPAG-5d8	CPAG-15	CPAG-4c1	CPAG-6c4A	CPAG-2d7	CPAG-4	CPAG-1c8	
I	55	0.216	0.320	0.052	0.154	0.176	0.291	0.034	0.178
N	40	0.046	0.052	0.022	0.012	0.023	0.257	0.038	0.064
L	50	0.110	0.058	0.028	0.012	0.235	0.065	0.026	0.076
S	41	0.321	0.318	0.052	0.143	0.023	0.274	0.031	0.166
F	36	0.038	0.243	0.091	0.016	0.176	0.235	0.106	0.129
M	40	0.047	0.209	0.071	0.176	0.176	0.257	0.124	0.151

Table S4. *Cancer irroratus*. Genetic differentiation (F_{ST}) between 7 sampled populations at 7 microsatellite loci. Significant departure from F_{ST} : * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. Tests significant at the 5% level (*) are not significant after Bonferroni adjustment. See Fig. 1 for location codes

F_{ST}	I	N	L	S	F	M
I		0.033** *	0.033** *	0.038** *	0.044** *	0.032** *
N			0.002	-0.004	0.023** *	0.022** *
L				0.004 (*)	0.024** *	0.026** *
S					0.011** *	0.013** *
F						-0.001
M						

Table S5. *Cancer irroratus*. Statistical support (logarithm of the likelihoods of the observed data and K) for a range of values for number of genetic clusters (K) within the dataset, simulated using BAPS and STRUCTURE (10 replicates) with and without prior information of the geographic location. The most likely structures indicated in bold. See Fig. 1 for location codes

	Clusters	Support						
		BAPS	Admix prior \pm SD		STRUCTURE		No admix \pm SD	
				K		K		K
1	No structure		-5968.09 \pm 0.28		-5967.94 \pm 0.25		-5968.03 \pm 0.31	
2	I vs. others	-6167.8	-5877.47 \pm 32.22	3.26	-6149.01 \pm 78.61	1.01	-5944.04 \pm 5.08	2.40
3	I N. L. S F. M	-6213.6	-5819.51 \pm 10.28	9.25	-6058.56 \pm 13.62	12.30	-5932.23 \pm 4.59	51.17
4	I N. L. S F M	-6291.3	-5888.06 \pm 59.84	5.80	-6128.1 \pm 35.75	1.47	-6155.34 \pm 116.85	0.47
5	I N. L S F M	-6377.2	-6044.5 \pm 88.06	0.16	-6442.77 \pm 138.96	1.75	-6433.69 \pm 106.16	0.49
6	I N L S F M	-6463.1	-6047.1 \pm 130.57	1.62	-6725.05 \pm 98.76	0.02	-6660.5 \pm 110.18	2.06

Table S6. *Cancer irroratus*. Unidirectional genetic distances (D_{LR}) between populations based on individual likelihood (log) values from GENECLASS. Distances below diagonal are based on the average likelihoods of assigning individual i sampled in population X to population Y, compared to assigning the individuals to their sampled population. Distances above diagonal are correspondingly based on the likelihoods of assigning individuals i in population Y to population X. See Fig. 1 for location codes

X	Y	I	N	L	S	F	M
I		0.000	2.054	2.275	2.561	2.718	2.147
N		2.314	0.000	0.922	1.199	1.506	1.898
L		2.289	0.803	0.000	1.212	1.435	1.711
S		2.812	1.020	1.006	0.000	1.627	1.639
F		3.635	2.076	2.158	2.219	0.000	1.531
M		2.803	2.246	2.553	2.050	1.429	0.000