

Supplementary material

Supplementary material - Appendix 1

Table A1 Genetic diversity statistics of black grouse samples (N=195) genotyped at 9 microsatellite loci: number of alleles per locus (N_A), allele ranges (in basepairs), observed and expected heterozygosity (H_O , H_E), inbreeding coefficient (F_{IS}), deviations of Hardy-Weinberg proportions (HW) are marked with an asterisk (p values adjusted for multiple testing using Benjamini-Yekutieli FDR).

Locus	N_A	Allele ranges	H_O	H_E	F_{IS}	HW
TUT1	9	205-237	0.55	0.81	0.32	*
TUT2	3	132-144	0.25	0.24	-0.02	ns
TUT3	7	154-178	0.73	0.72	-0.01	ns
BG15	12	164-208	0.78	0.72	-0.08	ns
BG16	7	148-172	0.69	0.70	0.02	ns
BG18	10	143-183	0.86	0.82	-0.05	ns
TUD6	7	183-197	0.72	0.69	-0.04	ns
BG19	8	158-190	0.48	0.50	0.04	ns
BG6	15	188-288	0.76	0.75	-0.01	ns
overall	8.67		0.65	0.66	0.02	*

Table A2 Analysis of molecular variance (AMOVA) for black grouse samples. Two structures were analysed: (1) clusters inferred by cluster analyses, (2) putative subpopulations.

Source of variation	d.f.	Sum of squares	Variance component	Percentage of variation	p value	Fixation index
(1)						
Between clusters	4	26.56	0.051	1.68	<0.001	$F_{ST} = 0.017$
Between individuals within clusters	190	594.54	0.143	4.70	<0.001	$F_{IS} = 0.048$
Within individuals	195	554.50	2.843	93.62	<0.001	$F_{IT} = 0.064$
Total	389	1,175.59	3.037			
(2)						
Between subpopulations	10	61.60	0.095	3.14	<0.001	$F_{ST} = 0.031$
Between individuals within subpopulations	184	559.49	0.098	3.24	0.013	$F_{IS} = 0.033$
Within individuals	195	554.50	2.843	93.61	<0.001	$F_{IT} = 0.064$
Total	389	1,175.59	3.037			

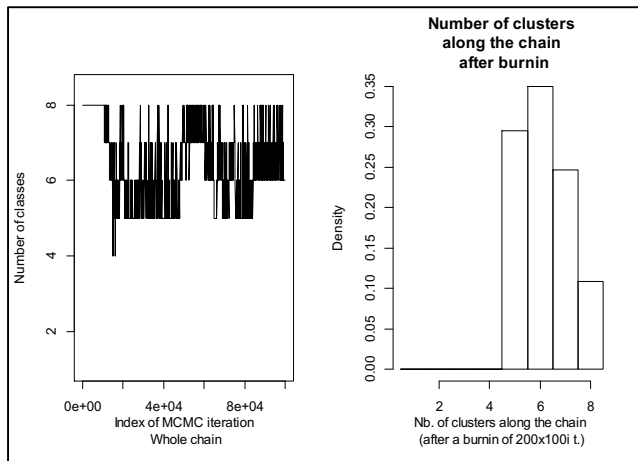


Figure A1 Graphical output of GENELAND analysis to choose the best number of clusters of 195 black grouse samples.

Table A3 GENELAND runs and their average log posterior probability for inference of optimal number of clusters.

Run	Number of populations	Average log posterior probability
20	6	-1935.756
13	6	-1953.885
16	6	-1963.969
4	6	-1973.352
6	6	-1993.062
18	6	-2043.045
12	6	-2045.508
8	6	-2059.959
9	6	-2070.438
3	6	-2086.643
7	6	-2103.621
1	6	-2122.914
5	6	-2128.190
14	6	-2183.804
11	5	-2205.300
2	6	-2206.328
17	6	-2213.829
15	5	-2236.006
19	5	-2294.664
10	5	-2323.737



Figure A2 Posterior probability of cluster membership for the most likely number of clusters $K=6$ and $K=5$ inferred from GENELAND analysis.