

Supplementary materials

Table S1. Microsatellite primers. Characteristics of the 12 primers used for the genotyping, showing the name of the locus, the primer sequences (F - forward, R - reverse), final concentrations for the primer mix (Primer conc.), allele size ranges of the Finnish golden eagle population, original species for which the primers were developed, and their corresponding reference. Multiplexing these loci was described in [39], except that one locus (Aa50) was removed from this study due to it being homozygous in our preliminary analyses.

Locus	Primer sequence	Primer conc. (μM)	Allele size range (bp)	Original species
Aa02	F: CTG CAG ATT TCA CCT GTT CTG R: CTT CCA GGT CTT GCA GTT TAC C	0.4	128–146	Spanish imperial eagle (<i>Aquila adalberti</i>) [92]
Aa04	F: TGC AGC TCA AAA GCA AAG G R: CAA CCC CAA CTC TCA CAC CT	0.25	117–159	Spanish imperial eagle (<i>A. adalberti</i>) [92]
Aa11	F: ACG AGC TTA TCT TTG ACC AAG C R: CTT TGT TTC AGC TGT TCC AGG	0.6	239–279	Spanish imperial eagle (<i>A. adalberti</i>) [92]
Aa15	F: TCA CTG ACC TGC CCT CTA CA R: CCA ACC CTC TAG TCG TCC AC	0.125	194–208	Spanish imperial eagle (<i>A. adalberti</i>) [92]
Aa26	F: GCA AAG GTA AAC TGC ATC TGG R: ATG CAC TAT TGG TAA ACA GGC A	0.125	139–155	Spanish imperial eagle (<i>A. adalberti</i>) [92]
Aa27	F: GAG ATG TCT TCA CAG CTT GGC R: AAG TCT CAG AGA CTG ACG GAC C	0.11	84–100	Spanish imperial eagle (<i>A. adalberti</i>) [92]
Aa35	F: GCA GCA GAA AGT GCA TAC GA R: GAC CAA ATG AAA TGC GCC	0.5	231–267	Spanish imperial eagle (<i>A. adalberti</i>) [92]
Aa36	F: ACA GGC CAG CAC CAA GAG R: TTT GGA GCC ATT GTT ACC GT	0.25	88–132	Spanish imperial eagle (<i>A. adalberti</i>) [92]
Aa39	F: TTC TGT TTT TCC ACT TGC TTG R: ATT GAG CTC ACA AAA ACA AAG G	0.8	182–200	Spanish imperial eagle (<i>A. adalberti</i>) [92]
Aa43	F: CCA CAC TGA GAA ACT CCT GTT G R: TTC CTG AGA GCT CTT CCT GC	0.125	103–129	Spanish imperial eagle (<i>A. adalberti</i>) [92]
NVHfr142	F: CCA CCC CTC TGC CAC TCA R: CCC CTG TCA GCT AAA CAC ATC AC	0.6	173–193	Gyr Falcon (<i>Falco rusticolus</i>) [93]
NVHfr206	F: ATC TAA TGG GCT TTC CTG GAT TT R: GAC ATT TTC CTC ATA GGC AAC TGA	0.25	153–169	Gyr Falcon (<i>F. rusticolus</i>) [93]

Table S2. Datasets used for different analyses with the number of samples used.

Analysis	Dataset	Number of samples
Microsatellite error rate calculations for the total dataset (Table S3)	Replicated samples from the complete dataset	372
Genetic diversity of microsatellite loci for the total dataset (Table S3)	Complete dataset	2215
Microsatellite error rates for the chick dataset (Table S4)	Replicated chick samples	41
Genetic diversity of microsatellite loci for the chick dataset (Table S4)	Chick samples	935
Genetic diversity and population structure (microsatellites)	Chick samples with a minimum of 75% genotyping success, one chick per territory	297
Genetic diversity and population structure (mtDNA)	Chick samples with a 100% amplification success of microsatellite loci; and from different nests to cover the distribution range of the species in Finland, one chick per territory	88
Turnover	Chick samples	935
Natal dispersal	Complete dataset	2215

Table S3. Characteristics of used microsatellite loci in the total dataset. Error rate per all loci (ER), percentage of successfully amplified alleles (%), polymorphic information content (PIC) of each locus, observed (H_o) and expected (H_e) heterozygosities, number of alleles (A), allelic richness (AR) based on a minimum of 1046 diploid individuals, inbreeding coefficients (F_{IS}) for each locus, and the mean values over all loci.

Locus	ER	%	PIC	H_o	H_e	A	AR	F_{IS}
Aa02	0.080	91%	0.478	0.503	0.528	9	8.50	0.048
Aa04	0.089	94%	0.677	0.723	0.706	14	13.26	-0.024
Aa11	0.063	88%	0.600	0.560	0.632	13	11.89	0.114
Aa15	0.086	97%	0.408	0.417	0.430	9	8.46	0.031
Aa26	0.048	73%	0.651	0.670	0.695	8	7.98	0.037
Aa27	0.063	90%	0.531	0.593	0.590	8	7.39	-0.005
Aa35	0.064	89%	0.578	0.548	0.645	17	14.36	0.149
Aa36	0.053	84%	0.777	0.726	0.804	21	20.50	0.097
Aa39*	0.025	47%	0.659	0.437	0.677	13	13.00	0.354
Aa43	0.071	99%	0.638	0.665	0.678	9	7.92	0.019
NVHfr142	0.027	80%	0.577	0.528	0.643	10	9.56	0.178
NVHfr206	0.011	78%	0.044	0.034	0.044	9	7.958	0.231
Mean	0.057	84%/88%**	0.552	0.534	0.589	12	10.90	0.095

Significant deviations ($P < 0.05$) from Hardy–Weinberg equilibrium expectations are in bold.

*Locus removed from further analyses.

**With locus Aa39 included and excluded, respectively.

Table S4. Characteristics of used microsatellite loci in the chick dataset. Error rate per all loci (ER), percentage of successfully amplified alleles (%), polymorphic information content (PIC) of each locus, observed (H_o) and expected (H_e) heterozygosities, number of alleles (A), allelic richness (AR) based on a minimum of 860 diploid individuals, inbreeding coefficients (F_{IS}) for each locus, and the mean values over all loci.

Locus	ER	%	PIC	H_o	H_e	A	AR	F_{IS}
Aa02	0.047	99%	0.480	0.547	0.536	6	3.15	-0.058
Aa04	0.089	99%	0.707	0.717	0.735	13	5.47	0.053
Aa11	0.023	98%	0.593	0.607	0.627	9	4.30	0.048
Aa15	0.021	100%	0.405	0.423	0.428	5	3.26	-0.049
Aa26	0.012	92%	0.655	0.701	0.702	7	4.27	0.016
Aa27	0.010	98%	0.527	0.563	0.587	7	3.24	0.090
Aa35	0.027	97%	0.584	0.611	0.648	7	3.73	0.063
Aa36	0.015	99%	0.787	0.752	0.813	16	5.88	0.109
Aa39*	0.030	68%	0.749	0.547	0.768	13	5.62	0.132
Aa43	0.011	100%	0.645	0.661	0.685	7	4.34	0.030
NVHfr142	0.000	95%	0.577	0.620	0.643	7	3.54	-0.026
NVHfr206	0.000	93%	0.033	0.035	0.034	3	1.34	-0.023
Mean	0.024	95%/97%**	0.545	0.567	0.585	7.91	3.87	0.033

Significant deviations ($P < 0.05$) from Hardy–Weinberg equilibrium expectations are in bold.

*Locus removed from further analyses.

**With locus Aa39 included and excluded, respectively.

Table S5. Mitochondrial haplotype information. Haplotypes found in this study (393 bp) with haplotype frequencies (number of individuals with a haplotype) and GenBank accession numbers to them. Also, here are the amalgamated haplotypes, i.e., haplotypes from previous studies to which haplotypes of this study match in a 338 bp alignment; H – Holarctic, M – Mediterranean, NA – North American, and EST – Estonian. The alignment to GenBank sequences resulted in a loss of two single nucleotide polymorphism positions, masking the divergence between some haplotypes found in this study: FIN1, FIN4, and FIN11 are amalgamated to H1; FIN3 and FIN6 are amalgamated to H12; FIN9 and FIN 16 are amalgamated to NA12. Three haplotypes (FIN5, FIN10, and FIN17) are newly discovered.

Haplotype, this study, 393 bp	Haplotype frequency	GenBank accession number, this study	Amalgamated haplotype, alignment 338 bp	GenBank accession number to the amalgamated haplotype
FIN1	54	OQ679875	H1	KR259260.1 [40]
FIN2	4	OQ679876	H4	KR259263.1 [40]
FIN3	4	OQ679877	H12	KR259271.1 [40]
FIN4	1	OQ679878	H1	KR259260.1 [40]
FIN5	1	OQ679879	-	-
FIN6	1	OQ679880	H12	KR259271.1 [40]
FIN7	1	OQ679881	M1	KR259251.1 [40]
FIN8	2	OQ679882	H2	KR259261.1 [40]
FIN9	2	OQ679883	NA12	MG491981.1 [71]
FIN10	1	OQ679884	-	-
FIN11	3	OQ679885	H1	KR259260.1 [40]
FIN12	6	OQ679886	H17	KR259276.1 [40]
FIN13	2	OQ679887	H14	KR259273.1 [40]
FIN14	3	OQ679888	EST-18, EST-25	MN105931.1, MN105938.1 [66]
FIN15	1	OQ679889	H10	KR259269.1 [40]
FIN16	1	OQ679890	NA12	MG491981.1 [71]
FIN17	1	OQ679891	-	-

Figure S1. Results from the Structure analysis of Finnish golden eagles using 11 microsatellite loci. (a) Mean LnP-values for $K = 1-5$. (b) Bar plots of genetic assignment of individuals for $K = 2$ to 5, where each bar represents an individual and colours represent the proportion of assignment to a cluster (K). The results show no population genetic structure of Finnish golden eagles.

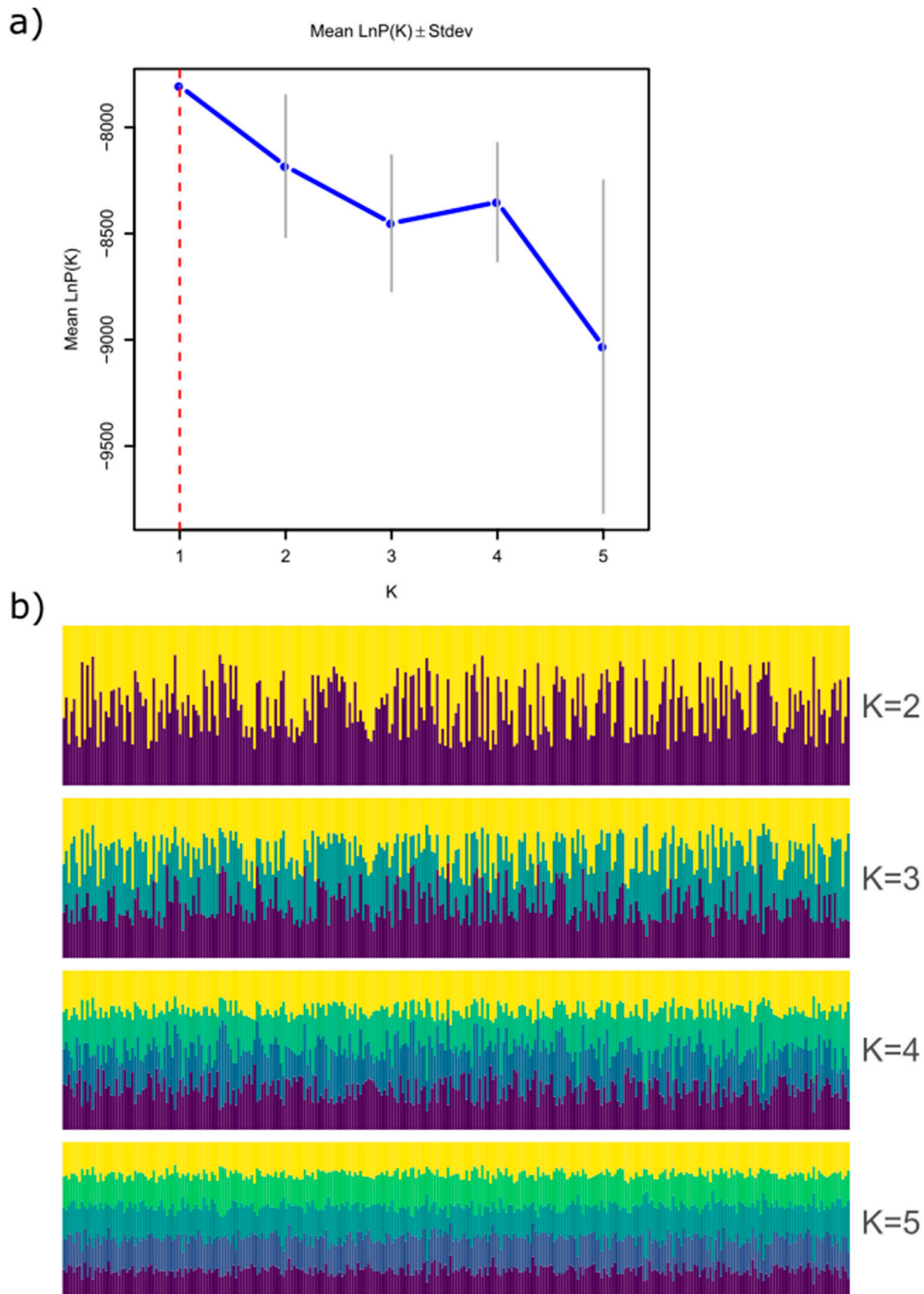
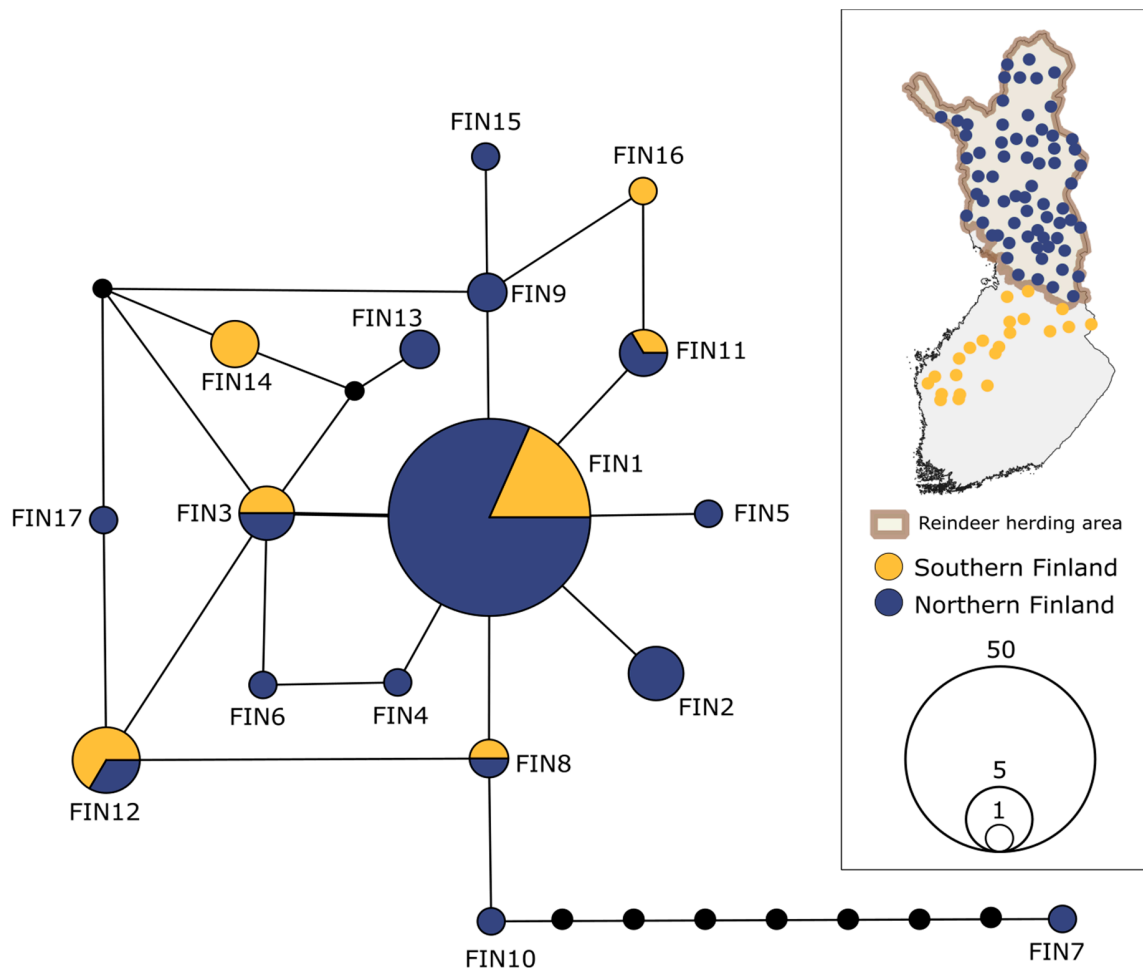


Figure S2. Median-joining haplotype network of Finnish golden eagles. The Northern Finland group includes individuals from the reindeer herding area, and the Southern Finland group - outside the reindeer herding area. In total, there are 17 haplotypes, of which 16 belong to the Holarctic lineage, and one (FIN7) - to the Mediterranean lineage [40]. Each line between haplotypes/nodes represents a single mutation step. The sizes of the circles reflect haplotype frequencies.



References to supplementary materials

39. Bielikova, M.; Ficek, A.; Valkova, D.; Turna, J. Multiplex PCR amplification of 13 microsatellite loci for *Aquila chrysaetos* in forensic applications. *Biologia* **2010**, *65*, 1081–1088.
40. Nebel, C.; Gamauf A.; Haring, E.; Segelbacher, G.; Villers, A.; Zachos, F.E. Mitochondrial DNA analysis reveals Holarctic homogeneity and a distinct Mediterranean lineage in the Golden Eagle (*Aquila chrysaetos*). *Biol. J. Linn. Soc.* **2015**, *116*, 328–340.
66. Nebel, C.; Gamauf A.; Haring, E.; Segelbacher, G.; Väli, Ü.; Villers, A.; Zachos, F.E. New insights into population structure of the European Golden Eagle (*Aquila chrysaetos*) revealed by microsatellite analysis, *Biol. J. Linn. Soc.* **2019**, *128*, 611–631; DOI: 10.1093/biolinnean/blz130.
71. Judkins, M. E.; van den Bussche, R. A. Holarctic Phylogeography of Golden Eagles (*Aquila Chrysaetos*) and Evaluation of Alternative North American Management Approaches. *Biol. J. Linn. Soc.* **2018**, *123*, 471–482; DOI: 10.1093/biolinnean/blx138.
92. Martínez-Cruz, B.; David, V.A.; Godoy, J.A.; Negro, J.J.; O'Brien, S.J.; Johnson, W.E. Eighteen polymorphic microsatellite markers for the highly endangered Spanish imperial eagle (*Aquila adalberti*) and related species. *Mol. Ecol. Notes* **2002**, *2*, 323–326.
93. Nesje, M.; Røed, K.H. Microsatellite DNA markers from the gyrfalcon (*Falco rusticolus*) and their use in other raptor species. *Mol. Ecol.* **2000**, *9*, 1438–1440.