

Supplementary Information

Tourani, M. et al. Spatial variation in red deer density in a transboundary forest ecosystem.

Model definition can be found here: <https://github.com/MTourani/OpenRepo/tree/master/BohemianCervus>

Table S1: Overview of the microsatellite markers used for individual identification of red deer *Cervus elaphus* samples in this study. The allele numbers represent the numbers of different alleles present in the population under study. The marker AMELXY was used for sex determination.

Marker	Length (bp)	Number of alleles	Reference
IDVGA55	195 - 209	11	[1]
BMC1009	282 - 306	14	[1]
TGLA53	151 - 193	18	[1]
BM203	214 - 236	19	[1]
CSSM16	152 - 162	6	[2]
CSSM19	139 - 169	14	[2]
Haut14	108 - 148	16	[2]
ETH225	132 - 170	15	[2]
AMELXY	228 - 282	2	[3]

Table S3: Total, jurisdiction-specific, and sex-specific estimates of red deer *Cervus elaphus* density and abundance with 95% credible interval in parentheses. BFNP: Bavarian Forest National Park, Germany; SFNR: Bavarian State Forest Neureichenau, Germany; SNP: Šumava National Park, the Czech Republic.

Region	Abundance (95% CI)			Density (95% CI)		
	Female	Male	Total	Female	Male	Total
SNP	990.4 (840 - 1166)	1061.6 (919 - 1230)	2052 (1836 - 2292)	1.7 (1.4 - 2)	1.8 (1.6 - 2.1)	3.5 (3.1 - 3.9)
BFNP	369.5 (287 - 473)	286.4 (220 - 370)	655.9 (547 - 786)	1.5 (1.2 - 2)	1.2 (0.9 - 1.5)	2.7 (2.2 - 3.2)
SFNR	46.6 (25 - 80)	97 (68 - 136)	143.6 (105 - 193)	0.3 (0.2 - 0.5)	0.7 (0.5 - 0.9)	1 (0.7 - 1.3)
Total	1406.4 (1229 - 1612)	1445 (1288 - 1626)	2851.4 (2609 - 3119)	1.4 (1.3 - 1.6)	1.5 (1.3 - 1.7)	2.9 (2.7 - 3.2)

Table S2: Genotyping error rates, i.e., allelic dropout (ADO) and false alleles (FA), as well as percentage of positive polymerase chain reaction (PCR) of genotyped red deer *Cervus elaphus* faecal samples collected in the Bohemian Forest Ecosystem. ADO and FA rates are denoted as percentage of all positive PCRs per microsatellite locus, as well as weighted average over all loci. H_{exp} stands for expected heterozygosity and H_{obs} denotes the heterozygosity observed in the data set.

Microsatellite	ADO (%)*	FA (%)	%PCR	H_{exp} (%)	H_{obs} (%)
Haut14	2.9	0.8	96	74	73
CSSM16	3.6	0.8	98	77	78
BM203	5.6	1.1	88	85	74
BMC1009	5.8	0.0	91	79	73
IDVGA55	2.9	0.4	98	83	83
CSSM19	3.3	1.1	82	78	68
TGLA53	4.4	1.0	95	86	85
ETH225	5.3	1.7	95	90	87
Mean	4.2	0.9	93	82	78

* For estimation of ADO, only heterozygote loci are used for all microsatellites, because ADO cannot be detected at homozygote loci.

Table S4: Covariate effects on red deer *Cervus elaphus* density including protected (i.e., non-intervention zones; β_{SNP_p} and β_{BFNP_p}) and unprotected regions (β_{SFNR} and β_{BFNP}), elevation (β_E), proportion of disturbance (β_R), and their interaction effect (β_{ER}).

Coefficients	Female			Male		
	Mean	Lower 95% CI	Upper 95% CI	Mean	Lower 95% CI	Upper 95% CI
β_{BFNP}	-2.8	-4.8	-1.4	-2.2	-3.8	-1
β_{BFNP_p}	0.2	-0.3	0.6	0.02	-0.5	0.5
β_{SFNR}	-1.9	-2.7	-1.1	-1	-1.5	-0.5
β_{SNP_p}	-0.4	-1	0.1	0.1	-0.4	0.5
β_E	0.03	-0.2	0.3	-0.3	-0.5	-0.1
β_R	0.7	-0.5	1.8	-1.9	-3.4	-0.4
β_{ER}	0.42	-0.3	1.1	2.1	1.3	2.8

References

- [1] Valière, N. *et al.* Importance of a pilot study for non-invasive genetic sampling: genotyping errors and population size estimation in red deer. *Conservation Genetics* **8**, 69–78 (2007).
- [2] Frantz, A. *et al.* Genetic structure and assignment tests demonstrate illegal translocation of red deer (*Cervus elaphus*) into a continuous population. *Molecular Ecology* **15**, 3191–3203 (2006).
- [3] Gurgul, A., Radko, A. & Słota, E. Characteristics of X- and Y-chromosome specific regions of the amelogenin gene and a PCR-based method for sex identification in red deer (*Cervus elaphus*). *Molecular Biology Reports* **37**, 2915–2918 (2010).