

## SAW project

### **INFERRING GENETIC PATTERNS OF ON-GOING RECOLONIZATION OF CENTRAL EUROPE BY ELUSIVE, LARGE CARNIVORES USING NOVEL SNP MARKER SYSTEMS FOR NON-INVASIVE SAMPLES**

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Many carnivores were largely or completely extirpated from Central Europe in the 18<sup>th</sup> and 19<sup>th</sup> centuries. For example, large species such as the Eurasian lynx (*Lynx lynx*) became extinct by the end of the 19<sup>th</sup> century, while smaller carnivores such as the Eurasian otter (*Lutra lutra*) survived persecution in small relict populations in remote areas. Due to the implementation of legal protection efforts, formerly absent carnivores have started to expand their ranges back into Central Europe since the second half of the last century, often supported by active reintroduction efforts.

All natural or human-mediated reintroduction involves small founder populations, below the long-term minimum viable population size, and often with reduced genetic variability. The recolonization of Central Europe by these carnivores is thus under intensive study by conservationists, ecologists and population geneticists. Concurrently, the source populations of these species outside of Central Europe are threatened by habitat loss and fragmentation, as well as human persecution. Thus, the future viability of these species in Central European and beyond is uncertain. In order to contribute to efforts to study and protect these species, the IZW joined a scientific network led by the Senckenberg Society for Nature Research.

In particular, the research network aimed to:

- Develop SNP-based genetic marker systems for fast, safe and reproducible genotyping based on non-invasively collected samples from five endangered carnivores (lynx, otter, bear, wolf, wildcat).
- Build a database with genotypic information for all relevant populations in Central Europe, as well as potential source populations in neighbouring regions.
- Determine the genetic status of Central European populations of all chosen model species, and investigate if and to what extent gene flow occurs between these populations and populations of neighbouring regions (i.e. potential source populations).

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#### Publications

Förster DW, Bull JK, Lenz D, Autenrieth M, Pajmans JLA, Kraus RHS, Nowak C, Bayerl H, Kuehn R, Saveljev AP, Sindicic M, Hofreiter M, Schmidt K, Fickel J (2018). Targeted re-sequencing of coding DNA sequences for SNP discovery in non-model species. *Molecular Ecology Resources*, in press. doi: 10.1111/1755-0998.12924

Bayerl H, Kraus RHS, Nowak C, Förster DW, Fickel J, Kuehn R (2018). Fast and cost-effective single nucleotide polymorphism (SNP) detection in the absence of a reference genome using semideep next generation Random Amplicon Sequencing (RAMseq). *Molecular Ecology Resources* 18: 107-117. doi: 10.1111/1755-0998.12717

Martin EA, Heurich M, Müller J, Bufka L, Bublly O, Fickel J (2017). Genetic variability and size estimates of the Eurasian otter (*Lutra lutra*) population in the Bohemian Forest Ecosystem. *Mammalian Biology* 86: 42-47. doi: 10.1016/j.mambio.2016.12.001

Bull JK, Heurich M, Saveljev AP, Schmidt K, Fickel J, Förster DW (2016). The effect of reintroductions on the genetic variability in Eurasian lynx populations: the cases of Bohemian–Bavarian and Vosges–Palatinian populations. *Conservation Genetics* 17: 1229-1234.  
doi: 10.1007/s10592-016-0839-0

Pajmans JLA, Fickel J, Courtiol A, Hofreiter M, Förster DW (2016). Impact of enrichment conditions on cross-species capture of fresh and degraded DNA. *Molecular Ecology Resources* 16: 42-55.  
doi: 10.1111/1755-0998.12420

Kraus RHS, VonHoldt B, Cocchiara B, Harms V, Bayerl H, Kühn R, Förster DW, Fickel J, Roos C, Nowak C (2015). A single-nucleotide polymorphism-based approach for rapid and cost-effective genetic wolf monitoring in Europe based on noninvasively collected samples. *Molecular Ecology Resources* 15: 295-305. doi: 10.1111/1755-0998.12307

#### Stakeholder Publications

Heurich M, Magg N, Fickel J, Förster DW, Müller J (2016). Gründe für die Stagnation der Luchspopulation. *Forst Praxis* 2/16: 19-21.

Fickel J, Förster DW (2016). Langfristige Perspektiven für den Luchs. *ÖKOJAGD* 3/16: 62-63.

Fickel J, Adelman W (2016) Die bayerisch-böhmische Population des Luchses benötigt Unterstützung – ANLiegen Natur 38(1): 40-41.

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