2.2. Genetic monitoring and recommendations at metapopulation level

Author: Christine Breitenmoser-Würsten
Reviewers: Michelle Müller, Carsten Nowak

Genetic monitoring is particularly important for (i) small, reintroduced and isolated populations, and (ii) populations that went through a severe historic bottleneck. Due to low effective population sizes (N_e) those populations are often affected by rapid loss of genetic diversity and increased levels of inbreeding. As all European lynx populations fall into one or the other category, a sound genetic monitoring is of pivotal importance for this species. As all reintroduced lynx populations show Effective Population sizes that are way below the level recommended for viable populations, they are in need of short- to long-term genetic management (Mueller et al. 2020).

All reintroduced lynx populations in Central and Western Europe with exception of those in Poland are considered part of the Carpathian lynx ESU (Evolutionarily Significant Unit). At the Bonn conference in 2019 (Bonn Lynx Expert Group 2021), the following recommendations have been established:

- Small and isolated populations should be genetically managed to minimise loss of genetic diversity (heterozygosity, allelic richness) and to keep the inbreeding coefficient F_{IT} below 0.15. If the inbreeding coefficient exceeds 0.25 (equivalent to full sibling mating) immediate action is needed to restore the genetic variability of the populations and decrease the inbreeding coefficient.
- A sufficient level of gene flow should be established within the local lynx metapopulation to reach these goals. If natural migration is not sufficient, assisted gene flow (assisted dispersal) has to be implemented. If local metapopulation dynamics (within an extant but fragmented population or between neighbouring reintroduced populations) is functioning either through natural gene flow or assisted dispersal, the population size of the population/metapopulation (Fig. 1.2.2) should not drop below an effective population size of 100 individuals, as an approximation to the $N_e = 100$ as lower limit of a population preventing short-term negative effects of genetic diversity loss and inbreeding Frankham et al. (2014).
- Consequently, the release of related animals should be avoided. Related animals and animals from inbred populations should not count fully, but e.g., 2 siblings as 1.75. Genotyping of each animal to be released is mandatory.

The sampling of material for genetic analyses needs to be included in monitoring protocols: Opportunistic sampling (e.g., from dead or captured lynx) has to be permanently implemented across the range. If a sample-size goal of 30 animals per generation (5 years) per population is not reached, sampling needs to be intensified. A common panel of 15 microsatellites should be used across the range by all laboratories involved in genetic monitoring of lynx. Calibration samples need to be exchanged between participating laboratories and a calibration table should be shared. Potential future extension or changes of genetic marker systems should be commonly agreed on by all involved genetic laboratories.

Recommendations:

1. Genetic monitoring needs to be established where it does not already exist and must become mandatory for all lynx populations in Continental Europe. This includes the tracking of genetic diversity and inbreeding over time, allowing to assess the effective population size (N_e) of (meta-)populations as well as gene flow between populations.
2. To establish an assisted metapopulation management: a system for assessing and exchanging animals (e.g., orphaned lynx) between reintroduced and other genetically deprived populations/subpopulations needs to be developed.
3. A permanent lynx genetics working group including experts from the laboratories involved in genetic monitoring and research should be established. This group should develop a more detailed protocol for genetic monitoring and conservation (genetic remedy of inbred populations, long-term genetic management of the metapopulations). Regular exchange of information between participating laboratories and with the *in situ* projects needs to be secured. Any new laboratory starting to work in lynx genetics is encouraged to join the working group.

Recommendation 1 has been implemented in various populations: Alps, Jura Mountains, Dinaric Range, and Harz Mountains. For the Jura Mountains, France has joined and provided samples to be included into the Swiss project. For Recommendation 2, work is under way, and Recommendation 3 has been implemented through the founding of the CElynx consortium (Linking Lynx Genetics Working Group). The focus of the work here is currently on implementing Recommendation 2.

References:

Bonn Lynx Expert Group. 2021. Recommendations for the conservation of the Eurasian lynx in Western and Central Europe. Cat News Special Issue 14, 78–86.

Frankham R., Bradshaw C. J. A. & Brook B. W. 2014. Genetics in conservation management: Revised recommendations for the 50/500 rules, Red List criteria and population viability analyses. Biological Conservation 170, 56–63.

Mueller S. A., Prost S., Anders O., Breitenmoser-Würsten Ch., Kleven O., Klinga P., Konec M., Kopatz A., Krojerovà-Prokešová J., Middelhoff T. L., Obexer-Ruff G., Reiners T. E., Schmidt K., Sindičič M., Skrbinšek T., Tám B., Saveljev P., Galsandorj N. & Nowak C. 2022. Genome-wide diversity loss in reintroduced Eurasian lynx populations urges immediate conservation management. Biological Conservation 266, 109442.