

International Exploratory Workshop

“Genetic status and conservation management of reintroduced and small autochthonous Eurasian lynx *Lynx lynx* populations in Europe”

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PROGRAMME

ABSTRACTS

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1.3. Review of the genetic research on lynx in Europe (Ch. Breitenmoser-Würsten, K. Schmidt, M. Sindičić, L. Paule & G. Obexer-Ruff)

Lynx went extinct in most of Central and Western Europe at the end of the 19th century and most of the autochthonous populations experienced a bottleneck of different extent and population numbers were about 10 times smaller than today. In the 1970s, re-introduction programs started in the Alps and in adjacent mountain ranges of Switzerland, Slovenia, Italy, Austria and France. Not all attempts were successful. Today we have in Europe a mosaic of large and small isolated autochthonous populations and several reintroduced populations of different size. We present an overview on lynx genetic research in different small populations and across Europe.

Poland - Lynx populations in the westernmost part of the species natural range (i.e. excluding the reintroduced populations) are highly fragmented across several forest patches in Poland, Lithuania and Belarus. Moreover, there is a large gap between these most western patches and the remaining, more contiguous range that stretches north-east across Latvia and Estonia and further to the east. The aims of the study were: (1) to determine the level of genetic variability of the lynx population in the most peripheral western patch of the species' distribution (north-eastern Poland) in comparison to lynx in the core area (Latvia and Estonia) and 2) to elucidate lynx population genetic structure across Poland, Latvia and Estonia. Based on microsatellite allele frequencies, we found the allelic richness in Polish lynx to be lower than that in lynx from Latvia and Estonia. We also found significant differentiation among the lynx populations, with the NE Poland population forming a distinct genetic group relative to the two other populations ($R_{ST} = 0.15$ and 0.22 , $P < 0.0001$). We suggest that genetic differentiation among lynx populations is the result of habitat insularisation that limits gene flow.

Croatia - The Dinaric population has been established in 1973 by reintroduction of three females and three males (among them a mother + son and brother + sister) from Slovakia to Slovenia, followed by their expansion to Croatia in 1974 and Bosnia and Herzegovina in 1984. Today, the population is considered endangered and isolated from any other population. Besides poaching, habitat fragmentation and lack of prey, loss of genetic diversity due to inbreeding is thought to be one of the causes of population decline in the past 10 years. The goal of this research was to evaluate the consequences of founder effect and inbreeding on genetic diversity of Eurasian lynx from Dinaric Mountains. A total of 94 samples dating from 1974 until 2010 have been analyzed. Additionally we included 16 samples from the Slovakian Carpathians. Genotyping of 20 microsatellite loci showed that the Dinaric population has a low genetic diversity.

Slovakia - The study provides basic characteristics of the genetic diversity of Eurasian lynx based on microsatellites markers. Samples from the Czech Republic, Romania, Russia and Slovakia were analyzed using 14 microsatellite loci. Tissue, bones and faeces were used as a source of DNA. The acquired genotypes were used for calculation of some genetic diversity characteristics. The obtained results indicate close relationships between Slovak and Czech samples as they probably come from one continuous population connected in the area of Kysuce in northern Slovakia and Jeseníky in northern Moravia. Populations from Western Siberia are genetically distant from the analysed European populations.

Switzerland - Because of the clandestine manner of some of the releases in Switzerland, most of the reintroductions remained obscure, but all together, there were not more than 14-16 animals re-

leased in the Swiss Alps and 8-10 in the Jura Mts., respectively. The two populations in Switzerland are today still relatively small and isolated. They consist of not more than 40-60 reproducing individuals. From this situation, the following questions arise: (1) Do the re-introduced populations have nowadays a reduced genetic variability compared to the Slovakian source population and other autochthonous populations in Europe due to the severe bottleneck created by the reintroduction? (2) What genetic signatures did the bottleneck leave on the evolving populations? (3) Do the two reintroduced populations differ genetically today from each other and the source population? (4) Is there geneflow between the two Swiss populations? To address these questions, genetic analyses were performed using microsatellites, which were developed in domestic cats and Canada lynx. A total of 530 samples from 13 populations were analysed with 22 microsatellites. The 8 autochthonous lynx populations from Europe showed heterozygosity values of 0.48-0.69 with 2.7-5.4 alleles per locus. Some of these populations went through a bottleneck in the 20th century or are very small today. The 5 re-introduced populations have a reduced genetic variability of various extents with heterozygosity values of 0.45-0.53 and 2.5-3.2 alleles per locus. In both Swiss populations, the loss of allele diversity was more severe than the loss of heterozygosity, and rare alleles have become less frequent compared to the source population. The populations in the Alps, in the Jura Mts. and in the Dinaric range have experienced an important genetic drift and are today distinct from the source population (F_{ST} 0.10-0.21), whereas the populations in the Vosges Mts. and in the Bavarian-Bohemian forest remained closer to the Carpathian lynx from Slovakia (F_{ST} 0.03 and 0.05, respectively).