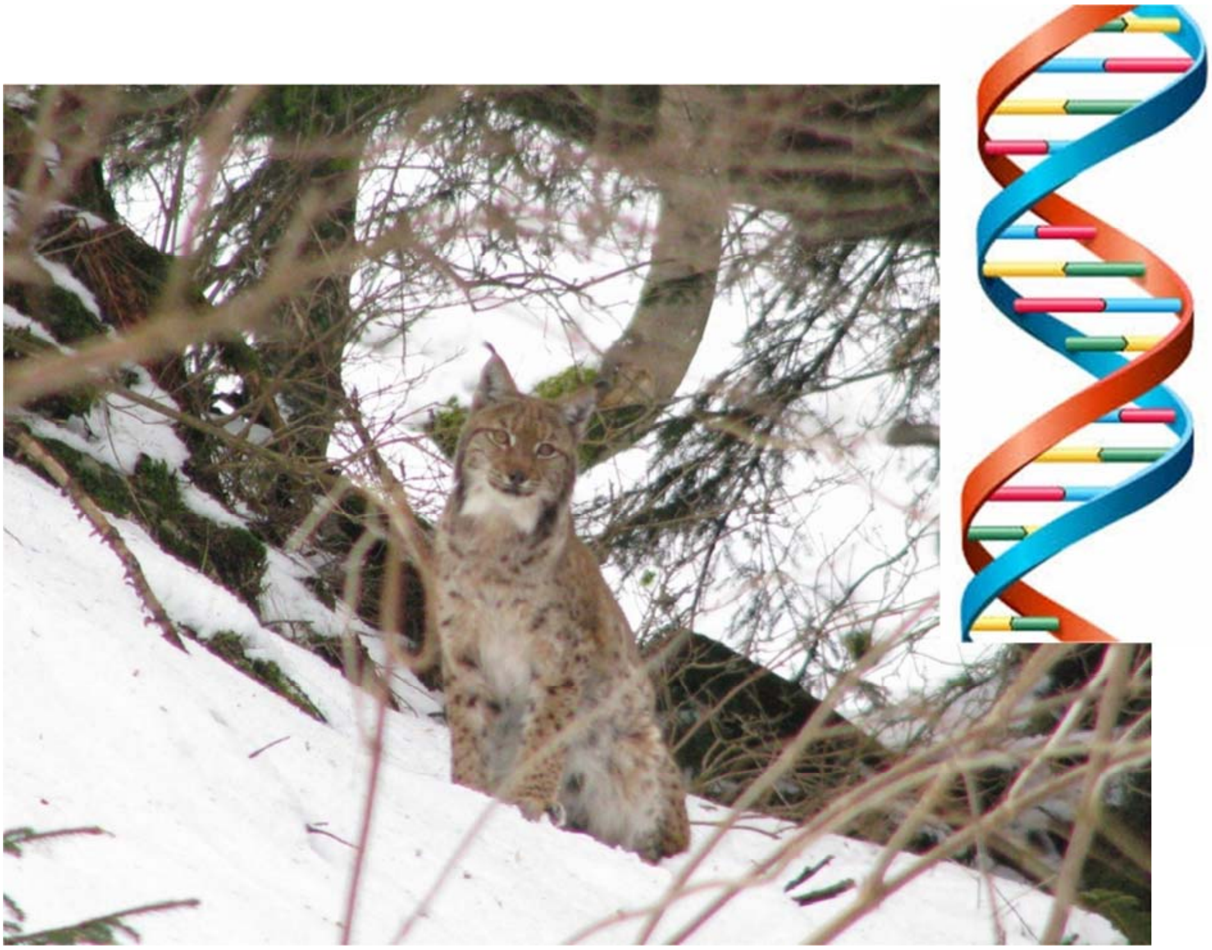
International Exploratory Workshop

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

Hotel Solsana, Saanen, Switzerland, 24-27 October 2011



PROGRAMME

ABSTRACTS

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3.5. To mix or not to mix? The phylogenetic map of lynx in Europe and the origin of released animals (Ch. Breitenmoser-Würsten, P. Wandeler, M. Sindičić, K. Schmidt & G. Obexer-Ruff)

The Eurasian lynx roamed once across the whole of Europe. But already around 1800 it has disappeared from all low land areas of western and Central Europe. The further decline culminated in a historic low around 1930 with an estimated number of some 700 lynx for the whole of Europe. After that all populations that made it through that low started to increase again. Reintroduction projects started in western and Central Europe in the 1970s. Lynx from the Carpathian Mts of Slovakia were released in Switzerland, Slovenia, Austria, Germany, Italy and France. Not all attempts were successful. Some of the releases were clandestine and the origin of the animals remained obscure.

Here we summarize the current knowledge on the phylogeny of the Eurasian lynx in Europe and the origin of the released animals in the reintroduction projects. So far seven mtDNA haplotypes found in animals in Scandinavia, Finland and the Baltics, the Carpathian Mts, the Balkans, the reintroduced populations in the Swiss Alps, Mongolia and Siberia have been published and are available at GeneBank. The mtDNA variability of the Eurasian lynx in Europe seems to be low to moderate. Two populations have only one haplotype: all animals analysed in Scandinavia have haplotype H1, and all animals in the Carpathian Mts have haplotype H4. The highest variability has been found in the Fenno-Baltic population. The population in the Balkans has two haplotypes H5 and H7 that have not been found in the rest of Europe. H5 has also been found in the Caucasus. The picture we find today is a combination of recolonization after the last ice age and recent isolation through fragmentation of the habitat. All reintroduced animals analyzed so far from the Alps and the Dinaric range share H4 with the source population in the Carpathian Mts.

The picture of the phylogenetic map based on mtDNA analyses has been confirmed by the analyses of nuclear markers, first for Scandinavia and the Fenno-Baltics, and now also for the rest of Europe. We have analysed all European populations with 22 microsatellites. The genetic structure found is supporting the results from mtDNA sequences. The following units can be distinguished: (1) Scandinavia, (2) Fenno-Baltics (including NE Poland), (3) Carpathian Mts and reintroduced populations with animals from there, (4) Balkans.

Additional to these findings, a study in Poland found mtDNA to show highly diversified genetic variability among populations with no haplotype polymorphism in Scandinavian and Carpathian lynx and high haplotype and nucleotide diversities in Latvia and Estonia, as well as in NE Poland with four new haplotypes (Ratkiewicz et al., unpubl. data).