

ABSTRACT

Robust monitoring combined with genetic analyses are important approaches to protect and manage large carnivore populations successfully. The aim of this master thesis is to analyse Eurasian lynx (*Lynx lynx*) population within whole Slovakia for the first time using 15 microsatellite loci. Noninvasive genetics is an effective tool for monitoring animal species with large home ranges and low population densities. Noninvasive samples including feces, hair, urine and buccal swabs were collected together with tissue samples from dead (mostly roadkill) individuals. 187 samples were collected between 2017–2019, resulting in 59 successful genotypes. Two samples were incorrectly determined in the field and excluded from further analyses since they were wildcat samples.

For population genetics analyses and demography, the dataset from the “*Velké šelmy 2*” project was extended with 98 genotypes in collaboration with the Institute of Vertebrate Biology CAS. Overall, 68 lynx individuals were detected in the dataset of 155 genotypes.

Relatedness analysis resulted in 67 significant relationships of the first degree and 9 significant relationships of the second degree. These results suggest a high relatedness among the whole population.

According to the present thesis, Slovakian lynx population has the third lowest genetic diversity of all European autochthonous populations and lower genetic diversity than the whole Carpathian population. Population size was estimated with large confidence intervals because of small sample size but it is still several times lower than hunters statistics.

Analyses of population and landscape genetics were first biased by related individuals in the dataset. In the Javorníky area, a family group previously described was detected. After related individuals were excluded from analyses, no population structure was detected. This suggests that even though Slovakian lynx habitat is fragmented due to deforestation and urbanization, it does not have influence on gene flow between separated areas.

There were no long distance dispersal events detected in the dataset. That indicates that gene flow with the rest of the Carpathian population is reduced.

Present thesis illustrates hurdles in research of large and elusive mammals and presents first results of population genetics analyses of the complete Slovakian lynx population. These data provide information about microevolution of large carnivores in anthropogenic landscape, which could be utilized also in conservation management.