

The aim of the master diploma work is to investigate origin of Czech populations and genetic variability of almost all Eurasian populations of the European beaver (*Castor fiber*). For our purposes we collected specimens from Czech populations, reintroduced population in Kirov district in Russia and all European and Asian refugia. At the end of the 19th century the species was on the verge of extinction due to overhunting, surviving only in eight isolated refugial areas. The population size at the end of the 19th century was estimated as 1 200 animals. The number of individuals has increased thanks to the legal protection and reintroductions. The current population size is estimated at 640 000. It is obvious that the populations of beaver have recently undergone severe bottleneck. Beaver was completely extirpated in the Czech Republic in the 18th century. Since the 80th of the 20th century beavers re-established in the Czech Republic due to migration from neighbouring countries and reintroduction programmes, however we knew only little about the origin of beavers in the Czech Republic. I showed that our beavers are derived from individuals in France, Germany, Norway and east Europe. Mitochondrial DNA of *Castor canadensis* has not been found in Czech beavers.

I studied microsatellite loci (first use for European beaver) and control region of the mitochondrial DNA (CR mtDNA) and I ascertained, that there are large differences between populations. The within-population variability of genetic markers is extremely low (max. 4 haplotypes CR mtDNA and 1 – 7 alleles per microsatellite locus). It corresponds to the strong bottleneck which reduced the effect of gene flow and on the other hand increased the influence of genetic drift, which resulted in discrete populations characterised by fixed alternative alleles. In Belarus and Russia we find six new CR mtDNA haplotypes. It indicates, that the variability in this areas is greater than previously suggested.