

In the last few centuries beavers passed through dramatic declining of the population size followed by expansion supported by reintroductions. The genetical variability is much decreased due to this bottleneck. Current beavers possess 31 known recent mitochondrial haplotypes, among which some were described independently several times. The haplotypes form two clusters, which serve as a base for dividing beaver populations into the west and east ESU. While microsatellite loci show moderate variability, the diversity of Y chromosome loci is very low. There are only ten described alleles of the DRB second exon, which belong to the MHC loci. No mitochondrial haplotype or MHC allele is shared between relict populations. This is not noticeable in samples from the time before the bottleneck. Described subspecies are therefore only the artefact of the recent bottleneck. Newly established populations comprise in many cases beavers of various origin and are more or less admixed. It seems, that the admixed populations have higher viability and conversely in some relict populations it is possible to find the evidence of the inbreeding depression. Thus, for reintroductions it is advantageous to use individuals from several source relict populations or to use beavers from admixed populations. Several species passed through the bottleneck and the recent expansions shows similarities with the population structure of the Eurasian beaver.