

Abstract

The Tatra chamois (*Rupicapra rupicapra tatrica*), an endemic mountain ungulate, occurs in the High Tatra Mts. (northern Slovakia and southern Poland). In the second part of the 20th century several chamois introductions occurred in Slovakia: Tatra chamois (from the High Tatra Mts.) were introduced into the Low Tatra Mts., while Alpine chamois (*R. r. rupicapra*) into the Veľká Fatra and Slovenský raj Mts. The High Tatra Mts. population underwent several population declines (bottlenecks) and all other Slovak populations were founded from only a few individuals (founder effect). Moreover, because the Low Tatra, Veľká Fatra and Slovenský raj are neighbouring mountain ranges, there is a potential risk of migration and hybridisation between the subspecies. Using 18 microsatellite loci, we studied neutral genetic variability, structure and potential hybridisation in chamois populations in Slovakia. The study is based on 193 samples: 95 tissue and 5 blood samples, and 88 faecal and 5 hair samples. Low genetic variability was found in all populations, the lowest one in High Tatra Mts. population. High values of fixation index, the number of private alleles, and factorial correspondence analysis indicated strong differentiation between the studied populations. Bayesian clustering divided Slovak chamois primarily according to subspecies and then into three distinct groups: (1) Tatra Mts. + Low Tatra Mts., (2) Veľká Fatra Mts., and (3) Slovenský raj Mts. In addition, the analyses indicated that hybridisation between the Tatra and Alpine chamois occurred in Low Tatra Mts., most probably as a result of migration from both Veľká Fatra and Slovenský raj Mts. Estimated extent of hybridisation was ca. 30%, but no F1 or F2 generation hybrids were detected, only backcross individuals with the Tatra subspecies. This suggests that hybridisation is not a common event and probably occurred earlier in the past. Using analysis in Bottleneck programme, recent population bottleneck was confirmed in all studied populations. Estimates of the effective population size (N_e) in OneSAMP programme suggest that N_e in all studied populations is very low, only 17-20 individuals. All chamois populations in Slovakia can be considered as very small and thus substantially threatened by genetic and demographic stochasticity. Classification of the Tatra chamois as critically endangered is therefore highly justified and both Tatra populations need strict protection.