Taxonomy and genetics

Genomic signature of bottleneck and founder effect in Alpine ibex populations in Slovenia

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In Europe, Alpine ibex (*Capra ibex*) was on the brink of extinction in the 19th century, with the only surviving population in Gran Paradiso, Italy, which numbered around 100 individuals. Extreme historical bottleneck and founder effect have strongly shaped the genetic make-up of recent reintroduced populations across Alpine arc. The two only existing populations in Slovenia, i.e. in the Kamnik-Savinja Alps and the Julian Alps, were established by individuals originating from Gran Paradiso as well as from Swiss and Austrian populations, reintroduced before also from Gran Paradiso in the 19th and 20th centuries. Past analysis of mitochondrial and immunogenetic diversity from recent samples revealed limited haplotype variation in Alpine ibex from Slovenia, with only one predominant mitochondrial haplotype present in both the Julian Alps and the Kamnik-Savinja Alps. The MHC genetic diversity in the same populations showed presence of only one functional allele (Caib-DRB*01).

The aim of this study was to investigate the signatures of inbreeding depression associated with founder events and population isolation in both populations using whole-genome sequencing at a 15-fold depth. Additionally, we included publicly available data on Alpine ibex from the NCBI database. Our analysis encompassed approximately 1 million unlinked nuclear SNPs as well as independent analyses of whole mtDNA and the Y chromosome. We demonstrated that, despite the rapid recovery of Slovenian populations and their increase in abundance during the 1960s, Alpine ibex exhibit persistent genomic signatures of historical bottlenecks, reintroduction events, and recent population declines. This is reflected in a low level of genome-wide genetic diversity compared to other established populations across the Alps. Our results highlight the urgent need to follow the results of the recent scientific research confirming that Alpine ibex is native to Slovenia; based on this, conservation actions aimed at improving genetic diversity of the species should be implemented as soon as possible. This is essential for increasing population viability and resistance to diseases.