Taxonomy and genetics

Genomic insights into hybridization and genetic introgression in European wildcats from the northern Dinaric Mountains and Pannonian Basin

Gerič, Urška[1]; Sollitto, Marco[1]; Šprem, Nikica[2]; Potočnik, Hubert[3]; Šnjegota, Dragana[4]; Ćirović, Duško[5]; Branković, Luka[1]; Bužan, Elena[1,6*]

[1] University of Primorska, Faculty of Mathematics, Natural Sciences and Information Technologies, Koper, Slovenia
[2] University of Zagreb, Faculty of Agriculture, Department of Fisheries, Apiculture, Wildlife Management and Special Zoology, Zagreb, Croatia
[3] University of Ljubljana, Biotechnical Faculty, Ljubljana, Slovenia
[4] University of Banja Luka, Faculty of Natural Sciences and Mathematics, Banja Luka, Bosnia and Herzegovina
[5] University of Belgrade, Faculty of Biology, Belgrade, Serbia
[6] Faculty of Environmental Protection, Velenje, Slovenia
* elena.buzan@famnit.upr.si

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European wildcat (*Felis silvestris silvestris*) is facing severe threats due to recent habitat loss, fragmentation, and ongoing hybridization with domestic cat (*Felis catus*). The ancestor of today's domestic cat originated from African wildcat (*Felis lybica*) in the Near East and Egypt approximately 10,000 years ago. Historical and recent hybridization with domestic cats poses a significant challenge to the conservation of the genetic integrity of wildcat populations across Europe. The present study investigates the genomic structure of European wildcat populations in the northern Dinaric Mountains and the Pannonian Basin, focusing on the presence and extent of recent hybridization in Slovenia, Bosnia and Herzegovina, Croatia, and Serbia. We employed whole-genome sequencing at 10-fold depth for 40 wildcat samples, complemented by publicly available data on the *Felis* genus, to analyse approximately 1 million unlinked nuclear single-nucleotide polymorphisms (SNPs) and complete mitochondrial genomes. Two combined approaches were employed for the analysis of mitochondrial genome variation. The first approach involves assembling and annotating coding sequences, respectively with NOVOPlasty and MitoZ, followed by multiple alignment using MAFFT and phylogenetic tree construction with BEAST2. The second approach entailed analysing mitochondrial SNPs to construct a hierarchical clustering tree and perform MDS plot. These analyses confirmed the presence of genetic introgression in wildcats from Serbia, specifically around the Beograd region, where a high population of stray cats poses a significant risk of hybridization. By leveraging advanced genomic tools, this study provides valuable insights to improve conservation strategies aimed at preserving the genetic diversity and integrity of European wildcat populations.