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# 34 IUGB CONGRESS

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# ABSTRACT BOOK

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# ABSTRACTS

## GENETIC STRUCTURE OF BALKAN CHAMOIS (*Rupicapra rupicapra balcanica*), CONSERVATION IMPLICATIONS

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### 4.S. Genetic structure and diversity of wildlife populations

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Balkan chamois (*R. r. balcanica*) is distributed across mountain chains in the Balkan Peninsula. Knowledge of the population genetic structure of Balkan chamois is limited and confined to regional studies. Therefore, the aim of this study was to use nuclear (20 microsatellites) markers to investigate the genetic structure of the subspecies across its distribution range and provide information on the connectivity levels of the different (meta)populations. We obtained muscle samples (preserved in 96% ethanol) from countries where hunting is allowed or from natural deaths and bone samples from hunters' private collections. We extracted DNA and successfully genotyped 79 individual samples of the Balkan chamois from six geographical populations and more are currently under study. Significant deviations from Hardy–Weinberg equilibrium were observed for three loci. In total, 115 alleles were detected across the 17 loci and the 6 study areas. The number of alleles ranged from 2 to 11 with a mean of 6.65. Observed heterozygosity ranged from 0.649 to 0.316 in Croatia and North Macedonia, respectively, while expected heterozygosity ranged between 0.592 in Montenegro and 0.303 in North Macedonia. The analysis of the genetic structure of the populations based on differences in the allele size (RST statistic) had the highest value of 0.316 between North Macedonia and Bulgaria and the lowest between Montenegro and Croatia (0,085). The STRUCTURE analysis indicated four clusters, one widespread across the

Peninsula, indicating similarity in the genetic structure of these populations, and three geographically confined (Bosnia and Herzegovina, Bulgaria and Serbia) ones. This knowledge about the population genetics of Balkan chamois will constitute the necessary starting point to assess the conservation status of the subspecies and design the necessary conservation strategies.

**Keywords:** Balkan chamois, genetic structure, genetic diversity, microsatellite

## THE DECLINE OF THE BREEDING POPULATION OF COMMON POCHARD (*Aythya ferina*) IN EASTERN EUROPE AND SIBERIA, AND ITS REASONS

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### 3.S. Wildlife and human-induced global climate change

A recent European review of the status of breeding Common Pochard population showed substantial decline since the 1980s (Fox et al., 2016). Our study has revealed that in Eastern Europe and Siberia, a particularly marked decline of the local breeding population was recorded during the last decades. The breeding population in the European Russia has declined from about 250,000 pairs in the 1990s to up to 100,000 pairs estimated in 2018. Up to 3-fold decline in numbers was recently recorded in certain regions of western and central Siberia. Simultaneously eastwards breeding range expansion of the species was observed with new records of breeding Common Pochards in east Siberia.

Common Pochard prefers eutrophic shallow lakes and floodplains rich in macrophytes and benthos organisms, also artificial wetlands (mostly fishponds) with abundant food resources. Many habitats of such types have been lost or degraded in Eastern Europe and Siberia during the last decades. It was mainly caused by recent land-use changes resulting in abandonment of large territories earlier used for agriculture and aqua-culture.

Climate warming is a major threat to ecosystems of small shallow lakes and ponds in the steppe zone of European Russia and Ukraine. Increased predation (particularly from invasive mammal species) is also important factor contributing to continued decline in the nesting abundance of the species.