

GENETIC STRUCTURE AND EXPANSION OF GOLDEN JACKALS (*CANIS AUREUS*) IN EUROPE AND THE CAUCASUS

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We analyzed 65 samples of golden jackals (*Canis aureus*) collected in south-eastern and central Europe, the Caucasus, and from Estonia (north-eastern Europe). Microsatellite markers and partial sequences of the mitochondrial control region were used to characterize the genetic structure of jackals in the sampled regions. The main aim of the study was to identify possible source populations of the golden jackals in north-eastern Europe. The analysis of 15 microsatellite loci revealed moderate levels of genetic variability: 89 alleles identified, resulting in allelic diversity close to 6.0. Observed heterozygosity was low (0.55) and significantly lower than heterozygosity estimated from Hardy-Weinberg equilibrium ($F_{IS} = 0.116$, $P < 0.05$ after Bonferroni correction for multiple comparisons). Only two mitochondrial haplotypes were identified. The first haplotype was detected in all sampling areas, whereas the other one was found only in the Caucasus. Bayesian analyses of population structure using STRUCTURE program indicated the presence of four genetic clusters, supported by the highest likelihood and delta K: the first was distributed mainly in Hungary and Romania, the second – in Estonia and the Caucasus, and the remaining two contained individuals of mixed ancestry from Slovenia, Croatia, Serbia, and Ukraine. Analyses using BAPS program, which included spatial information, suggested the presence of two genetic groups: the first comprising individuals from the Caucasus and Estonia, and the second containing all remaining animals. Spatial Principal Components Analysis also suggested that

Estonian population might have originated from the Caucasus. Similarly, some individuals in Ukraine appear to be genetically similar to the Caucasian population. In summary, our analyses indicated low levels of genetic diversity within *C. aureus*, especially for mitochondrial DNA. Moreover, we noted a clear distinction of the Caucasian population from jackals living in south-eastern Europe and possibly a Caucasian origin of the Estonian jackals. These results partly conflict with previous studies of the species that suggested a stepping-stone manner of dispersal. The close genetic connection between the Caucasus and the Estonian populations suggest that new populations can be founded from colonizers originating from remote areas.

Keywords: *long-distance dispersal, population genetics, microsatellites, mtDNA, Europe, the Caucasus*