

POPULATION GENETIC SURVEY OF THE GOLDEN JACKAL (*CANIS AUREUS*) IN THE SOUTHERN TRANS-DANUBIAN REGION

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The golden jackal (*Canis aureus*) is a widespread omnivorous and opportunistic mid-sized canid, distributed throughout southern Asia, the Middle East and south-eastern and central Europe. European populations have undergone significant population changes in recent decades. During the 20th century the size of the jackal populations increased in their distribution and abundance across Europe. Our main goal is to perform a genetic analysis of the golden jackal using 23 adapted dog microsatellite markers. Tissue samples were collected from individuals culled during legal hunting between 2011-2017 in Somogy and Baranya Counties. Our goal was to estimate genetic diversity and assess the genetic structure of jackals. Furthermore, we attempted to detect hybridization between golden jackals and other canids. Twenty-three microsatellites were optimized for multiplex PCR and used for genotyping. After recording the individual genotypes, we used GenAlEx software to calculate genetic diversity. In addition, we used PAST and STRUCTURE softwares to investigate the genetic structure, and to detect possible hybridization events between jackals and other canids. Of the 40 jackal samples 38 were successfully genotyped. Twenty of the 23 microsatellite markers were polymorphic; the number of alleles per locus ranged from 3 to 11, with an average of 5.45 alleles per locus. The observed (H_o) and expected (H_e) heterozygosity averaged 0.58 and 0.58, respectively. Both PAST and STRUCTURE clustering detected two groups among the golden jackal samples. F_{st} value, indicating the genetic distance between groups (subpopulations), was 0.073 calculated with STRUCTURE. Adding domestic dog ($n=12$) and grey wolf ($n=15$) samples to the jackal sample set, both PAST and STRUCTURE clustered the samples, into separate dog, wolf and jackal clusters; and no one of the samples showed any sign of hybridization. The adapted microsatellite marker set is suitable for population genetic studies in golden jackals. Heterozygosity values were moderate, and samples were divided into two groups. However, the very low F_{st} value indicates a very weak genetic separation of the groups. Domestic dog, grey wolf and golden jackal are

forming genetically distinct groups, and we could not detect any hybridization between them.

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