

Genetic structure of a brown bear (*Ursus arctos*) subpopulation in the extreme NW part of Greece.

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Greece hosts the southernmost brown bear (*Ursus arctos*) populations on the European continent. The minimum population size in the country is estimated at around 500 individuals inhabiting two separate geographical areas. The largest population occupies the area of Pindos Mountain range and is part of the wider Dinara-Pindos biological population whereas the other population nucleus occupies the Rhodope Mountain range in the East and is part of the wider Eastern Balkan population. The scope of this project is to investigate the genetic diversity and robustness of a brown bear subpopulation of the western nucleus located in the extreme NW part of Pindos range. This work is part of a wider project titled «Improving Human-Bear Coexistence Conditions in Municipality of Amyntaio–LIFE15NAT/GR/001108», in cooperation with the NGO “CALLISTO” project partner. Samples were collected, non-invasively, during field surveys in the study area from May to July 2017. Most samples were hairs (n=208), collected from a network of hair-traps with barbed wire attached to power poles covering the entire bear range in the prefectural unit of Florina. In addition, 8 stool samples were collected. DNA from 170 hair samples was successfully extracted. DNA samples were amplified and scored at ten microsatellite loci with ABI 3500 genetic analyzer (Applied Biosystems®). Each sample has been genotyped to estimate genetic parameters of the population including expected and observed heterozygosity values, number of alleles, Hardy–Weinberg equilibrium test and bottleneck effect. The effective population size was also calculated. Two sets of primers for SRY and ZF genes were used to calculate the sex ratio. Evaluation of the population status of bear population in Florina area is crucial for the efficient management of human-bear interactions and the proper management and conservation of the species both at national and trans-boundary levels. The population will also be genetically monitored in 2019.