

## NON INVASIVE GENETIC STUDY AND POPULATION MONITORING OF BROWN BEAR (*URSUS ARCTOS* L.) IN THE KASTORIA REGION, GREECE

Dimitris Tsaparis <sup>1,3</sup>, Nikoleta Karaiskou <sup>2</sup>, Yorgos Mertzanis <sup>3</sup>  
& Alexander Triantafyllidis <sup>2</sup>

<sup>1</sup>Section of Zoology-Marine Biology, Dept. of Biology, Univ. of Athens, Athens, Greece. Email: tsaparis@boil.uoa.gr

<sup>2</sup>Dept. of Genetics, Development and Molecular Biology, School of Biology, Aristotle University of Thessaloniki, GR-541 24 Thessaloniki, Macedonia, Greece. Emails: nikolbio@bio.auth.gr, atriand@bio.auth.gr

<sup>3</sup>NGO "Callisto"-Wild Life and Nature Conservation Society, Mitropoleos 123, GR-546 21 Thessaloniki, Greece. Email: mertzanis@callisto.gr

Population size and genetic diversity estimates are crucial for the conservation and the proper management of endangered species. Non invasive genetic sampling is used as a reliable alternative sampling method not only for the genetic study of rare or elusive animal species but for the estimation of their abundance as well.

The brown bear (*Ursus arctos*) population size in Greece appears to be generally stabilized, with positive trends at a local scale. Nevertheless, the species is still considered endangered and little is known about the genetic status and the exact size of local populations. The basic objectives of this study, which is part of an ongoing LIFE project (LIFE09 NAT/GR/000333), was to investigate the genetic diversity and genetic structure of the bear population in Kastoria region (NW Macedonia, Greece) and estimate its population size.

Samples were collected during field surveys in the study area from April to November 2011. The majority of samples were hairs (174 samples) that were collected with barbed wire attached to power poles. A permanent sampling network of 110 such hair traps was established in the study area and was revisited monthly from July to November. In addition, 46 scat samples were randomly collected and 15 tissue/blood samples from trapped/radio-tagged bears or bears victims of traffic accidents were also included in the present analysis. DNA from 76% of hair samples, 48% of scat samples and 80% of tissue/blood samples was successfully extracted. DNA samples were amplified for ten microsatellite loci. A complete genotype for 118 of these samples was obtained and the analysis indicated 63% of unique

genotypes. Further analyses will yield information on gene flow versus the K45 highway artificial barrier and overall population genetic variability.