



University of Utah

UNDERGRADUATE RESEARCH JOURNAL

GENERATING MINIMUM POPULATION SIZE ESTIMATE FOR BROWN BEARS IN
EASTERN TURKEY USING MULTILOCUS GENOTYPING

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Large carnivores are experiencing significant human-wildlife conflict as their large habitat requirements bring them into contact with expanding human settlements and infrastructure. Threats to large carnivore populations in Turkey are similar to threats to carnivores globally, which include reductions in size due to fragmented habitat, reductions in natural prey, vehicle collisions, and poaching. Despite the risks Turkey's large carnivores face, conservation efforts remain impeded by the poor documentation of local carnivore populations. Estimates of population size and trends remain unavailable for many large carnivore populations in the region.

Using a microsatellite analysis of scat samples, we obtained a minimum size estimate for a population of Eurasian brown bear (*Ursus arctos arctos*) in the Sarıkamış-Allahuekber Mountains National Park, eastern Turkey. The population relies heavily on anthropogenic food sources, resulting in conflict with surrounding human settlements. Our minimum population estimate will help inform future efforts to reduce conflict and promote further study into the population's health and viability.

From 2013-2015, scat detection dogs from the University of Washington's Center for Conservation Biology's Conservation Canines were used to collect bear scat samples. DNA was extracted following sample collection. For each sample, 8 different microsatellite loci were amplified using polymerase chain reaction and 8 primer pairs targeting each loci. An Applied Biosystems 3730xl capillary sequencer was used to distinguish alleles at each loci by fragment length. Each sample was subsequently associated with a set of alleles at each loci, or a "multilocus genotype". We collected 1,520 bear scat samples across all years and identified 157 viable bear samples to genotype. Logistic constraints were a limiting factor in our ability to generate enough data for capture-recapture analysis; therefore we focused on generating a minimum population estimate in the main study area. Taking a multilocus genotyping approach, our results identified 27 unique multilocus genotypes, which suggests a minimum population size of 27 bears. Our estimate can be used to investigate other indicators of population health, such as population density and genetic diversity, and will aid conservation efforts seeking to mitigate conflict as this brown bear population becomes increasingly exposed to human-dominated landscapes.

This is the first study to use multilocus genotyping as a means of estimating brown bear population size in the region. Our estimate can be used to investigate other indicators of population health, such as population density and genetic diversity, and will aid conservation efforts seeking to mitigate conflict as this brown bear population becomes increasingly exposed to human-dominated landscapes.