



Estimating effective population size of individual Eurasian brown bears (*Ursus arctos arctos*) by using noninvasive DNA samples

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Habitat destruction and fragmentation are major threats to biodiversity worldwide. One consequence of habitat fragmentation is the isolation of wildlife populations and reduction of genetic diversity. In Sarıkamış-Allahuekber Mountains National Park in eastern Turkey, a highly degraded forest harbors a Eurasian brown bear population (*Ursus arctos arctos*) that largely relies on anthropogenic food sources.

Monitoring and estimating population size and trends are key components in the management and conservation of large carnivores. In recent decades, techniques to estimate population size using genetic markers have become more common as a cost-effective approach to study these wide-ranging animals. Collecting scat samples is one noninvasive method to obtain genetic material for molecular fingerprinting.

We used scat detection dogs to collect scat samples within a sampling grid designed to produce data for spatial capture-recapture modeling. We collected 1,424 scat samples and have begun to genotype individuals using 19 polymorphic microsatellite loci. Preliminary results demonstrate that we have optimized our lab protocol for microsatellite analysis. From the initial 500 samples of extracted brown bear DNA, we have identified 65 samples with high quality and concentration by using a Nanodrop Spectrophotometer. We have confirmed 19 different microsatellite primers on each scat sample through amplification by polymerase chain reaction. We will run a fragment analysis on our samples to sequence microsatellites to identify individuals within this bear population inhabiting a human-dominated landscape.

Our overall goal for this project is to estimate effective population size, genetic isolation, and determine if effective dispersal corridors exist within the Sarıkamış bear population.

