

Genetic Diversity in Bobcat (*Lynx Rufus*) Populations in Northwest Nevada

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Population-level genetic analyses can provide important information on the health of wildlife populations and can be used to guide management decisions. Bobcats (*Lynx rufus*) are found all over Nevada and are trapped for fur purposes, yet little is known about their genetics. Our aim was to conduct the first genetic analysis on Northern Nevada bobcats from bone samples to obtain basic population-level genetic data. DNA was collected from jaw fragments donated by NDOW in 2019 and extracted using Qiagen DNeasy Blood and Tissue extraction kits. Samples were sent to the National Wildlife Research Center, who performed PCR and genotyped seven polymorphic microsatellites. Programs GENESOP and CERVUS were used to analyze the genotypes. We found all loci were polymorphic, ranging from 6-14 alleles and heterozygosity ranging from 0.60-0.90. The population sex ratio was 1.3:1, suggesting more males were captured by fur trappers. Overall, the population is more diverse than expected. Currently, the bobcat population appears to be genetically healthy even with trapping pressures and urbanization. Males appear to be trapped more frequently, likely due to their wider home ranges and more risk prone behavior, which is supported by other studies. This is the first year of data collection and is part of an ongoing project. We hope to continue to collect data from this population in order to determine genetic changes over time. Comparing these data with future samples will further the understanding of the population's genetic diversity as well as detect potential evolutionary changes related to inbreeding, migration, or selection. This research is the first to quantify population genetics of this bobcat population and maybe used to make management decisions in the future.