Using Historic Specimens to Provide Insight into Native Bighorn Sheep Genetic Diversity and Connectivity in Idaho

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ABSTRACT: Bighorn sheep *(Ovis canadensis*) have experienced severe population declines and population extirpations across the western US. One region where bighorn sheep were not extirpated is the Salmon River Drainage of Idaho. These native populations are a highly valuable and irreplaceable genetic and ecological resource. The goal of this study was to evaluate genetic diversity and connectivity among bighorn sheep in this region using a combination of current and historic specimens. Specifically, we addressed 4 questions 1) What are the levels of genetic diversity and population connectivity for native Idaho bighorn sheep? 2) Are Population Management Units (PMUs) genetically distinct? 3) What were historic levels of genetic diversity in native Idaho bighorn sheep? 4) How has diversity changed over time? We obtained 350 current samples from 5 PMUs, 43 historic samples (1989) from the Middle Main Salmon (MMS) and 34 historic samples (1923-1985) from Lower Salmon (LS) and Middle Fork (MF) using horn shavings from the Carrey Collection. We genotyped 15 microsatellite loci, eleven neutral and four adaptive. We observed the highest levels of genetic diversity in the historic samples from the Carrey Collection and from current samples in the core of the range. The Carrey Collection samples also had a much larger number of unique alleles (13) compared to the historic specimens from MMS (0) and current samples (3). Our connectivity and gene flow analyses indicated that PMUs were genetically distinct, but there was evidence for gene flow between PMUs. We found evidence for higher historic connectivity between the LS and MF PMUs compared to current samples from these regions. This is the first study in bighorn sheep to evaluate changes in genetic diversity over time using historic specimens and demonstrates that unique alleles and genetic diversity have been lost over time which has implications for fitness and adaptive capacity.

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KEYWORDS Connectivity; bighorn sheep; *Ovis canadensis*, genetic diversity; microsatellites; unique alleles.