
****AN INITIAL ASSESSMENT OF THE POTENTIAL OF GENOMIC ANALYSIS TO HELP INFORM BIGHORN SHEEP MANAGEMENT**

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Genetic research may be a useful approach for understanding factors that could impact productivity and restoration of bighorn sheep (*Ovis canadensis*) herds. For example, genetic consequences of inbreeding in small populations can impact recruitment and local adaptations can influence translocation success. This modest pilot study quantified genetic attributes of bighorn sheep populations with a range of different herd histories in Montana and Wyoming to investigate genetic similarity and differences, genetic heterogeneity and genetic distance. Employing an Ovine array containing about 700,000 single nucleotide polymorphisms (SNPs) with approximately 24,000 markers that are informative for Rocky Mountain bighorn sheep, we used whole genome genotyping to analyze genetic material. This technique represents a significant advancement in genetic analysis of bighorn sheep, as most previous studies have used microsatellites and less than 200 genetic markers. We analyzed approximately fifteen individuals from each of four different populations that we predicted would differ in genetic characteristics, due to population dissimilarities that potentially impacted their genetics, including origin (native/reintroduced), population size, bottleneck history, degree of connectivity, and augmentation history. We selected four populations that provided a spectrum of these herd attributes, including the Tendoys, Stillwater and Glacier National Park in Montana and the northeastern Greater Yellowstone Area in Wyoming. We present the results of this effort and examine expected and observed heterogeneity and genetic distance

estimates to evaluate the potential for links between genetics and herd demography. We discuss the utility of genetic analyses in improving knowledge of bighorn sheep populations and potential implications for bighorn sheep management.