An Initial Assessment of the Potential of Genomic Analysis to Help Inform Bighorn Sheep Management

ELIZABETH P. FLESCH, *Animal and Range Sciences Department, Montana State University, Bozeman, MT, USA 59717; elizabeth.flesch@gmail.com*
JENNIFER M. THOMSON, *Animal and Range Sciences Department, Montana State University, Bozeman, MT, USA 59717*
ROBERT A. GARROTT, *Fish and Wildlife Ecology and Management Program, Ecology Department, Montana State University, Bozeman, MT, USA 59717*
TABITHA A. GRAVES, *Northern Rocky Mountain Science Center, U.S. Geological Survey, West Glacier, MT, USA 59936*

ABSTRACT Genetic research may be a useful approach for understanding factors that could impact productivity and restoration of bighorn sheep 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. We used an Ovine array containing about 700,000 single nucleotide polymorphisms (SNPs) with approximately 24,000 markers that are informative for Rocky Mountain bighorn sheep. This technique represented a significant advancement in genetic analysis of bighorn sheep, because most previous studies have used microsatellites and less than 200 genetic markers. The Ovine array provided the capability to conduct whole genome genotyping of bighorn sheep and can increase understanding of population genetics. In addition, the Ovine array provides the potential to map informative SNPs to genomic areas of known function. We analyzed 11 to 16 individuals from each of 4 different populations that we predicted would differ in genetic characteristics due to population dissimilarities that potentially impacted their genetics. We examined differences in whether herds were native or reintroduced, population size, history of genetic bottlenecks, degree of connectivity, and augmentation history. The 4 populations we selected (Tendoys, Stillwater, and Glacier National Park (GNP) in Montana and the northeastern Greater Yellowstone Area (GYA) in Wyoming) provided a spectrum of herd attributes (Figure 1). The Tendoys herd was a small, introduced population on historical bighorn sheep range, which was started by two transplants in the 1980s. Additional transplants occurred in 1997 and 2002, following die-offs that occurred in 1993 and 1999. The Tendoys herd had strong potential for past bottlenecks to impact herd genetics and was also likely isolated from other bighorn sheep herds. In addition, we opportunistically included 2 samples from bighorn sheep that had been translocated from Wild Horse Island to the Tendoys. The Wild Horse Island herd was started by the transplant of 9 bighorn sheep in the 1930s-1940s and grew in number over time to a medium size, remaining isolated from other populations. Thus, there was a strong potential for past bottlenecks to impact genetics of this herd due to the small number of founding animals. Wild Horse Island bighorn sheep frequently serve as a source population for translocations, and examining this population could be informative for herds with initial reintroductions or augmentations from Wild Horse Island. The Stillwater population is a small, native herd with a moderate possibility for potential bottlenecks, and it may have some connectivity with the East GYA metapopulation. During the mid-1970s and early 1980s, the Stillwater population size ranged from 50 to 60, and the herd size decreased to below 40 in the mid-1980s and less than 30 sheep on average from 1989-1999. In recent years, there was

an increase in the population to a medium size. The GNP population represented a large, native herd that had high connectivity and mild potential for past bottlenecks. In addition to the Montana herds, we analyzed bighorn sheep across the east GYA in Wyoming (Wyoming hunt units 1-2). The Beartooth-Absaroka metapopulation also served as a baseline comparison of a large, native herd with high anticipated connectivity and genetic diversity. We are seeking to address important questions about the potential impacts of past management histories of individual bighorn sheep herds on their genetic attributes. We present the results and plan future research to evaluate the potential for links between genetics and herd demography. Genetic analyses may serve to improve knowledge of bighorn sheep populations and have potential implications for bighorn sheep management.

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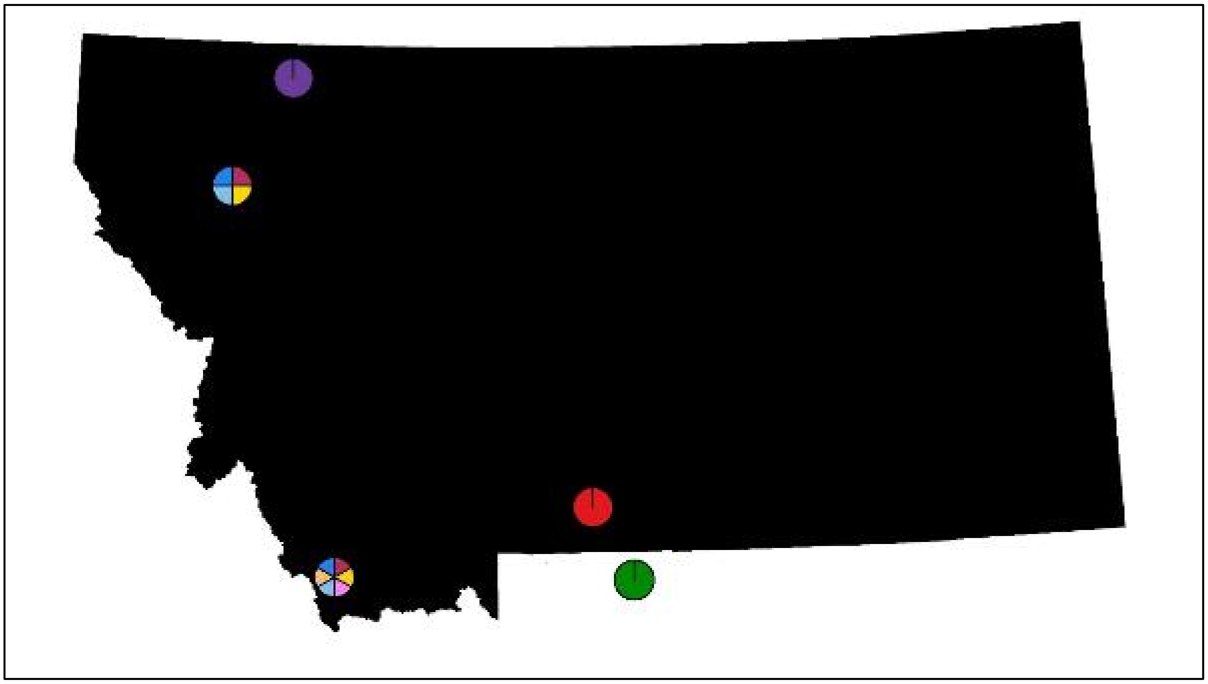

Figure 1. Hypothesized genetic composition of bighorn sheep herds in Montana and the east Greater Yellowstone Area (GYA) that were selected for this pilot study. Circles with one color symbolize native and large herds, as these herds have only one potential genetic source. Circles with multiple colors symbolize reintroduced and augmented herds, as these have multiple potential genetic sources caused by reintroduction and/or previous augmentations from multiple source populations.