



An Overview of Past and Present Genetic Studies of Bighorn Sheep: Reconciling Methods and Considering Applications for Management

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ABSTRACT: Bighorn sheep have been the focus of genetic research for decades. Because of small populations sizes, natural and anthropogenic habitat fragmentation, and a long history of bottlenecks and founder effects from translocation, managing low genetic diversity has been a concern across much of the present-day range of bighorn sheep. We review past, present, and possible future directions for studies of bighorn sheep that incorporate genetic tools or address genetic management. We consider two broad and not necessarily exclusive categories of studies or approaches: those intended to use genetic signals to infer phylogeography and phylogenetic relationships, demographic history, patterns of fragmentation and connectivity, or population size, and those intended to examine the consequences of genetic variation within populations, such as inbreeding, effects of genetic diversity on fitness, local adaptation, response to disease, and heritability of desirable traits. We provide a brief overview of different methods and questions, describe examples from past and present research, consider which types of methods and markers are most appropriate for different situations, and discuss how these concepts have been applied to management of wild sheep populations in North America. Finally, we identify areas of uncertainty and questions that bear examination in future research.

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