

MITOCHONDRIAL DNA VARIATION AND GENETIC POPULATION STRUCTURE IN ROCKY
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Abstract: Maintaining fitness and high adaptive potential in a species requires the maintenance of genetic variation both within and between populations. Transplanting individuals between genetically differentiated groups may cause outbreeding depression. On the other hand, if herds are not genetically differentiated, supplemental transplanting can prevent loss of genetic variation and concomitant inbreeding effects within small herds. Understanding the genetic population structure (i.e., distribution of genetic variation within and among populations) of bighorn sheep would help in making transplanting decisions that do not compromise the species genetic resources. The amount and distribution pattern (i.e., genetic population structure) of mitochondrial DNA (mtDNA) variation in Rocky Mountain bighorn sheep was assessed to determine relationships among populations and the usefulness of mtDNA analysis as a tool for conserving genetic variation in bighorn sheep. Restriction enzyme analysis was conducted on mtDNA from 292 individuals from 22 indigenous herds located throughout the entire geographic range of the Rocky Mountain subspecies of bighorn sheep. Eleven different mtDNA genotypes were identified. A phylogeographic analysis revealed relatively divergent mtDNA genotypes within herds, and several geographically widespread genotypes. This suggested that gene flow has occurred on a regional scale at some time in the past (perhaps during colonization of the Rocky Mountains) and that populations have not been subdivided by long-term barriers to gene flow. Significant differentiation in mtDNA genotype frequencies among local herds and among herds from 6 regions (Canada, central Montana, southern Montana, Idaho, Wyoming, and Colorado) suggests that little mitochondrial gene flow exists among current populations. The differentiation may be due to population fragmentation and bottlenecks during the last 200 years. Alternatively, because significant mtDNA frequency differentiation occurs on a microgeographic scale (i.e., among herds separated by only 4 to 15 miles) much of the observed mtDNA differentiation could be due to philopatric behavior. Female philopatry and population substructure may have existed for thousands of years. Although population differentiation is extensive for mtDNA variation, we cannot determine how extensive differentiation is for the nuclear genes which make up most of an organism's total genome. This study and the population fragmentation and die-offs of recent years, suggest a need for an assessment of population differentiation for nuclear genes in Rocky Mountain bighorn sheep. Thus, our lab (under F. Allendorf) in collaboration with J. Hogg are currently developing nuclear DNA analysis techniques (i.e. polymerase chain reaction and DNA sequencing) which will allow for a thorough assessment of genetic differentiation.