

## **\*\*Evaluating Bighorn Sheep Restoration Using Genomics**

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Wildlife restoration often involves translocation efforts to reintroduce species and enhance genetic diversity of small, fragmented populations. We examined the genomic consequences of bighorn sheep (*Ovis canadensis*) translocations and population isolation, to enhance understanding of evolutionary processes that affect population genetics and inform future restoration strategies. We conducted a population genomic analysis of 511 bighorn sheep from 17 areas, including native and reintroduced populations with contrasting translocation histories. Using the High Density Ovine array, we generated datasets of 6,155 to 33,289 single nucleotide polymorphisms and completed clustering, phylogenetic, and kinship analyses. Our study design maximized insight by employing standardized sampling of bighorn sheep herds, a standardized set of genomic markers, and a suite of contemporary analytical tools. Our analyses determined that most examined populations were isolated from recent, unassisted gene flow, including two pairs of native herds that had past connectivity but were recently fragmented. To identify which augmentation and reintroduction efforts made a genetic contribution, we synthesized genomic evidence across analyses to evaluate 24 different translocation events. We detected five successful augmentations and eight successful reintroductions based on genetic similarity with the source populations. A single native population founded most of the reintroduced herds, suggesting that genetic diversity of founders may have been more important to successful reintroduction than matching environmental conditions. Our results provide insight on genomic distinctiveness of native and reintroduced herds, the relative success of reintroduction/augmentation efforts and their associated attributes, and guidance for genetic rescue augmentations and reintroductions to aid in bighorn sheep restoration.