Surviving with Low Genomic Diversity: The Impacts of Reintroduction Management on Inbreeding and Genetic Load in Bighorn Sheep (*Ovis canadensis*)

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ABSTRACT: Bighorn sheep (*Ovis canadensis*) recovery throughout North America over the last century has been accomplished primarily through translocations from relict herds into unoccupied historical range. Yet the genomic consequences of reintroductions, including founder events, inbreeding depression, and genetic drift remain uninvestigated. This includes evaluating the risk of subsequent demographic/genetic rescue using stock from large, genetically diverse populations, as such individuals could introduce new deleterious recessive alleles. To characterize the effects of a founder event followed by complete isolation, we resequenced at 30x coverage 12 whole genomes from a 45-year-old introduced population of bighorn sheep in the Sespe Wilderness, California. This population was established from as few as 20 animals, has the lowest heterozygosity recorded for bighorn sheep, and anecdotally has shown potential phenotypic evidence of birth defects in the form of kinked tails. Yet the Sespe population has persisted at what is assumed to be near carrying capacity ($N \approx 60$) for decades. Size of runs of homozygosity suggested inbreeding was intense at the time of introduction but has been minimal in the last < 20 years. Compared to the source population ($n = 12$), and a genetically diverse reference population ($n = 12$), the Sespe individuals had a higher proportion of homozygous and fixed missense and loss-of-function mutations, which may reflect increased expression of deleterious alleles. Simulations of various augmentation scenarios are planned to evaluate extinction risk associated with introducing stock from various sized populations with differing genetic load. This study will guide future reintroductions and demographic/genetic rescue efforts for bighorn sheep throughout North America.

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