

Researchers study genetic outcomes of translocating bighorn sheep

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This bighorn sheep roams as part of the Absaroka herd near Cody, Wyo. University of Wyoming researchers led a study to evaluate the long-term impact of translocation actions on Rocky Mountain bighorn sheep in Wyoming. The research was published in a paper that appeared in the May 29 online issue of the *Journal of Wildlife Management*. Credit: Wyoming Game and Fish Department

Translocation is an important management tool used for nearly 100 years to increase bighorn sheep population numbers in Wyoming and to restore herds to suitable habitat throughout their historical range. Yet, translocation also can alter the underlying genetic diversity of managed wildlife species in both beneficial and detrimental ways.

To evaluate the long-term impact of [bighorn sheep](#) translocations, a University of Wyoming professor and postdoctoral researcher co-lead a study from 2015-19. The research group characterized statewide genetic structure and diversity by using microsatellite and mitochondrial DNA data in 353 indigenous and translocated Rocky Mountain bighorn [sheep](#) populations in Wyoming.

"The results of this study provide a comprehensive view of the level of genetic diversity in bighorn sheep in Wyoming. This is really important because bighorn sheep populations in Wyoming and throughout the West were driven down to such low numbers between the gold rush era and the 1960s," says Holly Ernest, a UW professor of wildlife genomics and disease ecology, and the Wyoming Excellence Chair in Disease Ecology in the Department of Veterinary Sciences and the Program in Ecology. "This loss of [population](#) numbers historically was due, in large part, to part overharvest, exposure to livestock diseases and loss of their habitat. In Wyoming, they perhaps existed in the hundreds of thousands pre-mid-1800s, but were driven down to as low as 2,000 total in Wyoming by the 1960s. Large losses of individuals often mean large loss of genetic diversity, which is a major foundation of healthy populations."

Ernest was the senior and corresponding author of a paper, titled "Bighorn Sheep Genetic Structure in Wyoming Reflects Geography and Management," that was published in the May 29 online edition of the *Journal of Wildlife Management*. The journal publishes manuscripts containing information from original research that contributes to basic wildlife science. Suitable topics include investigations into the biology

and ecology of wildlife and their habitats that have direct or indirect implications for wildlife management and conservation.

Sierra Love Stowell, a research genomicist and a UW postdoctoral researcher at the time (2016-18) of this work, was the paper's lead author. Roderick Gagne, a research scientist at Colorado State University and a UW postdoctoral researcher from 2015-17, and Doug McWhirter, a Wyoming Game and Fish Department wildlife biologist, were co-authors of the paper. Additionally, other wildlife biologists and officials from the Wyoming Game and Fish Department contributed to the paper.

Bighorn sheep are a key component of Wyoming's biodiversity and a species that provides important viewing and hunting opportunities.

Translocation is a tool used in wildlife management that involves the intentional, human-mediated movement of individual animals, populations or species from one area with release in another. Beyond the demographic effects of adding more individual bighorn sheep, translocated animals bring more genetic material that can increase genetic diversity and improve fitness in recipient populations. Translocation of bighorn sheep in Wyoming began in 1922 and still occurs today.

The study found there was high gene flow—genetic interchange due to movement of animals with resulting successful breeding—among herds that had [translocation](#) sources in common, and herds that received translocated individuals from other herds.

"We identified at least five genetic clusters of Rocky Mountain bighorn sheep in the major mountain ranges of Wyoming," Ernest says. "These genetic clusters generally align with current management units."

The [herd](#) units identified were in the Absaroka, Devil's Canyon, Jackson,

Kouba Canyon and Whiskey Mountain areas.



This Wyoming bighorn sheep is part of the Jackson herd, one of five distinct herds identified in Wyoming during a study that appeared in the *Journal of Wildlife Management*. Credit: Wyoming Game and Fish Department

For example, there is high gene flow among Devil's Canyon, Laramie Peak and Ferris-Seminole herds. Devil's Canyon, including the surrounding habitat in the Bighorn Mountains, received the most translocations of any herd in Wyoming, including translocation of bighorn sheep from Whiskey Mountain near Dubois; Morgan Creek, Idaho; Missouri Breaks, Mont.; and the Lower Deschutes River, Ore.

Laramie Peak also received translocations from Whiskey Mountain and Montana. The Ferris-Seminole herd was founded by translocation and continues to receive individuals from Devil's Canyon.

Ernest says the most interesting finding of the study is that bighorn sheep have maintained a distinctive population genetic structure in Wyoming, even with historical population losses and translocations.

"We found this intriguing and important, because we might have expected that the very large reductions in population sizes and extensive translocation events might have caused disintegration of population genetic structure, and an appearance of Wyoming bighorn sheep to be panmictic or 'all interbreeding,'" Ernest says. "But, they are not. They have distinctive populations."

The study used a panel of 38 variable microsatellite loci and 512 base pairs of mitochondrial DNA sequence to identify the genetic structure throughout the state and in translocation source herds; quantify the extent of genetic diversity within each genetic cluster; and estimate the degree of gene flow among herds.

In the early 1800s, the estimated number of bighorn sheep in Wyoming was between 150,000 and 200,000. Overharvest, habitat loss and livestock-transmitted disease outbreaks led to severe population declines. By the 1960s, bighorn sheep numbers had dwindled to about 2,000 before rebounding to roughly 7,000 in 1990.

Today's estimates are between 6,000 and 7,000 animals, with variable demographic rates between herds. Population rebound following the steep decline is attributed to management efforts, which include limiting harvest, preventing disease outbreaks and translocating individual sheep for reintroduction and demographic control.

The study's results provide a statewide assessment of genetic diversity and structure that will enhance management by understanding the outcomes of translocation, identifying the source of unknown individuals and parameterizing disease ecology models, Ernest says.

"The source herd identification of wandering bighorn sheep is important when determining if management actions, such as herd reductions, can be applied to reduce the likelihood of animals leaving the herd for extended forays," Love Stowell says. "Effective population sizes are low in most Wyoming herds, suggesting that managers should weigh the importance of maintaining gene flow for increasing genetic diversity and effective population size against the risks of disease transmission, outbreeding depression, phenology mismatch and other factors. Finally, this research provides a baseline for genetic monitoring in the face of future disease outbreaks or extreme weather events."

Outbreeding depression is described as interbreeding between two distinct populations that can lead to reduction in service and reproduction, Love Stowell says. Phenology mismatch is the timing of life events, such as lambing of bighorn sheep and their environment.

More information: Sierra M. Love Stowell et al, Bighorn Sheep Genetic Structure in Wyoming Reflects Geography and Management, *The Journal of Wildlife Management* (2020). [DOI: 10.1002/jwmg.21882](https://doi.org/10.1002/jwmg.21882)

Provided by University of Wyoming

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