

Project Title: Wyoming Statewide Bighorn Sheep Population Genetics, Year 3 of 3

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Project Type: Research

Affiliate: University of Wyoming with support from Wyoming Game & Fish Department and Wyoming Wild Sheep Foundation

Location of Project: state-wide Wyoming

Project Description

This represents a proposal for year-3 of the 3-year project. This 3rd year will complete a comprehensive statewide population genetic analysis of Wyoming bighorn sheep. Providing such an analysis will allow Wyoming Department of Game and Fish (WGFD) to better manage bighorn sheep by determining:

- 1) identities of genetically interbreeding populations (herds)
- 2) genetic signatures of past translocation events
- 3) gene flow among herds, genetics of migration and dispersal
- 4) herd-specific genetic diversity
- 5) genetic effective population sizes for each herd (numbers of individuals contributing to gene pool)
- 6) population assignment of individual bighorn sheep (wandering rams for example)

These data will form a foundation with which WGFD can monitor the genetic health of Wyoming's herds into the future. They will also provide better tools and reference data sets for forensic analyses, and provide critical data for understanding disease threats. Currently there is no such foundation, therefore no good way to track changes in genetic diversity, herd structure, and effective population sizes.

During the second year (2016-17), we acquired 593 additional samples from 28 hunt areas.

Please see details in attached report "Bighorn Sheep Research Activity 2016-17". We conducted 1094 DNA extractions and validated extraction methods for different sample types. We optimized PCR methods for sequencing ~500 base pairs of mitochondrial DNA. We have identified haplotypes for 238 individuals (plus 66 in preparation) and are documenting high diversity. We genotyped 255 individuals (plus 14 more in progress) at 40 microsatellite markers and 3 sex markers. We genotyped 36 individuals using the Illumina Ovine HD BeadChip, a technology developed to identify polymorphism at 600,000 loci. We received shared data from our collaborators at Montana State University on an additional 24 individuals from the Greater Yellowstone Ecosystem. We sequenced 92 individuals (plus another 92 individuals are in progress) at thousands of places in the genome after validating methods for library preparation. We are testing methods for identifying individuals and population clusters, and integrating these data with other data types.

Project Objectives

List of activities

- 1) Complete the collection of samples from animals captured for telemetry or collected by hunting.
- 2) Complete collection of data from WGFD for each sample, including geographic location, age, sex, and other key information.
- 3) Extract DNA from third year set of samples; prepare samples for genetic analyses.
- 4) Generate High Density Ovine SNP chip data, double digest restriction-site-associated DNA sequencing, microsatellites, and mitochondrial data.
- 5) Statistically analyze data – population genetic and genomic analysis; geographic analyses using landscape genetics techniques incorporating GIS.
- 6) Integrate translocation history with herd genetics
- 7) Communicate via reports and in-person presentations with WGFD Bighorn Sheep Working Group and collaborators. Write the third year/final report detailing findings. Write manuscript(s) for peer-reviewed publication.
- 8) Determine geographic gaps in sampling (some areas are not available) and provide recommendations to WGFD for future studies.
- 9) Recommend next steps for applying the findings of this current study to future research in genetic assessments of disease susceptibility (particularly for bighorn sheep response to pneumonia pathogens).

Project Goals

Completion of year 3 objectives will provide 1) a comprehensive view of statewide population structure and genetic diversity; and 2) information to guide recommendations for management and future research on bighorn sheep disease genetic susceptibility. These data and analyses will help address the main justifications and goals as stated in project description. The genome-wide data will also provide a foundation in host genetics to assist future genetic analysis of susceptibility to diseases that threaten bighorn sheep in Wyoming.

Project narrative/ budget justification

The project leads (Dr. Sierra Love Stowell and Dr. Holly Ernest, UW) have extensive experience leading and collaborating in genetics projects for trout (Love Stowell) and desert bighorn sheep (Ernest, California, Arizona, and publications including J. Mammalogy, a range wide genetic assessment), from prior and current work at Univ of Colorado Boulder (Love Stowell) and UC Davis (Ernest). Dr. Ernest will continue to use the resources of both her Wildlife Genomics and Disease Ecology lab and collaborations with the UC Davis Veterinary Genetics Laboratory. Publication list is here: <http://www.wildlifegenetichealth.org/publications/>
And details about our credentials are here: <http://www.wildlifegenetichealth.org/about-us/>

Next page for budget details

Total requested: \$57,436

Salary for bighorn sheep genomics postdoc: **\$ 28,670** (\$34.50/hour including fringe benefits)
(necessary personnel for items below – there are no other sources for the salary)

Genomic sequencing, microsatellite, mitochondrial, and SNP analyses: **\$25,886.**

Postdoc travel to meet with collaborating researchers / Wyoming GFD biologists: **\$880.** Vehicle rental / personal vehicle mileage \$420 (based on Univ. Wyoming mileage and fleet vehicle rates); Lodging/Food \$460 (3-4 nights).

Publication costs **\$2000**

We applied on 1/30/2017 for the Governors Big Game grant using these figures (plus here added the publication costs for journal paper). Therefore, we propose that this amount (\$57,436) be split between the Governors Big Game grant (proposal of 1/30/2017) and the WWSF grant (this proposal).