



Grant In Aid (GIA) Form

Project Title: _____

Project Type: _____
Waterhole/Transplant/Habitat/Research/Education/Other (Explain)

Affiliate: _____
Outfitter Organization/BLM/Game & Fish/Forest Service/Other (Explain)

Location of Project: _____
State/Territory/Area

Description Of Project:

Problem to be Solved:

Describe How You Propose Solving Problem:

Montana, Oregon, and Idaho have agreed to provide the necessary samples for DNA analysis via sample sharing agreements. These areas are the sources for past translocations into Wyoming. We have generated Wyoming-wide genomic SNP and microsatellite data for Wyoming bighorn sheep and will compare the MT, OR, and ID genotypes

BIOGRAPHY OF APPLICANT

Name: _____

Address: _____

Daytime Phone Number: _____ **Fax:** _____

E-mail: _____

Are you a current member of WY-WSF? _____ **Yes** _____ **No**



	Cost to be funded by WY-WSF Grant	Cost to be funded by other cooperators
Equipment.....	\$ _____	\$ _____
Services.....	\$ _____	\$ _____
Permanent, full time salaries will not be considered		
Publishing.....	\$ _____	\$ _____
Monitoring.....	\$ _____	\$ _____
Supplies.....	\$ _____	\$ _____
Please itemize then total		
Other (Specify).....	\$ _____	\$ _____
Totals	\$ _____	\$ _____

OTHER ORGANIZATIONS PROVIDING FINANCIAL AID OR SUPPORT OF THE PROJECT (Include any pending amounts applied for.): _____

ENDORSEMENT: I hereby agree to abide by the stated requirements of a WY-WSF grant. I also understand all WY-WSF funding stipulations and will provide all necessary reports if I receive a grant from WY-WSF.

Signature of Applicant _____

Title _____ **Date** _____

MEDIA CONTACTS: Please list one or more media sources in your area that we may contact with details of your project:

- 1) _____
- 2) _____
- 3) _____
- 4) _____

Project Overview

Title

Integrating genetic data with translocation history to inform scientific management of bighorn sheep

Synopsis

Translocation has been an important tool for wild sheep restoration and management since the early 20th century, involving the movement of more than 20,000 individuals around the United States and Canada. Given the importance, complexity, and expense of translocations, research is needed to understand the effects of translocation on recipient herds. Using a genetic approach, we will test whether translocation actually increases genetic diversity and fitness in recipient herds, focusing on bighorn sheep in Wyoming. This pilot project will help managers assess the effectiveness of translocation as a conservation strategy and provide a model that can be applied to evaluate translocations in other states.

Amount requested from WWSF

\$30,814

Project duration

2 years – we're in the second of two years for this translocation study

Amount requested per year

\$30,814 for this second year

Applicant names

Sierra Love Stowell, MA PhD
Holly Ernest, DVM PhD

Organization

University of Wyoming

Agency support

Dr. Mary Woods, Wyoming Department of Game & Fish
Hank Edwards, Wyoming Department of Game & Fish
Ryan Amundson, Wyoming Wild Sheep Foundation, Wyoming Department of Game & Fish,
Doug McWhirter, Wyoming Wild Sheep Foundation, Wyoming Department of Game & Fish

Project location

Wyoming bighorn sheep populations are the focus, and samples from reference populations from which bighorn sheep were translocated from: Idaho, Oregon, Montana, USA

Map

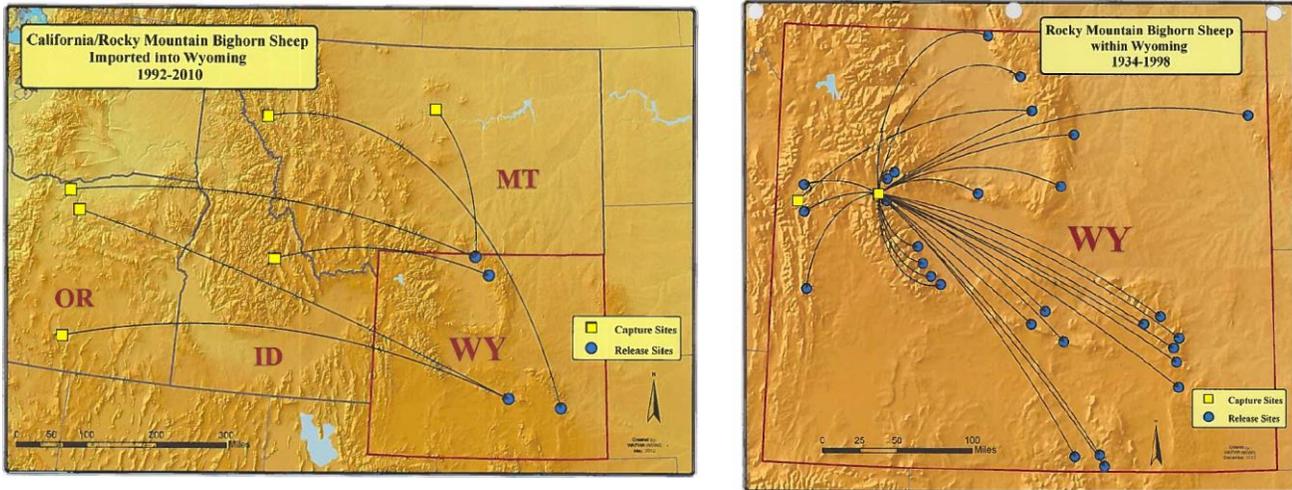


Figure 1: Bighorn sheep translocation history in Wyoming, 1934-2010. *Left* bighorn sheep imported into Wyoming from other states. *Right* translocations within Wyoming. (WAFWA Wild Sheep Working Group 2015)

Applicant Information

Applicant names

Sierra Love Stowell
Holly Ernest

Title

Postdoctoral Research Associate
Professor Wildlife Genomics and Disease Ecology, Wyoming Excellence Chair

Organization

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Project Description

Project description

Translocation has been an important tool for wild sheep restoration and management since 1922. More than 1,460 translocation projects have moved more than 21,500 bighorn sheep around the United States and Canada (WAFWA Wild Sheep Working Group 2015). Translocations are intended to augment declining populations and found new populations within the historic range of bighorn sheep. Beyond the demographic effects of adding more individuals, translocated individuals also bring new genetic material that can increase genetic diversity and improve fitness in recipient populations.

When planning translocations, considerations include how well the translocated individuals are adapted to the receiving habitat, how closely related the translocated individuals are to the receiving population, and the disease status of both the translocated individuals and the recipient population. Recent work highlights the potential for genetic mismatch between translocated individuals and their historic range (Malaney et al. 2015). Other work raises the question of genetic diversity in recipient herds depending on the number of source herds and whether those source herds had also received translocations (Olson et al. 2013). Given the importance, complexity, and expense of translocations, research is needed to understand the effects of translocation on recipient herds. By using a genetic approach, we will test whether translocation actually increases genetic diversity and fitness in recipient herds. This research will help managers assess the effectiveness of translocation as a conservation strategy and determine how much of the genetic legacy from the source herds (ID, OR, and MT) remains in Wyoming.

Project objectives

Research Questions:

- 1) What is the fate of translocated individuals?
 - a. Do translocated individuals breed and pass on their genes or do their alleles die out in the recipient population?
 - b. Does the genetic composition of modern herds reflect the genetic signal of source herds?
- 2) What is the effect of translocation on the recipient populations in terms of both genetic diversity and fitness?
 - a. Does translocation increase genetic diversity?
 - b. What is the relationship between demographic trends and trends in genetic diversity?
- 3) What is the role of source population in translocation success?
 - a. Are individuals translocated from some populations but not others more likely to breed in their recipient population?
 - b. Do translocations from particular populations confer greater benefits in genetic diversity and fitness?

WSF objectives

Enhance wild sheep populations and their habitats

Promote scientific wildlife management

How proposal addresses WSF objectives and benefits conservation/management

Enhance wild sheep populations and their habitats: Translocations are used to increase population size and expand bighorn sheep range. Given the risks and expense of translocation, research is needed to ensure that this conservation tool is used to its best effect.

Promote scientific wildlife management: Our research will provide estimates of genetic diversity and fitness in Wyoming's bighorn sheep herds and evaluate the effectiveness of translocations of increasing population size and genetic diversity. This work will also allow us to estimate population size, which is critical for modeling disease prevalence and spread and determining sustainable levels of harvest. Genetic data can be used to estimate population size when populations are difficult to census. We will communicate this work with the Wyoming Department of Game & Fish and other state management agencies, as well as the WSF, so that they may better plan future translocation efforts and account for genetic diversity in management plans.

How you propose meeting your research objectives

Wyoming is in the core of Rocky Mountain bighorn sheep range and is home to some of the largest and most continuously distributed populations. Wyoming herds have received 1,672 individuals during 71 translocation events, 6 translocations from sources outside Wyoming, and 65 translocations from other herds within Wyoming. Wyoming herds have also been the source for 23 translocation events and nearly 400 individuals translocated outside the state (Figure 1) (WAFWA Wild Sheep Working Group 2015). Our lab has already begun to develop genetic resources for Wyoming's herds as part of a state-wide genetic assessment of population health. Support from the Wild Sheep Foundation allow us to sample and analyze the herds outside of Wyoming that have served as sources for translocations into Wyoming. It will also support our ongoing analysis of herds in Wyoming so that we can estimate population parameters such as genetic diversity and demographic history more precisely. By starting with the recipient herds in a single state, we can provide insights into herds throughout the West and develop a workflow that can be applied to investigate additional herds.

Genetic methods are a powerful tool for studying population health and history. Without genetic data, understanding the effect of translocations would require detailed pedigrees and records of breeding success over long periods of time. With the exception of Ram Mountain in Alberta (Coltman et al. 2003), that kind of data is rare and will be difficult or impossible to collect. With enough genetic markers, we can infer past demographic events (did a population expand following the introduction of new individuals) and determine whether the genetic signal of source herds persists in the recipient herds. Genetic markers can also be used to reconstruct wild animal pedigrees, across multiple generations in some cases (Ernest et al. 2014, Riley et al 2014).

We propose to use complementary molecular genetic approaches: microsatellites and genome-wide variation. Each marker type provides information at different evolutionary time scales. Microsatellites are DNA sequences where a motif of a few DNA bases are repeated many times. The number of repeats varies among individuals and is heritable, so these markers can be

used to distinguish among individuals and families. Because microsatellites are thought to be rapidly evolving and non-coding, they can be used to estimate population genetic diversity and infer recent demographic events. Microsatellite data have been used in bighorn sheep to identify groups and barriers to gene flow (Buchalski et al. 2016), among many other applications.

Genome-wide data is especially interesting because by sequencing a greater number of loci across the entire genome, we increase the probability of identifying genes that are involved with traits of interest, such as disease resistance, migratory behavior, and growth rate (Kardos et al. 2015, Roffler et al. 2016).

Measures of success

- *Obtain genetic material from source herds outside of Wyoming
- *Genotype all targeted individuals
- *Detect genetic differences between source and recipient herds
- *Detect genetic signal of source in recipient populations
- *Detect genetic difference between recipient herds

Outcomes:

- *Establishment of a translocation genetics data base, and specific measures to assess translocation success from a genetic perspective
- *Information to guide more effective and successful bighorn sheep translocations
- *Yearly reports and presentations to WSF and WGFD
- *Enhanced collaboration between academic and agency entities
- *Peer-reviewed scientific publications and presentations to the scientific community
- *Dissemination to the public through website and radio presentations
- *Outreach materials for the National Bighorn Sheep Museum

Timeline

Year 1: completed:

- *Obtained 400+ blood and tissue samples from animals contacted in Wyoming in 2014-16, 400+ from 1996-2009
- *Established collaborations with Wyoming Game & Fish Department, Montana State University, and broader network of people researching and managing bighorn sheep
- *Obtained access to translocation history database from Western Association of Fish and Wildlife Agencies, Wyoming Game & Fish Department, Wild Sheep Foundation
- *Acquired Sample Sharing Agreements for samples from translocation source herds in ID, MT, and OR, targeting 20-30 individuals per herd depending on availability. Samples are on their way to our lab.

Year 2 – this proposal

- *Analyze samples from out of state source herds
- *Analyze samples from locales in Wyoming receiving translocations
- *Submit progress report to Wyoming Wild Sheep Foundation, National Wild Sheep Foundation, and Wyoming Game & Fish Department, present preliminary results at meetings.
- *Submit manuscript of findings for peer-reviewed scientific publication
- *Develop outreach materials for National Bighorn Sheep Museum

WSF Bighorn Sheep Goals by 2020

1. Bighorn Sheep Management Plans
2. Applied Disease Research
3. Population Management/Ewe Harvest

Project Budget Details**Amount requested from WSF**

\$30,814 for year 2 of this translocation project

Use of WWSF funds

Funds from WSF will be used to DNA-analyze samples from the out of state translocation sources used in Wyoming and complete WY recipient herd analysis. We will target at least 20 individuals from each source and recipient herds. Sample agreements for ID, OR, and MT are in place and samples are scheduled to arrive by Dec 2017. Analysis involves extracting the DNA from the hair, blood, or tissue sample, and then using that DNA in our approaches, microsatellite, and genomics.

Contracted Services: University of Oregon Genomics & Cell Characterization Core Facility,
Illumina Sequencing

Materials: reagents and plasticware for genomic DNA lab analysis

15% of temporary postdoc salary (for Sierra) for this work

Funding supplied by other sources: \$74,113