

# Teton Sheep Genetics Project

## Fall 2008 Update



The Teton Range bighorn sheep herd is a small, isolated herd that lives year-long along the crest of the range. Reduced genetic variation is one of the risks facing this relict population due to its potential association with disease and parasite vulnerability. Because of this concern, Grand Teton National Park personnel initiated a project to assess genetic variation and parasite loads in Teton Range bighorn sheep and the adjacent Jackson herd.

### PROJECT OBJECTIVES

- To determine the genetic variability and population genetic structure of Teton and Jackson bighorn sheep herds;
- To evaluate the health status of Teton and Jackson bighorn sheep herds;
- To determine the relationship between individual heterozygosity and parasite load and stress hormone levels;
- To assess the conservation status of these populations and develop a strategy to ensure the Teton Range herd's long-term viability and persistence based on project results.



Bighorn sheep rams in the Gros Ventre drainage.  
Photo by: John Stephenson



John Stephenson collecting fecal samples on the National Elk Refuge.  
Photo by: Sarah Dewey

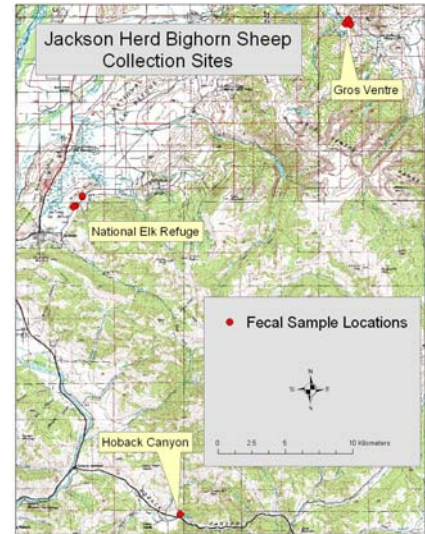
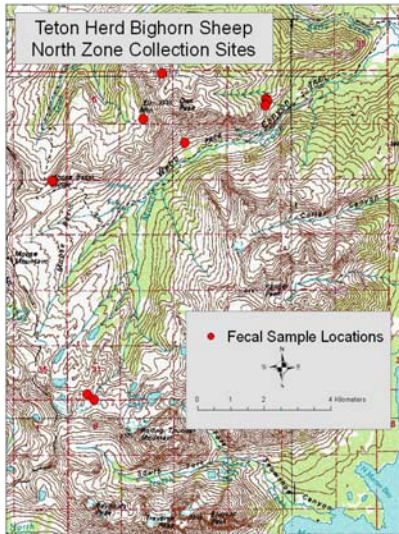
**To collect fecal samples, biologists watch sheep through binoculars and spotting scopes to classify animals and observe defecation. Samples are collected once the sheep move off.**

**Samples are then analyzed for genetic variation, lungworm and gastrointestinal parasites, and stress hormone levels.**

## SAMPLE COLLECTIONS & PRELIMINARY HERD HEALTH RESULTS

To date, a total of 111 fecal samples have been collected for genetic, parasite, and stress hormone evaluation. Fifty-three samples are from the Jackson herd and 58 samples are from the Teton herd. Five different gastrointestinal parasites (*Eimeria*, *Marshallagia*, *Moniezia*, *Thysanosoma*, and *Trichuris*) were detected in Teton Range sheep. Egg counts suggest the parasite burden is rare to light. Lungworm counts were low (Teton herd summer) to moderate (Teton herd winter, Jackson herd spring).

### Maps of Collection Sites



### ONGOING WORK

Genetic analysis is ongoing at the University of Montana and should be complete by summer 2009. The genetics work will enable us to quantify genetic diversity (heterozygosity, allelic richness) within and among populations, evaluate evidence for genetic bottlenecks, evaluate evidence of relatedness between populations, and evaluate evidence for recent genetic interchange between populations. A better understanding of the genetic status of this small population will inform long-term management strategies for the herd.

### PROJECT COOPERATORS

- Wyoming Game and Fish Department
- National Elk Refuge
- Bridger-Teton National Forest
- Caribou-Targhee National Forest
- Wyoming State Veterinary Lab
- University of Montana
- Wyoming Cooperative Fish and Wildlife Research Unit

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- Greater Yellowstone Coordinating Committee
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- 1% For the Tetons
- National Park Service BRMD
- Wyoming Chapter of Foundation for North American Wild Sheep
- University of Wyoming-NPS Research Station
- Grand Teton Association