## **INVESTIGATOR'S ANNUAL REPORT**

National Park Service

All or some of the information provided may be available to the public

Reporting Year:		Park:	
2005		Grand Teton NP	
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Permit#: GRTE-2005-SCI-0038			
Park-assigned Study Id. #: GRTE-00094			
Project Title:			
Pilot study: The feasibility of non-invasive fe	ecal sampling for genetic and		
parasite studies in the Grand Teton National Park/National Elk Refuge bison herd.			
Permit Start Date: Jul 07, 2005		Permit Expiration Date Dec 31, 2005	
Study Start Date: Jul 07, 2005		Study End Date Dec 31, 2005	
Study Status:			
Continuing			
Activity Type: Research			
Subject/Discipline: Animal Communities / Wildlife			
Objectives:			
This pilot study will allow us to determine a set of loci that have the highest amplification rate from fecal samples, and calculate genotyping error rate,			
before broadening the scope of a larger conservation genetics study of the JBH. Concurrent fecal samples for parasite studies will provide information regarding associations between genetic variation and parasite load, and establish seasonal differences in parasite communities within the JBH. It may			
also be possible to genotype parasites in future studies to identify specific populations of parasites present within bison subpopulations, which would allow us to track movement of parasites between host populations, and study transmission dynamics. It is imperative to conduct this initial pilot study in			
order to establish a set of protocols to be used for future, expanded studies.			
The historical and ecological significance of the JBH warrants careful scientific investigation with respect to their potential genetic contribution to future			
bison conservation efforts. In addition to the Yellowstone bison herd, it is the only free ranging, wild bison herd in the United States descended, in part,			
from a continuously wild herd, with historic and cultural ties to the Greater Yellowstone Ecosystem (Halbert 2003). Proposed management plans for the JBH, aimed at limiting population size to decrease the perceived risk of brucellosis transmission to domestic livestock, and habitat degradation, has been			
in the public eye for several years. The publicity generated by these contentious issues has created a public interest in scientific approaches to			

conserving this herd for the future.

The bison of GTNP /NER provide a unique opportunity for research with respect to the conservation of our national s last wild, free ranging herd. Noninvasive DNA sampling can offer genetic information relative to their significance for restoration of wild bison as a species. In addition, non-invasive genetic studies can broaden our understanding of population dynamics within wild, free ranging bison herds. These studies may also contribute to the development of critical management strategies directed at conserving genetic diversity and evolutionary potential within the JBH.

## Findings and Status:

A pilot study, funded by the Boyd Evison Foundation, is currently underway to determine a set of loci that have the highest amplification rate from fecal samples, and calculate genotyping error rate, before broadening the scope of a larger conservation genetics study of the Greater Yellowstone Area bison. Preliminary results reveal that we have successfully extracted small quantities of bison DNA from fecal samples collected during the summer. We anticipate greater quantities of DNA from the winter fecal samples, due to increased dietary roughage, resulting in a higher rate of epithelial cell shedding. We have screened over 50 microsatellite loci, both neutral and selective, and are in the process of optimizing a subset of over 30 loci to use in the larger study.

We began our initial field season this past summer, collecting fecal samples from over 47 bison in Grand Teton National Park. Samples from each individual were preserved in 95% ethanol for DNA studies. Concurrent fresh samples were collected as well, and analyzed for parasites at the Washington State University Veterinary Laboratory. We will collect another set of fecal samples from bison at their wintering areas in January for further genetic and parasite studies.

The summer season parasite studies revealed an aggregation of Dictacaulus (lungworm) species in the Grand Teton bison when compared to the the Yellowstone bison herd. However, there was no significant difference in parasite species richness between Yellowstone and Grand Teton bison populations. Comparisons between age groups revealed greater parasite loads in the youngest and oldest animals.

For this study, were one or more specimens collected and removed from the park but not destroyed during analyses? No

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Fill out the following ONLY IF the National Park Service supported this project in this reporting year by providing money to a university or college			
Full name of college or university:	Annual funding provided by NPS to university or college this reporting year:		
The University of Montana	5875		