Project Summary
Rocky Mountains Cooperative Ecosystem Studies Unit

Project Title: Conserving Genetic Diversity in Yellowstone Bison

Discipline: Natural Resources
Type of Project: Research
Funding Agency: National Park Service
Other Partners/Cooperators: University of Montana; USDA-Forest Service
Effective Dates: 9/15/2008-3/31/2010
Funding Amount: $25,000

Investigators and Agency Representative:

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Project Abstract: Evidence suggests that maintaining breeding groups of 1000 to 2000 bison in each of the central and northern herds should retain 90-95% of rare alleles in Yellowstone bison over the next 200 years. However, there is substantial uncertainty in this estimate due to population substructure (i.e., distinct breeding herds, influence of matrilineal groups) and inter-annual variation in population size due to recurrent, large-scale culls to reduce the risk of brucellosis transmission to cattle. Thus, there is uncertainty regarding potential effects of risk management operations to the genetically diverse population of bison, and how to best manage and conserve existing heterozygosity and allelic diversity.

The National Park Service will provide the University of Montana with: additional fecal samples collected from bison in the northern range and central interior breeding groups for extracting DNA and assessment of current levels of genetic diversity, and relevant information on the demography and population substructure of the Yellowstone bison herds. The University of Montana researchers will then estimate the current distribution of genetic diversity (i.e., heterozygosity, allelic diversity) and gene flow between the two primary breeding herds; devise a computer model that simulates an idealized population of bison (i.e., no overlapping generations, no substructure, equal contributions to reproduction) and evaluates the potential effects of management influences (e.g., removals) similar to those experienced since 2000 (directed by the Interagency Bison Management Plan) on genetic diversity over 100-200 years; come up with a mathematical simulation model that incorporates the best available estimates of demography, genetic diversity, age structure, population substructure, and polygamy for Yellowstone bison breeding groups and simulates management influences similar to those experienced since 2000, with different recovery rates, to evaluate potential effects to genetic diversity over 100-200 years; compare results from the idealized and realistic population models to test the effects of age structure, population substructure, polygamy, and management influences on rates of loss of genetic diversity (heterozygosity and allelic richness); and perform an objective assessment based on modeling and other information of the abundance per primary breeding herd needed to preserve 90 and 95% of current level of genetic diversity values. This assessment should assume continued fluctuations in breeding herd and population abundance.

Outcomes with Completion Dates:

1. Report by November 30, 2008 on results and inferences from haplotype and microsatellite analyses of genetic samples collected from bison in the

central and northern breeding herds of Yellowstone National Park during 2005-2008, including estimates of the current distribution of genetic diversity and gene flow between the two primary breeding herds.

2. Final Draft Report by September 30, 2009 that includes (1) a mathematical computer simulation model that simulates an idealized population of bison (i.e., no overlapping generations, no substructure, equal probability of reproduction) and evaluates the potential effects of management influences (e.g., removals) similar to those experienced since 2000 (directed by the Interagency Bison Management Plan) on genetic diversity over 100-200 years, (2) mathematical simulation model that incorporates the best available estimates of demography, genetic diversity, age structure, population substructure, and polygamy for Yellowstone bison breeding groups and simulates management influences similar to those experienced since 2000, with different recovery rates, to evaluate potential effects to genetic diversity over 100-200 years, (3) a comparison of results from the idealized and realistic population models to test the effects of age structure, population substructure, and management influences on rates of loss of genetic diversity, (4) assessments of appropriate herd and overall population abundance necessary to preserve 90 and 95 percent of current levels of genetic diversity (e.g., estimation of effective population size (Ne) and the Ne/N-census ratio), (5) recommendations regarding genetic monitoring (e.g., samples, timing, locations, loci) to ensure Yellowstone would have the statistical power to detect a genetically significant loss of diversity over time, and (6) draft copies of the modeling code, assumptions used in the model, initial inputs and specific analyses used to assess statistical power to detect a change during long-term monitoring, laboratory and model output, genotyping, databases, and analyses created during this project by September 30, 2009, (7) final closeout and reports finalized by March 31, 2010.

Keywords: Yellowstone NP, bison, genetic diversity, computer models, genetic monitoring, University of Montana