RM-CESU -Project Report, FY 07

Project Title:
Predicting Disease Spread in Greater Yellowstone Elk Using DNA

Park: Yellowstone NP

Funding Source: Rocky Mountains CESU Research Funding

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Project Description:
The Greater Yellowstone Area supports world-renowned herds of elk that provide significant visitor enjoyment and benefits to local economies through guiding and sport hunting. Elk have strong, ramifying effects on other species and processes in the ecosystem, including predators, scavengers, vegetative production, soil fertility, and plant diversity. Unfortunately, these magnificent elk herds also transmit diseases such as brucellosis, sarcoptic mange (scabies), septicemic pasteurellosis and, perhaps, Yersiniosis to other wildlife and domestic livestock. In addition, they may soon be infected with chronic wasting disease, which was detected approximately 130 miles from the park in the Bighorn Basin area of Wyoming during 2003. There is no vaccine or known treatment for this contagious, fatal disease which is transmitted by direct animal-to-animal contact or, indirectly, through the environment.

A critical need for developing feasible strategies to minimize the adverse conservation, economic, and social effects of these diseases is information on disease transmission pathways through the Greater Yellowstone Area. This project will address this need by identifying

elk DNA markers in non-invasively collected fecal and tissue samples that can be used to assign individuals to their population of origin and estimate sex-specific rates of gene flow and movement among elk populations. This information can then be used by natural resource managers throughout the Greater Yellowstone Area to track the origin and spread of diseases, and predict the risks and geographic routes of transmission.

Objectives and Methods:

The specific objectives and methods are to: 1) identify 4 new microsatellites that are highly polymorphic in elk; 2) identify maternally-inherited mitochondrial DNA markers (mtDNA) useful for assessing female elk movements and population connectivity; 3) optimize the analysis of microsatellite and mtDNA markers from fecal samples.

Project Results:

We have obtained elk tissue, blood or fecal samples from 6 populations across the GYA. We have isolated DNA from over 300 elk.

We have identified 5 new microsatellites that are highly polymorphic according to genotyping a test panel of 8 elk from across the GYA. It is exciting that 3 of the 5 microsatellites are in or near disease-related genes; these loci might help us test for effects of disease on elk populations and to identify markers informative for elk movement (e.g., assigning elk to a population of birth/origin). We will genotype approximately 240 elk with 4 or 5 of the new loci in the next few months. This will include some elk fecal samples.

We have identified a highly polymorphic mtDNA fragment that identifies 9 haplotypes (alleles) among 15 GYA elk. We have extracted DNA from over 300 elk samples and will sequence for mtDNA them in the next month. This will help us test for population structure and female-biased dispersal rates.

Expected Final Report:

Final data and report expected in May, 2008. This will include names of loci and estimates of elk gene flow and movement across the GYA.