# Genetic Diversity & Paternity Analysis of Endangered Canadian Sage-Grouse

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Sage-Grouse (*Centrocercus urophasianus*) are classified as endangered in Canada and are rapidly declining throughout their range in the United States. The remaining leks (communal breeding and display grounds) in southeastern Alberta and southwestern Saskatchewan have experienced a population reduction of 66%-92% over the past 30 years. There has not been any research on the genetic makeup of the Canadian population and only limited research on the American populations. I am hoping to conduct the first and most comprehensive genetic assessment of the declining Canadian Sage-Grouse population. This will be accomplished through the sequencing of multiple microsatellite loci (tandemly repeated segments of DNA) and extensive population and paternity analyses. Genetic data will be used to determine the extent of inbreeding and relatedness between and within the different leks in Alberta and Saskatchewan, the genetic relatedness of Canadian and American populations, and the genetic structure and mating hierarchy present within the Canadian leks. It will also provide an estimate of the effective male population size, reveal potential inbreeding avoidance mechanisms, and will determine if there are possible genetic causes for the low chick survival and recruitment seen in the past 30 years. It will also allow us to assess if supplementing the population with birds from the U.S. is a viable and effective option for species recovery and management. Verifying possible causes for the decline may ultimately result in the stabilization of Sage-Grouse populations in Canada through the development and implementation of strategic management plans.

Over the next year, I will determine the paternity of over 100 complete or incomplete broods of Sage-Grouse chicks from 5 different leks in southeastern Alberta. The samples that I will extract DNA from were taken during a related ecological study and include adult blood and plucked or molted feathers, unhatched, hatched, and predated eggs, and feather samples from chicks of captured broods. DNA will be amplified via polymerase chain reaction (PCR) to create large amounts of DNA that can be used for microsatellite sequencing. This consists of running each sample on a polyacrylamide sequencing gel with several fluorescently labeled microsatellites. The data will be used to assess if any of the broods were fathered by multiple males and if one male fathered the majority of the offspring at a specific lek each year using population genetics software programs such as CERVUS (to assign paternity to each offspring). I will also examine if chicks fathered by a particular male were more successful at reaching sexual maturity than those fathered by other males. Once I establish paternity for all of the successful and unsuccessful nests, I will assess whether more successful males have greater heterozygosity at the loci tested and estimate the male effective population size which can be used for population modeling. I will also examine the genetic diversity of the Canadian population (n = 1000). I will use polymorphic microsatellites to evaluate the extent of inbreeding and relatedness between and within the different leks present in Alberta and Saskatchewan. This will be accomplished using programs such as GENEPOP (to assess the genetic diversity of the population) and analysis methods such as probability of identity, expected heterozygosity, and departure from Hardy-Weinberg Equilibrium. Since there are multiple breeding locations in Alberta and Saskatchewan, I am hoping to look at whether the genetic makeup of each lek is distinct. This will allow me to determine if there is migration of genes between the different Alberta leks and between provinces. I would also like to look at geographic distance and habitat fragmentation as causes of genetic differentiation of the populations.