

MEG AND BERT RAYNES WILDLIFE FUND
Current Status Report
January 15, 2018

Name of Applicant: Beth Mendelsohn

Mailing address: 1174 Snowy Range Road, Laramie, WY 82070
bmendels@uwyo.edu

Website address: www.wildlifegenetichealth.org

Contact information for the person responsible for directing the funding:

Holly Ernest, DVM, PhD

University of Wyoming, Department of Veterinary Science

hernest@uwyo.edu (307) 766-6605

Grant Spending:

Total received	\$4,732
Genomic sequencing of 85 samples	\$2,099*
Genomic sequencing of 115 samples (partially covered cost)	\$1,239**
One-month graduate student summer stipend for data analysis	\$1,394***
Total spent	\$4,732

*Cost is higher than budgeted in the grant application (\$1,695) because we decided to sequence 150 base pair long fragments instead of 100. This substantially increases the amount of data per fragment, and leads to the discovery of more genetic markers.

**The cost for sequencing at the same facility increased to \$2,147. Another funding source covered the remaining balance.

***Cost of summer stipend was \$53 more than originally estimated.

Objectives and Achievements:

The goal of this project is to assess the genetic health of the population of Great Gray Owls in northwest Wyoming. This project is an ongoing MS thesis. Through the funding from the Meg and Bert Raynes Wildlife Fund, significant progress was made in 2017.

I am using next generation sequencing technology to find and begin to analyze genetic differences from over 150 owls. We are generating genetic sequence data from owls in California, Oregon, Idaho, Montana, Canada and Wyoming

Achievement 1: Completed genomic sequencing of DNA from 100 individual owls from Wyoming. The first sequencing run was less successful than planned, but after modifying the methods, the second sequencing run produced more success. Individuals from Alberta, California, Idaho, Oregon, and Montana were also sequenced.

Achievement 2: Found 9,494 genetic markers in the form of single nucleotide polymorphisms (SNPs). These SNPs are used to analyze differences between individuals at many locations across the genome.

Achievement 3: Tested for population structure within the Wyoming population and between other populations in western North America. Found significant evidence for population structure across the range, indicated by clustering of geographically separate groups into distinct genetic groups. See Figure 1.

Achievement 4: Generated genotypes for 90 owls from the Jackson Hole study area. This data is currently being analyzed to test for population structure, inbreeding, genetic diversity, and other measures within the Wyoming population. The data will be used to estimate relatedness between individuals and help determine natal and breeding dispersal biology. Data generated from owls in other nearby populations is being used to determine connectivity or isolation of the populations, and will serve as a comparison to the Wyoming population.

Achievement 5: This research was presented at the annual Wyoming Chapter of the Wildlife Society conference in Jackson in December 2017. I also shared the importance of genetics studies for wildlife with young attendees of the Teton Raptor Center's annual Raptorfest in June 2017.

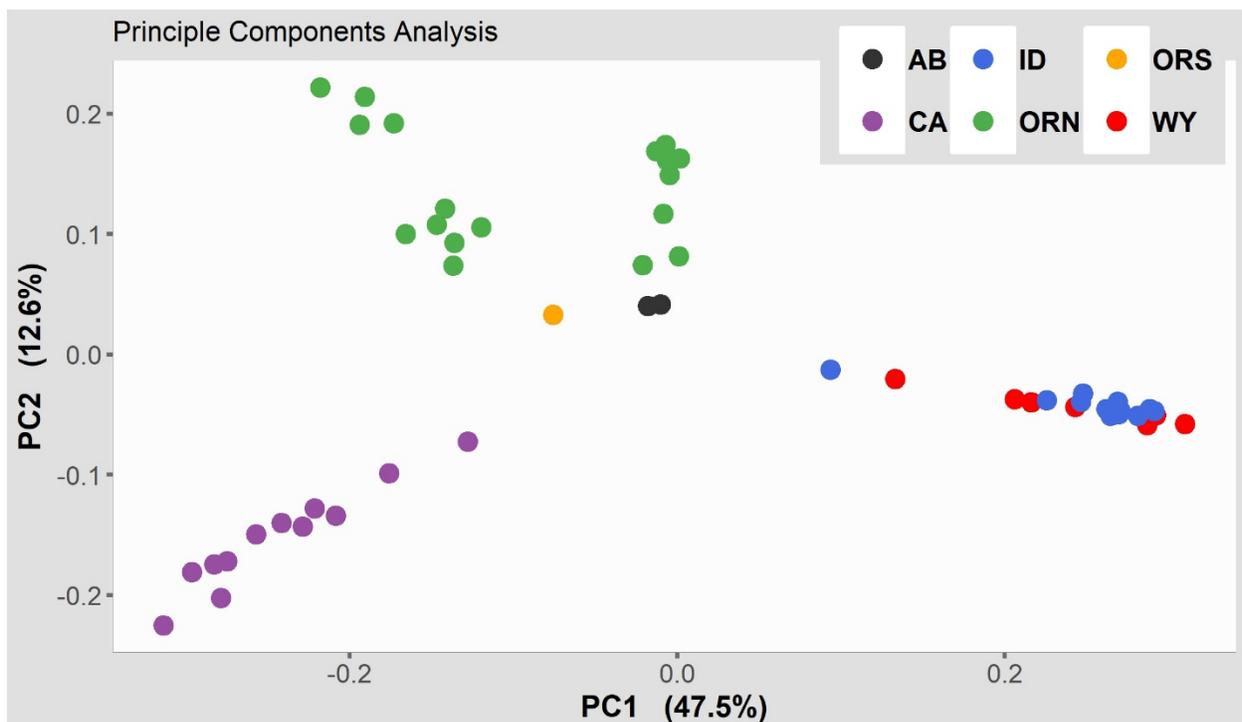


Figure 1. Principle Components Analysis of Great Gray Owls (N=52) using 9,494 SNPs. Samples from Alberta = 2, California = 12, Wyoming = 7, Idaho = 12, Oregon = 19. All individuals have data at >50% of loci. PC1 axis explains 47.5% of the genetic differences, PC2 axis explains 12.6% more of the difference. Wyoming and Idaho GGOWs cluster together, California GGOWs form their own cluster, and Oregon owls cluster in between the two groups, with Alberta in the center.

Conclusions:

The scope of this project was originally to explore the range-edge dynamics of the Great Gray Owl through genetics. Although the original idea remains, the goals have been modified to a narrower scope that will be achievable given the samples available and data generated. I will compare populations in different parts of the range that represent edge or isolated populations. I will also look at gene flow and connectivity to look for range-edge effects. This research will provide a valuable basis to assess the genetic population health of the Great Gray Owls in Wyoming and other areas in the west. The results will contribute to a better understanding of how habitat changes and environmental changes could affect the species.

Further analyses will be completed using the data generated thanks to the Meg and Bert Raynes Wildlife grant. The anticipated completion of the data analysis is August 2018. Publication of results and completion of the master's thesis are planned the fall of 2018. As the results presented above are preliminary, final results and a final report will be provided to the MBRWF when complete.