

MEG AND BERT RAYNES WILDLIFE FUND
Current Status Report
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Using Genomics to Understand the Population Dynamics and Further Conservation of Great Gray Owls in Jackson Hole

Grant Spending

Total Received: \$3,240
Total Spent: \$1,800
Remaining: \$1,440

Project Summary and Update

We previously genotyped 92 individual great gray owls sampled from Jackson Hole between 2013-2016 using thousands of genetic markers (single nucleotide polymorphisms) for between-population analysis of great gray owls in western North America. For this project, we are using these data to gain a within-population assessment of population health, breeding strategy, and dispersal. We are using the single nucleotide polymorphisms to compare the genotypes of individuals to determine the kinship coefficient for each pair of individuals and the genetic relationship between them. We are using these data to assess our project objectives.

We have assessed all previously genotyped samples for our three project objectives. To complete this project, we need to finalize the analyses and write up the results. However, we have identified a need for more samples to clarify several of our objectives and have an additional ca. 40 samples from 2017-19. We are currently in discussions with the lab at University of Wyoming to determine if/how we can get those additional samples genotyped to bolster our existing dataset. Given our results using the 2013-16 dataset, we do not feel like we have sufficient data to publish a full manuscript. Adding our additional DNA samples to the analysis would greatly increase our power to publish these results. The samples must be run in the same lab using the same techniques as the previous samples in order to do the combined analysis. We are currently working on a plan to accomplish this task.

We are hopeful to complete the project in 2020 with the addition of the 2017-19 samples. To that end, we sequestered some of the granted funds to continue analysis and complete reporting in 2020.

2019 Project Updates

OBJECTIVE 1: Evolutionary potential. The ability of the population to adapt to perturbations, expand, etc.

Results:

- *Effective Population Size:* Effective population size is an indicator of the number of successfully breeding individuals, not the total population size. Generally, it is the number of individuals that contribute genetic material to subsequent generations. So, only owls that successfully breed are counted in the effective population size estimate. There are other owls that have not yet bred or not yet had a successful nest that produced young that survived to reproduce themselves.

We were able to estimate the effective population size (N_e) of our population to approximately 71 individuals. This size is significantly larger than other smaller, more isolated populations of Great Gray Owls in California and Oregon. This generally indicates that this population has a healthy number of breeders given the long lifespans of this species and the opportunity for high lifetime reproductive success of breeding owls that have already secured territories.

- *Inbreeding:* We did not find any evidence of inbreeding. We calculated the inbreeding coefficient, F_{IS} to be -0.11. This coefficient is usually between 0 – 1, and being below zero indicates the opposite of inbreeding resulting in an excess of heterozygotes in the population. Theoretically, this could mean that there is negative assortative mating occurring within this species (individuals selecting mates that are not related). We plan to explore this further.
- *Genetic diversity:* We used nucleotide diversity to assess the genetic variation within this population. We found that the diversity of this population is higher than other populations of Great Gray Owls included in our west-wide study, but still low compared to other species of birds. This indicates that this population may have low genetic diversity. Low genetic diversity can lead to low evolutionary potential, or the ability of the population to respond to changes in environment.

Discussion:

While relating effective population size to the minimum viable population size is near impossible, we can make some good inferences of the population health in Jackson Hole using data from other areas and demographic studies in conjunction with our results. For example, the N_e in Jackson Hole is larger than other, more isolated populations. While the population of great gray owls in California is threatened, it appears that the population there is low but stable. Having a much larger N_e in Wyoming (coupled with little-to-no inbreeding) points to a more robust population here. However, the overall low genetic diversity may be problematic if large perturbations to the population exist. With low diversity, the ability to genetically adapt to changes may be limited.

Future Goals:

We would like to compare effective population size to estimated total population size based on our demographic studies (e.g., nest density in modeled nesting habitat with annual production/mortality). We also plan to verify the inbreeding estimate using other measures to assess inbreeding.

OBJECTIVE 2: Breeding strategy. Territoriality, multiple paternity, mate selection.

Results:

- *Multiple paternity:* We did find possible evidence of multiple paternity in at least one nest, meaning that the female at that nest likely copulated with more than one male. Unfortunately, we do not have all adults sampled and cannot conclusively determine the paternity and maternity of nestlings across multiple years.
- *Disassortative mating:* We found evidence of owls breeding with individuals that are less related to them than a random individual out of the population. With our current sample we only have 3 nesting pairs where both adults were genotyped – two of these pairs are less related than would be expected by random, and one pair is slightly related. We have additional samples we are hoping to genotype to include in this analysis.
- *Nest-site fidelity:* We found some evidence for nest site fidelity over multiple years where both adults at the nest were the same, but we also found some evidence of one adult switching nests. More data would be very helpful to explore this further.

Goals:

Increase the number of nests with adults and fledglings sampled to look for more evidence of multiple paternity. We have additional samples from 2017 that we are hoping to genotype to further this analysis and increase statistical power. More nesting pairs and offspring relationships would help us explore disassortative mating further and adding more samples across more years would help draw conclusions about nest-site fidelity.

OBJECTIVE 3: Dispersal

Results:

We did not find a strong signal of isolation-by-distance, meaning that individuals that are closer together geographically are not more likely to be more genetically related. This indicates that dispersal distances are high, and within our study area dispersal is not limited. We found some close relatives to one of the wandering juveniles, indicating that it could be from a nest within the territory, but none of the other nine juveniles could be traced back to a known, sampled territory, indicating they were likely from unknown nests or territories that are outside the study area.

Goals:

Add more samples to increase the probability of detecting dispersal of juveniles within our study area if it is occurring.