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Conservation of Sharp-Tailed Grouse (*Tympanuchus phasianellus columbianus*) Through Fecal DNA Extraction

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Abstract

Columbian Sharp-tailed Grouse (*Tympanuchus phasianellus columbianus*) are the rarest of the six extant Sharp-tailed Grouse subspecies. This subspecies experienced a 90% range contraction over the last century and have been extirpated from several states (Figure 1). In Washington alone, populations that once numbered hundreds of thousands of individuals now consist of fewer than 1,000 birds. Conservation efforts—including conservation translocations and habitat management—are underway to help bolster this imperiled subspecies across their range. However, little is known about the ecology of this charismatic species and the factors that may be contributing towards higher rates of decline.

The collection of fecal pellets presents an opportunity to better understand Columbian Sharp-tailed Grouse across their range, by providing information on their diet and host ID. As a HERC Fellow in the Conservation Genetics Lab at Boise State University, I have been exploring the potential to use non-invasively collected fecal samples to understand how we can best capture different DNA types, which can be used to better inform the conservation and management of this charismatic grouse.

Conservation of Sharp-Tailed Grouse (*Tympanuchus phasianellus columbianus*) Through Fecal DNA Extraction

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Understanding one of North America's most Charismatic, but Underrecognized Grouse Species

INTRODUCTION

Columbian Sharp-tailed Grouse (*Tympanuchus phasianellus columbianus*) are the rarest of the six extant Sharp-tailed Grouse subspecies. This subspecies experienced a 90% range contraction over the last century and have been extirpated from several states (Figure 1). In Washington alone, populations that once numbered hundreds of thousands of individuals now consist of fewer than 1,000 birds. Conservation efforts—including conservation translocations and habitat management—are underway to help bolster this imperilled subspecies across their range. However, little is known about the ecology of this charismatic species and the factors that may be contributing towards higher rates of decline.

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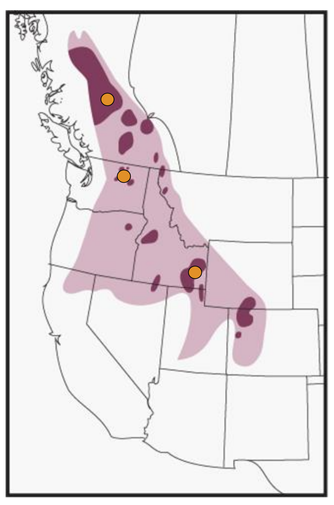


Fig 1. Range of Columbian Sharp-tailed Grouse (left)**,** with previous distribution in light purple and current distribution in dark purple.Collection sites for this study denoted with orange circles. Image of Columbian Sharp-tailed Grouse and their fecals seen to the right.

PROJECT GOALS

- Subsample fecal pellets from across the range to assess diet and host DNA.
- Compare DNA extraction protocols to see whether host DNA can be extracted from grouse fecal pellets.
- Develop customized database of plants for downstream diet analyses
- Expand my professional skill sets and networks to prepare for a career in wildlife conservation.

Downstream Applications:

- What are grouse eating across their range, and is this different in various management scenarios (e.g., translocation sites, conservation reserve program)?
- What are the demographics of these populations (e.g., sex ratio, genetic diversity, gene flow)?

METHODS

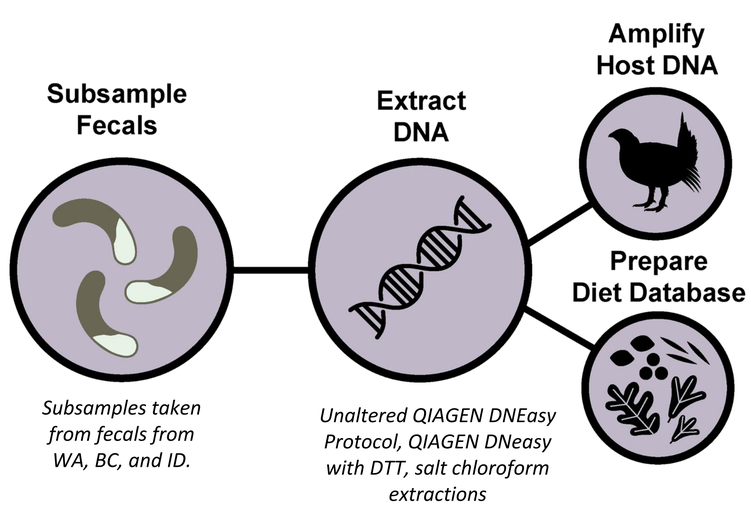


Fig 2. Schematic detailing the scientific methodology of this HERC Fellowship. Briefly, fecal pellets were subsampled in sterile environments. DNA was extracted using three different protocols. Host DNA was amplified using sexing primers for grouse. Diet database was prepared using GenBank, searching for the trnL p6 locus.

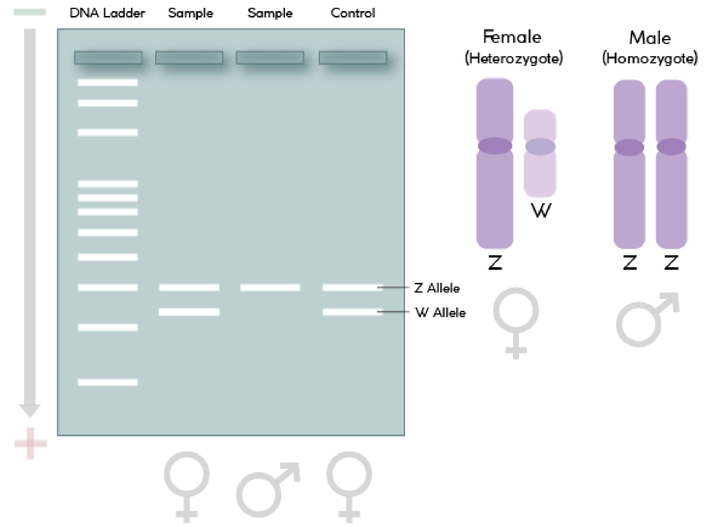
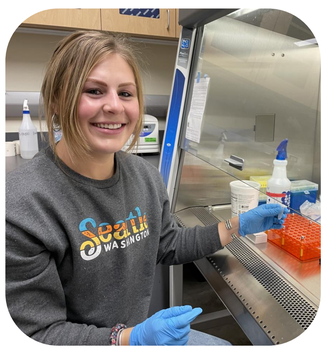
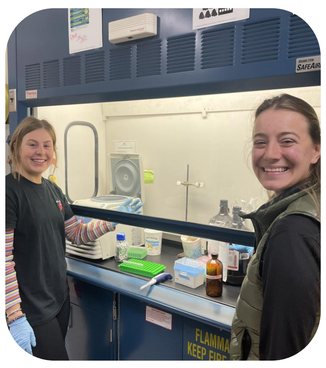


Fig3. Schematic for sexing avian DNA. Briefly, extracted DNA is amplified for markers (e.g., CHD) that are specific to the avian sex chromosomes. Because females have two different sex chromosomes (i.e., Z and W), they produce two different sized DNA fragments through the PCR process. In contrast, males have two copies of the same sex chromosome (i.e., Z) and produce a fragment of the same length.

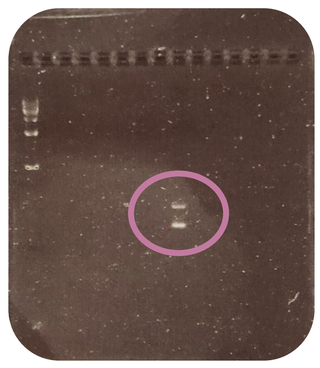
RESULTS & PRODUCTS



Subsampled ≈164 fecal samples for downstream diet and host DNA analyses.



Extracted DNA from fecal samples using column and salt-chloroform protocols.



Conducted PCR and gel electrophoresis for avian sexing primers. There was no DNA amplification from fecals DNA extractions.

Created plant trnL database for Washington and Eastern Idaho, including 110 plants.

NEXT STEPS

- Modify the PCR protocol for more cycles and new taq polymerase.
- Work with conservation practitioners to collect more samples in eastern Idaho, Washington, and British Columbia.
- Sequence trnL (diet) from fecal samples in summer 2023.
- Educate others regarding the noninvasive approach fecal sampling offers to scientific pursuits.
- Start MSc Research at BSU in Fall 2023!

REFERENCES & ACKNOWLEDGEMENTS

Conservation Genetics Lab
at Boise State University