

Dr. Joseph Cook,

My name is Jessica Scales and I am completing my first year as a PhD student in Dr. Jeff Good's lab at the University of Montana. For my dissertation research, I am continuing the work of Dr. Mafalda Ferreria in the white-tailed jackrabbit (*Lepus townsendii*) system (see attached pdf) to look at genome-wide adaptive variation, as well as expanding into black-tailed jackrabbits (*Lepus californicus*) to explore their overall population genetic structure and determine whether there is contemporary hybridization in overlapping populations of both species.

Anthropogenic pressures such as climate change, habitat fragmentation, predator shifts, and direct mortality from hunting and poisoning have resulted in local and regional extirpation alongside range contraction in white-tailed jackrabbits¹. Climate change stressors are of particular interest as the species exhibits unique seasonal camouflage patterns that have evolved in response to variation in seasonal snow. Previous research has dissected the genetic basis of seasonal coat color and used these inferences to predict the potential for future adaptive responses to widespread loss of seasonal snow duration². However, the extent to which predicted patterns of camouflage mismatch parallel overall adaptive potential and vulnerability is unclear. In addition, niche overlap and competition in combination with clear evidence of historic introgression³ make consideration of black-tailed jackrabbits a key part of the conservation plan for white-tailed jackrabbits in the central and southern plains.

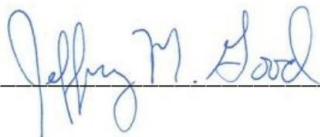
To do this, we would like to start by sequencing a large sample of genomes from available museum samples across the respective ranges of both species to investigate adaptive potential to climate change by examining how allele frequencies have changed locally across space and time. Specifically, we are targeting geographic regions where the species ranges overlap and areas that were under-represented in the published dataset to prevent redundancy. We then plan to augment museum samples with additional field collections (opportunistic and targeted) represented by vouchered specimens whenever possible, to the extent that local permitting allows.

I am reaching out for two reasons. First, given your broad interest in mammalian phylogeography, I wanted to check and see if anyone in your research group is pursuing overlapping questions in either of these systems. If so, we would welcome the opportunity for synergy and collaboration between our projects. Second, as the MSB has among the best representation of these species of any collection, we are very interested in collecting tissue and, as relevant, phenotypic data from MSB samples (e.g. winter specimen images and/or quantitative spectrometer coat color measurements). We will be using highly sensitive whole genome sequencing protocols that do not require very much material for DNA extractions and are prioritizing preserved tissue whenever possible. However, for skin samples, this will require some destructive sampling of skin tissue from the ventral incision or lip. As I have a long list of desired samples (77 frozen tissue and 38 skins) that I would like to request access for (see attached specimen list), would the most efficient approach be to coordinate a trip to the MSB for me to directly collect samples, or to assist with your staff in sample collection? Ideally, this would occur sometime this summer but we're flexible and appreciate that this is a large request during a likely busy time of year and we want to be respectful of you and your staff's time.

Thank you for your time and consideration,



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References

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