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**Historic and contemporary effective population sizes for six populations of Canada lynx**

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Project Description

The US Fish & Wildlife Service recently announced the completion of a scientific review of Canada lynx *(Lynx canadensis)* populations in the contiguous United States, concluding that the species no longer warrants protection under the Endangered Species Act and should be considered for delisting due to recovery (FWS 2017). However, the review also acknowledges the need for reliable estimates of historic and contemporary population size for each of the six populations. Demographic history, including bottlenecks, migration patterns, range expansions and changes in population size is of great interest to conservation biologists (Miller et al. 2012). Past events may influence the genetic health, diversity, and connectivity of contemporary populations and thus their likelihood of adapting to change and persisting on the landscape.

The Canada lynx is a wide-ranging felid that has evolved morphological, behavioral, and physiological specializations unique to its northern boreal forest habitat and heavy reliance on its primary prey, the snowshoe hare *(Lepus americanus)*. Due to their elusive nature, wild cats are especially difficult to monitor and study at meaningful scales, and thus demographic data are often unavailable to guide appropriate conservation action or test hypotheses regarding population viability (Gompper et al. 2006). In collaboration with an interdisciplinary team of experts from field biology, genomics, and bioinformatics we have completed the first assembled, annotated reference genome for Canada lynx (Koepfli et al. 2015). In this project, we aim to use our Canada lynx reference genome and additional population-level genome sequence data to address critical knowledge gaps in lynx demography. Ultimately our goal is to translate our findings into recommendations for state and federal partners designing and implementing management strategies for lynx conservation.

Whole genome resequencing (WGR) is a powerful tool for addressing fundamental questions about wild populations that have not been resolved using traditional genetic methods. Low-coverage whole genome resequencing is a population-based approach that aims to produce data (e.g. allele frequencies) from multiple genomes and requires the availability of a reference genome. We aim to perform low-coverage whole genome resequencing of Canada lynx from six populations in the contiguous US (Northern Maine, Northeastern Minnesota, Northwestern Montana/Northeastern Idaho, North Central Washington, Greater Yellowstone Area, Western Colorado). The generated sequence data will be aligned to our Canada lynx reference genome, mined for genome-wide variation, and used to infer population structure, reconstruct demographic history, and estimate current population sizes (Reed et al. 2005).

Samples and Methods

We have access to a wide collection of tissue samples from the Smithsonian Institute Frozen Collection as well as State and Federal agency partners, which frequently biobank samples from vehicle mortalities and Canada lynx incidentally caught during the fur-trapping season. Two adult lynx from each of the six populations will be selected for whole genome resequencing. An average genome coverage of 18X per individual is required for proper inference of demographic history using common methods. High molecular weight DNA will be extracted from the samples, prepared in libraries and sequenced on a next generation platform at the University of Massachusetts Amherst under the supervision of technical advisers Dr. Warren Johnson (Smithsonian Institute) and Dr. Ravi Ranjan (UMass Genomics Resource Lab). The amount of tissue and DNA required for library preparation is relatively small. Therefore, the remaining tissue and extracted DNA will be stored as part of the NHC Natural History Collection, available for future work on genetics or other research endeavors.

Budget

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| **Item** | **Description** | **Cost** |
| Qiagen HMW DNA kit | Extract DNA from tissue | $316 |
| Lab consumables (price based on previous experience) | Tips, tubes, kimwipes, ethanol, agarose, Qubit reagents | $150 |
| Shipping and dry ice | Shipping tissue samples | $50 |
| Illumina sequencing low-coverage whole genome resequencing (academic rate) | Cost includes use of DNA probes, IDT xGen library preparation, and sequencing | $290/sample x 12 = $3,480 |
|  | **Total** | **$3,996** |

References

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