PhD Position – Climate-mediated genomic variation in Canada lynx and snowshoe hares (Trent University)

The Integrative Wildlife Conservation Lab at Trent University (Ontario, Canada) is seeking a PhD student to investigate climate-mediated genomic variation in Canada lynx and snowshoe hares, two iconic species of the North American boreal forest. Building on long-term ecological research on both species and an established framework for whole-genome or genome-wide sequencing and analysis, this project will examine whether genomic structure and signatures of selection exhibit predictable spatial and temporal patterns associated with environmental variation across their ranges. Both lynx and hares undergo pronounced population cycles, and variation in selection and genetic structure may arise through cyclic dynamics and related environmental stressors affecting productivity and survival. This project will evaluate how genomic variation reflects local environmental conditions and population phase, and how these patterns can be incorporated into a landscape genetics framework to assess future connectivity, fragmentation, and climate-associated adaptation. The student will have flexibility to develop independent research questions within the overarching objectives of the project.

The project will address questions such as:

- How does genomic structure vary across the sympatric distributions of Canada lynx and snowshoe hares?
- Do patterns of genetic diversity and gene selection covary between species, and to what extent does this variation reflect local environmental conditions?
- Do patterns of genetic diversity and gene selection vary across population cycles and is this variation associated with changes in natural stressors?
- Do signatures of selection correspond to environmental gradients associated with climate change, and how might future climate scenarios influence genomic variation and local adaptation?
- How might climate-mediated changes in habitat connectivity affect gene flow among environmentally differentiated populations?

The student will develop and apply contemporary genomic, bioinformatic, and landscape ecology approaches, including whole-genome and/or transcriptome sequencing and/or genotyping-by-sequencing (3RAD). From these data the student will conduct population genomic analyses (phylogeography, population-assignent, Fst, Ne, inbreeding coefficients), , and landscape genetics (isoloation by distance, resistance and environement, signatures of selection). These will be integrated with Species Distribution Models (SDMs), climate projections, and spatial environmental data to generate predictive maps and quantify related patterns and uncertainty. The project is supported by existing whole-genome resources (including partial genome annotation) for both species (forthcoming) and extensive archived tissue samples collected over more than a decade.

Qualifications

- MSc in Ecology, Genetics, Evolutionary Biology, or a related field

- At least one senior-authored peer-reviewed publication
- Strong quantitative and computational skills, including experience with R and bioinformatic workflows
- Interest in climate adaptation, landscape genetics, and integrative ecological genomics
- Ability to link ecological and evolutionary questions with genomic data

Start date: Flexible (2026). Fully funded for 4+ years.

To apply, please send a CV, unofficial transcripts, a brief statement of research interests, and contact information for two references to dennismurray@trentu.ca. Review of applications will begin immediately and continue until the position is filled. See www.dennismurray.ca for additional details.

Dennis Murray

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