PARIS
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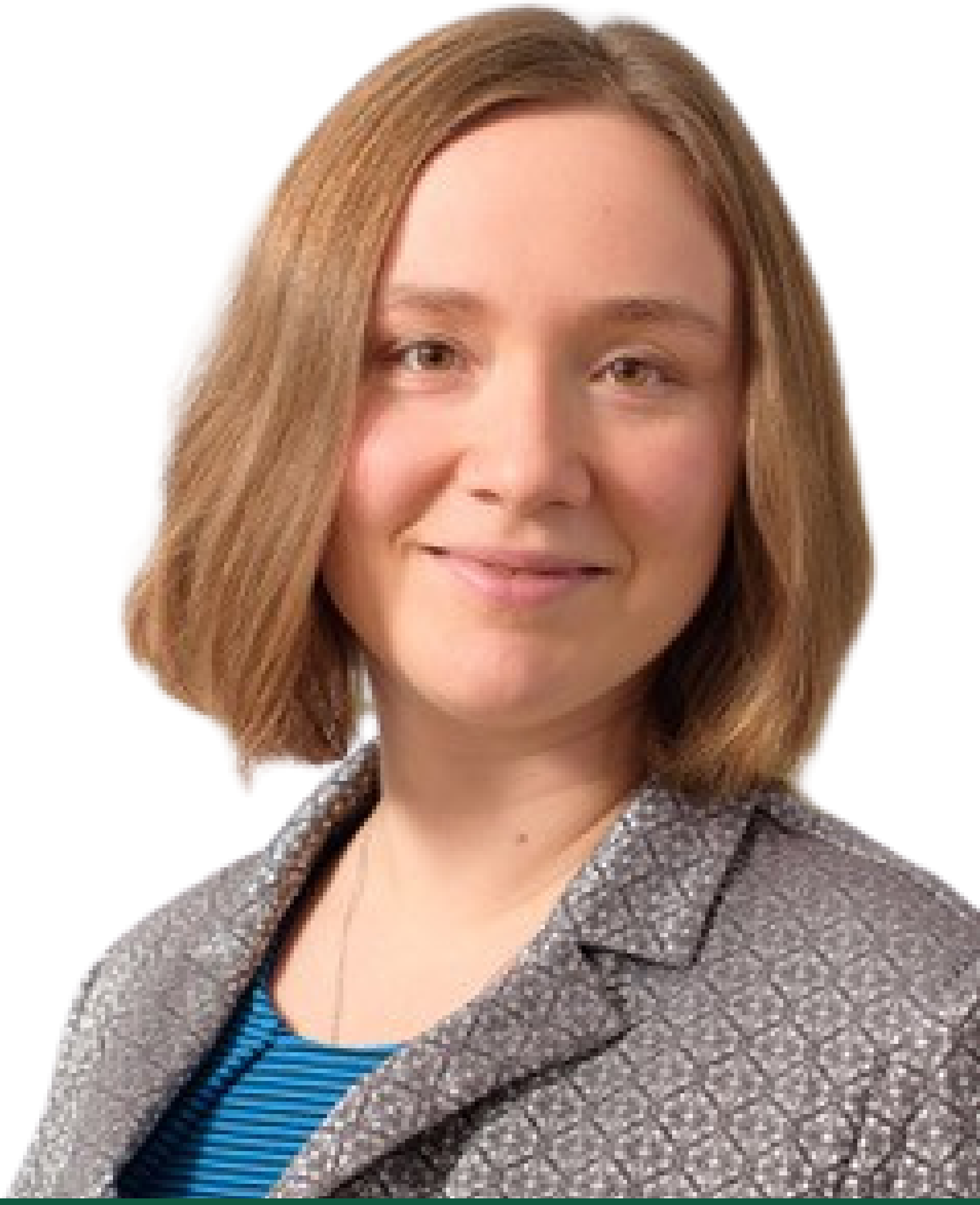
Lecture Series Environment & Biodiversity

Whole-genome insights into migration, reproductive isolation and genetic erosion



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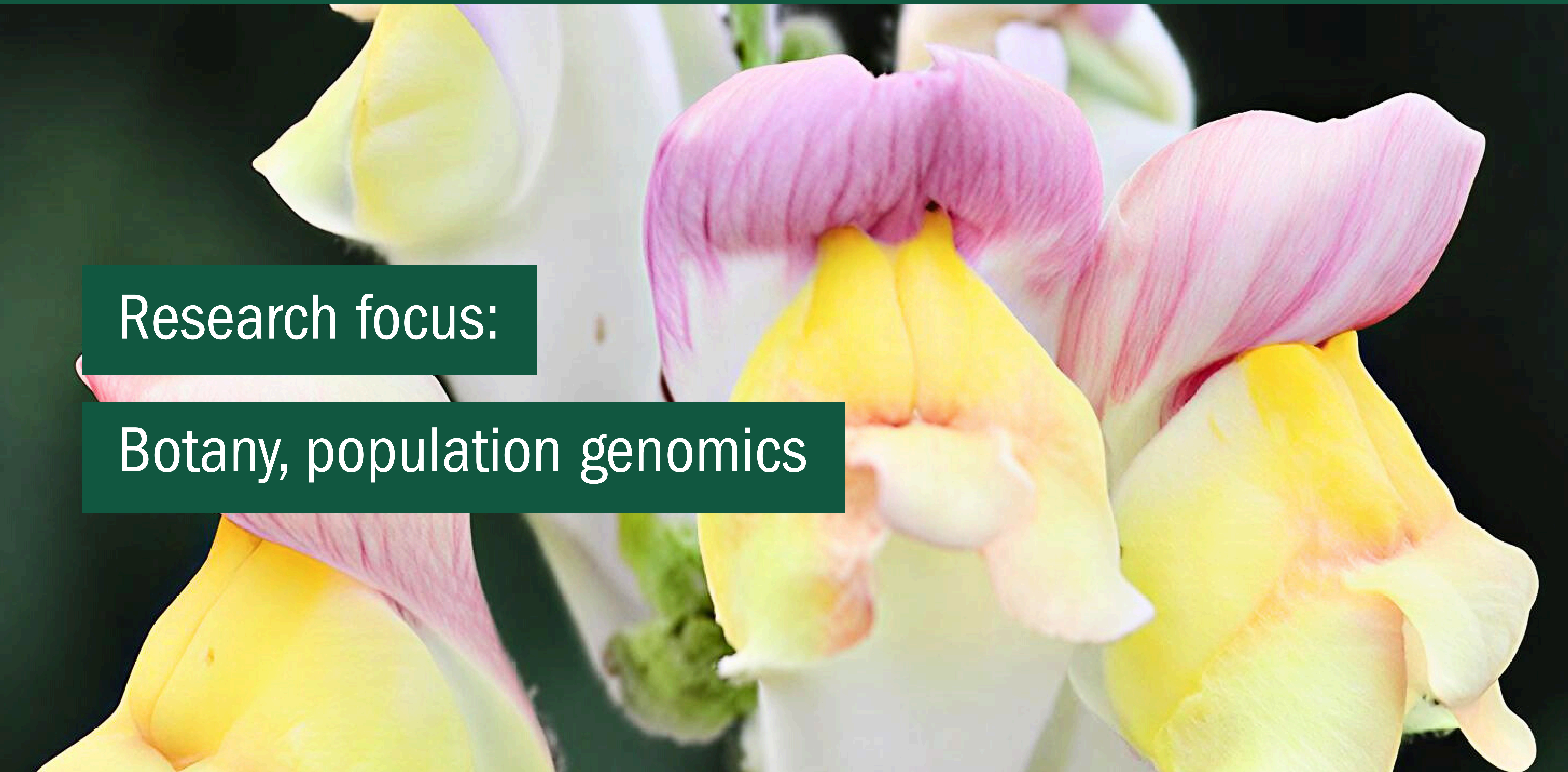
Host: Dominique Groffman, MSc.

Friday, January 16, 2026, 2:00 PM
NLW-Faculty, Room 421, 2nd floor



Research focus:

Botany, population genomics

Abstract

Whole-genome sequencing allows us to revisit classic questions in ecology and evolution by linking traits and population patterns to genome-wide signatures of demographic history and adaptation. I will illustrate the power of such data with three examples: 1) revealing hidden population structure in migratory butterflies (Vanessa cardui), 2) identifying the genetic basis of a reproductive barrier in snapdragon (Antirrhinum majus), and 3) examining the consequences of loss of genetic diversity in a vulnerable warbler species (Phylloscopus ijimae).

- Earlier work suggested that the cross-continental migrant butterfly Vanessa cardui forms a single panmictic population across Europe and North Africa. We asked whether this apparent panmixia extends from South Africa to the Arctic. Whole-genome scans instead revealed a previously hidden hemispheric migratory divide, associated with a single major chromosomal inversion that separates two alternative migratory types.
- Snapdragons (Antirrhinum majus) have two flower colour morphs that form an extensive hybrid zone. However, the long-term persistence of this polymorphism implies a barrier to gene flow. Whole-genome analyses reveal that flower colour loci disproportionately underlie this barrier, a pattern only detectable at whole-genome resolution.
- Vulnerable Phylloscopus ijimae warblers had not previously been genetically characterised, and standard measures of genetic diversity