

9-1-2012

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Recommended Citation

Novak, Kelly and Runck, Amy, "Phylogeography of Southern Red-Backed Voles in North America" (2012).
Student Research and Creative Projects 2012-2013. 33.
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Phylogeography of the Southern Red-backed Vole (*Myodes gapperi*)

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Introduction

The southern red-backed vole (*Myodes gapperi*) inhabits the forests of the Hudsonian and Canadian life zones of central and southern Canada and the Rocky and Appalachian mountain ranges (Figure 1; Hall 1981). Fossils document the species in North America dating back to the Middle Pleistocene, where it was believed to persist in refugia south of the Cordilleran and Laurentide ice sheets during the last glaciation (Figure 2; Hibbard et al. 1965; Graham 1976; Runck and Cook, 2005). Upon the retreat of these ice sheets, populations of southern red-backed voles are thought to have expanded into previously glaciated areas around 12,000 years ago. We examined the phylogeographic patterns of Eastern and Northern populations (Figure 1) of the southern red-backed vole in response to the climatic fluctuations of the Late Pleistocene. We used microsatellite DNA in order to test for contemporary gene flow among the different *M. gapperi* lineages.

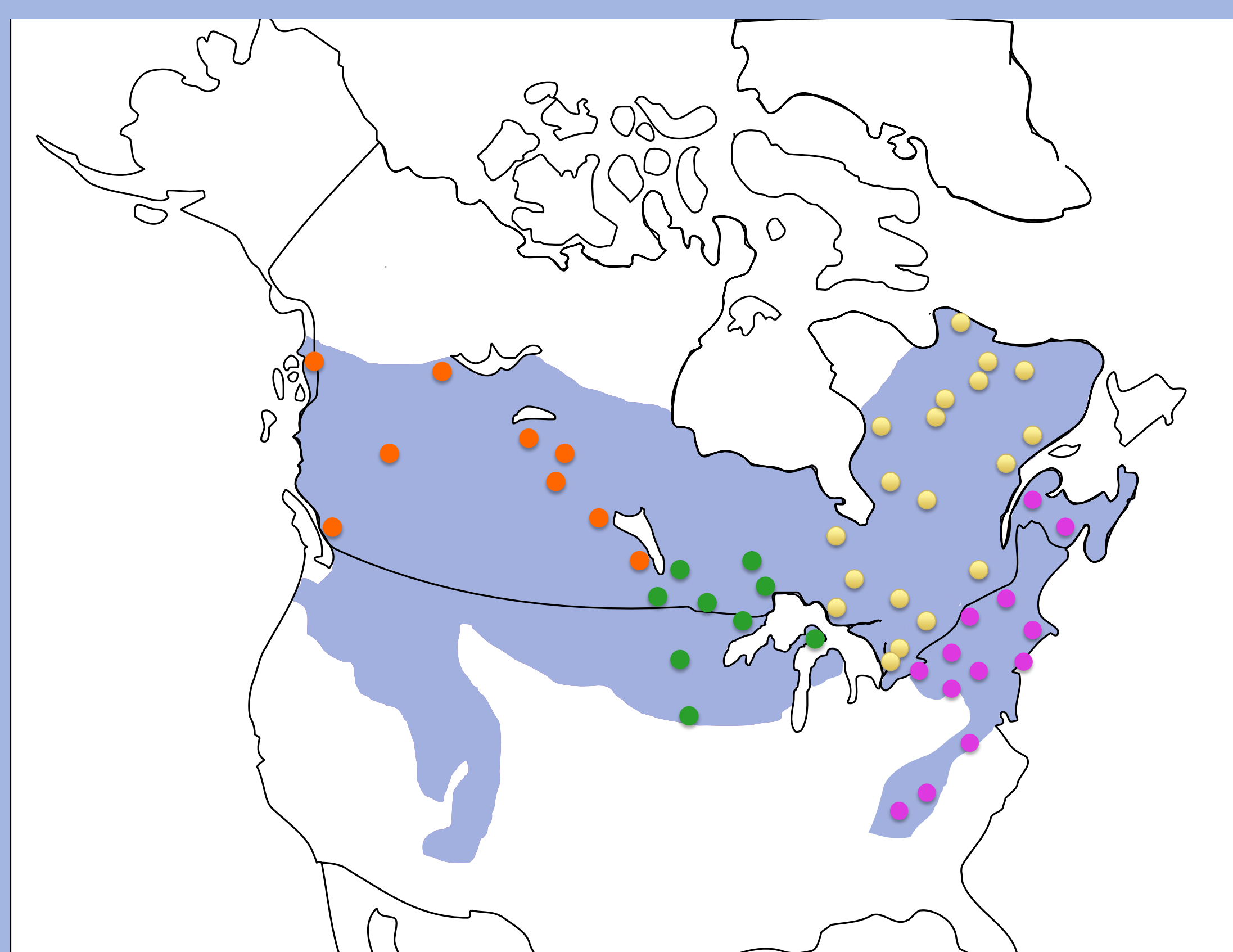


Figure 1. Distribution of *M. gapperi* shown in blue. Sampling localities are indicated by dots.

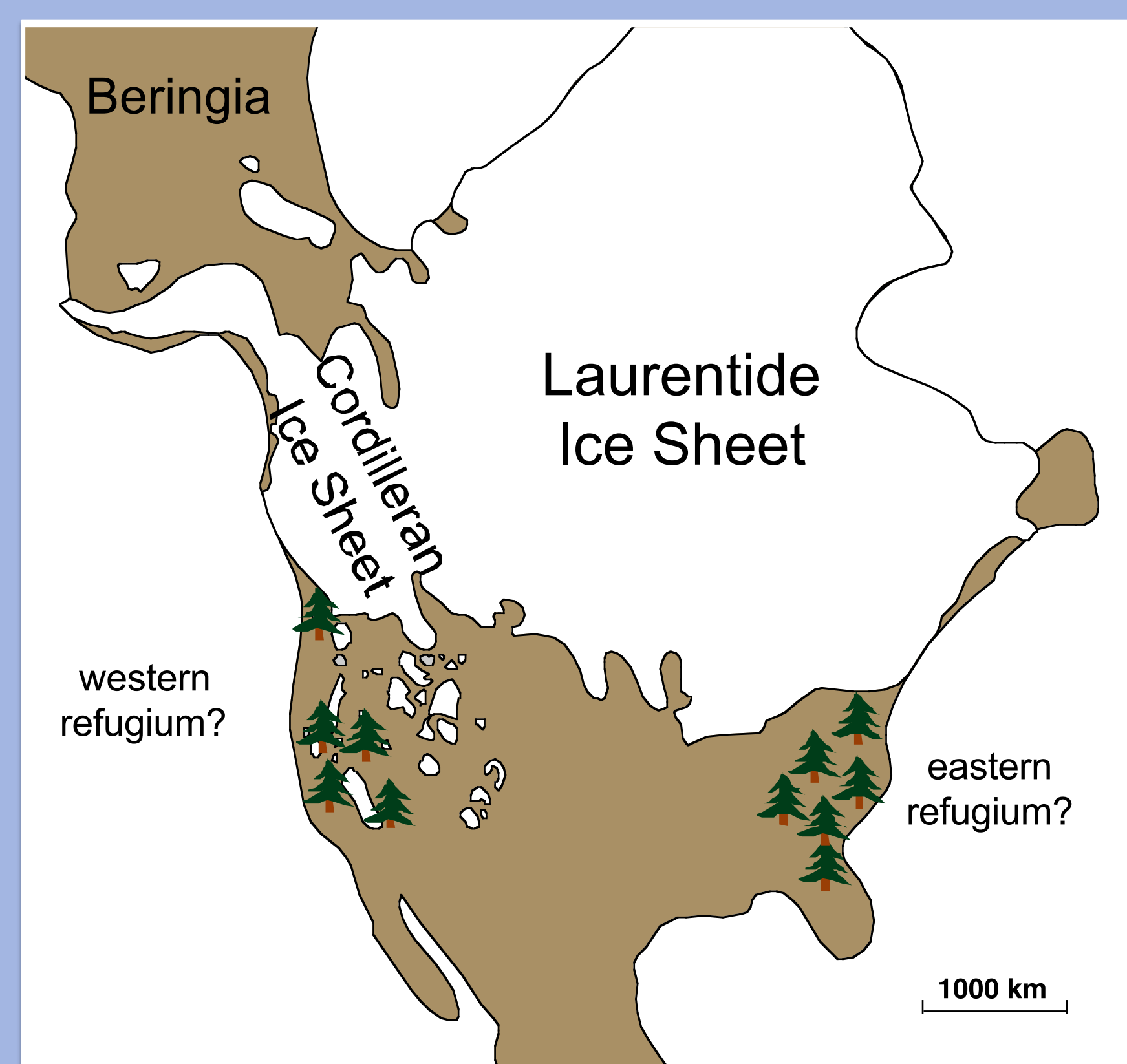


Figure 2. Map of North American ice sheets ca. 18,000 years before present. *M. gapperi* is hypothesized to exist in refugia south of the ice sheets.

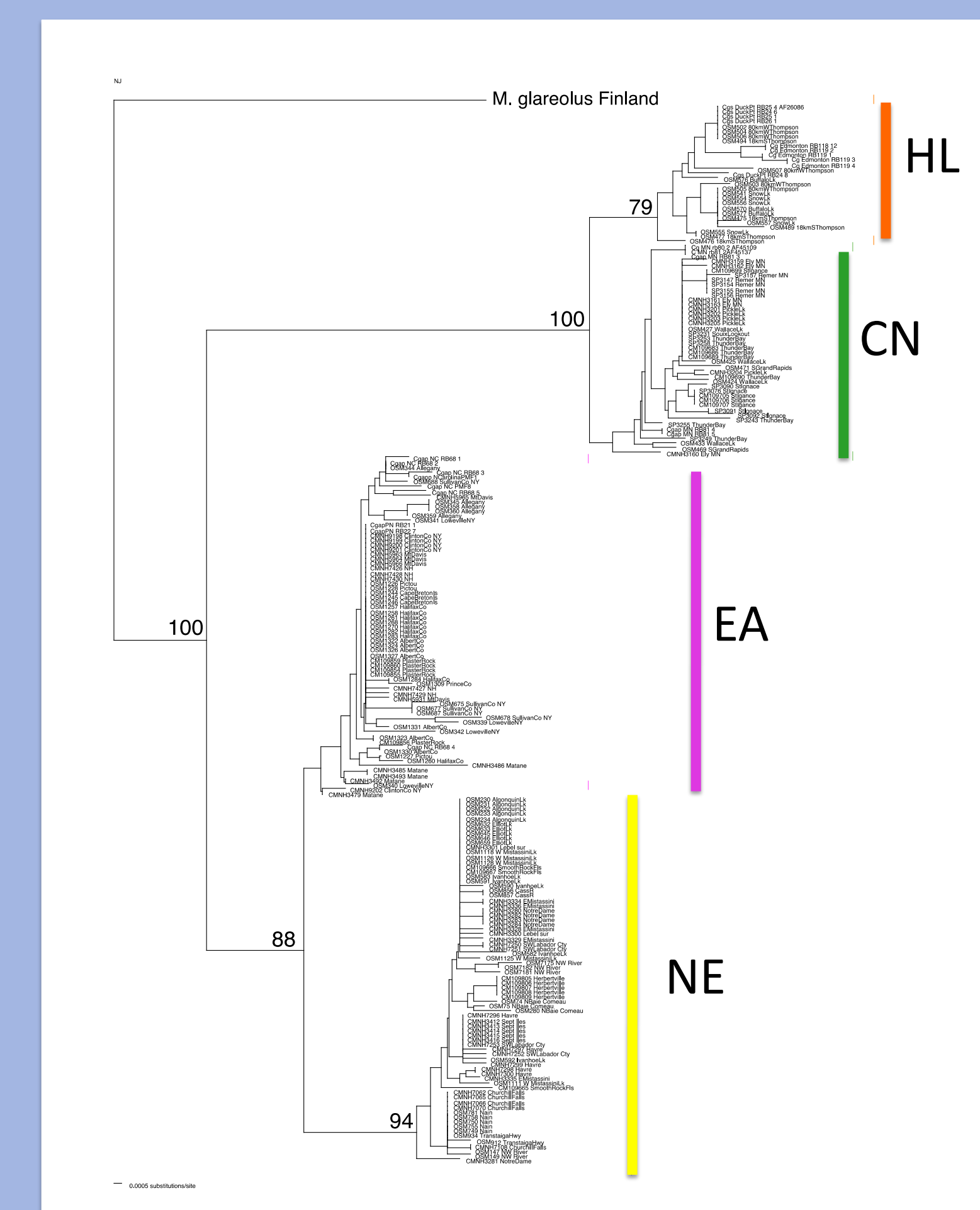


Figure 3. Phylogeographic relationship of *M. gapperi* using the Neighbor-joining algorithm. Lineages are color-coded to correspond with sampling localities in Figure 1. Numbers above the branches are bootstrap values > 65 based on 10,000 bootstrap replicates. *M. glareolus* was included as an outgroup.

	NE	EA	CN	HL
NE	-			
EA	0.24	-		
CN	0.53	0.47	-	
HL	0.54	0.42	0.27	-

Table 1. Pairwise F_{ST} values among the different lineages of *M. gapperi*.

Methods

- DNA was isolated from 237 red-backed voles from 50 localities
- 600 bp of the mitochondrial cytochrome *b* gene were amplified and sequenced
- Phylogeographic trees were constructed to show the genetic relationships of the voles from the different localities
- Microsatellite DNA was amplified at 3 loci (MsCg7, MsCrb05, and List 3-5) from populations across northeastern North America
- Analyses were conducted to determine if gene flow exists among the different lineages

Results

- 4 major lineages were uncovered with the cytochrome *b* gene: Central (CN), High latitude (HL), Eastern (EA), and Northeastern (NE) (Figure 1 & 3), which are identified by more than 2% sequence differentiation in cytochrome *b*
- Microsatellite data showed moderate levels of genotypic differentiation with $F_{ST} > 0.2$ among the different lineages (Table 1)

Conclusions

- Two major clades were recovered, an eastern- containing the NE and EA lineages, and central- containing the CN and HL lineages. The levels of sequence divergence exceed 2% among the four lineages and suggest that during the Pleistocene, voles existed in separate refugia.
- The voles in the HL lineage appear to be descendants of a more central North American refugium. These voles may have persisted in the Driftless Region, which has been shown to be a refugium for other forest-associated species, such as the eastern chipmunk (*Tamias striatus*; Rowe et al. 2004)
- Preliminary analyses of microsatellite data show moderate levels of differentiation among the lineages ($F_{ST} > 0.2$) which suggest that these lineages are reproductively isolated from one another. Thus, these lineages may be on a trajectory to speciate from one another.

Future Directions

- Increase sampling from the Driftless Region to determine if this region was a refugium for the CN and HL lineages
- Increase the number of microsatellite loci to further test for interbreeding among the lineages.

Funding: National Science Foundation, Winona State Undergraduate Research Grant.

RESEARCH / CREATIVE PROJECT ABSTRACT / EXECUTIVE SUMMARY
FINAL REPORT FORM

Title of Project
Phylogeography of Southern Red-backed Voles in North America

Student Name Kelly Novak
Faculty Sponsor Amy Runck, PhD
Department Biology

Abstract

Climate change has altered species distributions and has lead to species forming as they live in isolated refugia. I propose to examine microsatellite alleles from the southern red-backed vole (*Myodes gapperi*) in order to test whether or not previously identified distinct lineages of these voles can interbreed. If they are no longer interbreeding, this will give us insight on how climate change can affect species distributions and contribute to speciation.

The end product of this project in electronic format has been submitted to the Provost/Vice President for Academic Affairs via the Office of Grants & Sponsored Projects Officer (Maxwell 161, npeterson@winona.edu).

Student Signature Kelly Novak Date 2/4/13

Faculty Sponsor Signature Amy M Runck Date 4 Feb 2013