PHYLOGEOGRAPHIC ANALYSIS OF NORTH AMERICAN MOOSE

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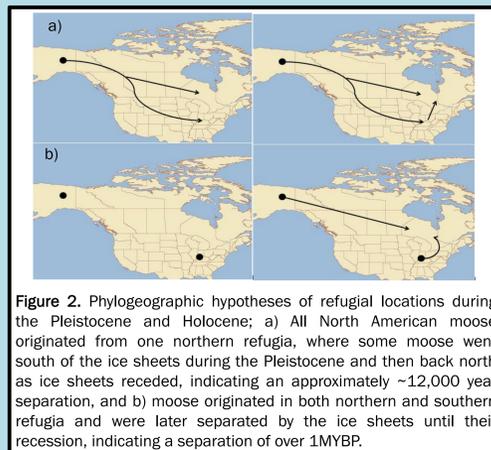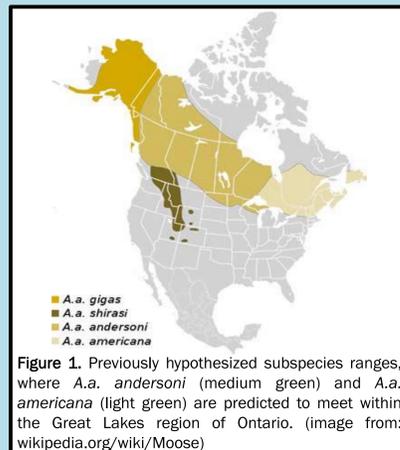4. Trent University, Department of Biology, Peterborough, Ontario
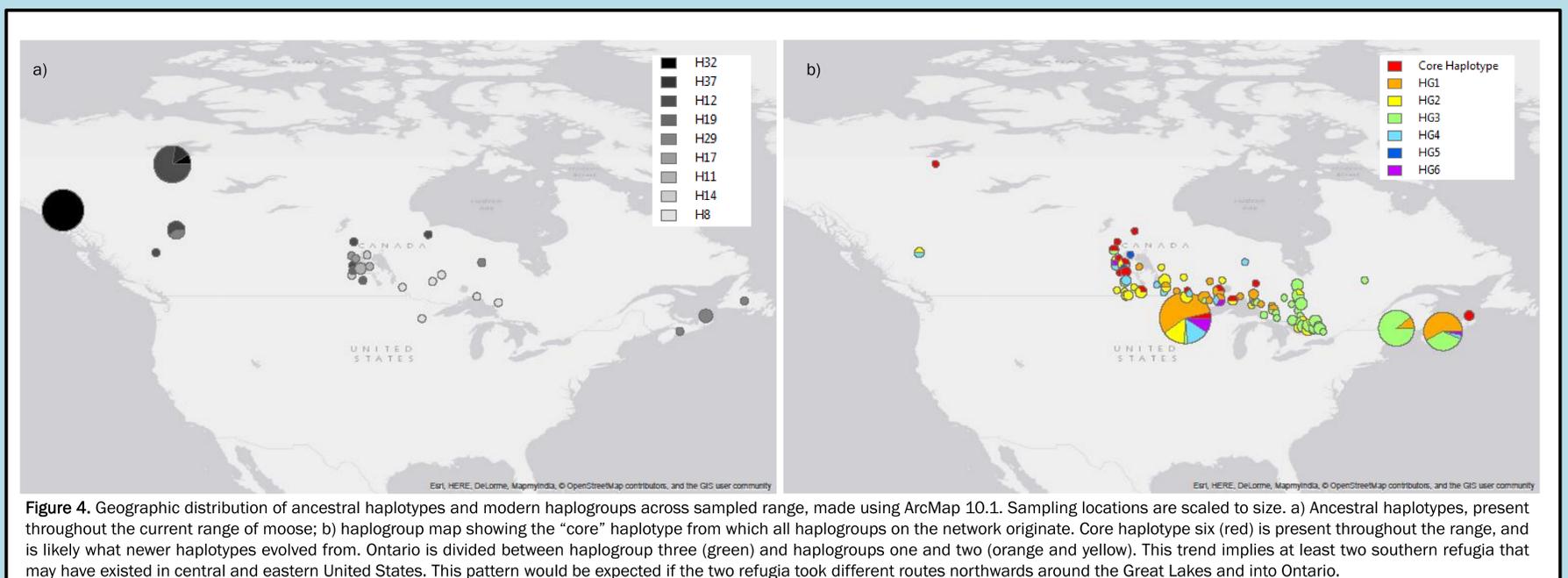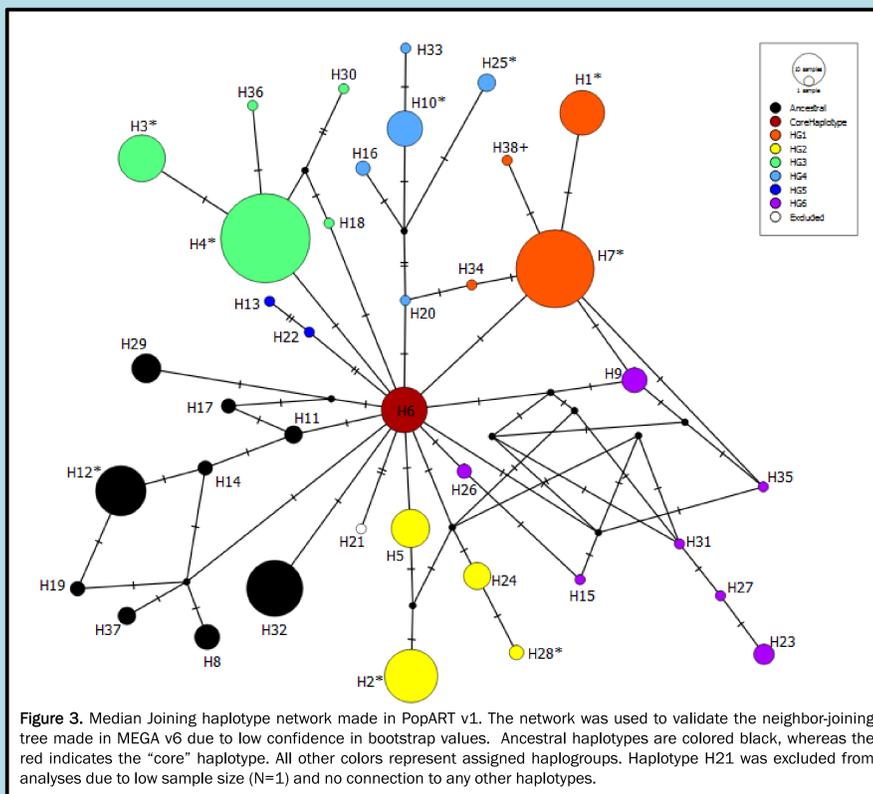*meredithpurcell@trentu.ca

I. Introduction

- Work within the last decade has provided support for the designation of four different subspecies of moose in North America (Figure 1). There are several hypotheses which attempt to explain the phylogeographic history of moose, and how their range has adjusted over time to their current distribution (Figure 2).
- This project further investigates these hypotheses to determine subspecies ranges and phylogeographic history using the mitochondrial DNA (mtDNA) control region of 366 moose across Canada. Of particular interest is **whether moose existed in southern refugia during the Pleistocene, rather than one single northern refugium.**

Figure 1. Previously hypothesized subspecies ranges, where *A.a. andersoni* (medium green) and *A.a. americana* (light green) are predicted to meet within the Great Lakes region of Ontario. (image from: wikipedia.org/wiki/Moose)

A.a. gigas
A.a. shirasi
A.a. andersoni
A.a. americana

Figure 2. Phylogeographic hypotheses of refugial locations during the Pleistocene and Holocene; a) All North American moose originated from one northern refugia, where some moose went south of the ice sheets during the Pleistocene and then back north as ice sheets receded, indicating an approximately ~12,000 year separation, and b) moose originated in both northern and southern refugia and were later separated by the ice sheets until their recession, indicating a separation of over 1MYBP.

II. Results

- A median-joining network (Figure 3) supported the phylogenetic relationships identified in a neighbor-joining tree.
- Visualization through haplotype and haplogroup maps displayed relationships between moose across North America, identifying ancestral haplotypes present throughout the range as well as haplotypes not present in northern populations (Figure 4). This is indicative of **admixture as a result of a period of separation during the Pleistocene.**
- Two possible refugia gave rise to a separated distribution of haplogroups in central Canada.

Figure 3. Median Joining haplotype network made in PopART v1. The network was used to validate the neighbor-joining tree made in MEGA v6 due to low confidence in bootstrap values. Ancestral haplotypes are colored black, whereas the red indicates the "core" haplotype. All other colors represent assigned haplogroups. Haplotype H21 was excluded from analyses due to low sample size (N=1) and no connection to any other haplotypes.

III. Future Work & Conservation Implications

- Continuing with a **full genome approach** would allow for identification of more variation between subspecies.
- Sequences will also be analyzed with **Approximate Bayesian Criterion (ABC) methods**, which allows for testing of multiple phylogeographic hypotheses to determine which scenario is most likely to account for current haplotype distributions.
- As some moose populations along the southern range periphery have begun to decline, others are remaining steady, and much interest has been targeted upon understanding why they are experiencing a differential decline.
- **Understanding the evolutionary history of moose is essential to understanding their differential success in the face of climate change. Future management practices would need to incorporate this knowledge in order to explain current declines and identify at-risk populations.**

Figure 4. Geographic distribution of ancestral haplotypes and modern haplogroups across sampled range, made using ArcMap 10.1. Sampling locations are scaled to size. a) Ancestral haplotypes, present throughout the current range of moose; b) haplogroup map showing the "core" haplotype from which all haplogroups on the network originate. Core haplotype six (red) is present throughout the range, and is likely what newer haplotypes evolved from. Ontario is divided between haplogroup three (green) and haplogroups one and two (orange and yellow). This trend implies at least two southern refugia that may have existed in central and eastern United States. This pattern would be expected if the two refugia took different routes northwards around the Great Lakes and into Ontario.