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Importance

- The Northern Bog Lemming, *Mictomys (Synaptomys) borealis* is currently pending a federal decision for protections under the Endangered Species Act
- M. borealis* is one of the most data deficient species among all North American small mammals despite its large distribution and inherent rarity (Fig. 1).
- We investigate the evolutionary history of northern bog-lemmings and highlight issues with conserving rare species.
 - Test validity of taxonomy and systematic relationships
 - Assess phylogeographic structure and history, rangewide
 - Test validity of sub-species designations
 - Assess genomic diversity regionally

Methods

- Tissue samples (muscle) were obtained on loan from museum collections and DNA recovered from salt extraction
- Analyses included:
 - Phylogeny estimation (mtDNA tree using BEAST; SNP tree using RAXML)
 - Clustering analyses of SNPs (DAPC, STRUCTURE)
 - Genomic diversity stats (Heterozygosity)
- The mitochondrial Cytochrome-b gene (1143bp) was sequenced with Sanger methods
- Thousands of nuclear loci were obtained through ddRADseq
- To assess specimen availability, we searched ARCTOS and GBIF, downloading all available specimen vouchers with georeferenced locality and date of collection information
- Plotted specimen acquisition and availability through time.

Discussion

- The lack of modern samples throughout this taxon's broad distribution severely limits interpretation of modern molecular methods and hinders management decisions (Figs. 1, 2)
 - Except for contemporary sampling in eastern Beringia, sampling has decreased through time and is generally extremely limited
- Both mitochondrial and nuclear trees support northern bog-lemmings as *Mictomys*, a monotypic genus, and **not** *Synaptomys* as popularly recognized (Figs. 3, 4)
- Clustering analyses and trees support most current sub-species designations reflecting regional divergence in multiple glacial refugia including Southeast Alaska (Figs. 4, 5, 6).
- Southern and coastal island populations appear of highest conservation priority based on diversity (Fig. 7)
- Possible gene flow suggests ongoing evolutionary complexity

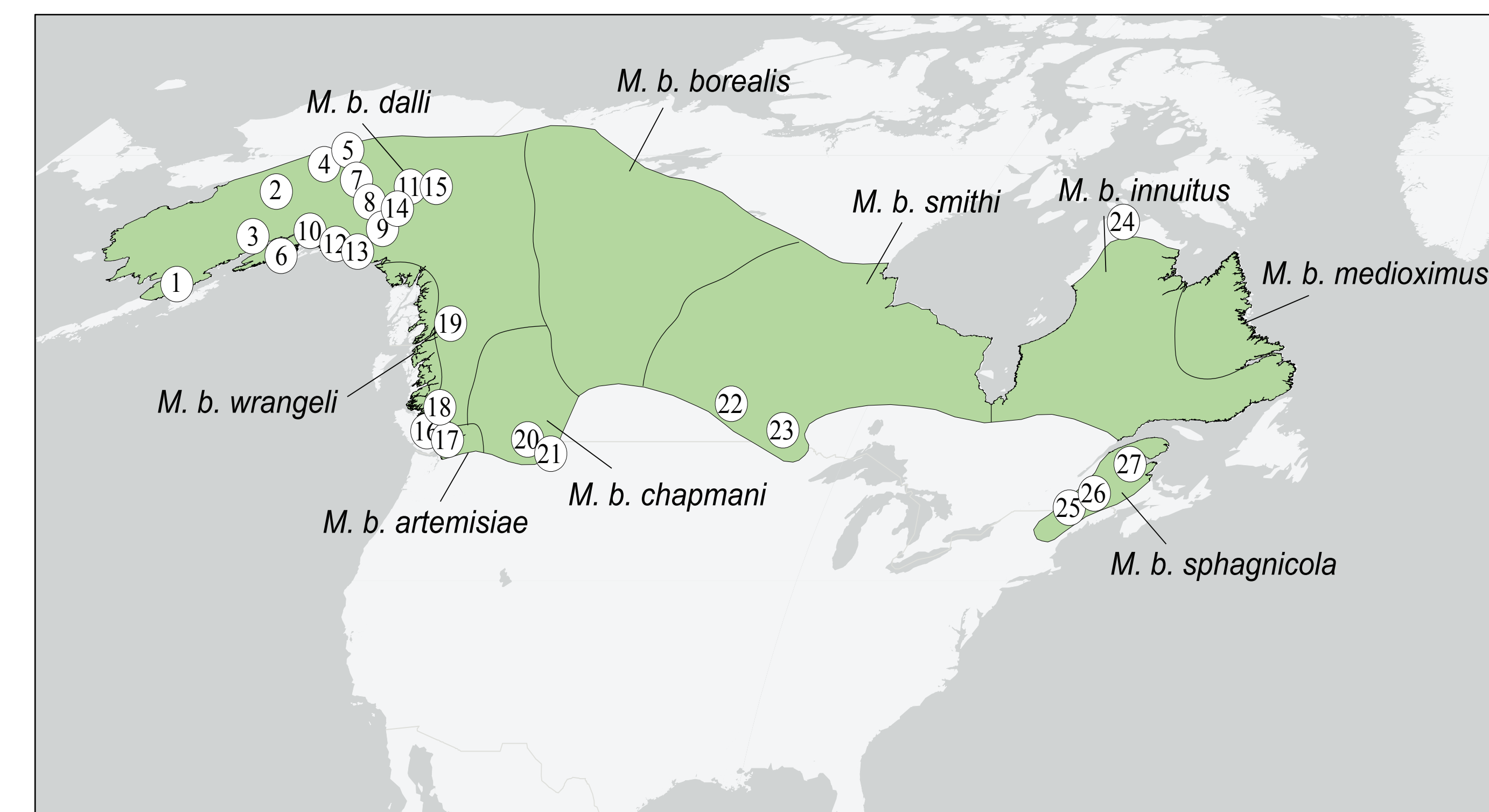


Figure 1. Map of the distribution of *M. borealis* (green shading) estimated subspecies ranges, and localities of specimens used for genetics.

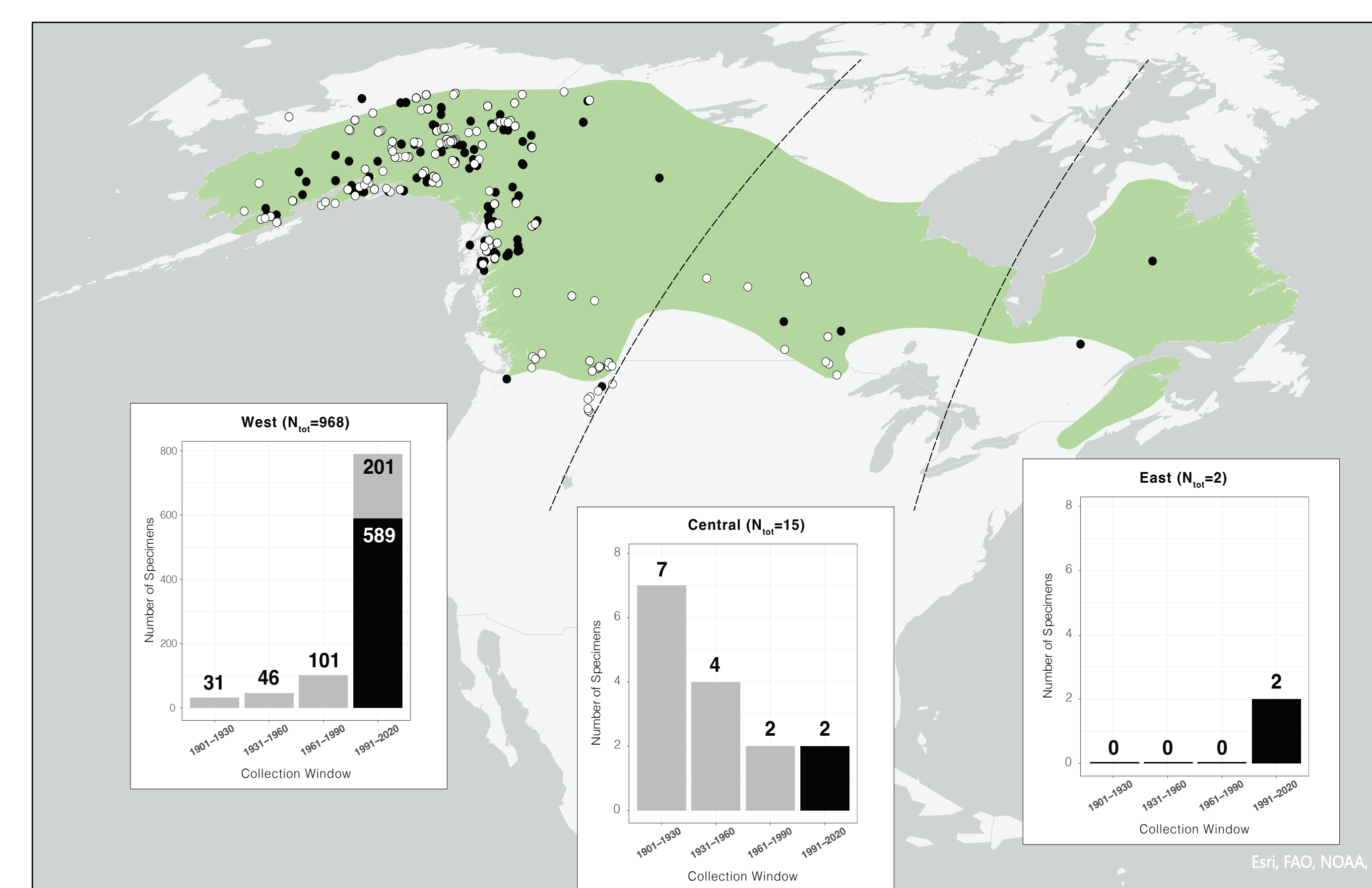


Figure 2. Distribution of georeferenced samples of *M. borealis* from ARCTOS database. Samples are divided by longitude (West, Central & East) and binned by 30-year collection intervals. Black bars in plots and black dots on map represent specimens with genomic resources.

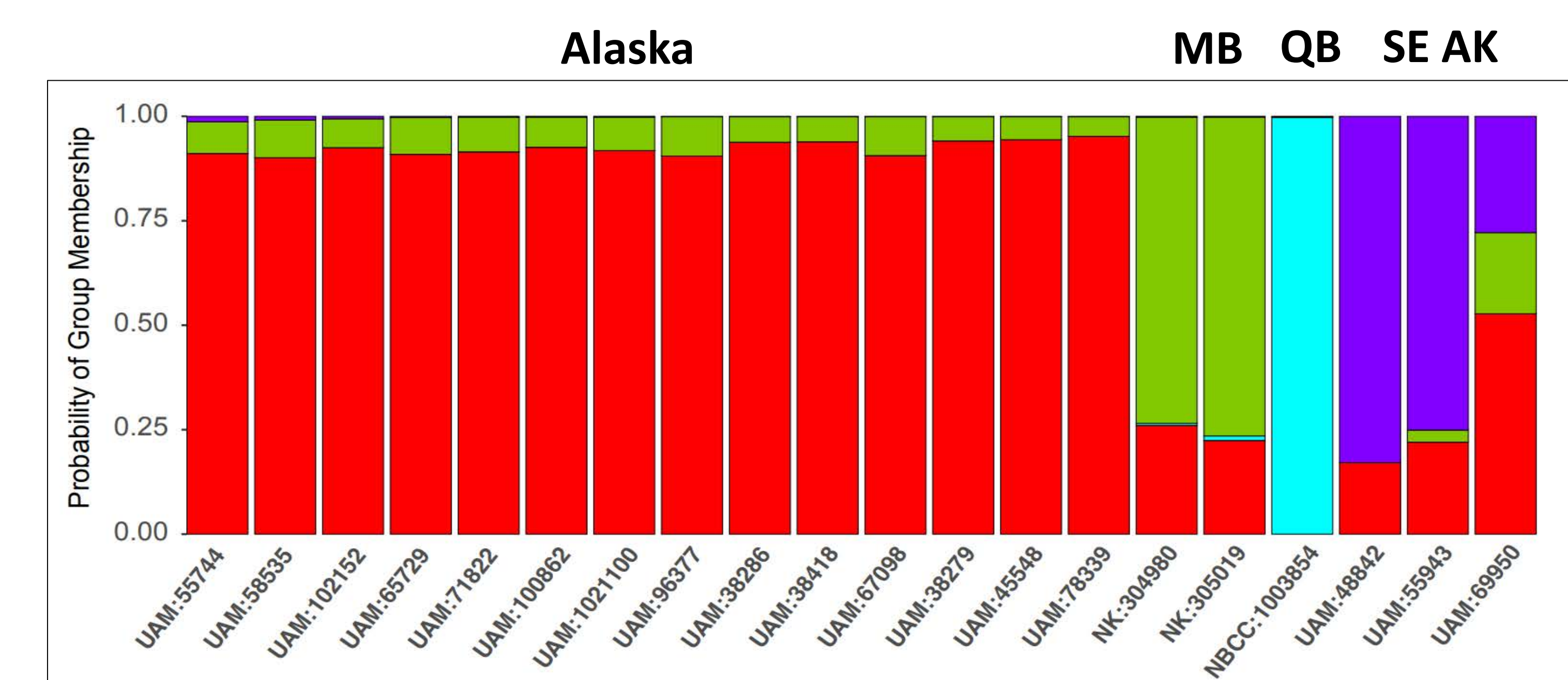
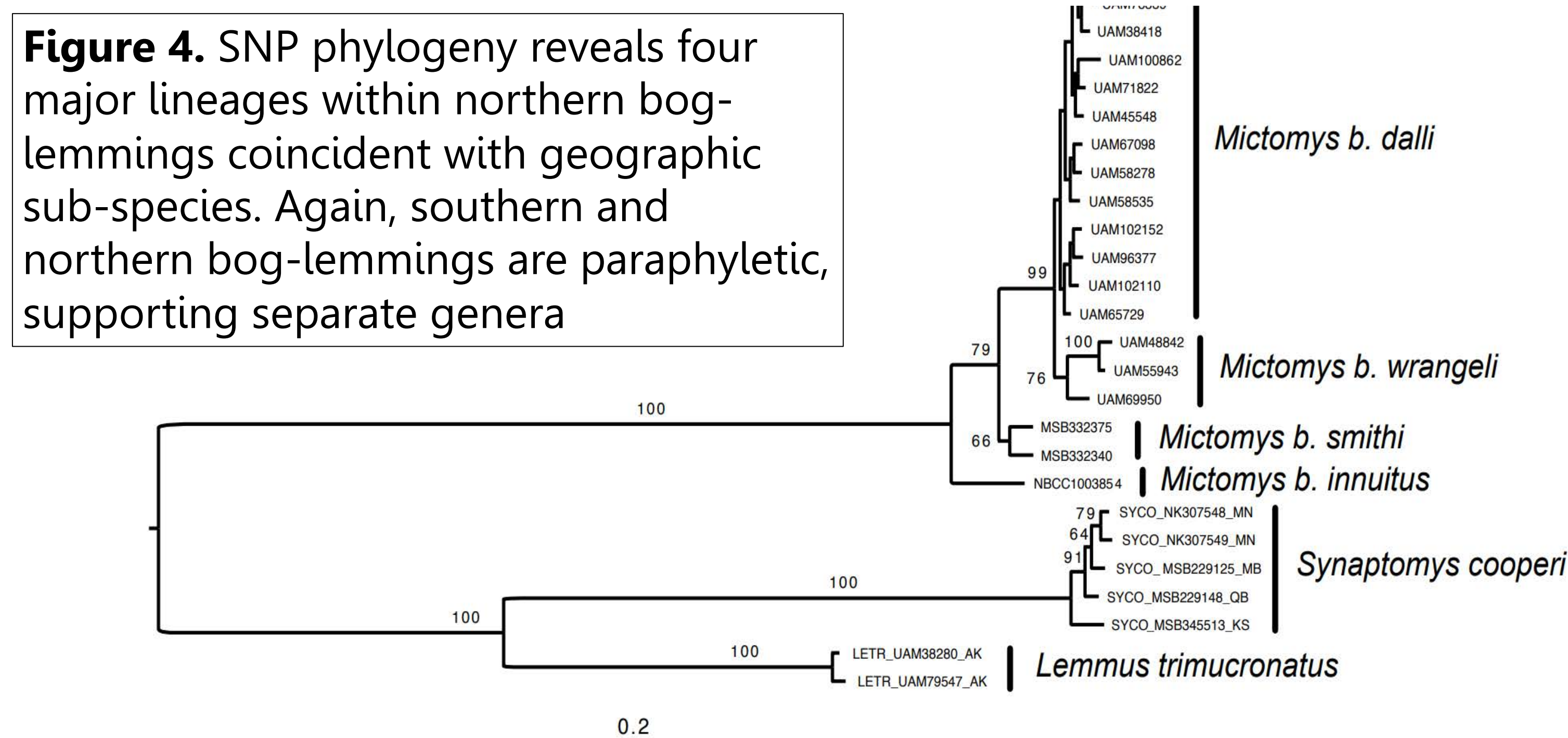
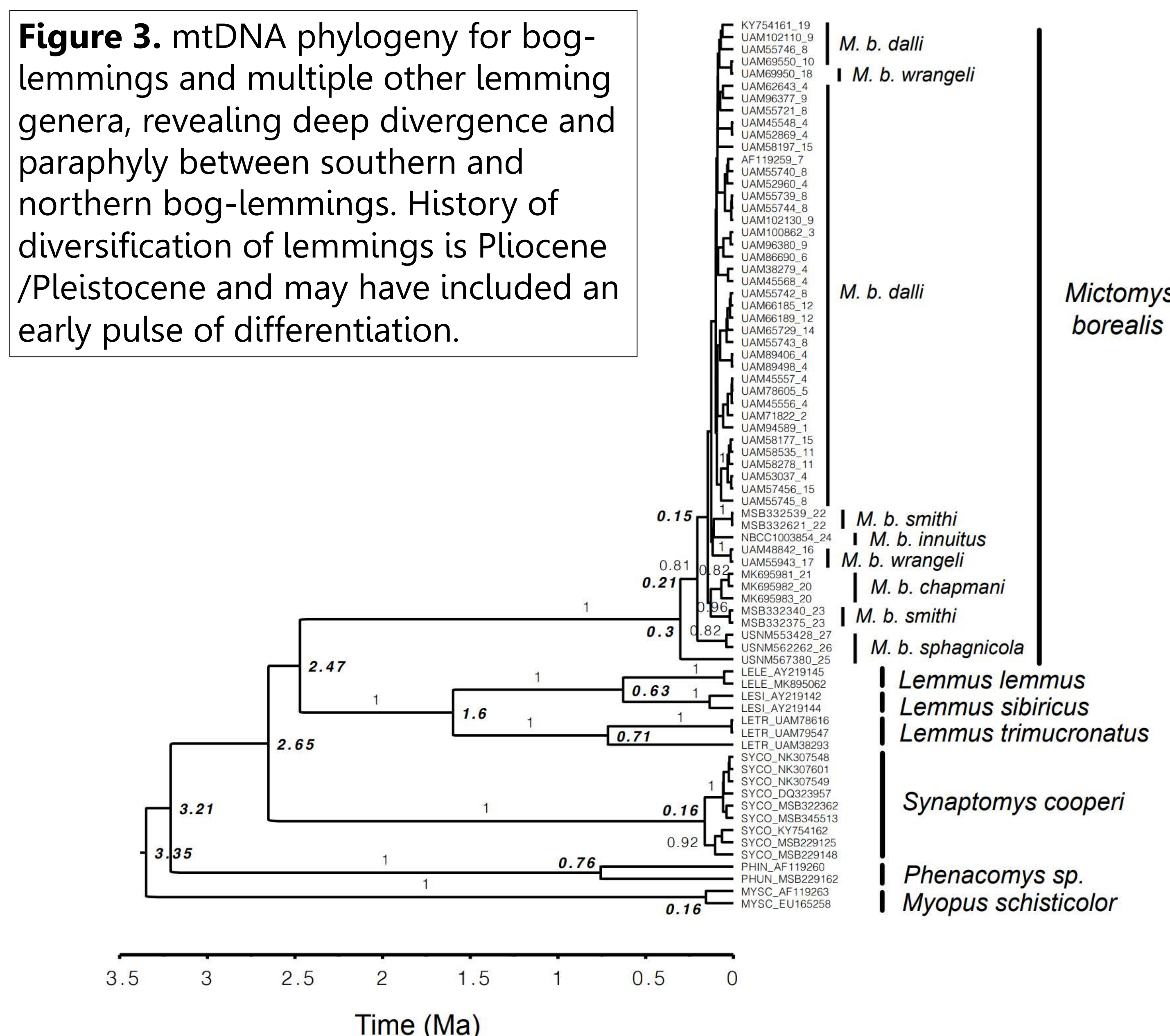


Figure 5. Structure plot showing proportional assignment of alleles among samples in four distinct geographic clusters.

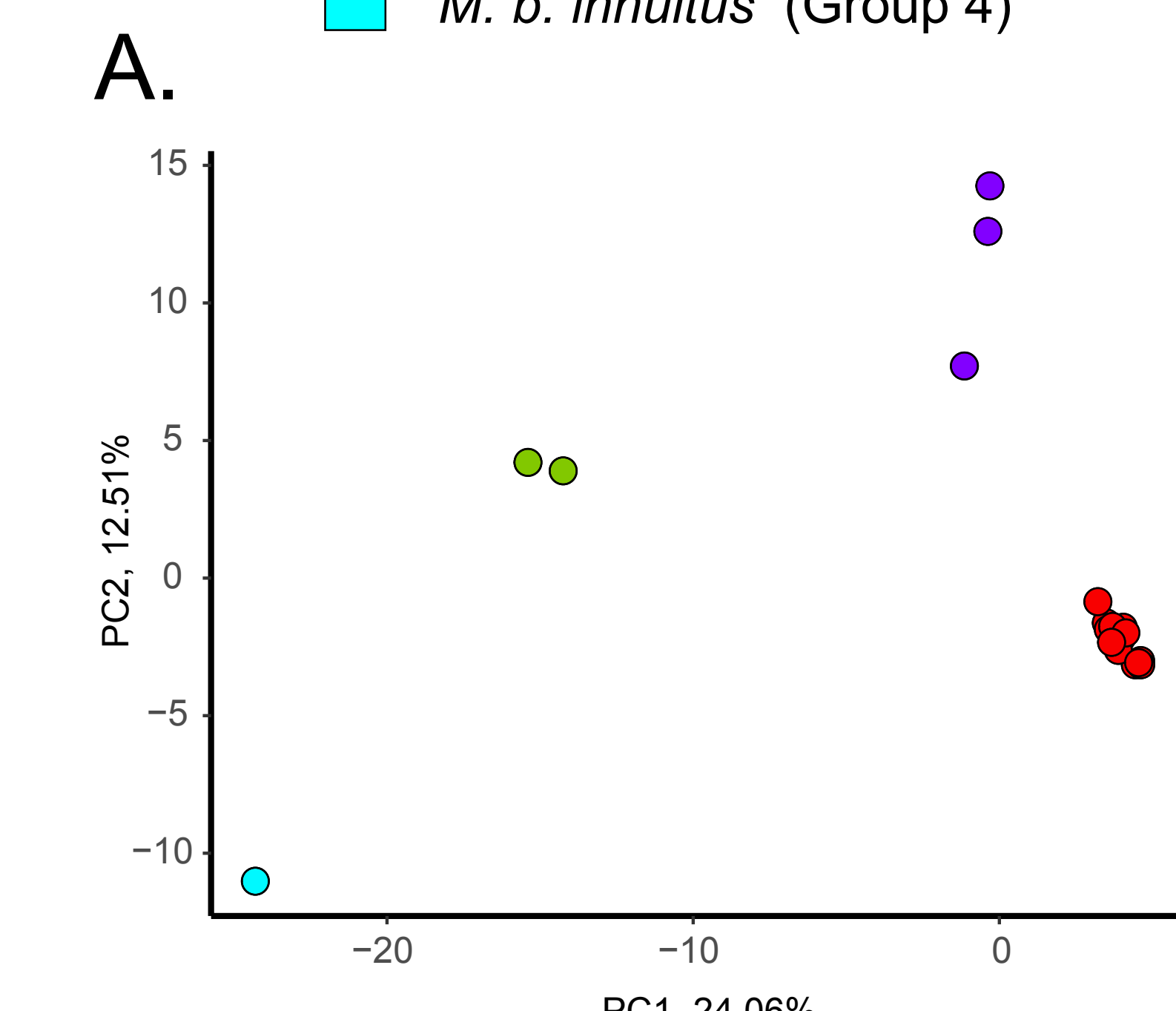


Figure 6. DAPC plot showing spatial genomic differentiation between samples clustered by geography. Clear separation exists across first two axes.

Figure 7. Observed Heterozygosity based on SNP data shown in bean plots. Dots represent individual samples