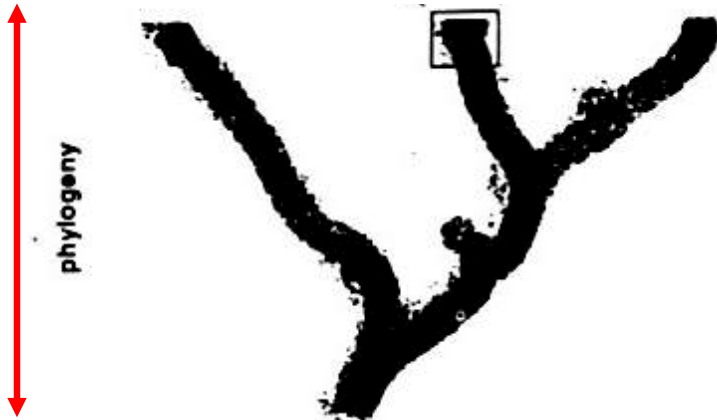
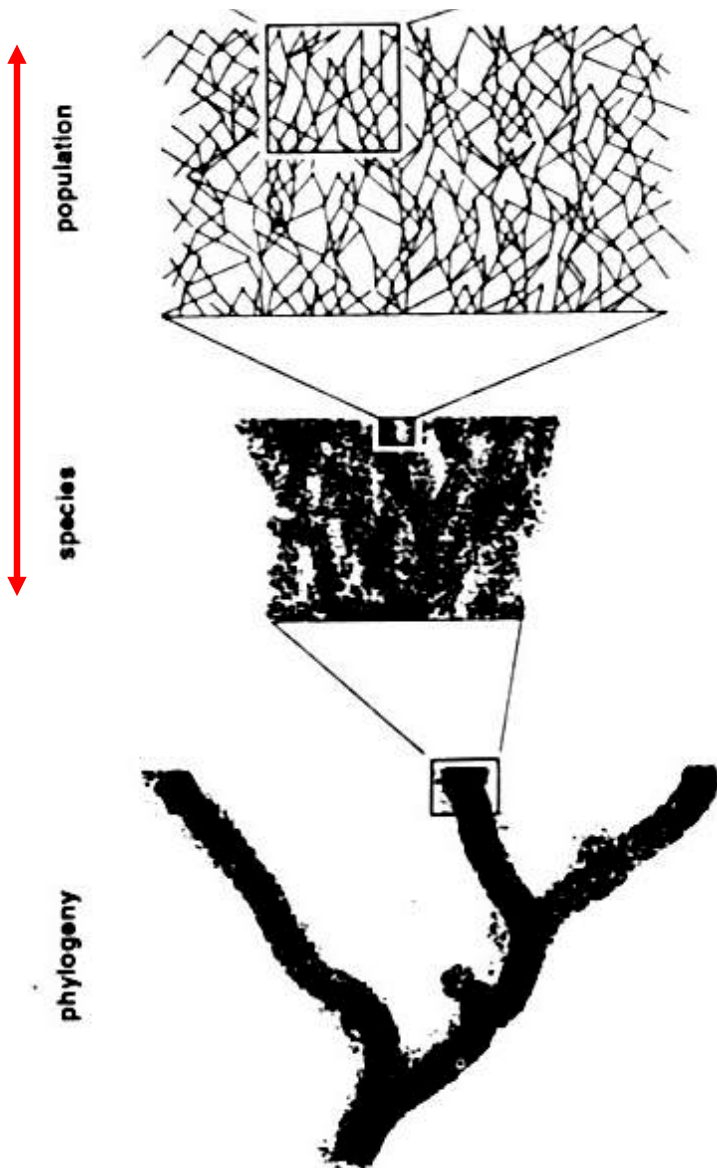


Phylogeography — Historical Biogeography of the Species



Historical biogeography traditionally deals with relationships among species, genera, and higher taxonomic groups and the areas they occupy

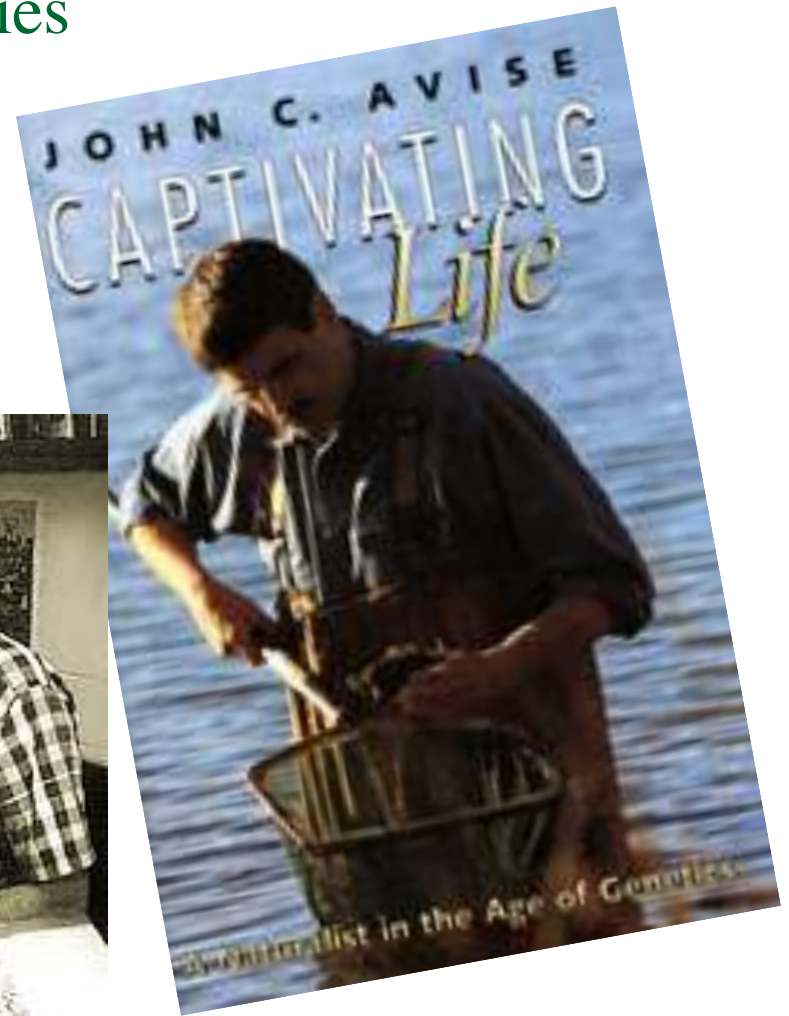
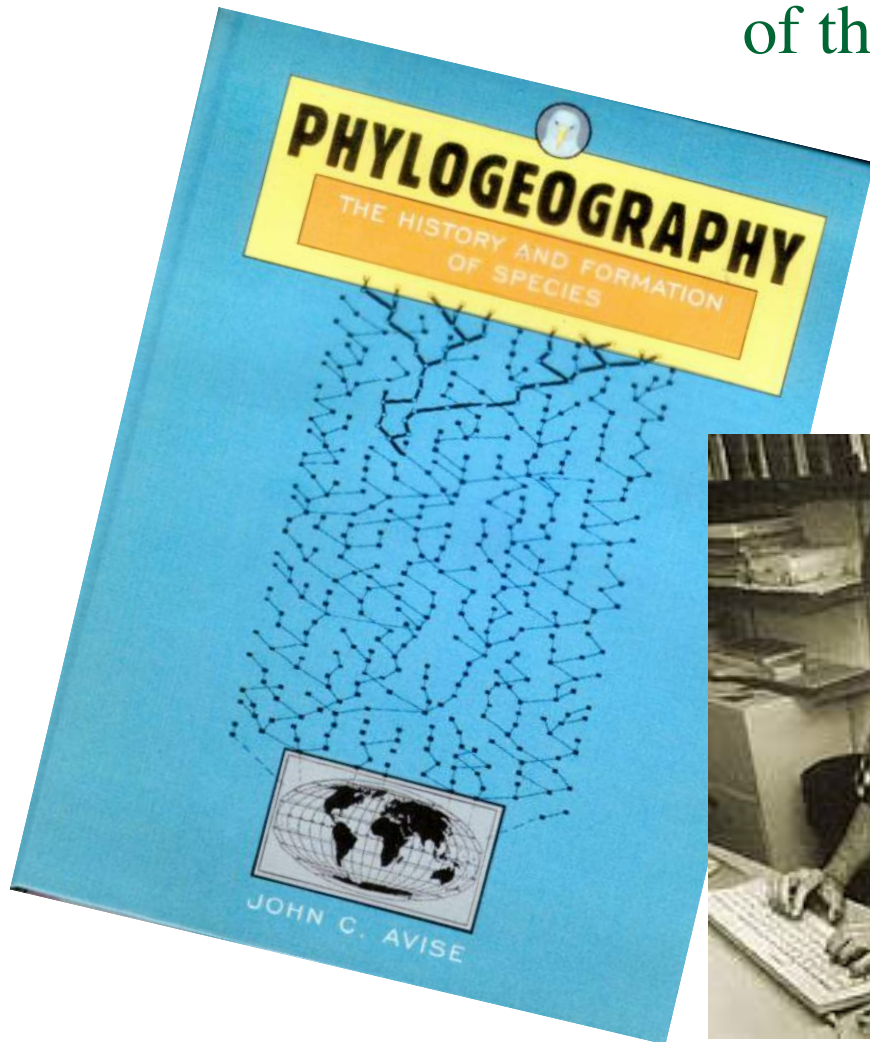
Phylogeography — Historical Biogeography of the Species



Due to advances in DNA sequencing and fingerprinting methods, historical biogeography has recently begun to integrate relationships of **populations within species** and the areas they occupy

Historical biogeography traditionally deals with relationships among species, genera, and higher taxonomic groups and the areas they occupy

Phylogeography — Historical Biogeography of the Species



John Avise, animal geneticist at University of Georgia, coined the term “**phylogeography**” to describe “the history and formation of species” from a geographical perspective

Phylogeography — Historical Biogeography of the Species

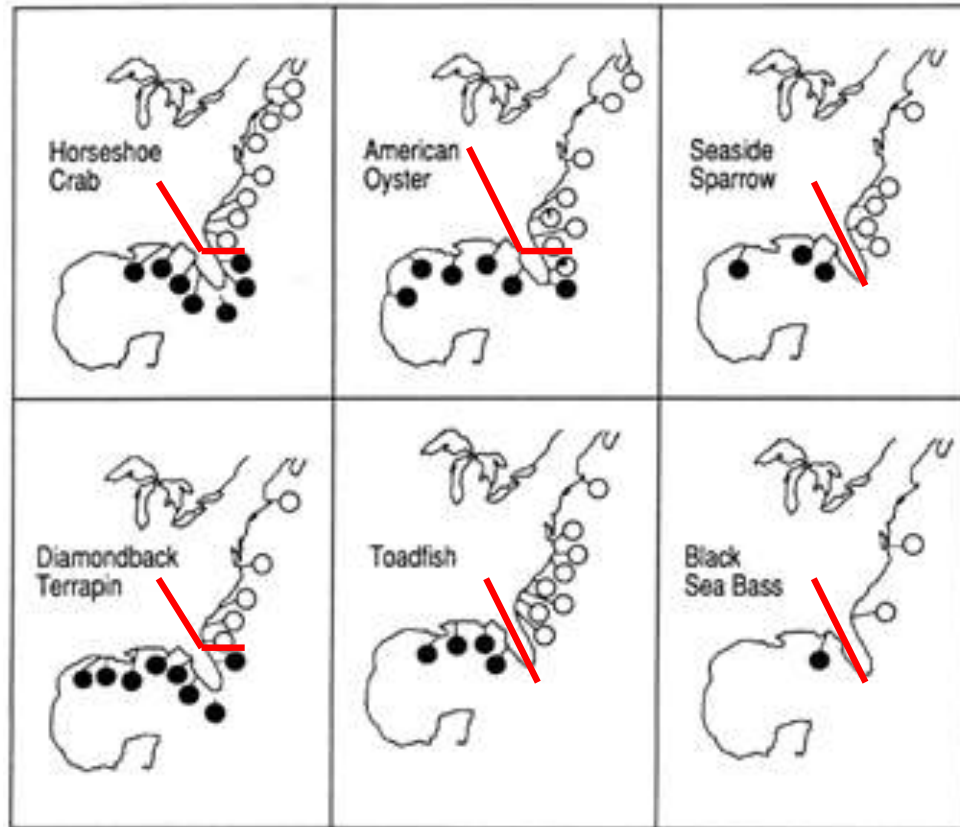


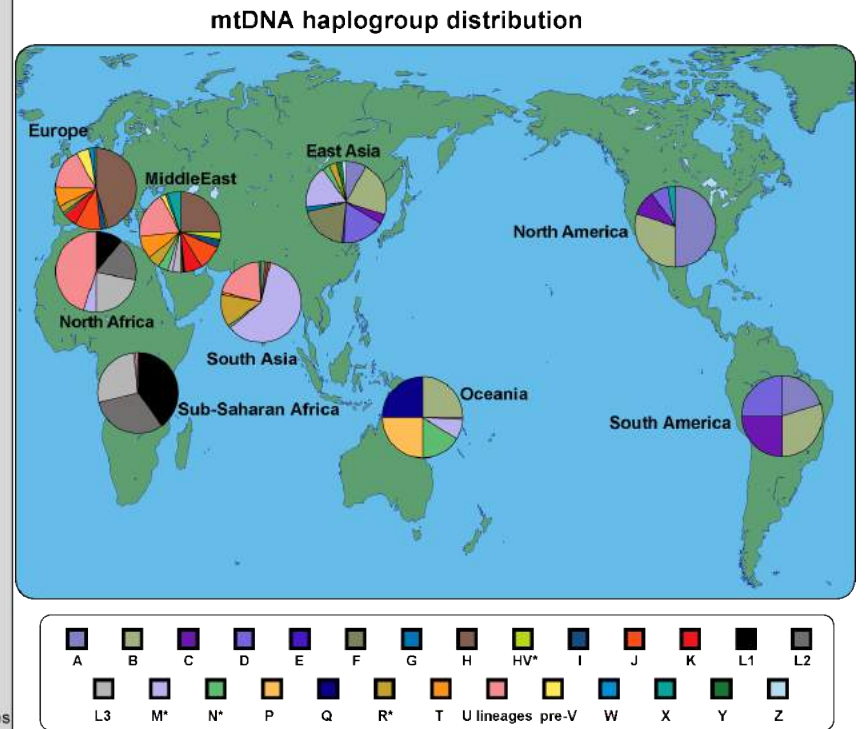
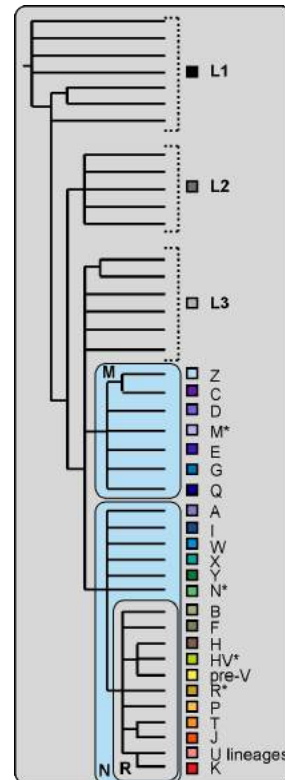
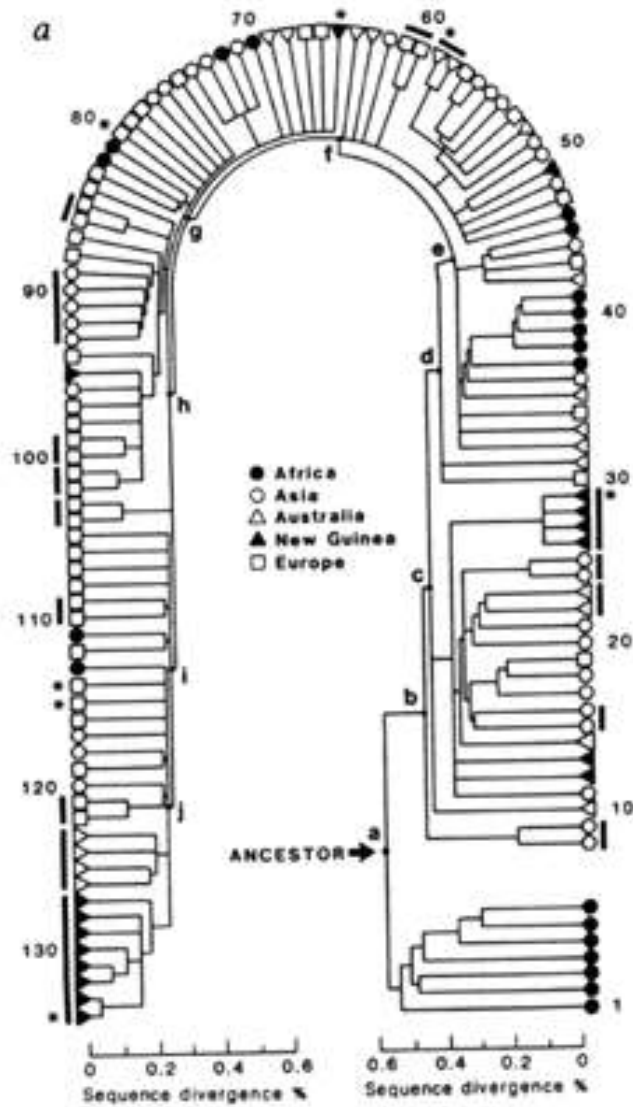
Figure 6.9. Geographic distributions of mtDNA genotypes within each of six maritime taxa (from Avise, 1992). Shown are pie diagrams summarizing frequencies of the two fundamental clades in populations of each species.

The classic phylogeographic analysis by Avise and his students involved the identification of a strong geographical signal within species **separating populations** from the **Atlantic seacoast** from the **Gulf of Mexico seacoast**.

The presence of two quite distinct genotypes within all these unrelated species has been explained by **Pleistocene** glacial and inter-glacial events

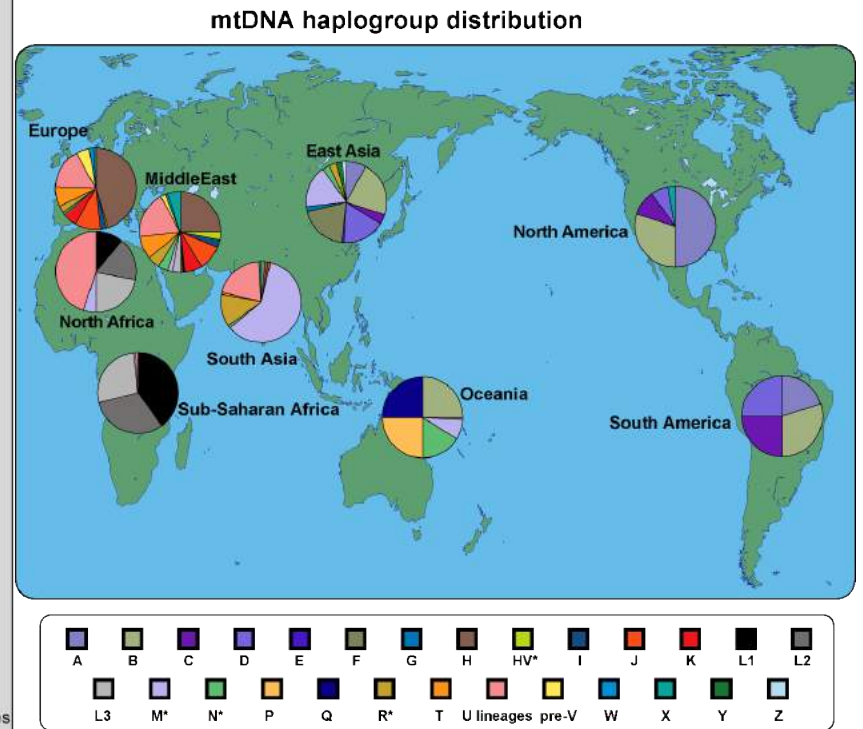
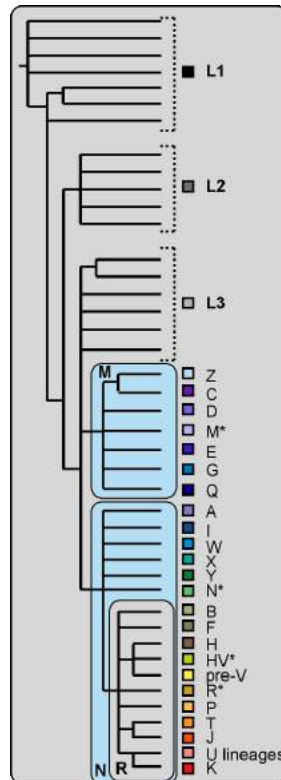
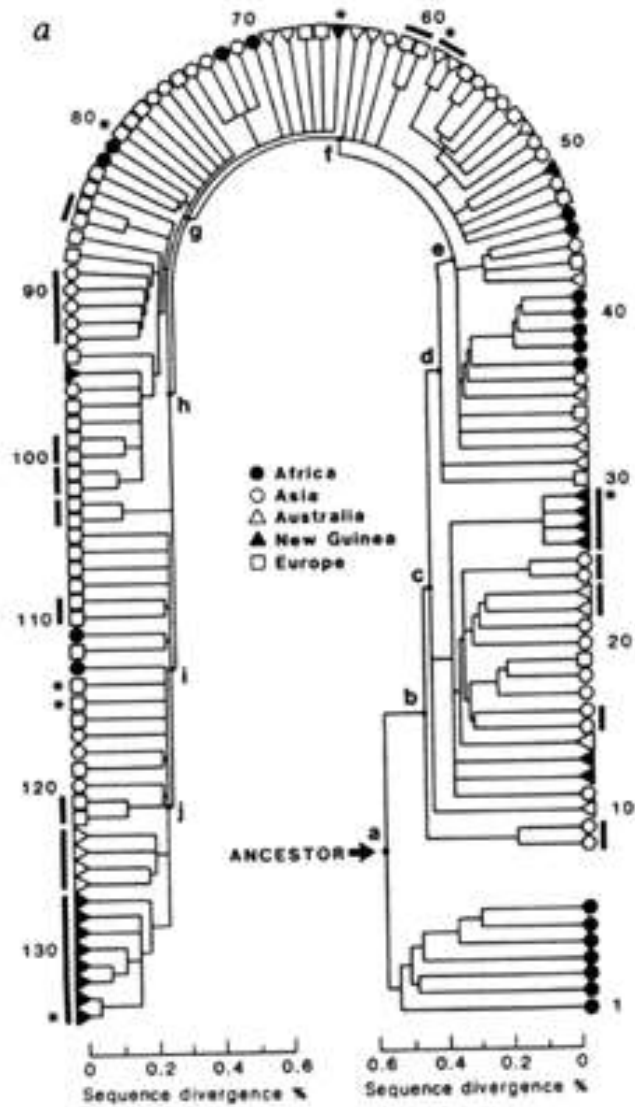
Phylogeography — Historical Biogeography of the Species

One of the most debated issues in phylogeography is the geographical origin of *Homo sapiens* - the “Eve hypothesis” as maternally inherited mitochondrial DNA (mtDNA) is often used



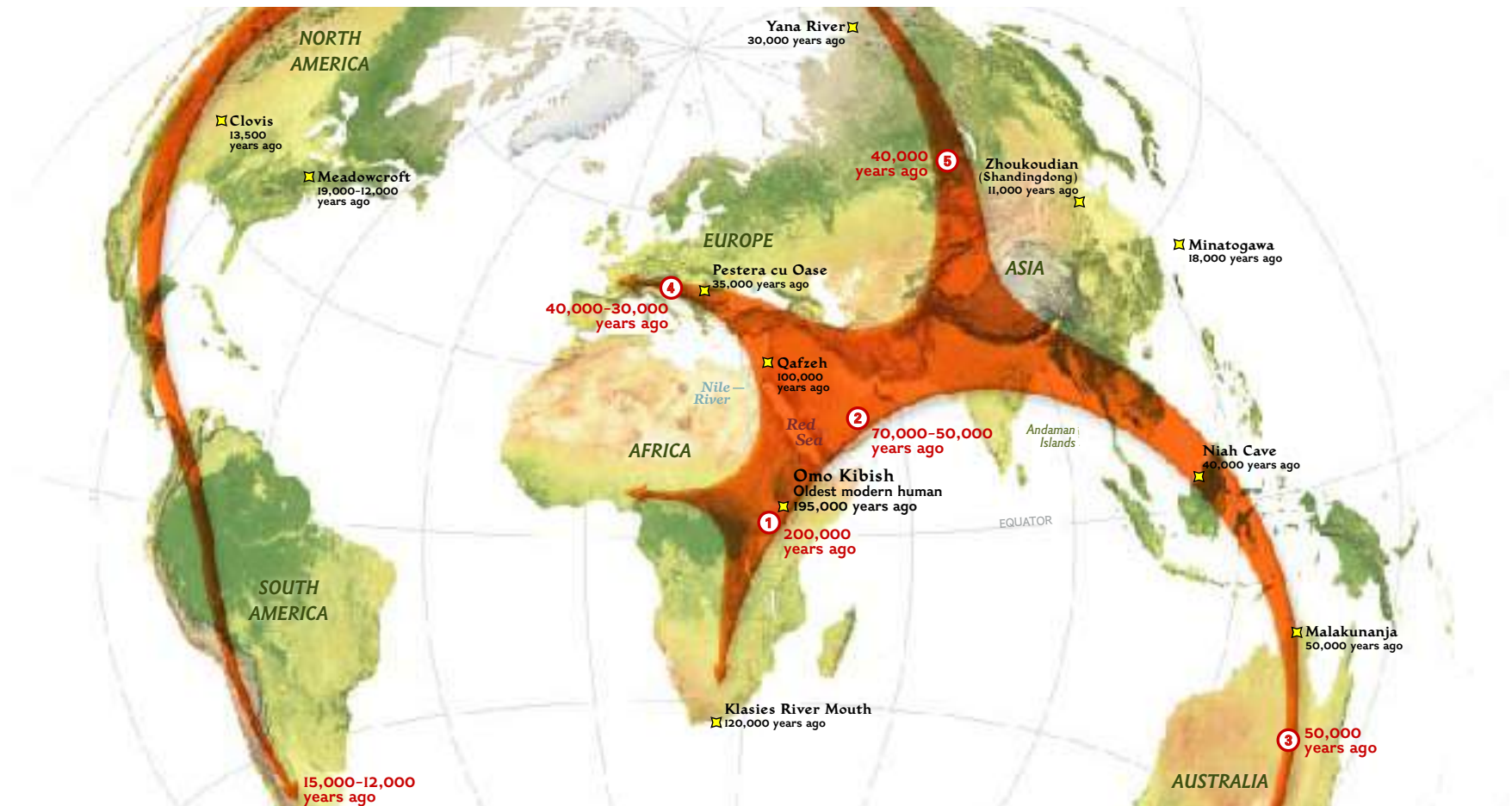
Phylogeography — Historical Biogeography of the Species

The “out-of-Africa” scenario is mostly supported - as shown here - and is consistent with the fossil record.



Phylogeography — Historical Biogeography of the Species

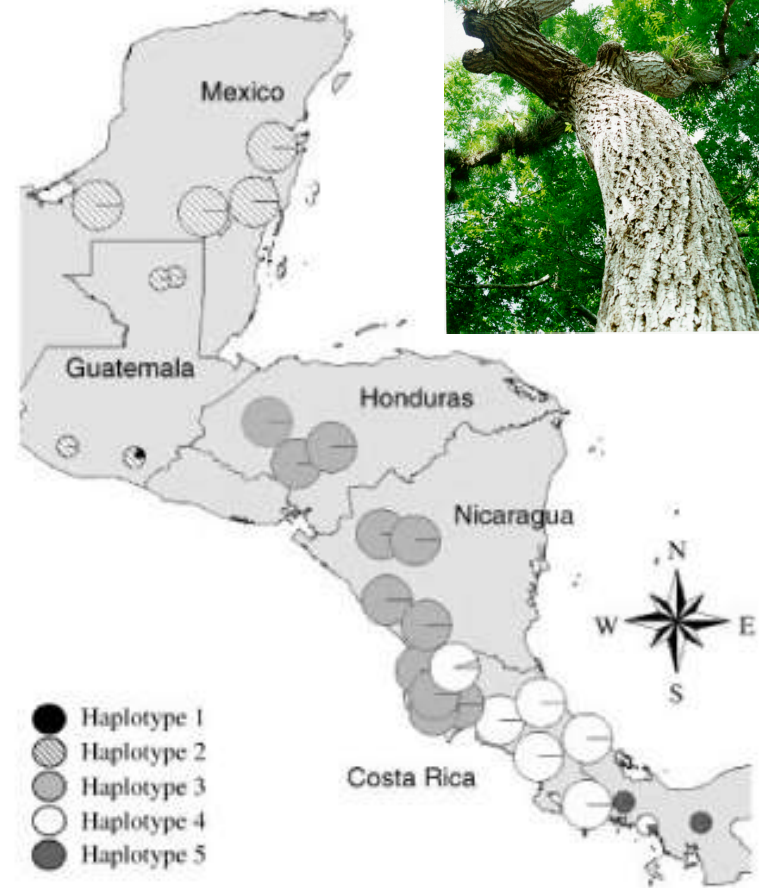
The “out-of-Africa” scenario is mostly supported - as shown here - and is consistent with the fossil record. However, different ways of analyzing DNA support an “out-of-Asia” scenario as well.



Phylogeography — Historical Biogeography of the Species

Steps in a phylogeographic study

1. Sample populations widely **across geographical range** of species
2. Sample multiple individuals from each population to **access levels of variation in DNA** [cpDNA, mtDNA, or nuclear genes]
3. Identify and quantify **genotypes for each population** [haplotypes if cpDNA or mtDNA]



Map of the populations and distribution of haplotypes of *Cedrela odorata* (Spanish cedar) across Mesoamerica (Cavers et al. 2003)

Phylogeography — Historical Biogeography of the Species

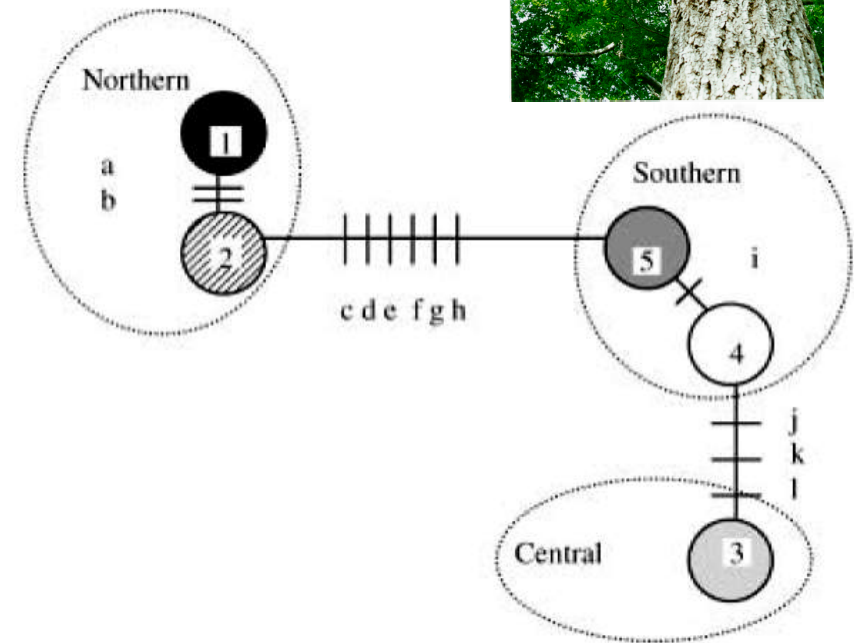


Steps in a phylogeographic study

4. Construct “species” tree/network for the haplotypes

5. Overlay geographical distributions onto the tree/network

6. More recent Next Gen Sequence data allow for more sophisticated *Structure Analysis*



“Species” tree of five haplotypes and their geographic locations for *Cedrela odorata* (Spanish cedar) (Cavers et al. 2003)

Phylogeography — Historical Biogeography of the Species

Example 1: Cryptic invasion of a non-native genotype of *Phragmites australis* (**common reed**) into North America (Saltonstall 2002)



Kristin Saltonstall

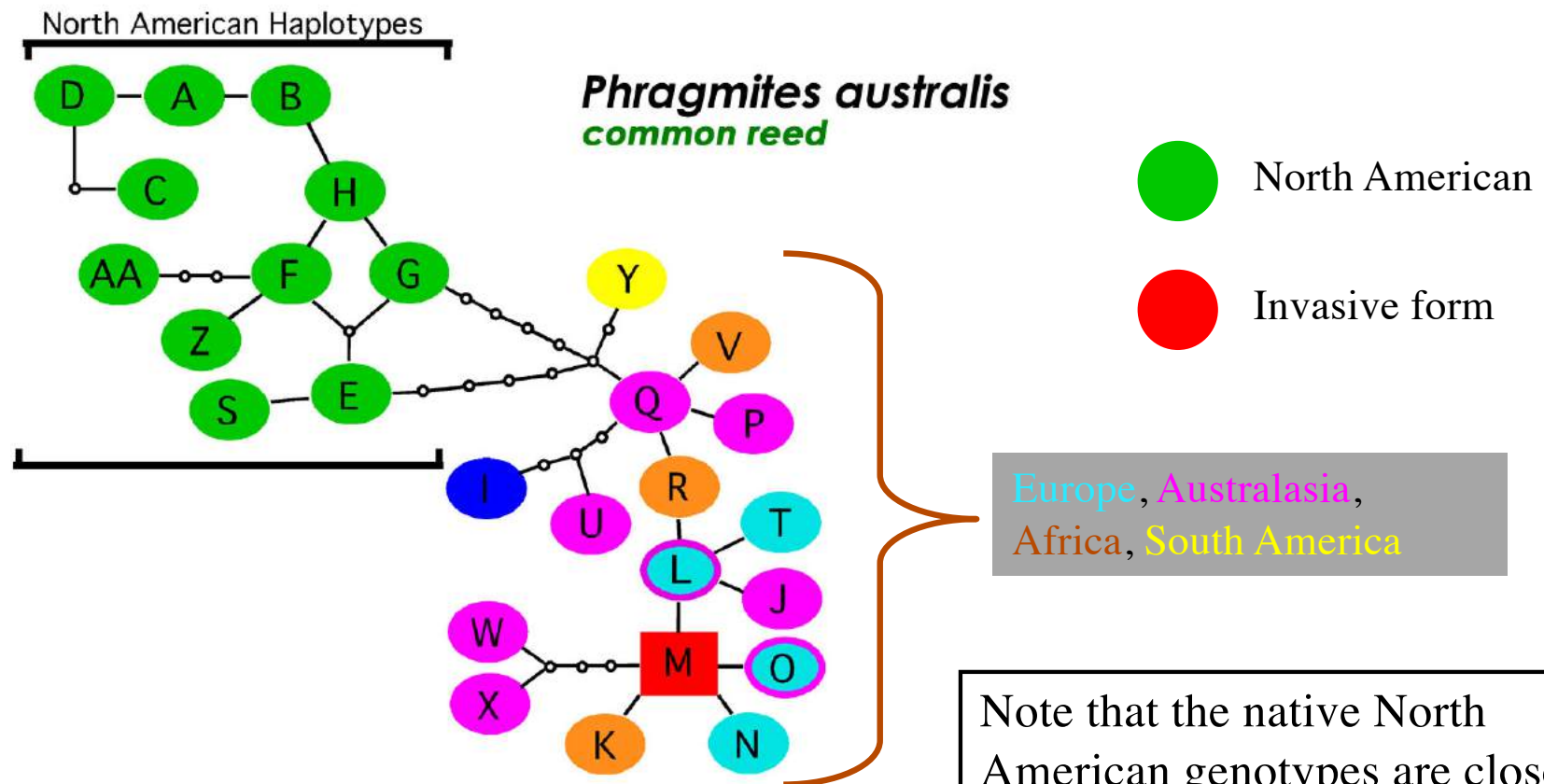


Native population in Great Lakes



Invasive population in Great Lakes

Phylogeography — Historical Biogeography of the Species



Network tree for all genotypes

Note that the native North American genotypes are closely related and they are unrelated to the invasive form from the Old World

Phylogeography — Historical Biogeography of the Species

a) Native Haplotypes Before 1910



Genotyping of common reed from herbarium specimens *prior to 1910* indicates the widespread presence of **11 native genotypes** and **1 southern genotype** also seen in South America and Asia

Phylogeography — Historical Biogeography of the Species

a) Native Haplotypes Before 1910



b) Invasive Haplotype Before 1910



Genotyping of common reed from herbarium specimens *prior to 1910* indicates the widespread presence of **11 native genotypes** and **1 southern genotype** also seen in South America and Asia

A few populations scattered from Connecticut to Maryland prior to 1910 also exhibited the **invasive genotype**

Phylogeography — Historical Biogeography of the Species

a) Native Haplotypes Before 1910



b) Invasive Haplotype Before 1910



c) Native Haplotypes After 1960



Genotyping of common reed from modern populations (both herbarium specimens *after 1960* and extant populations) indicates the same distributions of genotypes

Phylogeography — Historical Biogeography of the Species

a) Native Haplotypes Before 1910



b) Invasive Haplotype Before 1910



c) Native Haplotypes After 1960



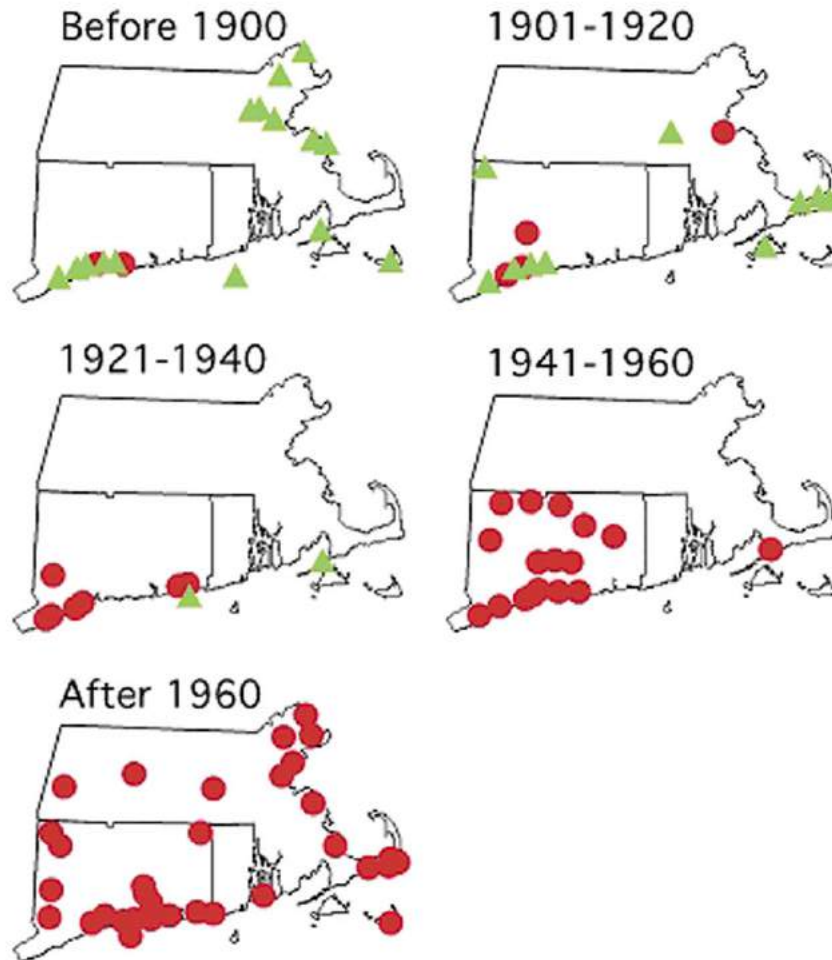
d) Invasive Haplotype After 1960



Genotyping of common reed from modern populations (both herbarium specimens *after 1960* and extant populations) indicates the same distributions of genotypes

However, the **invasive genotype** has dramatically spread across North America since 1910

Phylogeography — Historical Biogeography of the Species



The “invasive” nature of the **introduced common reed** is more dramatically seen in the time sequence of genotyping of pre-1900 to modern populations

The **native North American** genotypes are systematically replaced by the invasive form along the eastern seaboard of Connecticut, Rhode Island, and Massachusetts

Phylogeography — Historical Biogeography of the Species

Example 2: Population relationships within disjunct
species

Chloe Drummond 2018



Western North
American
disjuncts:

Thimbleberry,
Devil's-club,
Monkshood

Phylogeography — Historical Biogeography of the Species

- Pleistocene glacial cycles
(~ 2.5Mya – 11,000 Ya)
- Wisconsin Glacial Episode
(~ 75,000 Ya – 11,000 Ya)
- Last Glacial Maximum (LGM)
(~22,000 Ya)

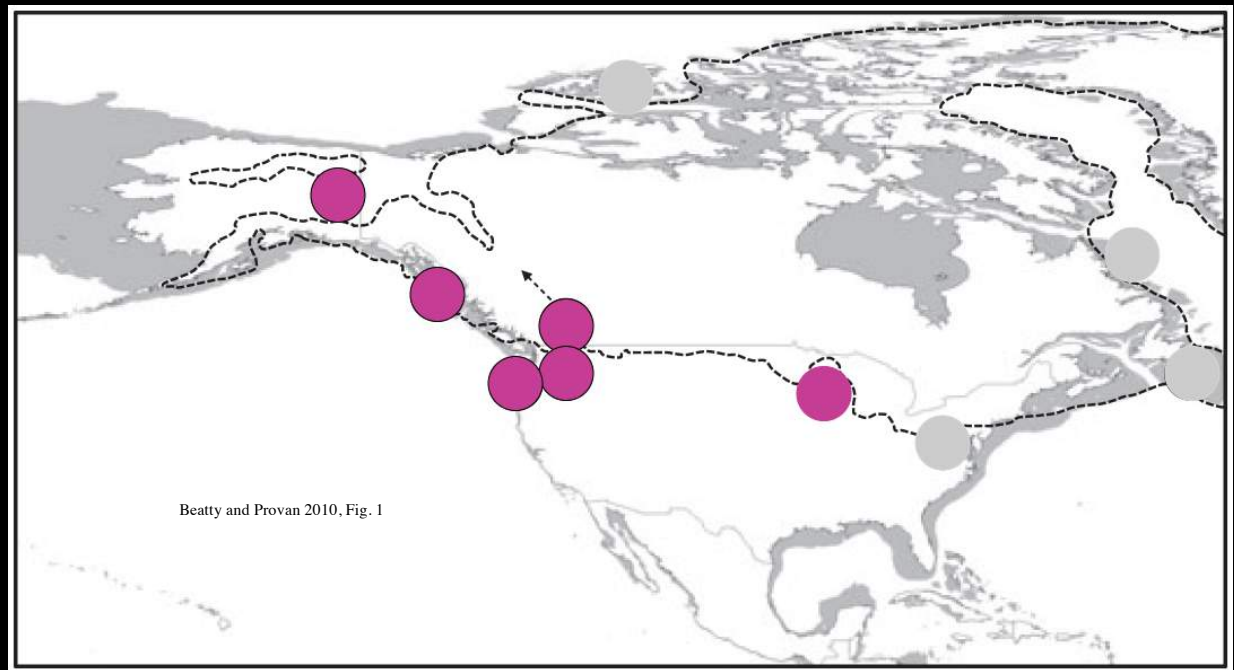


Phylogeography — Historical Biogeography of the Species

A. Persistence in GLR **refugium** during last glacial cycle with re-colonization of glaciated regions

B. **Peri-glacial migration** to the GLR as ice was melting

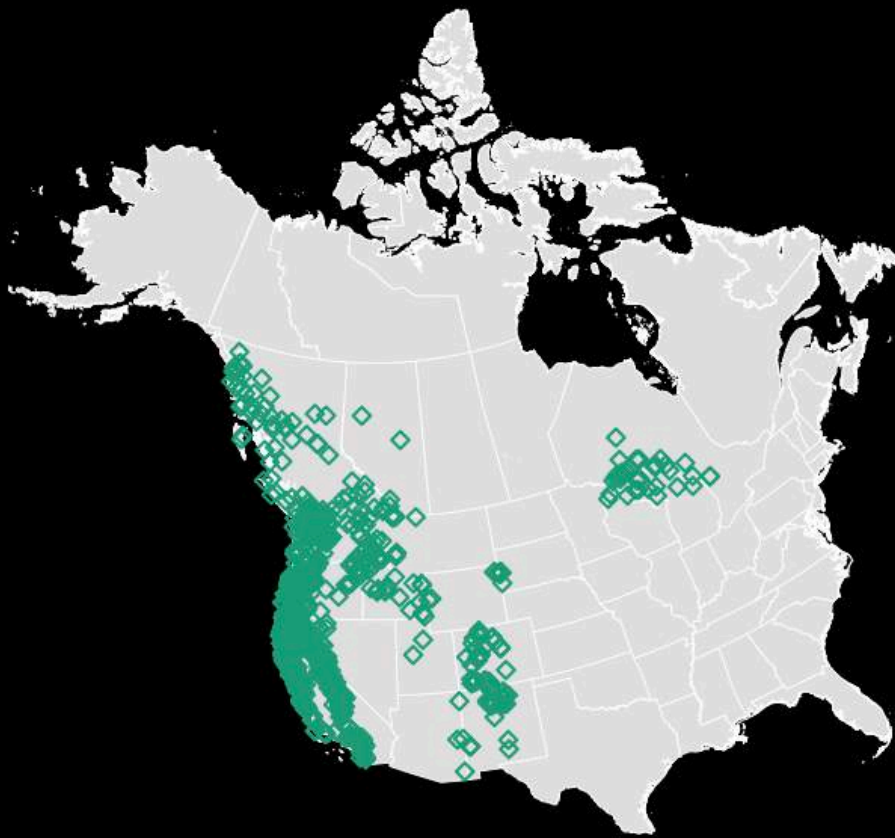
C. **Long-distance dispersal** to the GLR — founder event



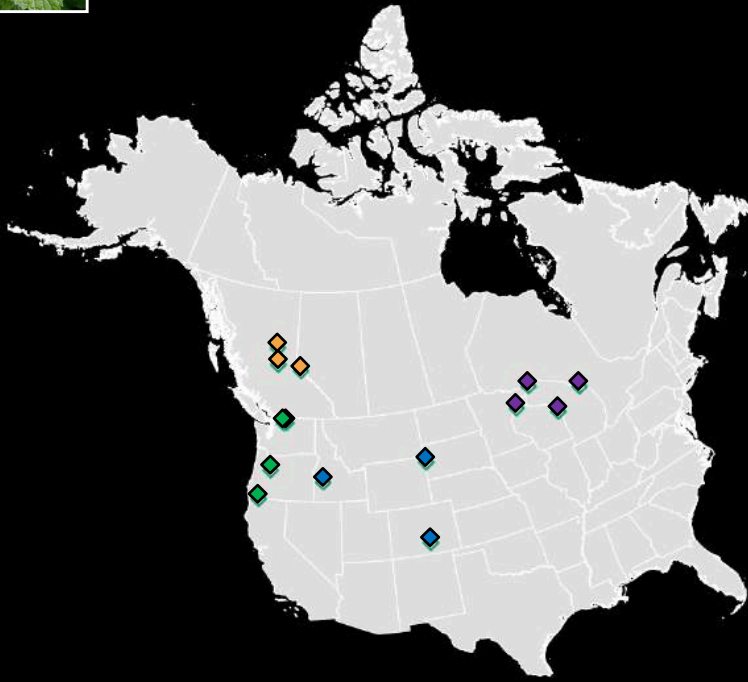
● = putative Pleistocene refugia

Phylogeography — Historical Biogeography of the Species

Example 2: Population relationships within disjunct
species — *Rubus parviflorus* (thimbleberry)

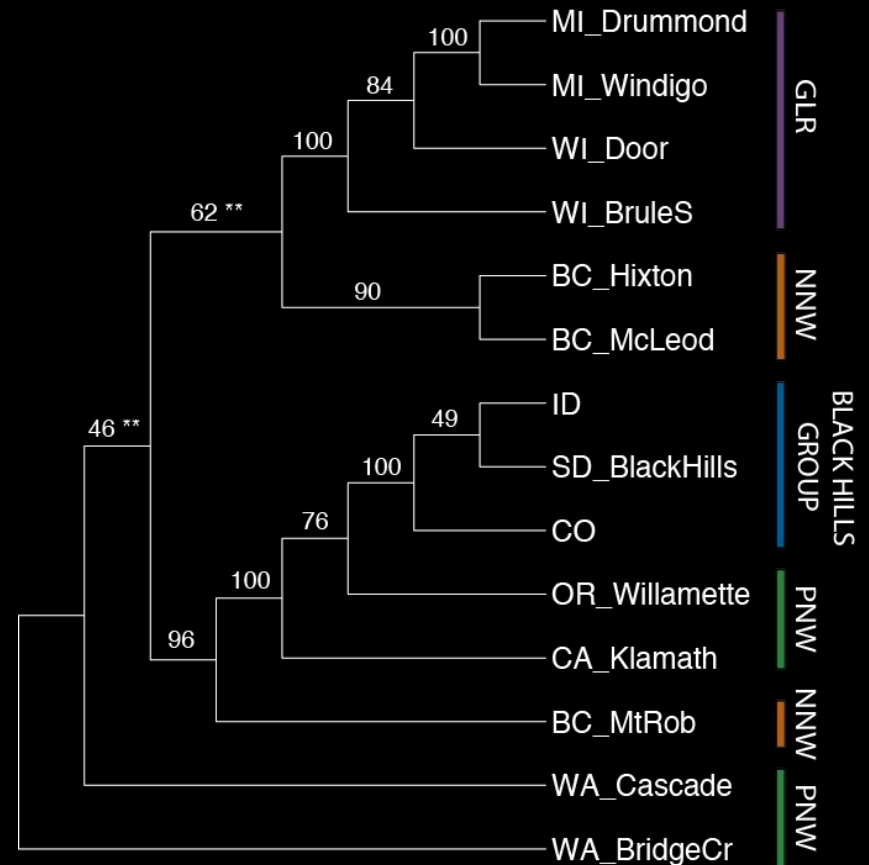


Phylogeography — Historical Biogeography of the Species



Genotyping-by-sequencing
(GBS)

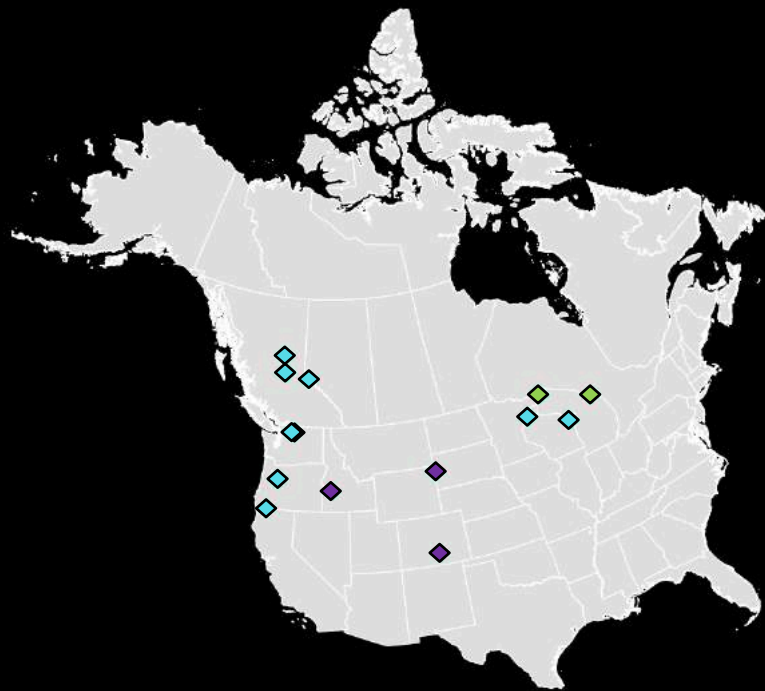
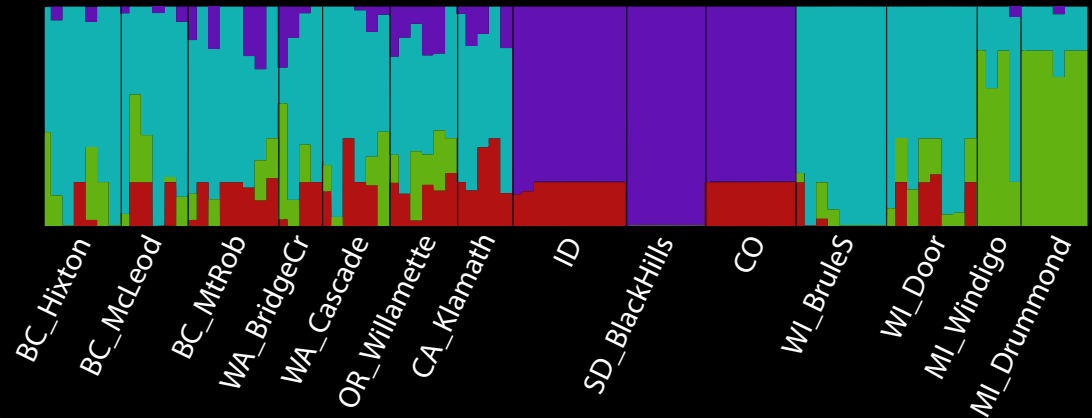
28,512 SNPs



Phylogeography — Historical Biogeography of the Species



Rubus parviflorus K = 4 mean population assignment



- GLR populations **not** from restricted refugium or founder event
- Expansion or migration from BC to the GLR along the receding glacier
- Black Hills did **not** serve as a dispersal stepping stone

Phylogeography — Historical Biogeography of the Species

Example 2: Population relationships within disjunct species — *different stories for different species*



Periglacial migration



Dispersal & founder event



Mid-continental origin and E & W migration