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EVOLUTIONARY LESSONS FROM CALIFORNIA PLANT PHYLOGEOGRAPHY

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Introduction

- Purpose
- Phylogeography
- Concequences of being a plant
- Case study 1 and 2
- Conclusions
- Closing statements and questions

Purpose

To take a fresh look at how environmental factors influence the role of Selection. Discuss 5 characteristics of plants that intensify the impact of selection, and illustrate this with 2 case studies that used modern tools to generate genome wide sequence data.

What is phylogeography?

Phylogeography documents the spatial distribution of genetic lineages that result from demographic processes, such as population expansion, population contraction, and gene movement, which are shaped by climate fluctuations and the physical landscape.

Consequences of being a plant

- Sessility – plants are stationary once established
  - Easy to track distribution
  - Must survive and reproduce in same location
- Leptokurtic pattern of gene flow
  - Through pollen and seeds
  - Majority exhibiting local dispersal
- High reproductive output
  - But only a few seeds land in the right environment– resulting in strong selection
- Environmental influence on gene flow
  - Isolation by distance will almost always be involved in plant phylogeography
- Longevity
  - Local environment will influence size and reproduction
  - Longer life will produce greater genetic diversity
  - Longevity can help prevent extinction
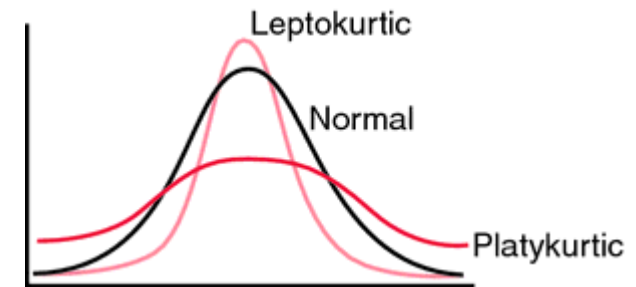
Case study 1

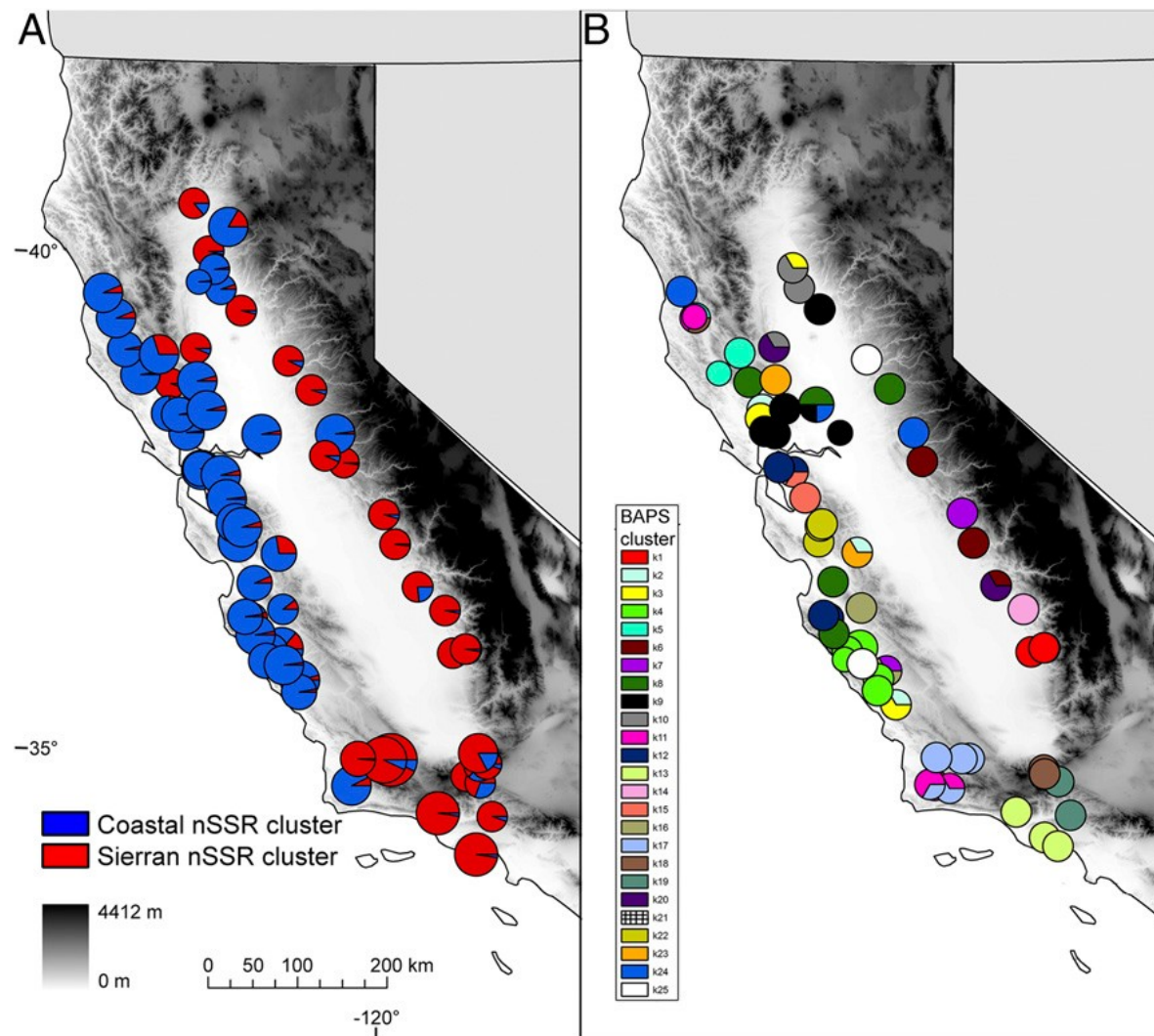- Evolutionary lessons from a California endemic oak, *Quercus lobate*.

Fig. 1. Maps of genetic structure of *Q. lobata* inferred from the nuclear and chloroplast microsatellite genotypes.
(A) STRUCTURE analysis of nuclear microsatellites.
(B) Genetic clusters using BAPS.
Pie charts represent the proportion of genetic assignment to each inferred genetic cluster.
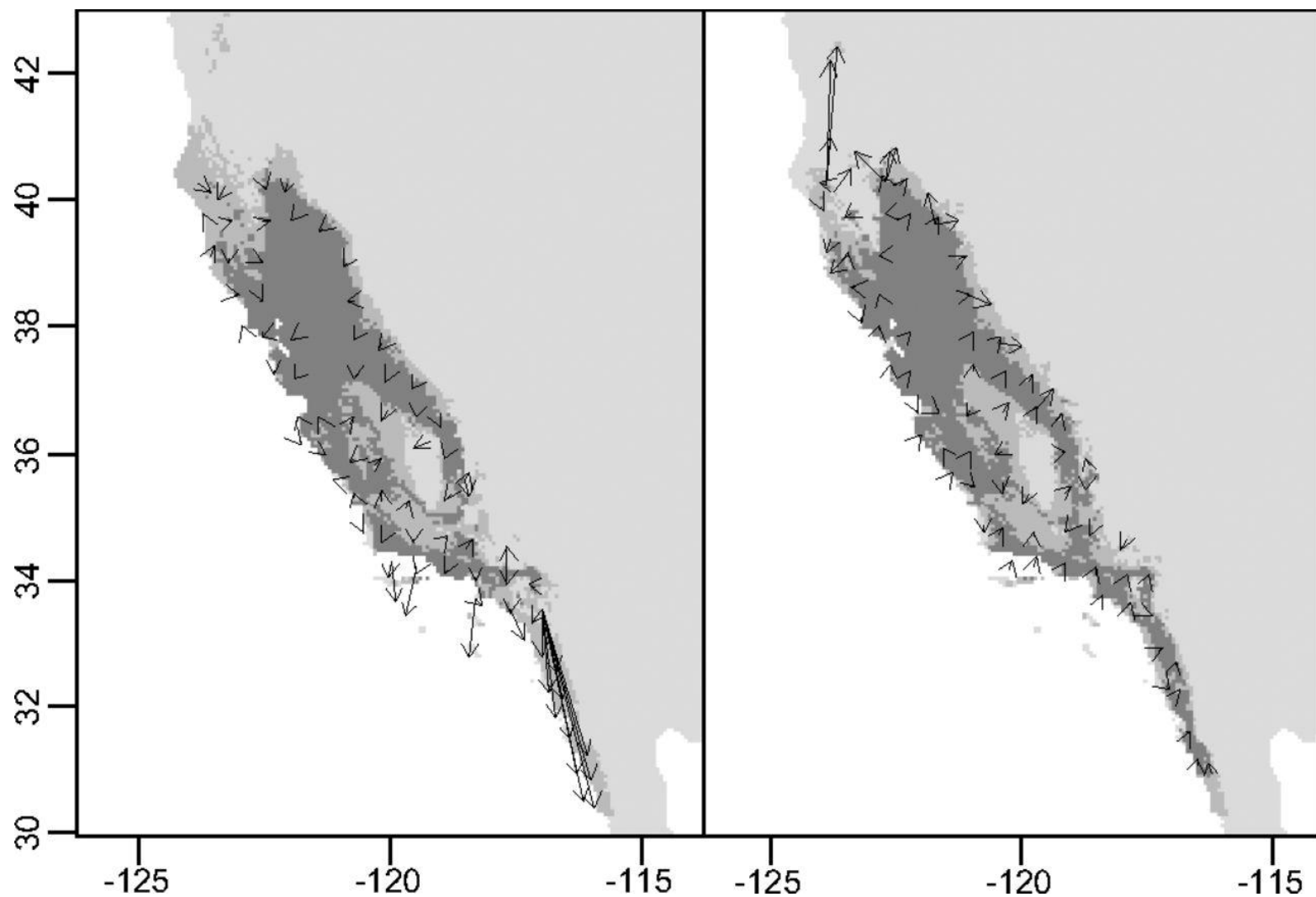Background gradient (gray scale) represents elevation

Fig. 2. Vectors represent the local migration direction of *Q. lobata* during recent interglacial and glacial periods predicted by species distribution models.
(A) Predicted movement from the last interglacial period (~120 ka) to the Last Glacial Maximum (21 ka).
(B) Movement from the Last Glacial Maximum to the present.
Dark gray background represents areas where *Q. lobata* was inferred to be present in both time periods, medium gray indicates present in one time period, and background light gray is present in no time period.

Case study 2

- Evolutionary lessons from California's state lichen, *Ramalina menziesii*.
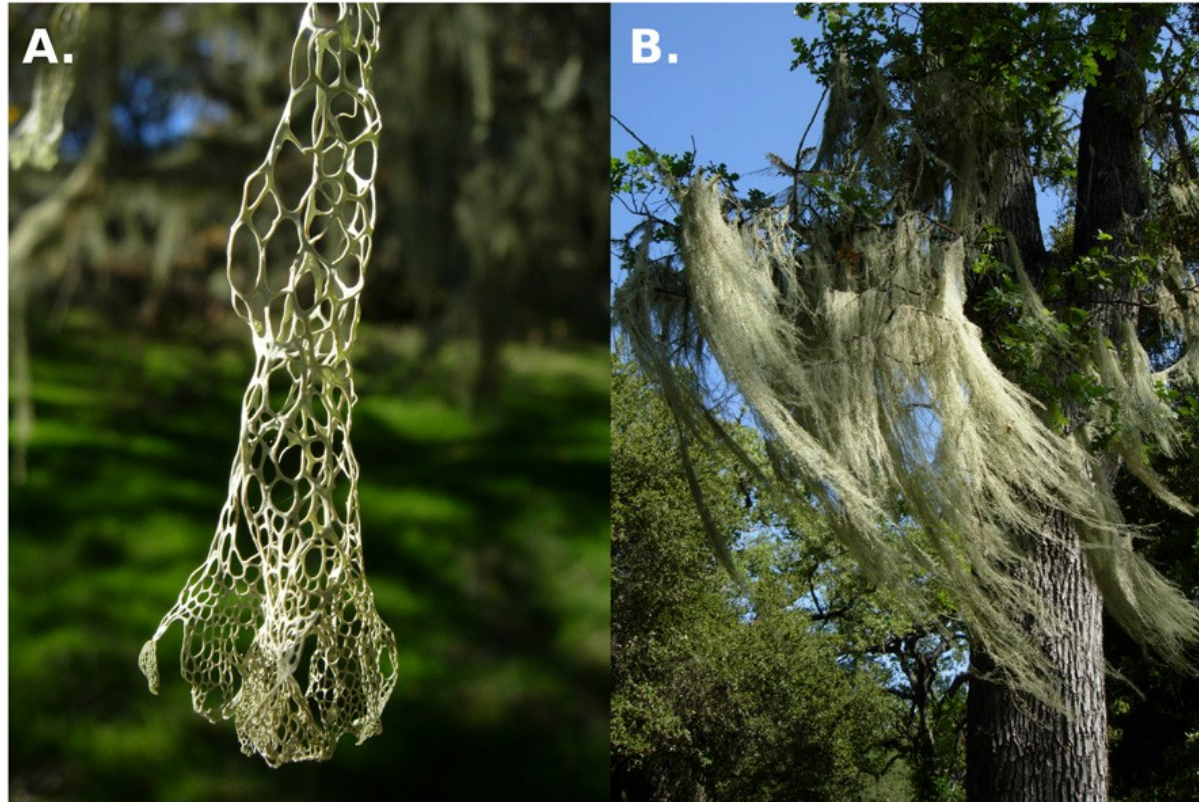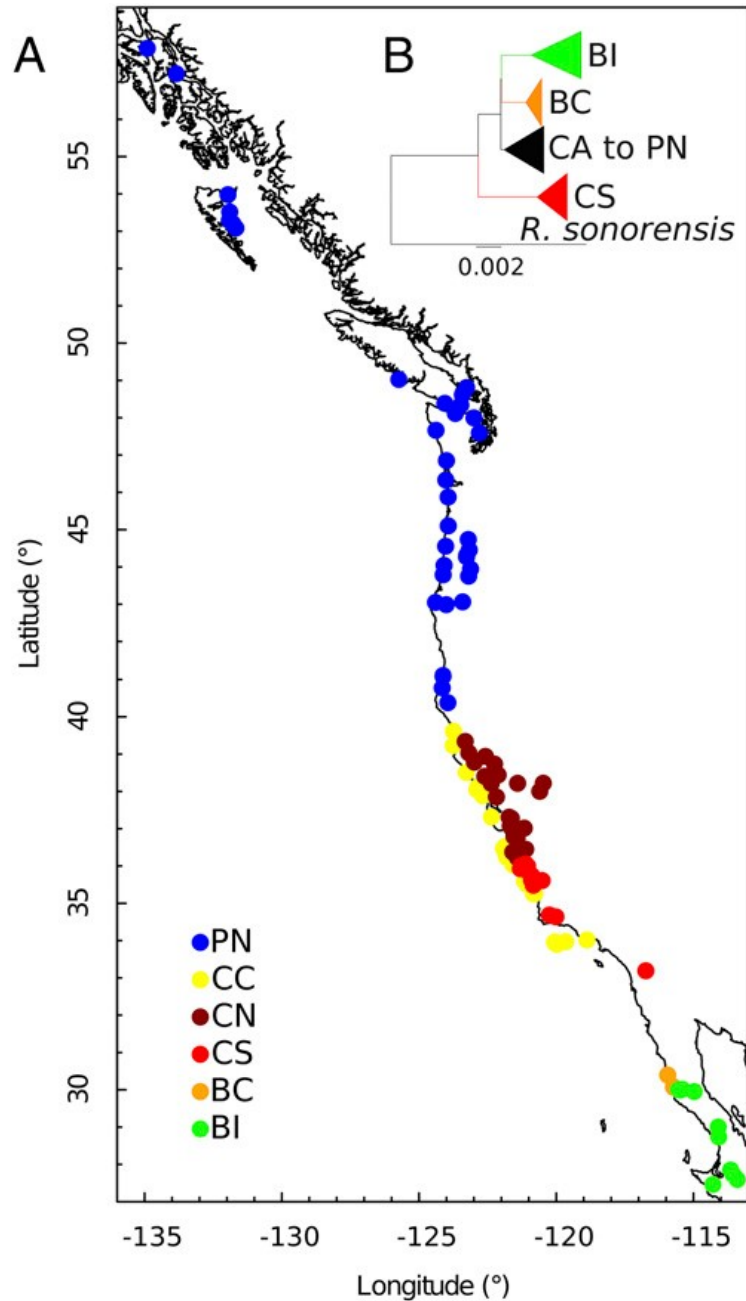
Fig. 5. Spatial distribution of sampling sites and clades of the lichen forming fungus *R. menziesii* along western North America.
(A) Sampling sites, color-coded by ecoregion.
(B) Bayesian Markov Chain Monte Carlo tree generated in BEAST on the basis of four nuclear genes, with ecoregion specific clades color-coded as indicated in the figure. AK, Alaska; BCC, Baja California coastal; BCI, Baja California interior; CA, California; CAI, California interior
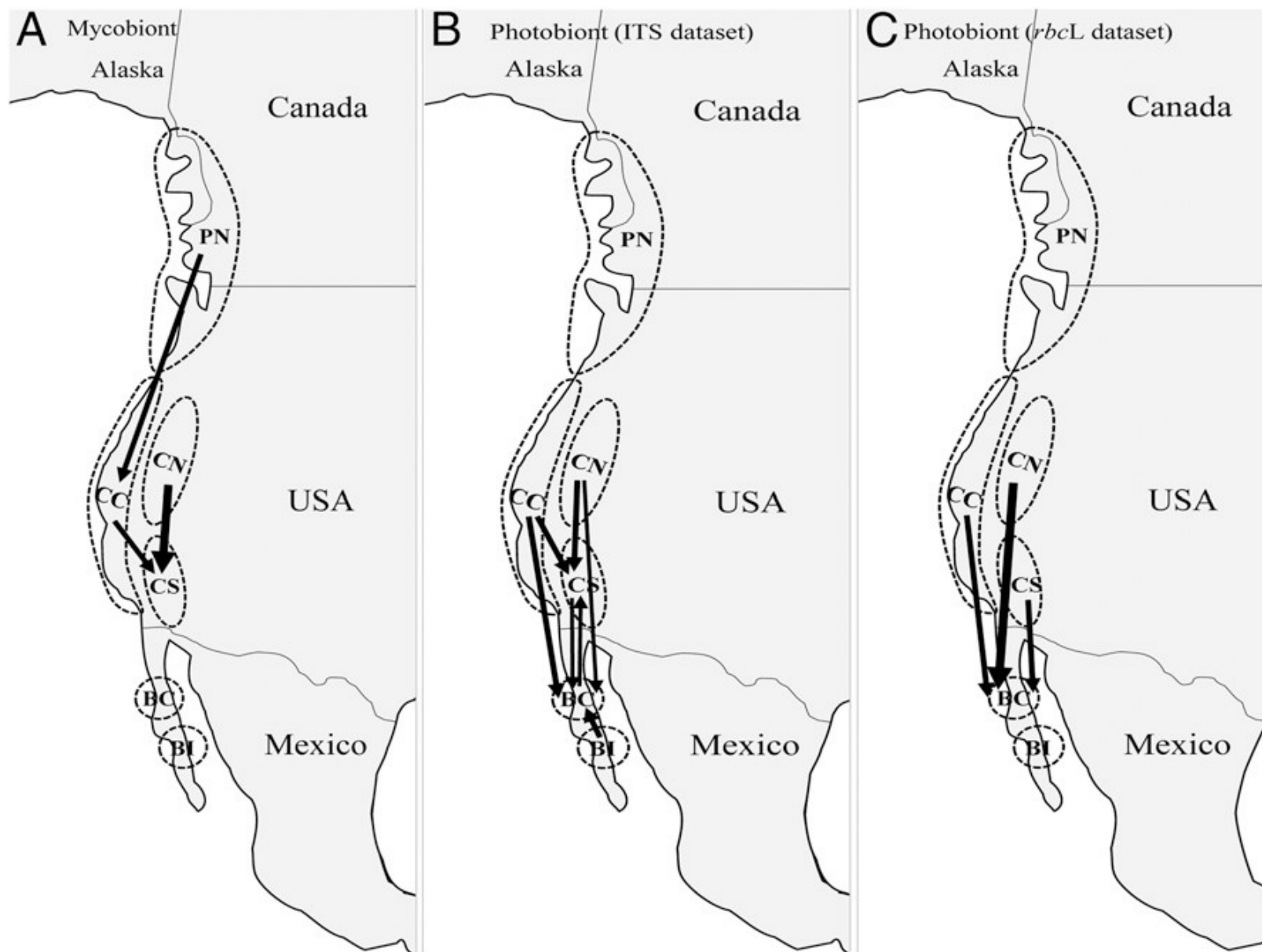
Fig. 6. Comparison of recent migration patterns of *R. menziesii* and *T. decolorans* across ecoregions as inferred from coalescent analysis for three kinds of markers:
(A) fungal nuclear genes,
(B) *T. decolorans* nuclear gene, and
(C) *T. decolorans* chloroplast gene

Conclusions

- These 2 case studies have helped us to see that regions with high environmental heterogeneity and high species diversity is the contribution of natural selection in the response of species to climate fluctuations and the presence of major physical barriers.

- Previous pylogeography studies used neutral demographic patters that appeared to show concordance among multiple species that highlights shared impacts of neutral demographic processes.

- Increasingly, however, through the use of next generation sequencing datasets used to look at large numbers of loci, we are finding that co-occurring species are responding individualistically.

- This will allow us to examine the history of movement of not just species but the processes that led to the shifts in species distributions.

- Future studies that use the new genomic tools that include neutral and adaptive genetic markers will more accurately model species-specific shifts in species distributions due to climate change.

In Closing

- The main problem I had with this paper...
  - Compilation of other sources/peoples work
  - Required lots of additional reading of source material to understand this paper

QUESTIONS?