Developing and Validating Genomic Models for Climate-Transfer Risk In Coastal Douglas-fir (*Pseudotsuga menziesii var. menziesii*)

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Plant Animal Genome

Forest Trees Workshop

1/11/2026

Trees are limited in their capacity to migrate and adapt to changes in climate

Natural history limitations for tree species

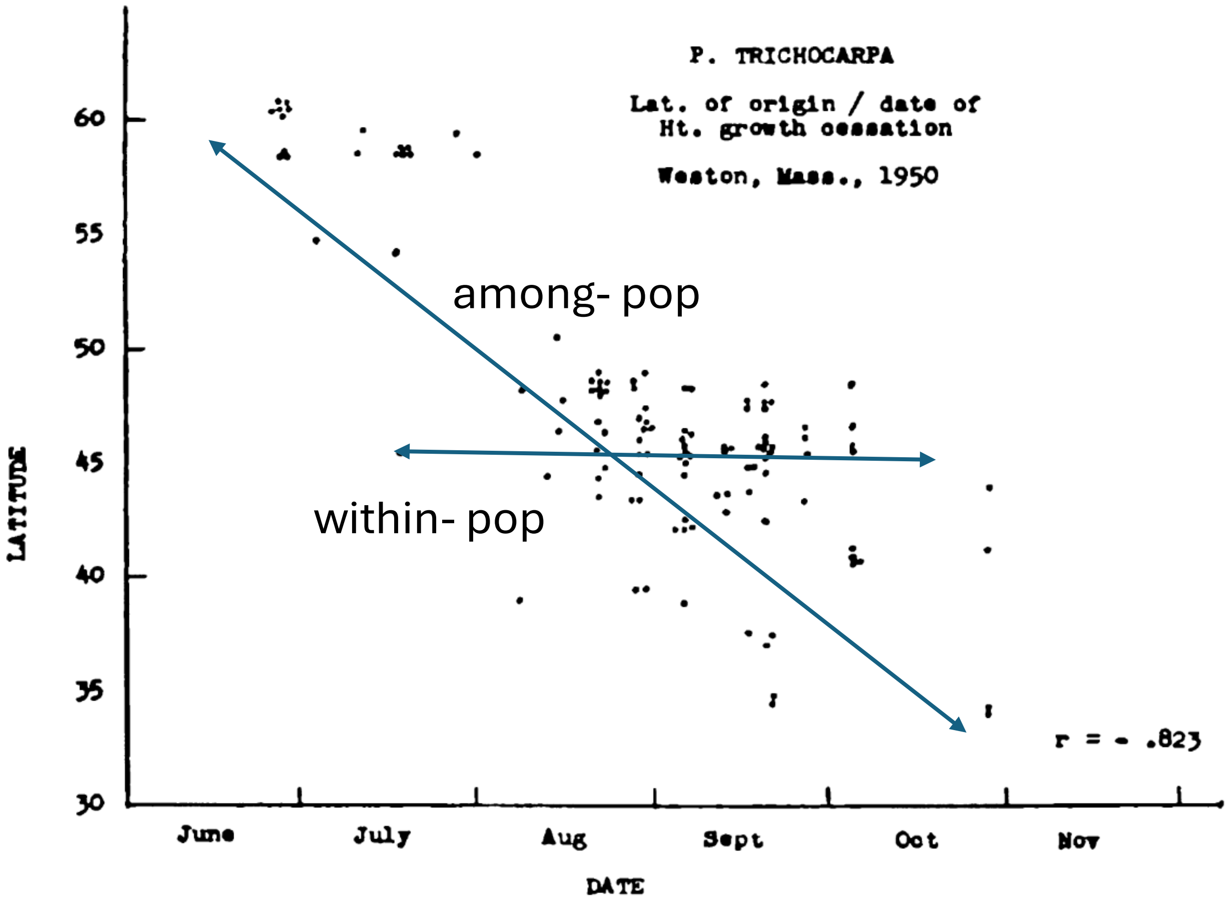
- Long generation times
- Migration rates (100m/yr) << rate of climate change

Likely seeing early effects of climate change in marginal habitat at “trailing edge”

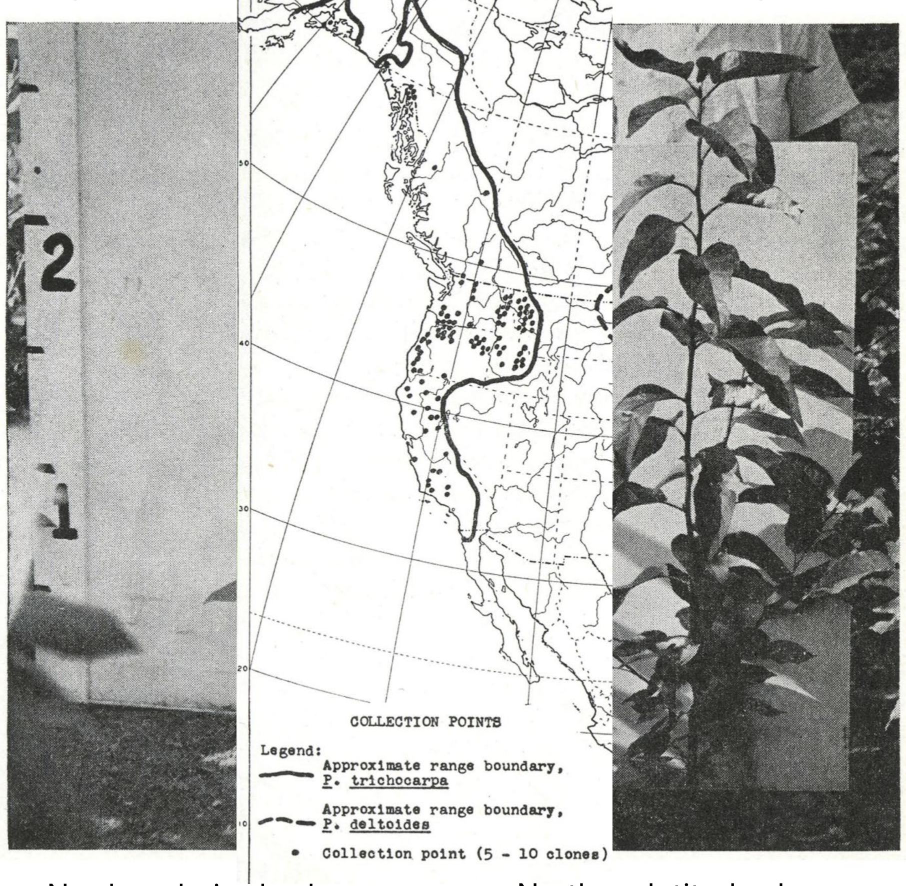
Credit: Chris Adlam, © Oregon State University

Douglas-fir dieback in Applegate valley, So OR

Populations have different potential to respond to climate change due to differences in genetics



Huge impact of provenance variation on growth



Northern latitude clone grown in MA (short day)

Northern latitude clone grown in AL (long day)

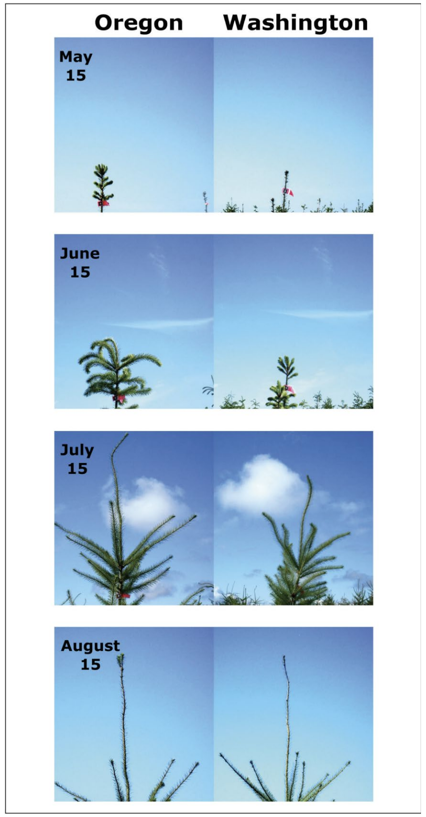
Pauley, S., Perry., T. ,*J. Arnold Arboretum*. 1954

Important traits have high among-pop variation in Douglas-fir

(Van Rooij, M. *Annals of Plant Science*, et al. 2024)

Cregg, B., MSU Extension, 2017)

Cold injury (fall/spring)



Harrington, C., St. Clair, B.
Western Forester. 2017

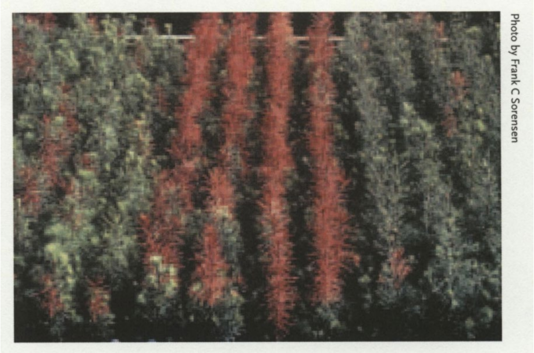
Bud set/growth cessation

Forest management greatly influences adaptive capacity of forests

Provenance trials

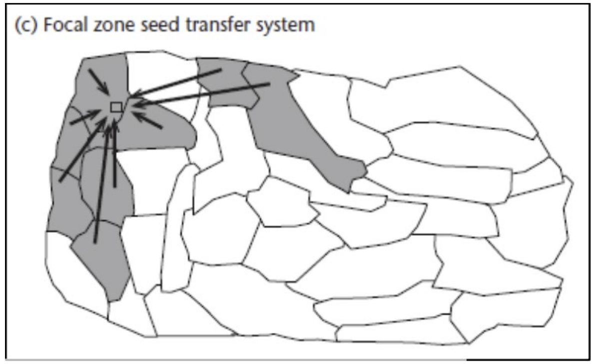
Hernandez *et. al.*, PSW-GTR-146 ,1993

Common garden studies

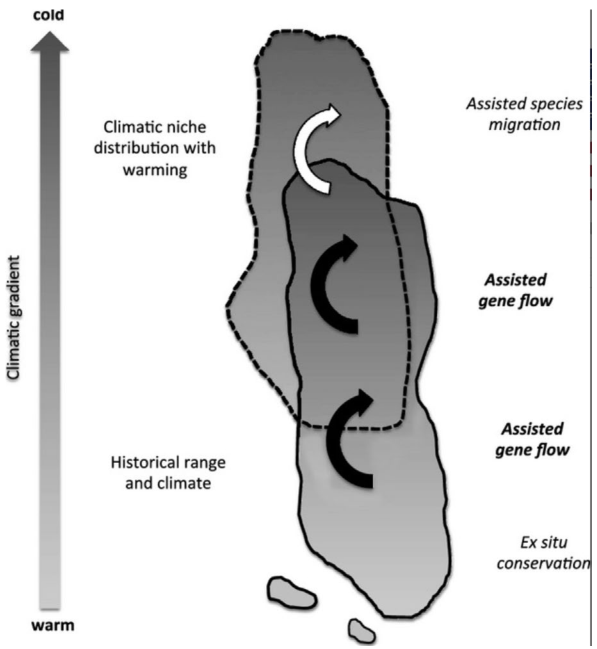


Johnson G.R., *et al. Native Plants*, 2004

Seed transfer guidelines



O’Neill *et al*. 2017. B.C. Tech. Rep. 099.



Aitken, S., Bremmels, J., *Evol. Appl.*, 2015

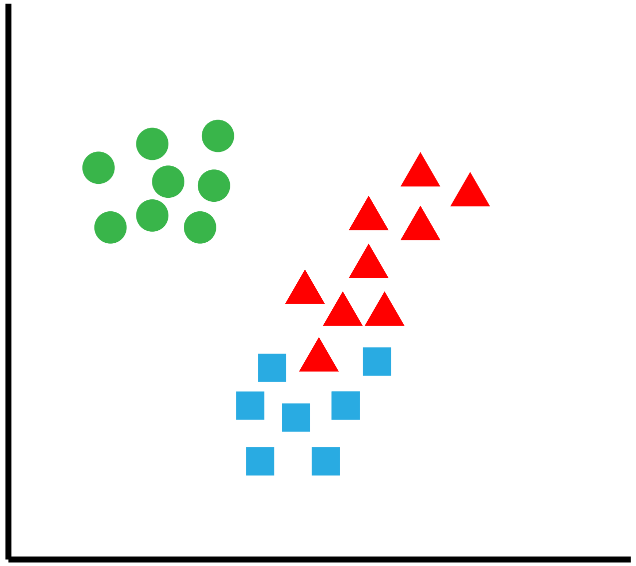
Risks

- Future maladaptation
- Current maladaptation

How do we decide where to plant for future climates?

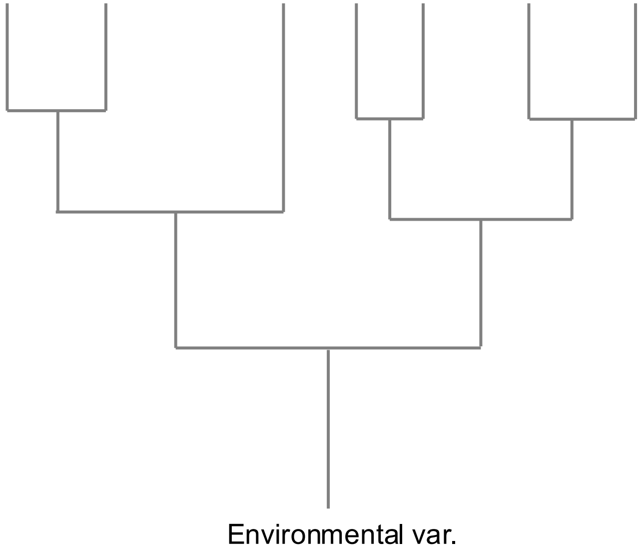
Oregon Department of Forestry

Can genomic information be used to manage seedlots under uncertainty?

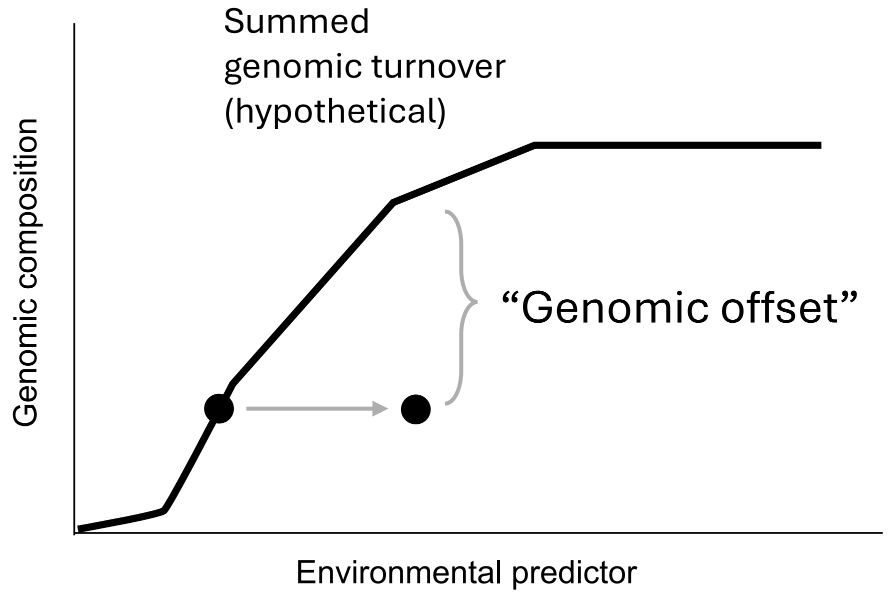


Genomic variation within and among pops

Decision tree



Model environmental predictors That explain variation among & within pops



Project suitability of genetic material in different (e.g. future) climate

Predictions from genomic models require robust empirical validation

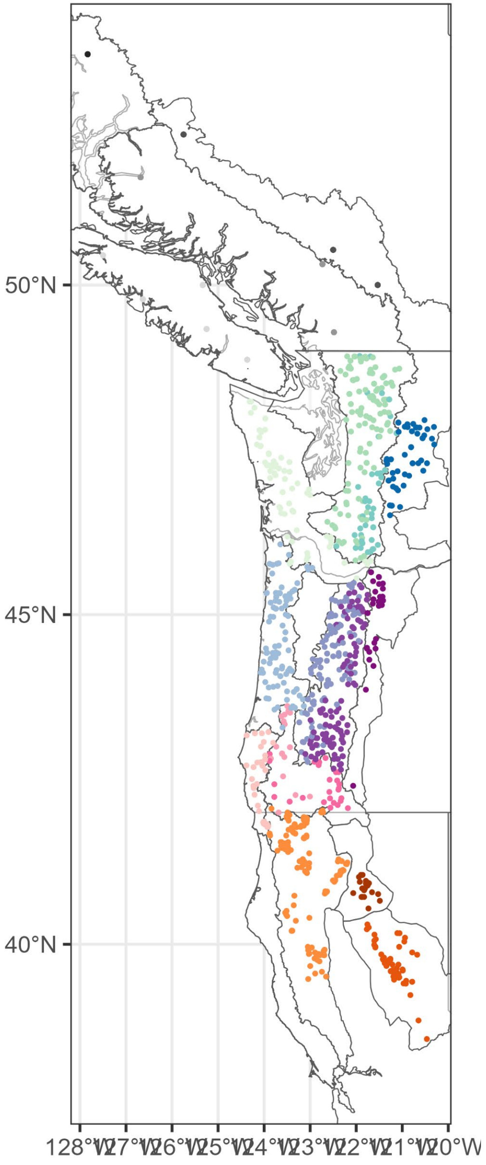
Benefits

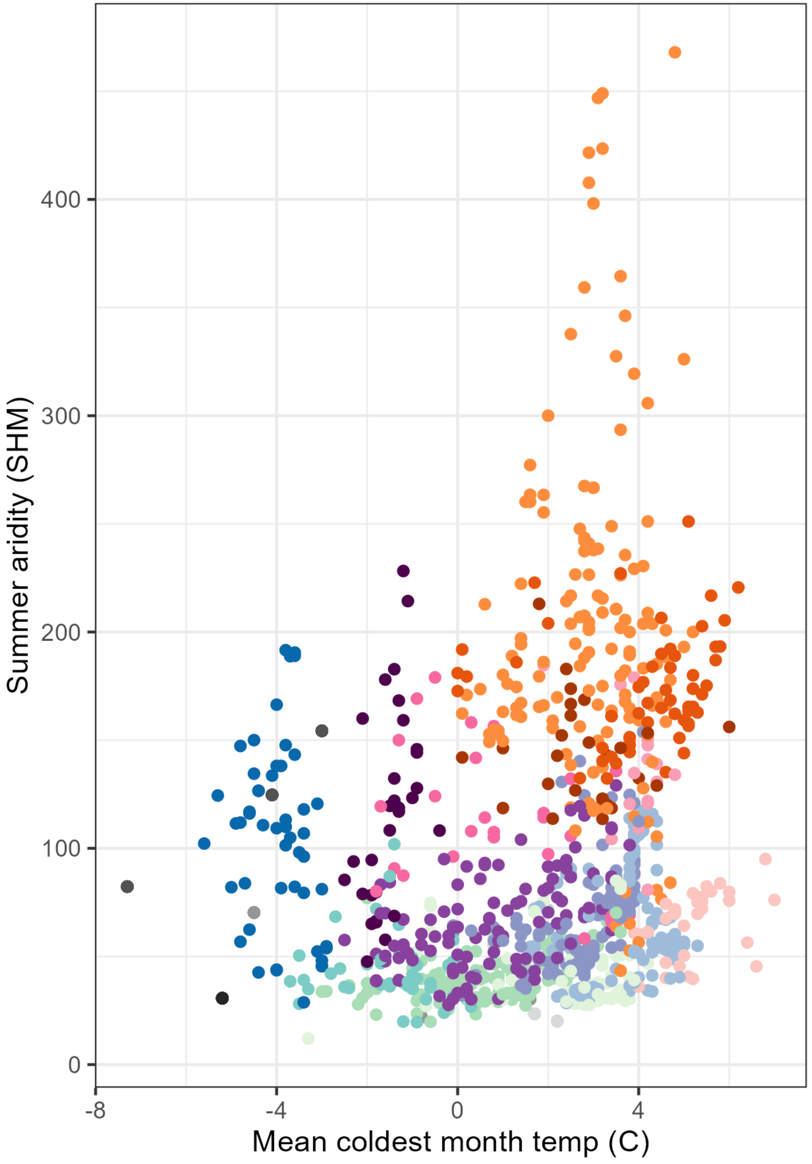
- Phenotypes are expensive
- Larger samples sizes
- High resolution data

Concerns

- Fitness proxies
- Population structure mirrors adaptive clines
- Complex genetic architecture

Developing model of genomic “offset” in coastal Douglas-fir

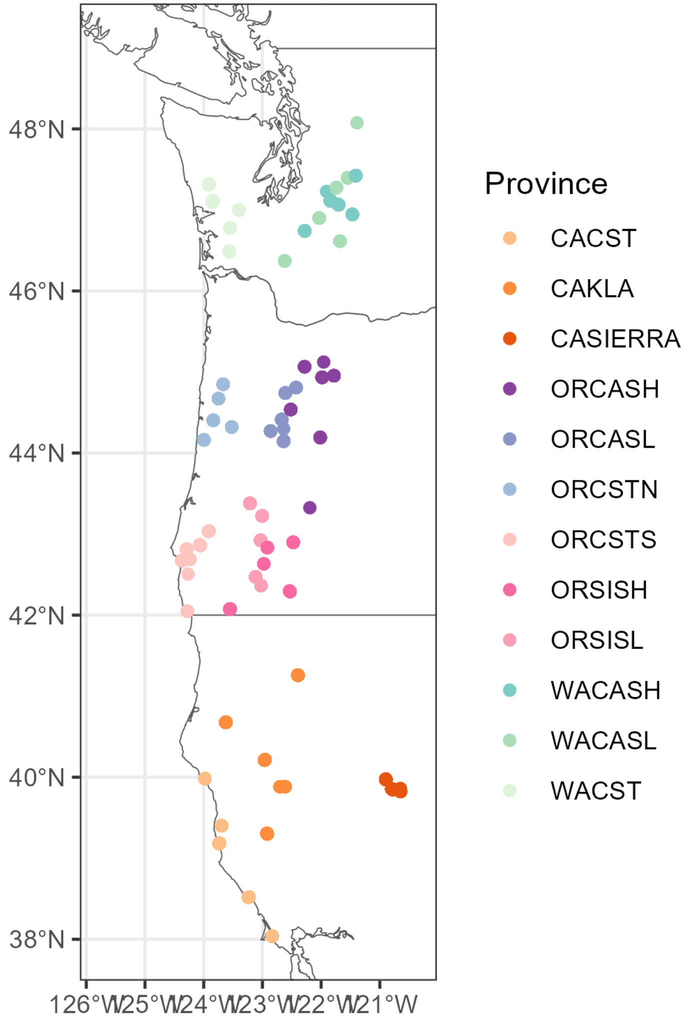




Samples grouped into provinces

- Underlying seed zones (1966)
- Groupings based on Omernik level III ecoregions

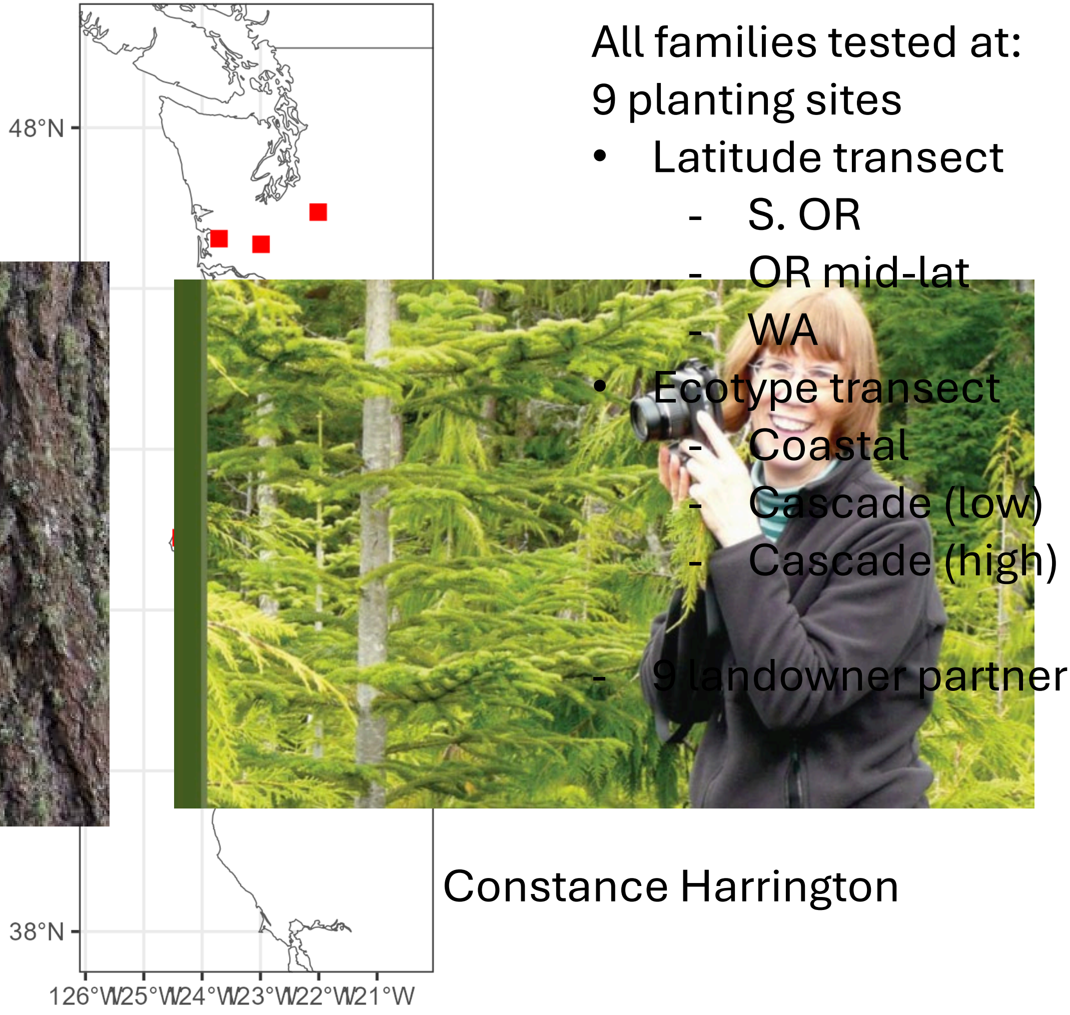
Using Seed Source Movement Trials for empirical validation of genomic model of climate drivers of adaptation in coastal Douglas-fir



- 120 families from 60 populations
- Populations from 12 provinces
- Populations selected from previous genecology study
- 806 trees genotyped

Brad St. Clair

All families tested at:
9 planting sites
- Latitude transect
  - S. OR
  - OR mid-lat
  - WA
- Ecotype transect
  - Coastal
  - Cascade (low)
  - Cascade (high)
- 9 landowner partners

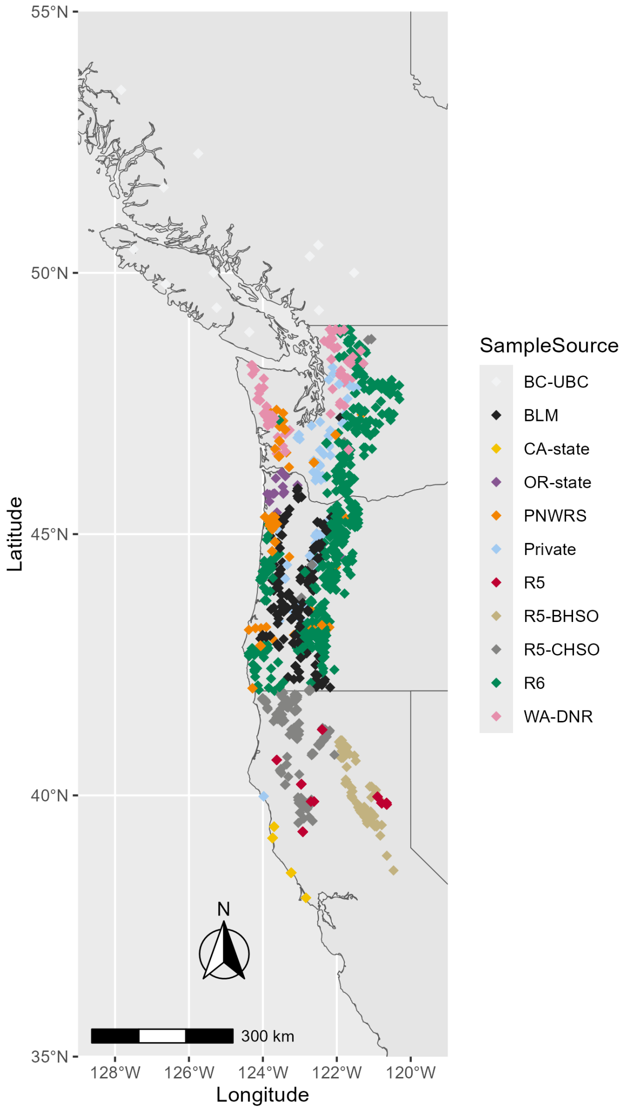


Constance Harrington

Characterizing range-wide genomic variation in coastal Douglas-fir using an Axiom array

- Is variation in genomic markers found mostly among or within populations?
- Are there outliers that would inform model development?
- Which if any populations have data that appear to be affected by ascertainment bias?
- How well does a preliminary model capture variance?

Samples span range of coastal variety



Lisa Crane, USDA R5

Sally Aitken, UBC

Brad St. Clair

Jeff deBell and co., DNR

Rafael Candido-Ribeiro, UBC

2276 trees were genotyped for 18732 polymorphic high-resolution loci

DNA extracted from germinated cotyledons or dried needle tissue

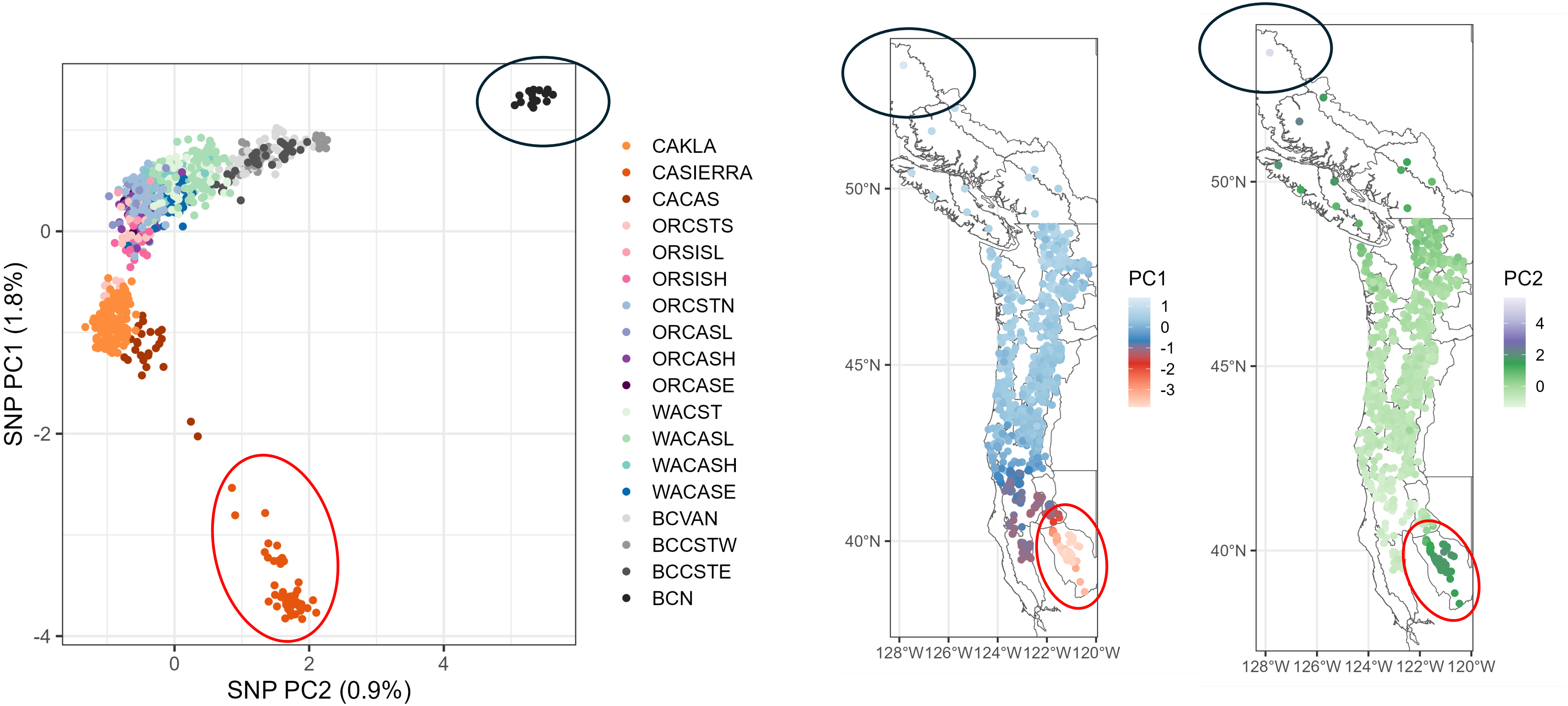
Sample quality thresholds for ThermoFisher Axiom Array analysis

	dQC	CR	N
best workflow	>=0.90	0.97	2023
dual workflow	>=0.82	0.9	253
total			2276

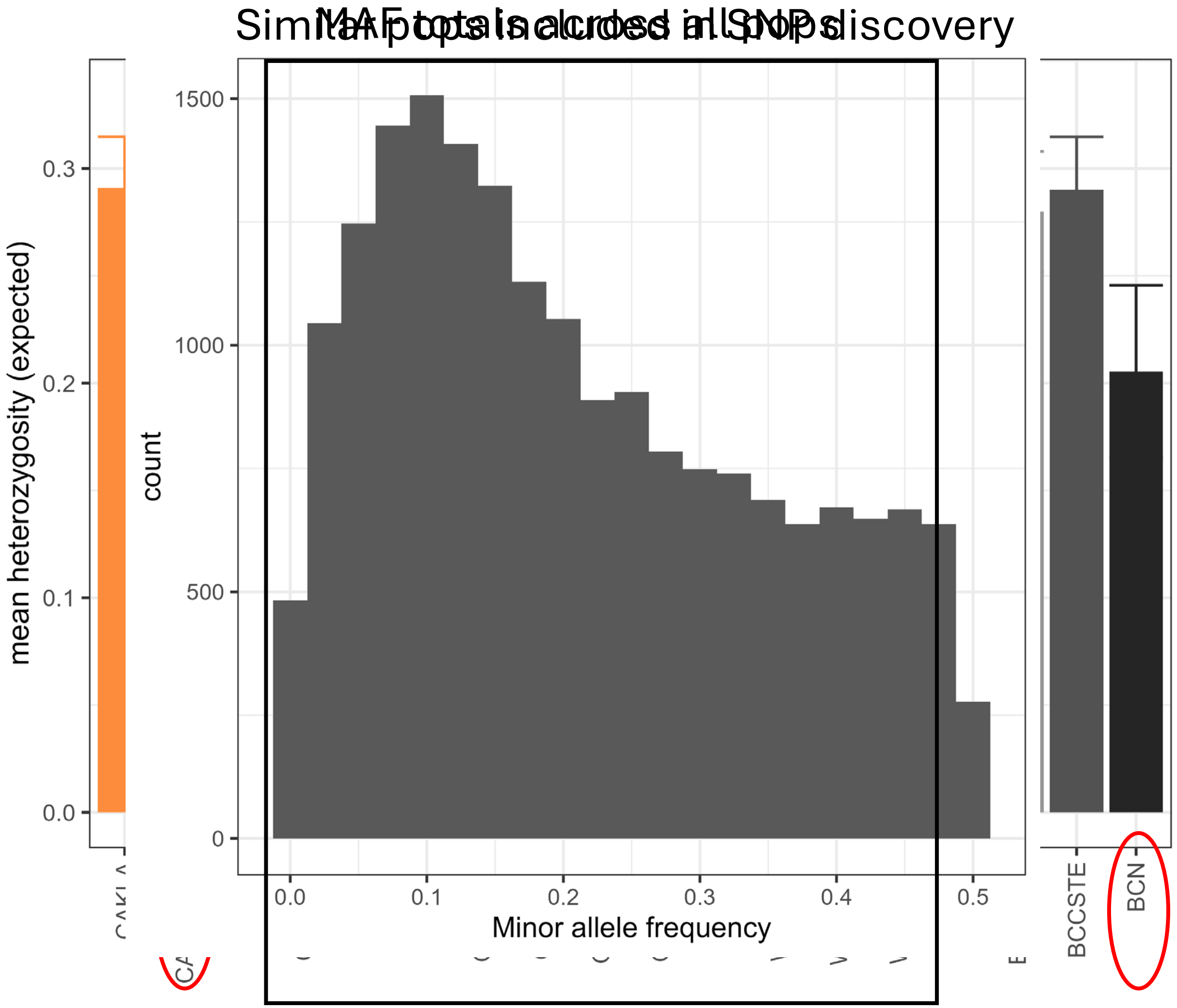
SNP categories from current and previous genotyping

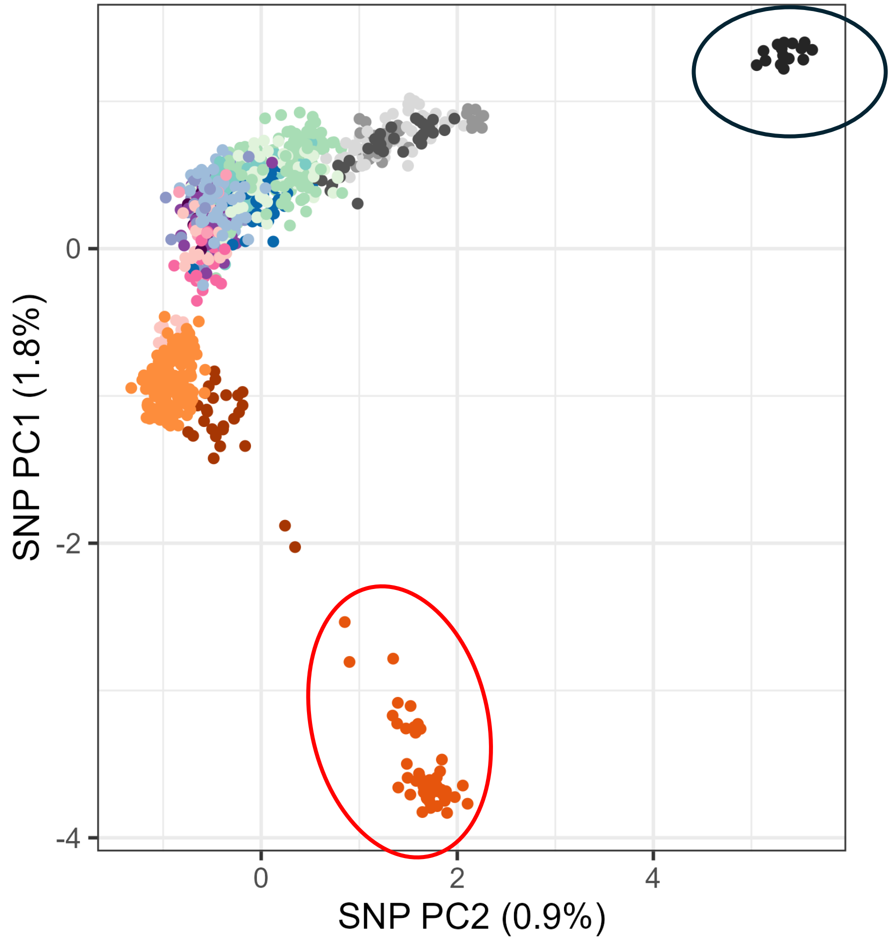
SNP category	2025_SNPs	2015_SNPS
Polymorphic|High Resolution	25081	18732
Polymorphic|NoMinorHomozygote	9307	9396
Monomorphic|HighResolution	8409	8224
LowCallRate	3760	4800
OffTargetVariant|Other	11712	16534

Genomic variation is high within populations but with outlier populations

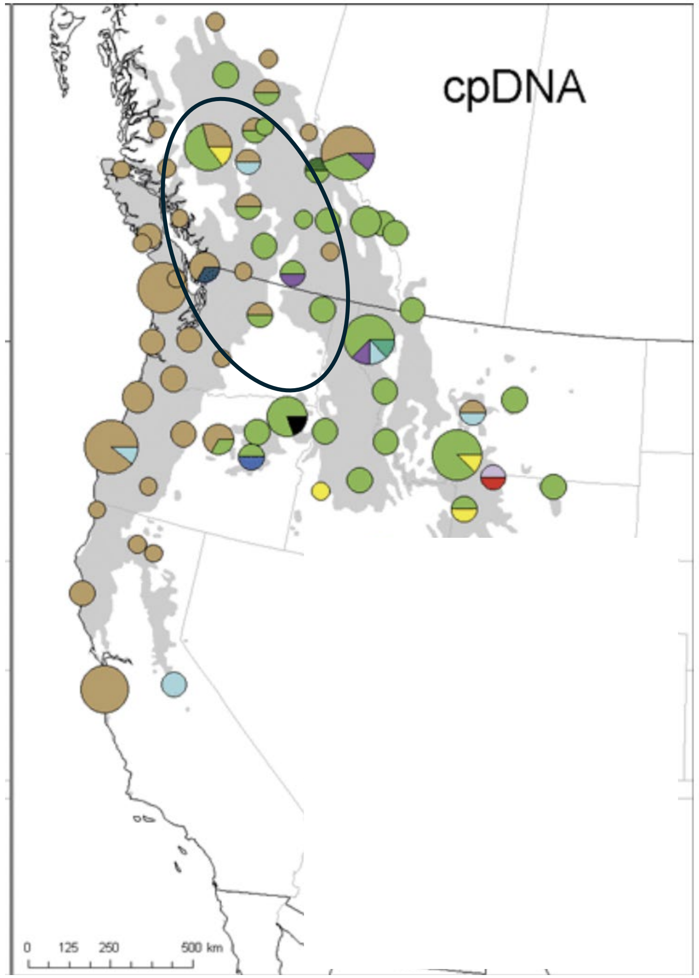


Outlier populations have more rare alleles and lower genetic diversity (exp. heterozygosity)

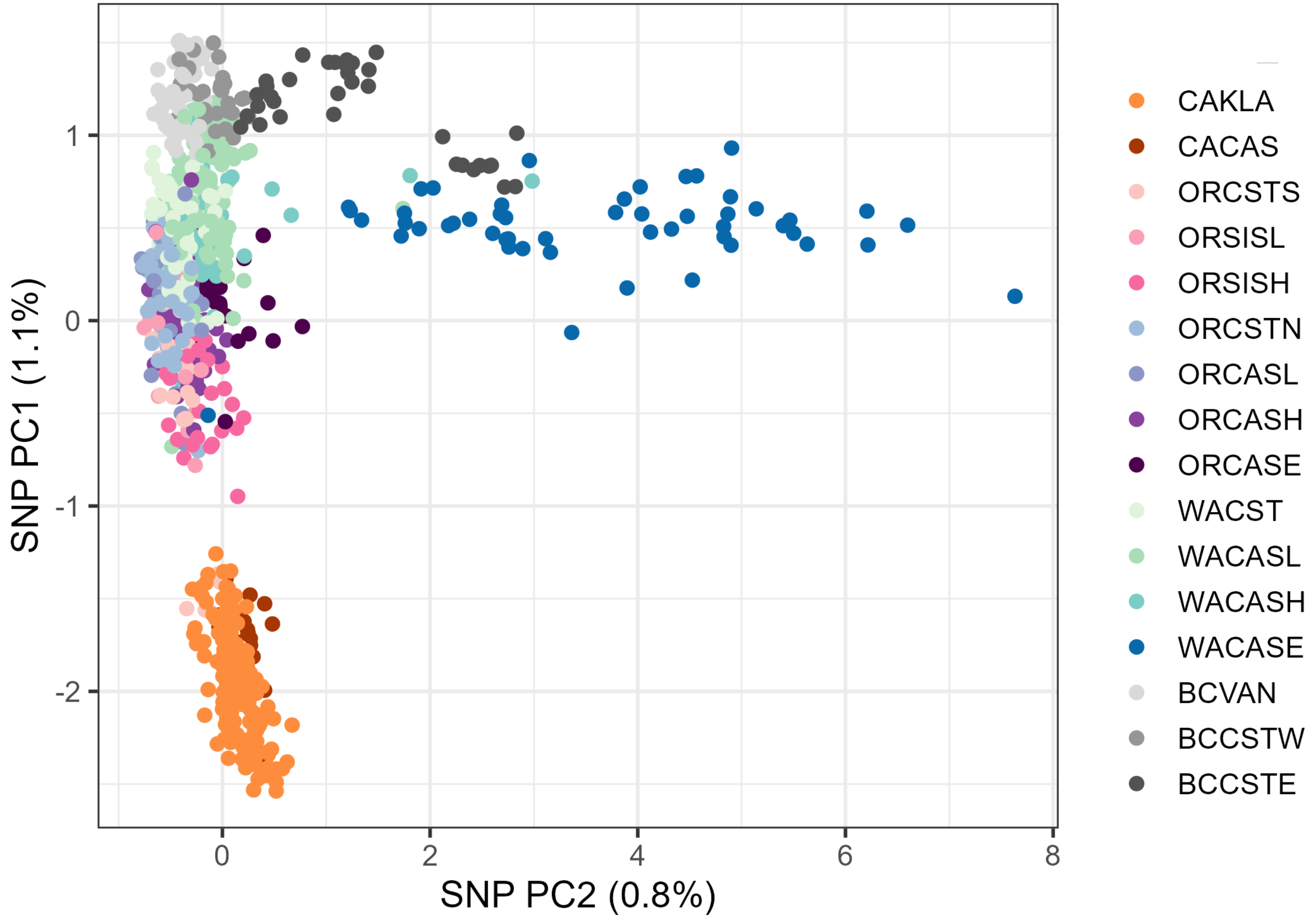




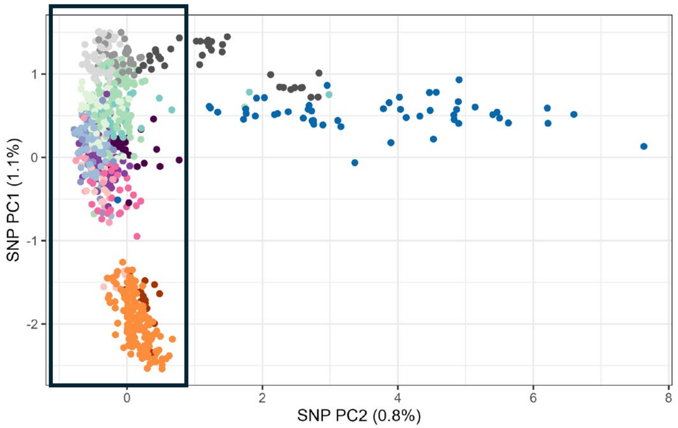
PCA of population w/o outliers reflects gene flow with interior variety

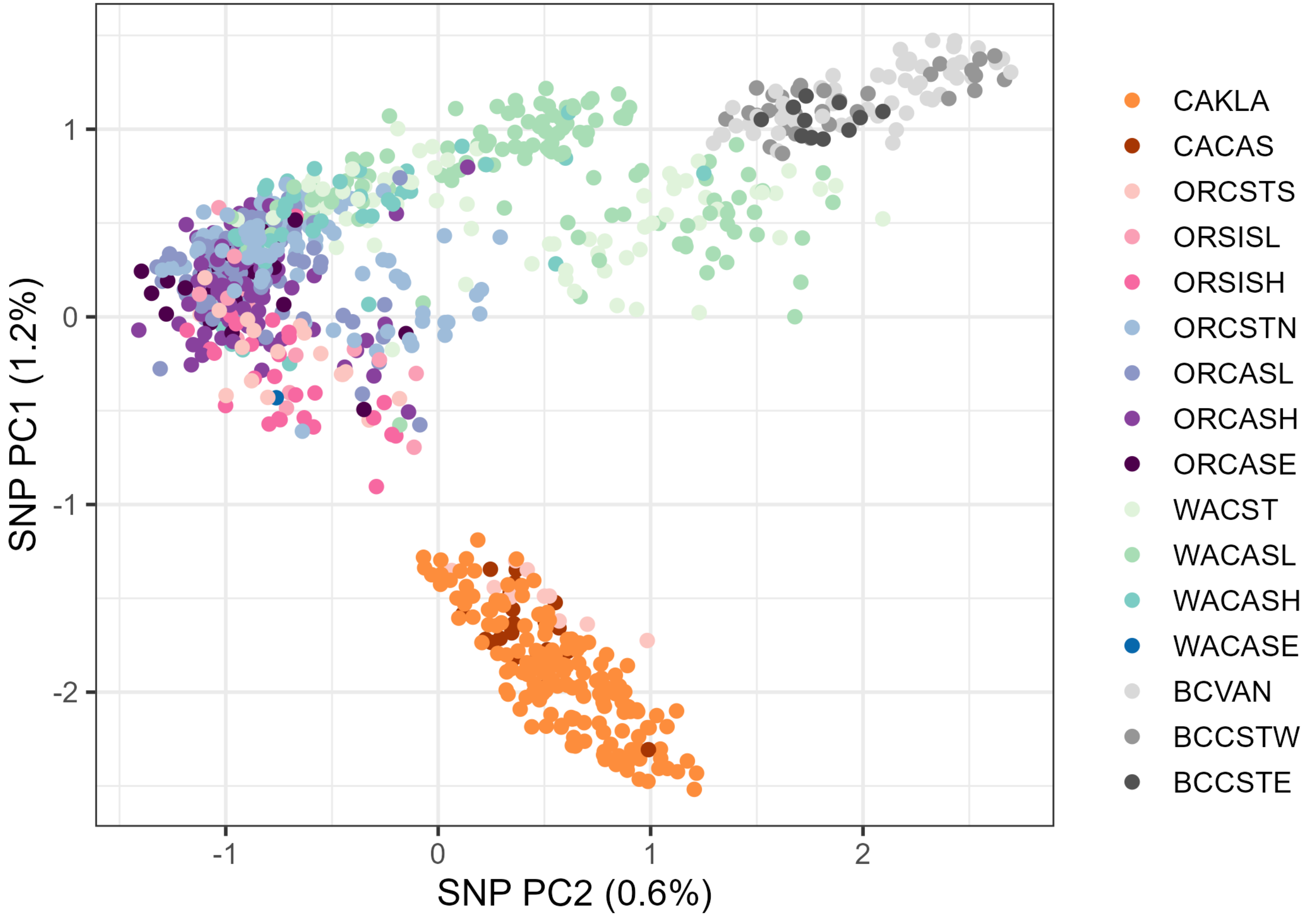


Gugger, P. *et al.*, *Mol. Ecol.*, 2010



Klamath/Mendocino populations are distinct within core of coastal dataset





Summary

- Unique genetic clusters detected reflect dynamic population structure and history
    - Varietal admixture
    - Post-glacial migration
- Genomic variation for SNPs is mostly found within populations
- Populations differences in genetic diversity may have leverage on model outputs
    - Analyze common alleles only?
    - Focus on core of population?

Next steps

- Tree genotypes from diverse geographic and climatic range in Douglas-fir will be useful for developing genomic model of climate adaptation
- Compare genomic predictions and phenotypes from SSMT
  - Fitness traits
  - Economic traits

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