The National Forest Genetics Laboratory

Latitudinal cline in genetic structure identified from a range-wide collection of Pacific madrone (*Arbutus menziesii* Pursh)

The Future of Pacific Madrone
Puyallup, Washington. 19 – 20 April, 2016

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United States Department of Agriculture

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The National Forest Genetics Lab (NFGEL)

Using genetic information to make informed management decisions.

177 Different Plant Species Studied

56 Different Conifers

329 Different Management Projects

Genetic Projects

- **Genetic Improvement**
- **Orchard and Breeding Support**
- **Conservation**
- **Restoration**
- **Taxonomy**
- **Climate Change Implications**
- **Forensics – Timber Theft**

Arbutus. iStock

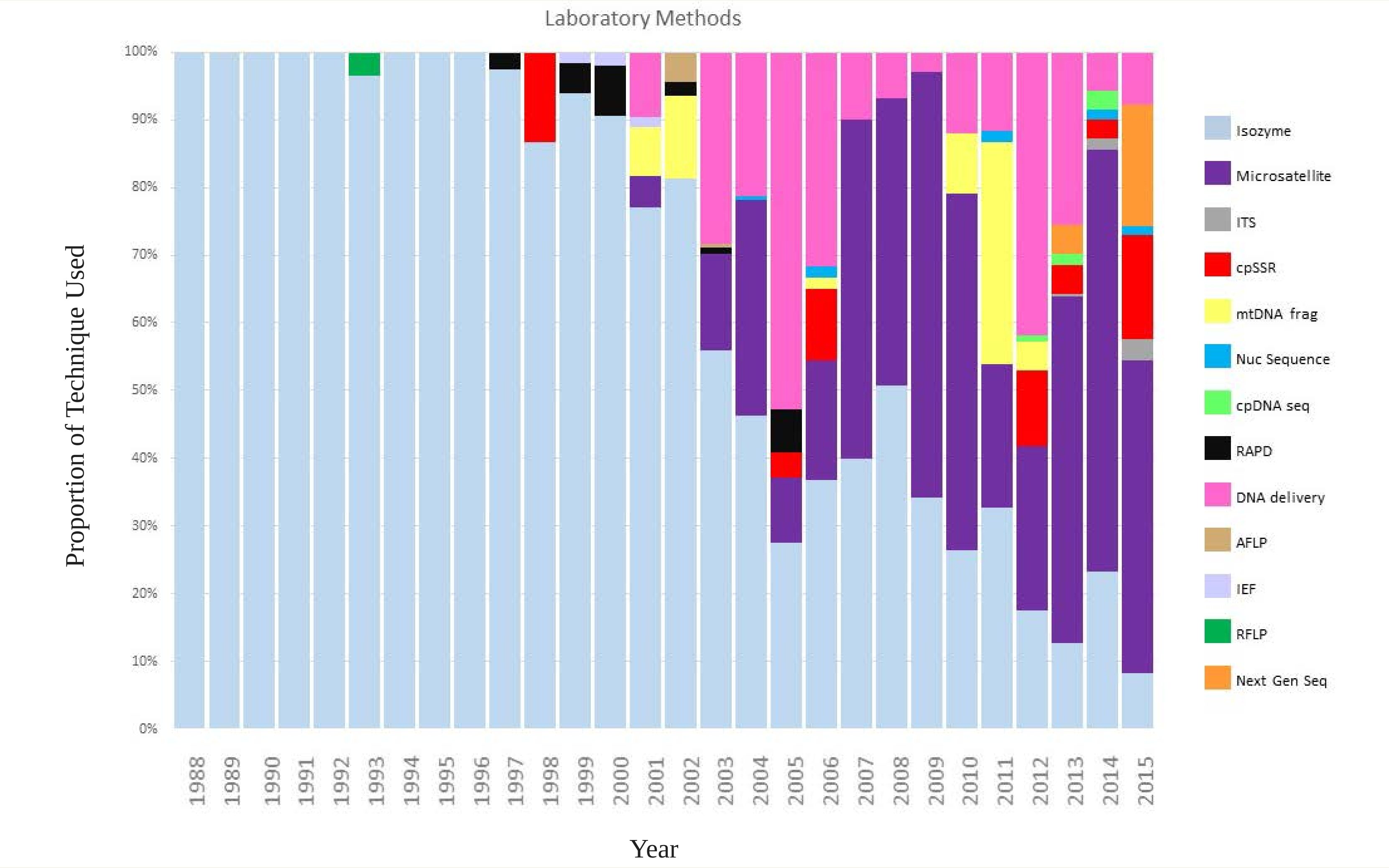
What makes a molecular genetic technique a good assessment tool?

- Can it address the management objective?
- Can we answer the question/objective within the management timeframe?
- Availability of markers without additional development.
- Is the marker system reliable and reproducible over time (data compatibility)?
- Lowest cost marker.

Prioritization of Work

- Strategic alignment
- Value to customer
- Availability of existing technology
- Availability of sample material
- Importance to risk mitigation
- Leverage potential
- Project costs

Overview and Trends



Pacific madrone (*Arbutus menziesii* Pursh) genetic study

Objectives:

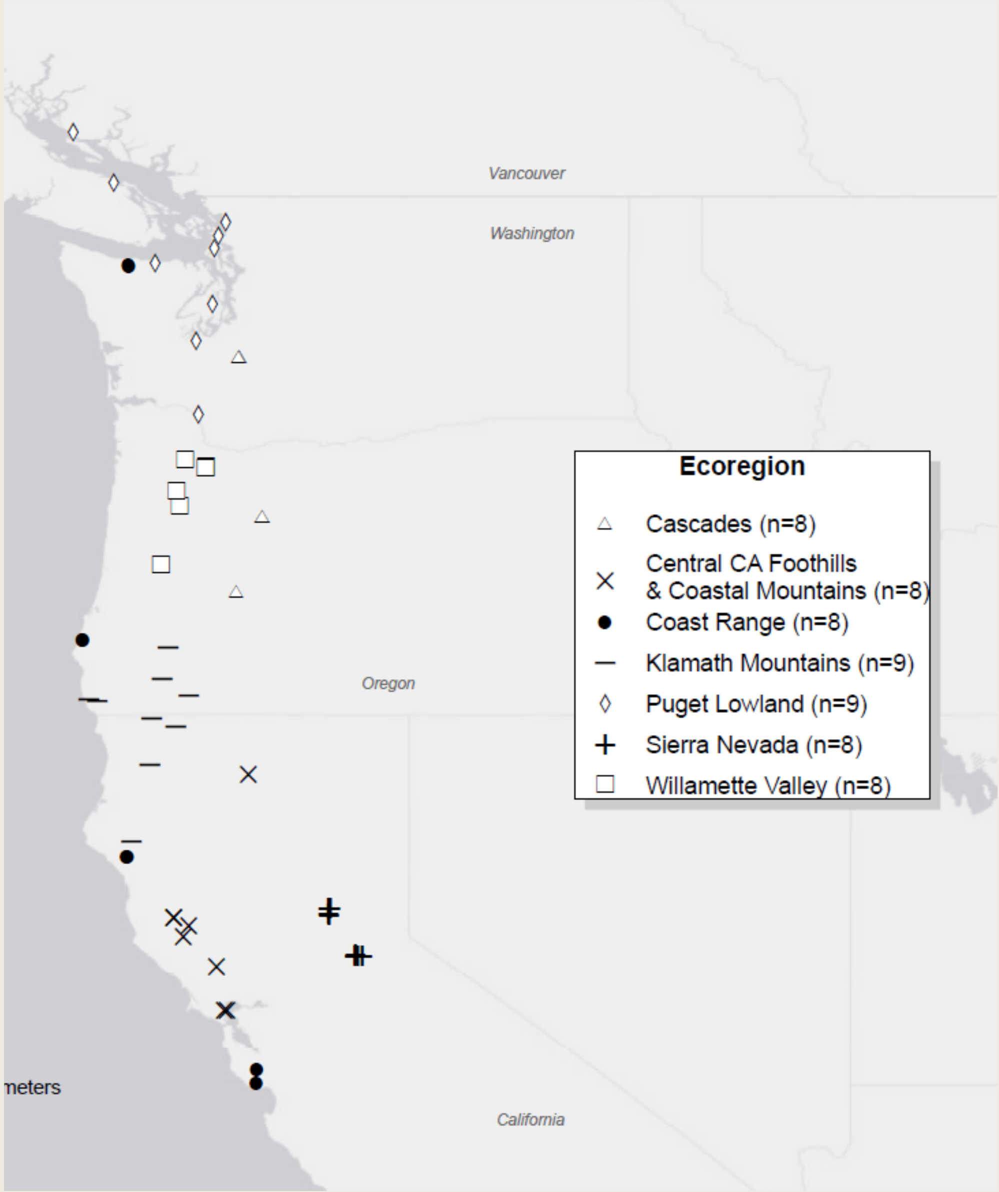
- Assess genetic variation in a geographically wide-ranging subset of Pacific madrone from the common garden experiment.
- Determine if isozyme data are sufficient to describe half-sib families and population structure in order to inform ongoing quantitative genetic studies.
- Availability of neutral genetic markers would benefit the analysis and interpretation of the adaptive genetic variation measured from the common garden experiment.

Arbutus. iStock

Methods

SAMPLING

- Fifty-eight Pacific madrone samples (one sibling from 58 half-sib families)
- One sample of Texas madrone (*A. xalapensis* Kunth)
- One sample of strawberry tree (*A. unedo* L.)
- Samples were grouped by 7 ecoregions



Results

19 isozyme loci.

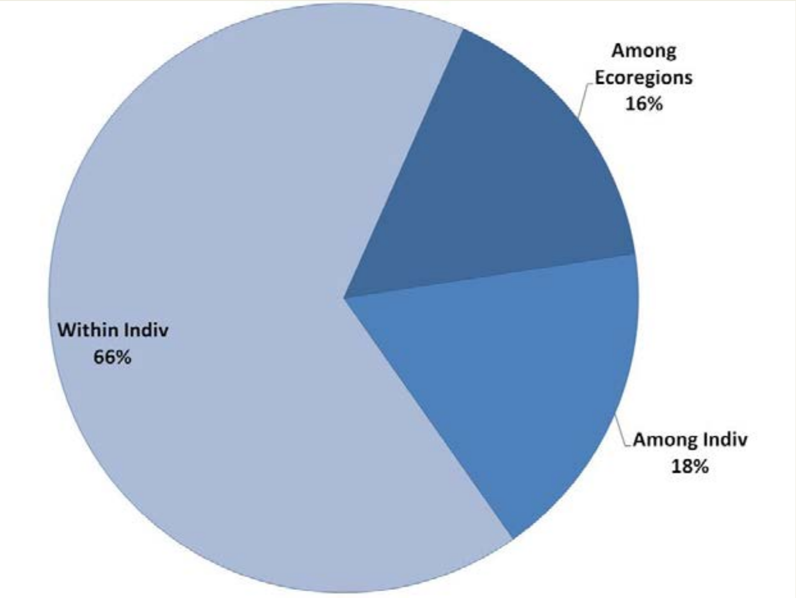
Genetic Variation

Low levels of genetic diversity

(40% loci were polymorphic, a maximum of 3 alleles per locus, and mean heterozygosity of 0.16).

Genetic Differentiation

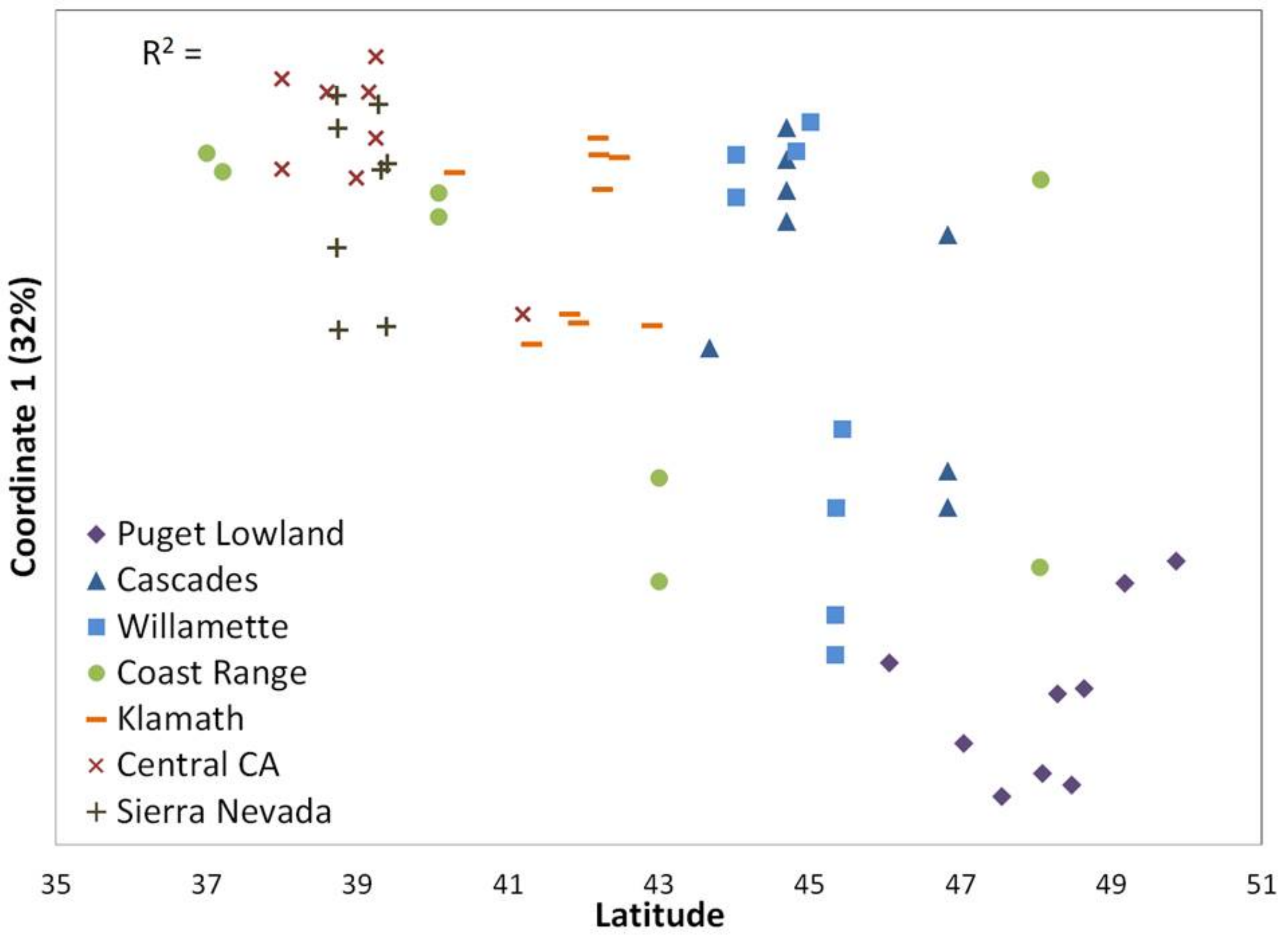
Significant allele frequency variation was detected, indicating ecoregions are genetically differentiated across the landscape ($F_{ST} = 0.16$, $P < 0.001$).

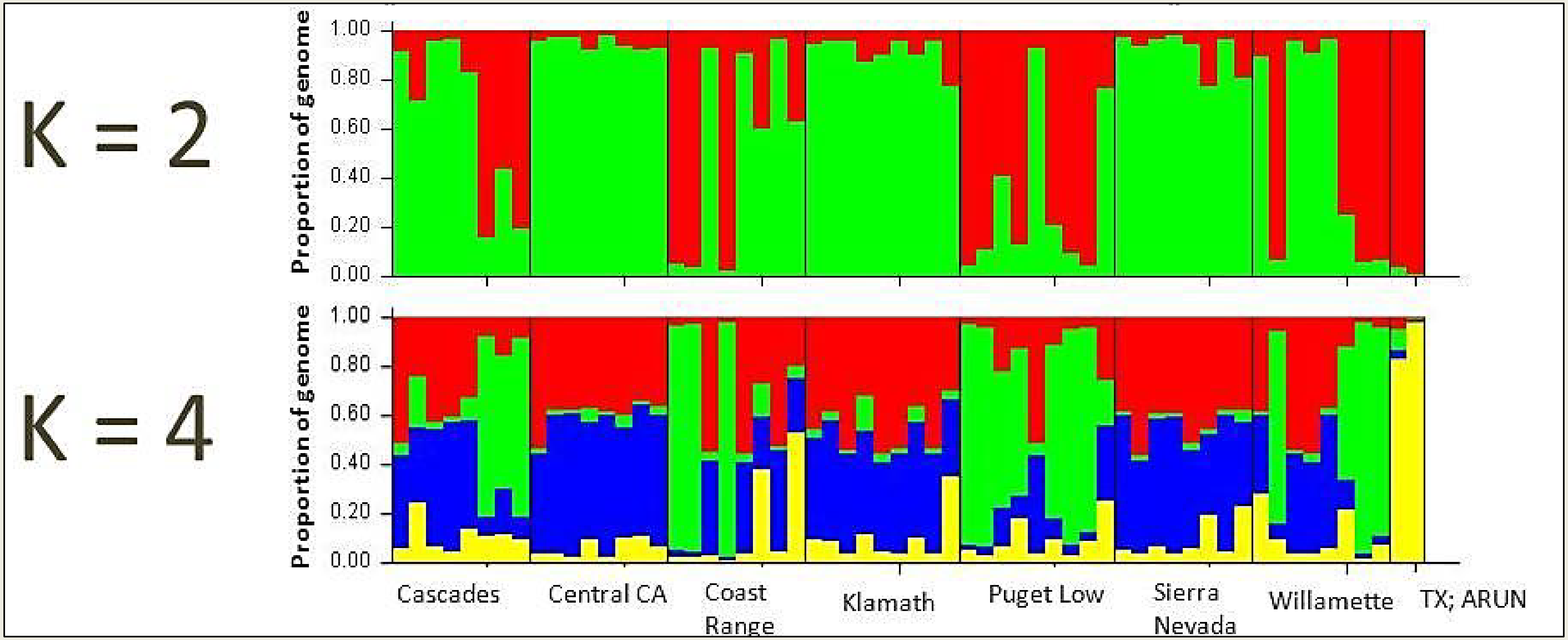


Results

Landscape Patterns

Tests of isolation by distance and correlation with latitude indicate the genetic differentiation occurs across a latitudinal and elevational cline.





Klamath Mountains, Central California, and the Sierra Nevada distinct from Puget Lowland.

Collections from the Cascades, Willamette Valley, and Coast Range were variable, likely reflecting the long latitudinal range of these ecoregions.

Conclusions

- There is a significant latitudinal cline in genetic variation.
- Low levels of heterozygosity - biparental inbreeding and fine-scale genetic structure due to limited seed dispersal. Consistent with Beland et al. (2005) (AFLPs of northern populations).
- Coast Range small but negative (F = -0.015), potentially reflecting an inaccurate designation of this ecoregion.
- Given the low number of alleles per locus and low variation observed within many ecoregions, isozyme markers will likely be insufficient to examine fine-scale spatial structure or within-family variation in the full common garden collection.
- Alternate DNA technologies may be required to gain sufficient power to address all of the project objectives.