



The National Forest Genetics Laboratory

Integrating Molecular Genetics into Seed Management Programs

2017 National Native Seed Conference

February 13-16, 2017

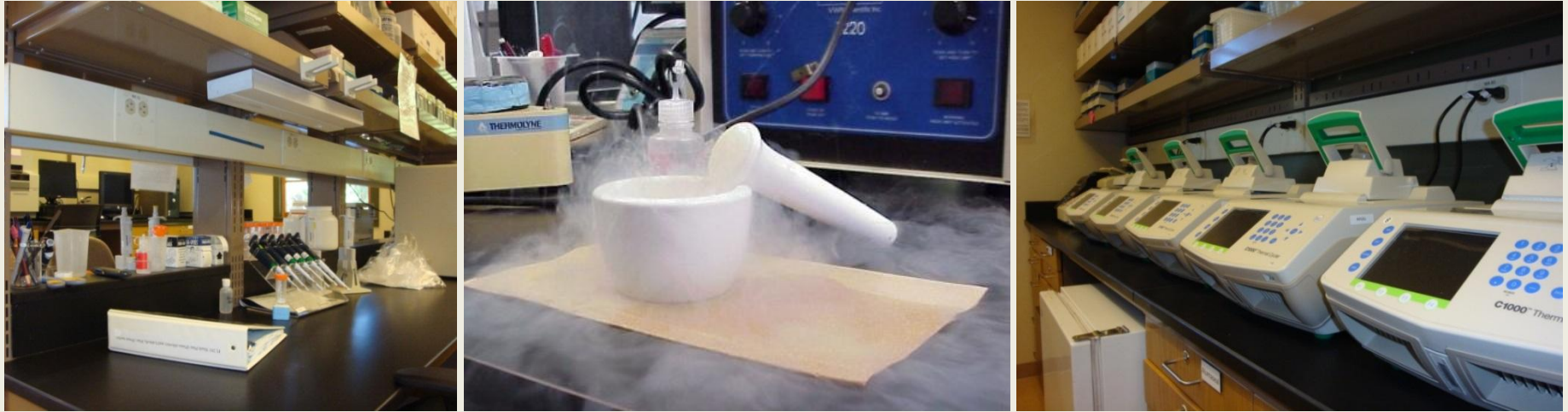
Valerie Hipkins



U.S. FOREST SERVICE

Caring for the land and serving people

Outline



- **NFGEL Organization and Purpose**
- **Lab technology as applied tools**
- **Examples**

The National Forest Genetics Lab (NFGEL)

Using genetic information to make informed management decisions.

177 Different Plant Species Studied

56 Different Conifers

Genetic Projects

Conservation

Restoration

Taxonomy

Genetic Improvement

Seed Collections

Orchard, Nursery and Breeding Support

Climate Change Implications

Forensics – timber theft; poaching

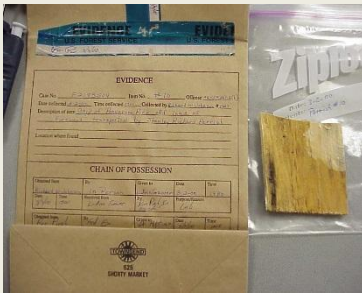


What makes a molecular genetic technique a good management tool?

- **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.**

Management Questions

- Identify cultivars
- Identify source or population
- Assess levels of genetic variation
- Determine individual relatedness
- Determine taxonomy
- Identify pollen and seed contamination
- Verify crosses
- Clone, ramet, and family identification

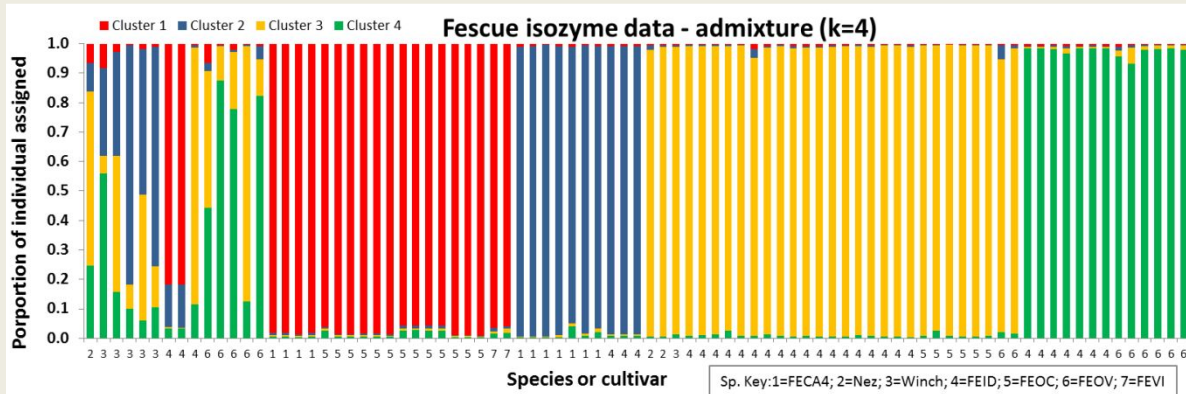


Identification

(Species identification and cultivar detection in Fescue)

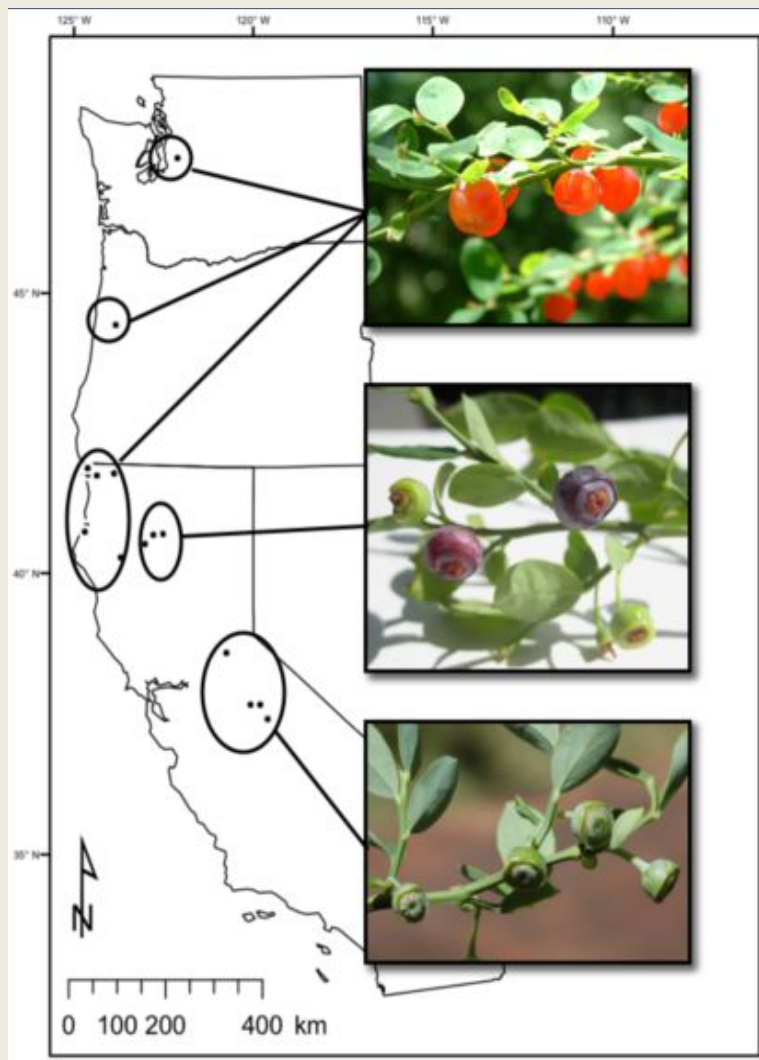
Objective 1: Are “wild” seed collections really Idaho Fescue, or are they at least one of 5 ‘like’ species native to Montana.

Objective 2: Do the “wild” seed collections include some NRCS “cultivar” releases, or hybrids between the cultivars and wild-type Idaho Fescue.



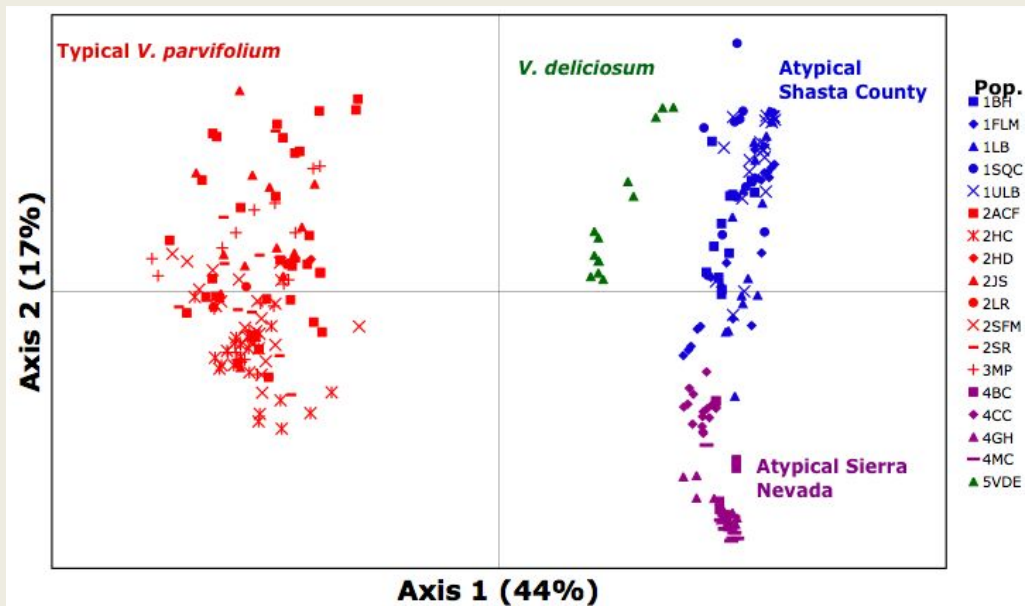
[Mary Frances Mahalovich, Susan Rinehart]

Taxonomy/Population Genetics



Vaccinium parvifolium (huckleberry)

[Project Cooperators: Julie Nelson, Len Lindstrand]



Golden Chinquapin (*Chrysolepis chrysophylla*)



Pete Veilleux, East Bay Wilds. USFS

- **What is the level and distribution of genetic diversity within species**
- **How different are the northern-most disjunct populations from rest of range**
- **Are there varietal level genetic differences among the ‘shrub’ and ‘tree’ forms**

MARKER CHOICE

Allozymes: low variation obtained in tests

Microsatellites (SSRs): pulled over from other Fagaceae (oaks, European chestnut)

16 loci, 716 trees, 23 stands

(~\$20,000; 1 yr)

2b-RAD: Next Generation Sequencing approach for genome-wide genotyping

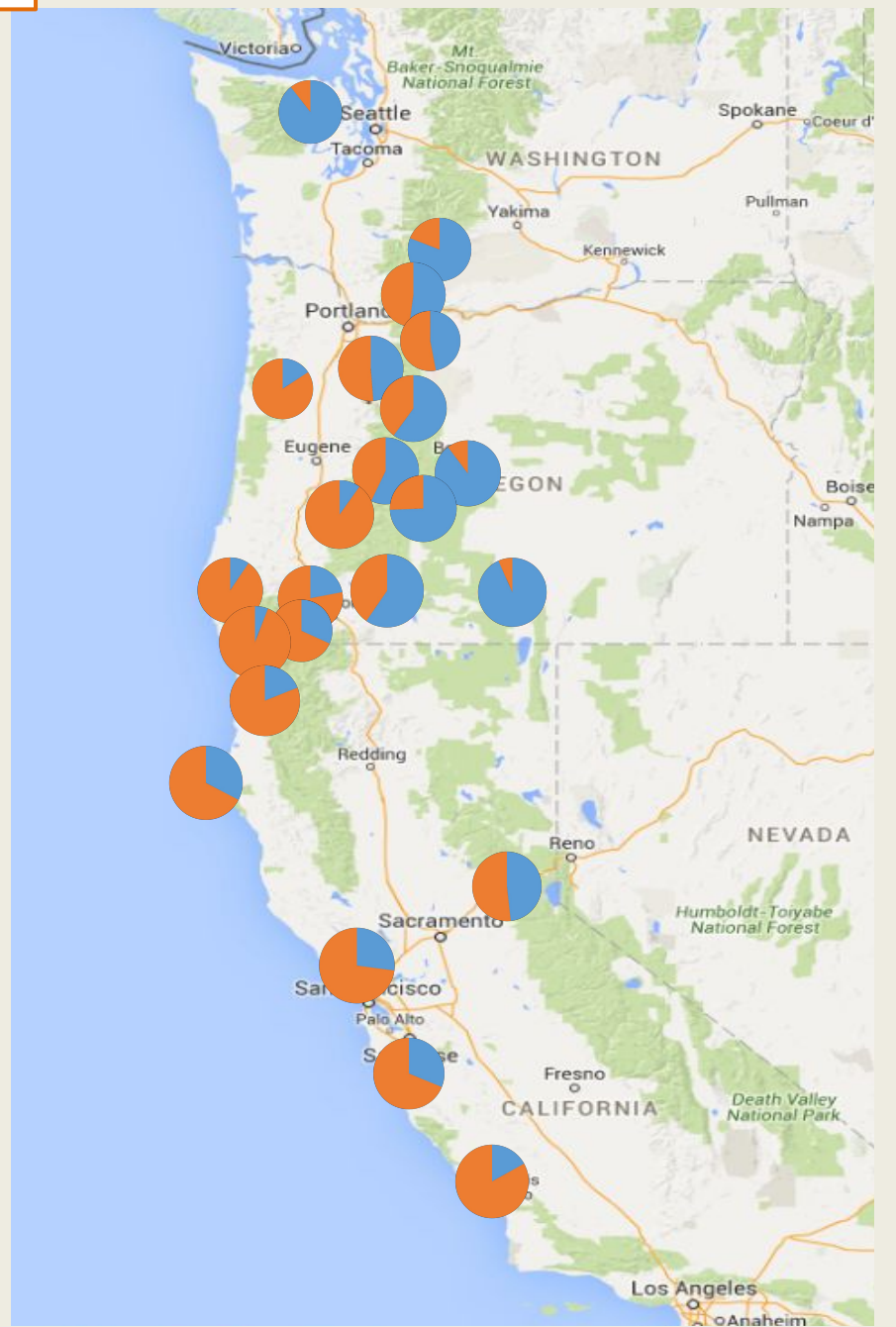
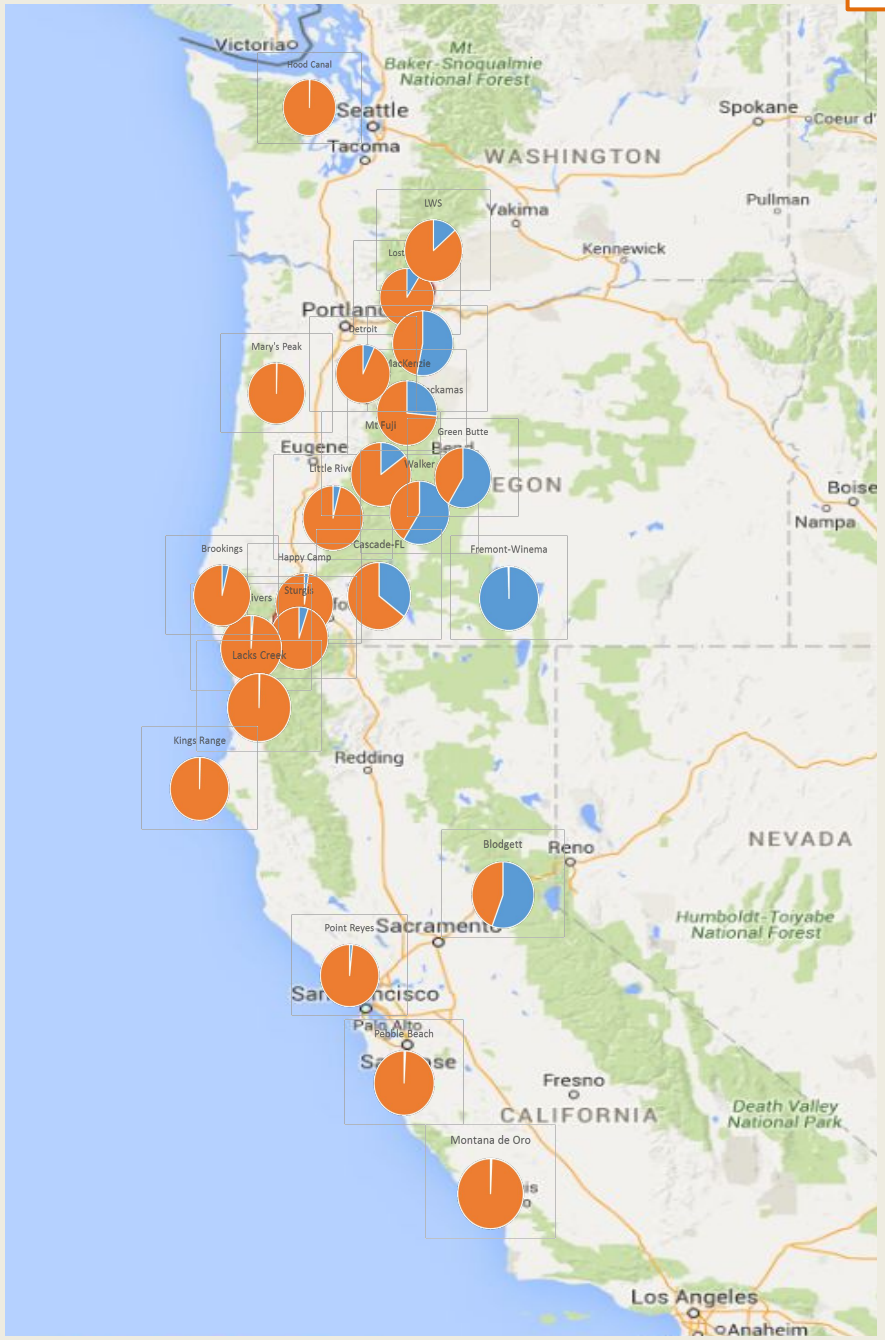
(restriction site-associated DNA (RAD), based on sequencing fragments produced by type IIB restriction endonucleases)

628 samples, 2021 SNPs with coverage $\geq 20X$ (~\$75,000; 2.5 yrs)

2b-RAD: Population STRUCTURE

K=2

SSR: Population STRUCTURE



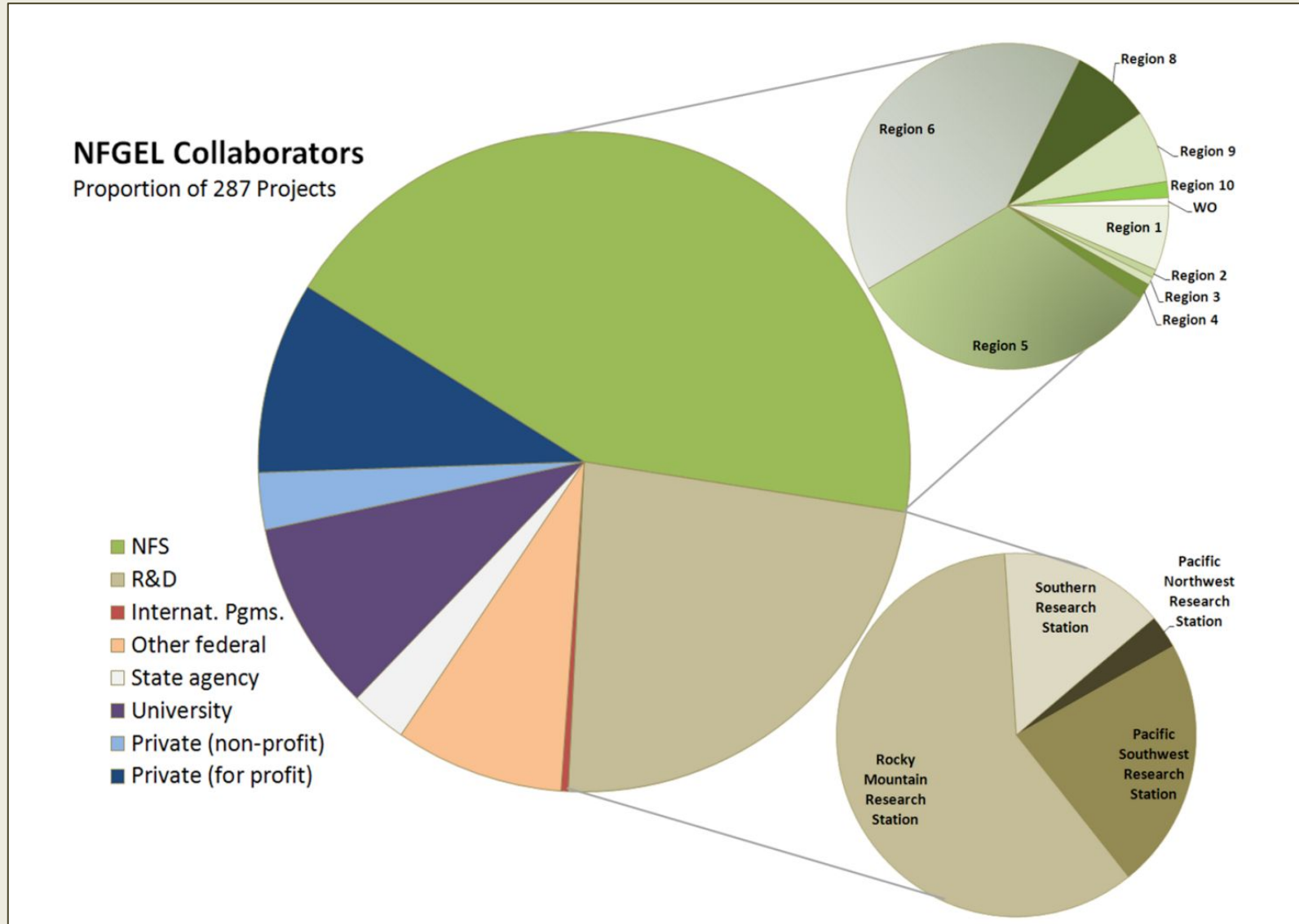
HYBRIDIZATION



Longleaf (*Pinus palustris*) and Shortleaf Pines (*P. echinata*) X Loblolly Pine (*P. taeda*)
Whitebark Pine (*P. albicaulis*) X Limber Pine (*P. flexilis*)
Butternut (*Juglans cinerea*) X Japanese Walnut (*J. ailantifolia*)
Sisyrinchium sarmentosum* X *S. idahoense
***Oenothera wolfii* (Wolf's evening primrose) X *O. glazioviana* (garden escape)**

Management Needs by Collaborator

Thank you to all NFGEL partners and collaborators



Markers for Applied Purpose

Ability to address management objective drives all work and dictates to organization of the project:

- **What marker(s) will get run**
- **Number of samples to collect**
- **Location of samples**
- **Tissue to collect**
- **What kind of data will be obtained**
- **When the data will be obtained**
- **Cost/sample determination**



The preceding presentation was delivered at the

2017 National Native Seed Conference

Washington, D.C. February 13-16, 2017

This and additional presentations available at <http://nativeseed.info>

