Integrating Molecular Genetics into Seed Management Programs

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Outline

• NFGEL Organization and Purpose

• Lab technology as applied tools

• Examples
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.
Overview and Trends
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*)

- 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 ≥ 20X (~$75,000; 2.5 yrs)

[Project cooperator: Andy Bower]
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)
Thank you to all NFGEL partners and collaborators.
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

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