Pacific Northwest Tree Improvement Research Cooperative
Annual Report
2010-2011

Oregon State University College of Forestry
Department of Forest Ecosystems and Society
Glenn Howe, Lauren Magalska, Ron Beloin, J. Bradley St.Clair, Scott Kolpak, Oguz Urhan

http://www.fsl.orst.edu/pnwtirc/
PACIFIC NORTHWEST TREE IMPROVEMENT RESEARCH COOPERATIVE

Oregon State University College of Forestry
Department of Forest Ecosystems and Society

2010-2011 Annual Report

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The Pacific Northwest Tree Improvement Research Cooperative (PNWTIRC) was formed in 1983 to conduct research in support of operational tree improvement in the Pacific Northwest. Emphasis is on region-wide topics dealing with major coniferous species. Membership has included representatives from public agencies and private forestry companies in western Oregon, western Washington, and coastal British Columbia.

OUR MISSION IS TO:

- Create a knowledge base concerning genetic improvement and breeding of Pacific Northwest tree species.
- Develop reliable, simple, and cost-effective genetic improvement methods and apply these methods to solve tree-breeding problems.
- Promote effective collaboration and communication among public agencies and private industries engaged in tree improvement in the region.

All participants provide guidance and receive early access to research results. Regular and Associate members provide financial and in-kind support and are represented on the Policy/Technical Committee. This committee is responsible for making decisions on program strategy and support, identifying research problems, establishing priorities, and assisting in the planning, implementation and evaluation of studies. Because Contractual Participants provide less financial support, they have no voting rights on the Policy/Technical Committee. Liaison Members provide no financial support and have no voting rights. The PNWTIRC is housed in the Department of Forest Ecosystems and Society at Oregon State University.
PNWTIRC PARTICIPANTS

Regular Members
Cascade Timber Consulting
Bureau of Land Management
Forest Capital Partners
Green Diamond Resource Company
Longview Timber Company
Olympic Resource Management
Oregon Department of Forestry
Oregon State University
Plum Creek Timber Company
Port Blakely Tree Farms
Rayonier
Roseburg Forest Products
Stimson Lumber Company
Washington State Department of Natural Resources

Associate Members
Starker Forests

Contractual Participants
Lone Rock Timber Company

Liaison Members
Inland Empire Tree Improvement Cooperative
Northwest Tree Improvement Cooperative
USDA Forest Service, Pacific Northwest Research Station
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<td>• PNWTIRC accomplishments for 2010-11</td>
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<td>• Seed Transfer Tool</td>
<td>Ron Beloin</td>
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<td>• CTGN survey</td>
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<td>Budget and Other Business</td>
<td>Glenn Howe</td>
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<td></td>
<td>• Budget presentation and vote</td>
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<td>• Elect new Policy/Technical Committee Chair</td>
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<td>1:30-2:10</td>
<td>Conifer Translational Genomics Network</td>
<td>Glenn Howe</td>
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<td>• Douglas-fir SNP chip</td>
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<td>Miniaturized Seed Orchard Project</td>
<td>Scott Kolpak</td>
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<td>2:55-3:00</td>
<td>Wrap-up and adjourn</td>
<td>Glenn Howe</td>
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PNWTIRC Annual Meeting 2011

September 14, 2011
Pacific Northwest Tree Improvement Research Cooperative
Department of Forest Ecosystems and Society
Oregon State University

PNWTIRC personnel

2010-2011
- Director – Glenn Howe
- Research Coordinator – Scott Kolpak
- Program Manager – Liz Etherington
- Graduate students – Lauren Magalska, Oguz Urhan
- Policy/Technical Committee Chair – Sara Lipow
Highlights of 2010-2011

Site characterization research
- Data analyses and interpretations were completed during the summer
- Lauren will defend her thesis on September 16, 2011
- Lauren will present her conclusions to PNWTIRC members today
Highlights of 2010-2011

**Wood quality research**

- Published manuscripts

- Funded a CAFS proposal entitled “Early genetic selection for wood stiffness in Douglas-fir and western hemlock” and began the associated research
  - Scott Kolpak and Oguz Urban will discuss

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**Miniaturized Seed Orchard Study**

- Trees were stimulated with girdling and calcium nitrate
- We measured the 2011 cone crop and completed the first analyses of crown volume and the cone crops in 2010 and 2011
- Scott will discuss

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Highlights of 2010-2011

Publications by PNWTIRC personnel


Highlights of 2010-2011

Presentations by PNWTIRC personnel


Highlights of 2010-2011

Presentations by PNWTIRC personnel

  *Presenter

  *Presenter


Collaborations and grants

- **CAFS**  *Center for Advanced Forestry Systems*. B. Goldfarb; H. Allen; H. Burkhart; T. Fox; G. Howe; K. Jayawickrama; R. Meilan; C. Michler; S. Strauss. NSF Industry-University Cooperative Research Center Program, 2007-2012, $1,450,000 (total), $250,000 (OSU).

- **CTGN**  *Conifer Translational Genomics Network*. D. Neale; T. Byram; D. Harry; G. Howe; D. Huber; S. McKeand; J. Lee; N. Wheeler; J. Wegrzyn. USDA NRI Coordinated Agricultural Project Program. 2007-2011, $5,900,000 (total), $1,043,594 (OSU).

Collaborations and grants


CAFS

**National Science Foundation**

*Industrial Innovation Partnership (IIP) Division*

*Industry / University Cooperative Research Centers*

**Center for Advanced Forestry Systems**

North Carolina State University – Jose Stape
Oregon State University – Glenn Howe
Purdue University – Charles Michler
University of Florida – Eric Jokela
University of Georgia – Michael Kane
University of Idaho – Mark Coleman
University of Maine – Robert Wagner
University of Washington – David Briggs
Virginia Tech – Thomas Fox
First 5 years
- $50K/yr ($26.9K operating funds) for dues of 150-300K
- $70K/yr ($37.7 operating funds) for dues >300K

Second five years
- $25K/yr ($13.4K operating funds) for dues of 150-300K
- $35K/yr ($18.8K operating funds) for dues >300K

Matching funds
- OSU reached the 300K threshold through contributions to PNWTIRC (Howe), TBGRC (Strauss), CIPS (Maguire), and BLM Density Management Study (Puettmann)
OSU CAFS proposals in 2011

**Proposed continuing proposals**

- Effects of site and genetics on Douglas-fir growth, stem quality, and adaptability (Howe)
- Early genetic selection for wood stiffness in Douglas-fir and western hemlock (Howe)
- Overstory cover dynamics in thinned stands and riparian areas (Puettmann)
- Floral transcriptomics of eucalypts (Strauss)

PNWTIRC plans for 2011-2012

**Site characterization study (PNWTIRC/CAFS/NWTIC)**

- Defend thesis and publish results

**Miniaturized seed orchard study**

- Develop work plan and outline for final MSO report
- Measure flowering, bud phenology, and crown volume
- Measure cone and seed yields in the fall of 2012

**Wood quality (PNWTIRC/CAFS/NWTIC)**

- Complete the field work for the PNWTIRC/CAFS study entitled “Early genetic selection for wood stiffness in young Douglas-fir and western hemlock”
PNWTIRC plans for 2011-2012

SNP-based marker-assisted selection in Douglas-fir

- Write a proposal for a new PNWTIRC study to investigate the potential for SNP-based marker-assisted selection in Douglas-fir
- Test new SNP chip and begin genotyping second-cycle selections

Cold hardiness testing

- Facilitate cold hardiness testing by the NWTIC

Climate change subproject (TAFCC)

- Continue to facilitate the activities of the Taskforce on Adapting Forests to Climate Change
- Submit a proposal to the AFRI Climate Change Program with PNWTIRC participation
Identifying Site Characteristics that Explain Variation in Douglas-fir Productivity and Stem Form

Lauren Magalska
Department of Forest Ecosystems and Society
College of Forestry
Oregon State University

Agenda

• Introduction
• Project Objectives
• Materials and Methods
• Results and Discussion
• Future Work
• Conclusions
Introduction

- What did I do?
- Why did I do it?
- Why is it unique?
- How does it fit into the bigger picture?

What I Did...

- Identified site characteristics that explain variation in Douglas-fir site productivity and stem form
- Site characteristics include climate, soils, and topography
- Site productivity was measured as
  - Mean individual tree height and diameter increments
  - Total volume and basal area per hectare
  - Site mortality (%)

What I Did…

- Stem form was measured as incidents/tree of stem forking and ramicorn branching, and % stem deflect/tree (sinuosity)

Why I Did It

- Site productivity and stem form are directly related to:
  - Profitability of owning forestland
  - Return on silvicultural investment
- Current methods of assessing site productivity have limitations
- Douglas-fir response to near-term climate change needs to be better understood
- Availability of NWTIC genetic tests
Forest Productivity Models

- Empirical Growth and Yield Models
- Mechanistic Models

Climate Change

- Projections
  - Uncertain changes to precipitation
  - Summer warming, more pronounced inland
  - Greater winter warming than summer warming in the western Cascades
  - Increased CO₂
- How will Douglas-fir respond?
- Which climate site characteristics should be investigated in detail?
Why is it unique?

- Tree improvement programs
  - Breeding zones
  - Parent trees (families)
  - Progeny trees
  - Progeny test sites
- Site characteristic relationships with stem form
- Unique geographic study area

The Big Picture

- Douglas-fir is an economically important species in OR and WA
- Competitive market
  - Low cost imports
  - Alternative land uses
- Maintenance and improvement of timber quantity and quality will help OR and WA timber producers remain competitive
- Understanding the relationships among Douglas-fir productivity, stem form and site characteristics is key
Materials and Methods

- Progeny Test Sites
- Site Characteristics
- Variable Selection

Progeny Test Sites

- Site locations
- Measurements of trees at each site
- Site characteristics
Site Locations

- 191 NWTIC progeny test sites in Oregon and Washington
- Measured between 1967 and 2005
- Elevation 15 to 1090 meters
- Average of 3500 trees per site (400 to 9400)

Site Measurements

- Measured variables
  - Height at three ages (~ages 5, 10, 15)
  - DBH at three ages (~ages 5, 10, 15)
  - Mortality at three ages (~ages 5, 10, 15)
  - Stem forking
  - Ramicorn branching
  - Sinuosity
- Calculated variables
  - Individual tree periodic annual growth rates for height and DBH over 6 growth periods
  - Total volume/ha (~ages 5, 10, 15)
  - Total BA/ha (~ages 5, 10, 15)
Site Measurements

- Site means were calculated by program
- Adjusted to remove mean genetic differences among sites
- Site means were calculated for
  - HT response group (6 periodic annual height growth rates)
  - DBH response group (6 periodic annual DBH growth rates)
  - Biomass response group (Total volume and total BA at 3 ages)
  - Site mortality at 3 ages (Mortality response group)
  - Incidents of stem forking, ramicorn branching and sinuosity per tree

Site Characteristics

- Climate
  - ClimateWNA
  - 35 climate site characteristics
  - 7 periodic growth climates
- Soils
  - NRCS SSURGO
  - 3 soils site characteristics
- Topography
  - USGS DEM
  - 2 topographic site characteristics
- Total of 40 site characteristics
Data Summary

- Across-program data
  - 7 datasets
  - 24 response variables (DBH, HT, stem forking, etc.)
  - 40 independent variables (MAT, slope, AWC, etc.)
- Within-program data
  - Variation explained by program and sowing year has been removed

Variable Selection

- Variable importance study
- Issues
  - Nature of relationships
  - Interactions
  - Colinearity
  - Strength of the biological signal
Approach

- Hierarchical clustering of site characteristics
- Three-pronged variable selection
  - Simple correlation (Corr)
  - Linear regression (LR)
  - Random forest (RF)

A Few Words on Random Forests

- Non-parametric analysis
- Automatically incorporates interaction terms
- Robust to collinearity among the independent variables
Issues

- Nature of relationships – Use analytical methods that describe both linear and non-linear relationships (LR and RF)
- Interactions – automatically included by RF
- Colinearity – RF is robust, Corr captures simple relationships
- Biological signal – separate real from artifacts using three-pronged approach, importance scores and rank correlations

Importance Scores

\[ I_i = \sum_{k=1}^{n} r_{ik}^2 + R_{ik}^2 + VI \cdot \hat{R}_{ik}^2 + GDI \cdot \hat{R}_{ik}^2 \]
Consistency

- Each response group had a Corr, RF, LR and total importance score for both the across- and within-program data.
- Spearman’s rank correlations were used to judge consistency of importance scores among analytical methods and response groups for the productivity measures.

Results and Discussion

- Site Characteristic Groups
- Consistency
- Site Productivity
- Stem Form
Site Characteristic Groups

PRECIP

- Amount and timing
- Adequate water supplies required for growth
- Late season precipitation may lead to multiple flushing
- Expected to explain variation in site productivity, specifically MAP

MAP
MSP
PPT_sp
PPT_sm
PPT_at
PPT_wt
TEMP1

- Temperatures affect the induction and release of endodormancy
- Expected to explain variation in site productivity, specifically DD<0°C

TEMP2

- Growing season temperatures and length affect growth
- NFFD and MAT may explain variation in productivity
- Extreme temperatures may cause injury and mortality
- eFFP and EMT may explain variation in stem form
Dry

- Summer drought and relationships between temperature and precipitation
- Critical in this region
- Early ecodormancy, reduced photosynthesis and growth
- Expected to explain variation in site productivity, specifically SHM

Topography

- Slope and cosASP did not cluster with any other site characteristics
- Influences light intensity, PAR, temperature and drought stress
- Ability of slope and cosASP to explain variation in site productivity is dependent on importance of other site characteristics
Soils

- AWC, TPD and clay did not cluster with any other site characteristics
- Douglas-fir productivity has been linked to soil moisture
- AWC expected to explain variation in site productivity
- TPD and clay influence AWC
- TPD and clay expected to have diminished importance if AWC explains variation in site productivity

Moderate to Low Consistency

Rank correlations between analytical methods

<table>
<thead>
<tr>
<th>Response</th>
<th>Corr vs RF</th>
<th>Corr vs LR</th>
<th>RF vs LR</th>
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</thead>
<tbody>
<tr>
<td>Across-program</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Biomass</td>
<td>-0.07 (0.66)</td>
<td>-0.27 (0.09)</td>
<td>0.01 (0.96)</td>
</tr>
<tr>
<td>DBH</td>
<td>0.39 (0.01)</td>
<td>-0.06 (0.70)</td>
<td>0.47 (&lt;0.01)</td>
</tr>
<tr>
<td>HT</td>
<td>0.05 (0.74)</td>
<td>-0.03 (0.87)</td>
<td>0.48 (&lt;0.01)</td>
</tr>
<tr>
<td>Mortality</td>
<td>0.33 (0.03)</td>
<td>0.28 (0.07)</td>
<td>0.08 (0.62)</td>
</tr>
<tr>
<td>Within-program</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Biomass</td>
<td>0.11 (0.48)</td>
<td>-0.13 (0.43)</td>
<td>0.02 (0.91)</td>
</tr>
<tr>
<td>DBH</td>
<td>0.26 (0.10)</td>
<td>0.09 (0.57)</td>
<td>0.13 (0.42)</td>
</tr>
<tr>
<td>HT</td>
<td>0.33 (0.03)</td>
<td>0.15 (0.34)</td>
<td>0.32 (0.04)</td>
</tr>
<tr>
<td>Mortality</td>
<td>0.08 (0.63)</td>
<td>-0.01 (0.93)</td>
<td>0.09 (0.57)</td>
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</table>
Moderate Consistency

Rank correlations between response groups

<table>
<thead>
<tr>
<th>Response</th>
<th>Across-program</th>
<th>Within-program</th>
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<tbody>
<tr>
<td>DBH vs HT</td>
<td>0.24 (0.12)</td>
<td>0.52 (&lt;0.01)</td>
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<tr>
<td>DBH vs Biomass</td>
<td>0.24 (0.13)</td>
<td>0.25 (0.11)</td>
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<tr>
<td>DBH vs Mortality</td>
<td>0.02 (0.92)</td>
<td>-0.20 (0.20)</td>
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<tr>
<td>HT vs Biomass</td>
<td>0.35 (0.02)</td>
<td>0.41 (0.01)</td>
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<tr>
<td>HT vs Mortality</td>
<td>0.44 (&lt;0.01)</td>
<td>-0.09 (0.59)</td>
</tr>
<tr>
<td>Biomass vs Mortality</td>
<td>0.16 (0.31)</td>
<td>-0.18 (0.26)</td>
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</table>

Consistency… or lack thereof

- Weak biological signals over a relatively narrow range of site characteristics
- Sources of inaccuracy and random variation
  - ClimateWNA
  - SSURGO
- Differences in analytical methods
- Large number of independent variables in relation to the number of observations
- Some responses may not be explained by the site characteristics
Site Productivity Results

Across-program

Site Characteristics

Within-program

Response Groups

Site Productivity Results

Cold Season Temperatures

Across-program

Site Characteristics

Within-program

Response Groups
Cold Season Temperatures

- Most consistently important
  - **TEMP1**
    - DD<0°C for DBH and HT response groups
    - TD for biomass response group
  - **TEMP2**
    - Tmax_wt for DBH and biomass response groups
    - NFFD for HT response group
    - Temperatures at the beginning and end of the growing season for mortality response group

Site Productivity Results

Available Water Capacity

<table>
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<tr>
<th>Across-program</th>
<th>Within-program</th>
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Site Characteristics
Available Water Capacity

- Explained variation in DBH response group
- PRECIP and DRY did not consistently explain variation

Why Would AWC Explain Variation?

- More accurately – why would AWC explain variation but PRECIP and DRY do not?
- Amount of precipitation may not be as important as the ability to store it
- High AWC potentially mitigates summer drought stress
- Temporal resolution of response and independent variables may influence the importance of precipitation and summer dryness
- ClimateWNA may not model PRECIP and DRY site characteristics well
Slope, cosASP, TPD, Clay

- No evidence to support that these site characteristics explain variation in site productivity
- Importance may be masked by interactions with other site characteristics

Stem Form Results

Across-program

Within-program
Stem Form

- No evidence to suggest that any of the SCGs or individual site characteristics explained variation in stem form
- Small amount of variation explained
- Lack of consistency
- Different set of site characteristic may be important (insect, disease, mechanical damage)

Future Work

- General relationships have been identified, but there is ample opportunity for continued work
- Continue to refine the analytical approach
- Define approaches for reducing the number of independent variables
- Increase the sample size
  - Conducting analysis without soils data, increase sample size by 97 sites
  - Continue mapping NWTIC progeny test sites
Future Work

- After important site characteristics are identified, predictive modeling under future climate scenarios
- Environmental transfer distances
  - GxE
  - Adaptability
  - Seed transfer guidelines

Conclusions

- Identified site characteristics that explain variation in Douglas-fir site productivity
  - Cold season temperatures
  - Available water capacity
- Attempted to identify site characteristics that explain variation in Douglas-fir stem form, but results were inconsistent
- Understanding the relationships among Douglas-fir site productivity, stem form and site characteristics is essential to the maintenance and improvement of the timber industry in OR and WA
Conclusions

- Study identified general relationships
- Laid the groundwork for future studies on Douglas-fir productivity, stem form and related site characteristics

Acknowledgements

My Committee:
Glenn Howe
Scott Holub
Doug Maguire (a.k.a. Robin Rose)
Jeff Stone

The NWTIC:
Keith Jayawickrama
Denise Cooper
Terrance Ye

Jim Smith
Jeff DeBell
Sara Lipow
Randall Greggs
Dan Cress
Rich Kelly

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Annie Simmonds
Elaine Blampied
James Crawford

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Early genetic selection for wood stiffness in juvenile Douglas-fir and western hemlock

Scott Kolpak¹, Oguz Urhan¹, Glenn Howe¹

¹Pacific Northwest Tree Improvement Research Cooperative
Department of Forest Ecosystems and Society
Oregon State University

Genetics of wood stiffness

Trend toward shorter rotations, faster growth

- More wood from the juvenile wood core
- Juvenile wood:
  - Lower wood density
  - Higher microfibril angle
  - Lower stiffness
  - More shrinkage
Past research on wood quality traits of ‘mature’ Douglas-fir (25 years old)

- Stiffness is heritable and **substantial gains** are possible
- HM200 MOE has a high genetic correlation \((r_g = 0.92)\) with bending MOE
- ST300 MOE has a moderate genetic correlation \((r_g = 0.57)\) with bending MOE
- **Acoustic velocity** can be used instead of acoustic MOE to evaluate wood stiffness (**no strong need to measure density**)
- Selection for bending stiffness or **acoustic velocity = no large adverse effects on growth**

**Wood stiffness publications:**

Wood stiffness in juvenile Douglas-fir and western hemlock

**There is a strong interest in improving stiffness in younger trees (e.g. 6 – 12)**
- Trees of these ages are being measured for inclusion into seed orchards and future breeding
- No wood quality traits have been incorporated beyond 1st cycle breeding populations

**There are challenges to applying research tools and methods from older trees to younger trees, and to western hemlock**
Wood stiffness in young trees: Challenges and unknowns

**Phenotype**
- Wood anatomy is different, mostly juvenile wood and sapwood
- Branches on small trees may adversely affect 'standard' measurement protocols
  - *Secondary branches in hemlock*
- Acoustic tools may not work well on small trees
- Differences between Douglas-fir and western hemlock

**Genetics (young trees)**
- Heritabilities, genetic gains, juvenile-mature wood correlations are unknown

### Project goals

<table>
<thead>
<tr>
<th>Project goals</th>
<th>Progress</th>
<th>Location</th>
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<tbody>
<tr>
<td>(1) Evaluate alternative methods for measuring wood stiffness on young trees of Douglas-fir (DF) and western hemlock (WH)</td>
<td>Field work done</td>
<td>Operational plantations</td>
</tr>
<tr>
<td>(2) Estimate genetic parameters and genetic gains for juvenile wood stiffness in DF and WH</td>
<td>Ongoing</td>
<td>Progeny sites</td>
</tr>
<tr>
<td>(3) Develop optimal measurement and selection scenarios for improving juvenile wood stiffness in DF and WH</td>
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<tr>
<td>4) Estimate age-age correlations for DF wood properties</td>
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Acoustic tools being tested

Juvenile stiffness work phases

Phase 1: Phenotype – Evaluate acoustic tools and techniques in operational plantations

Phase 2: Genetics

- Estimate genetic parameters and genetic gains for juvenile wood stiffness in progeny sites
- Develop measurement protocols and selection scenarios for improving juvenile wood stiffness in operational programs

Phase 3: Age-age correlations – Estimate age-age correlations for Douglas-fir wood properties
Phase 1 objectives

**Tools** - Evaluate standing-tree acoustic tools for measuring acoustic velocity (AV) in young trees
- Robustness
- Correlations with log-based tools (HM200)

**Methods** - Evaluate the same-face method of probe placement versus the opposite-face method

**Whorls** - Compare alternative standing-tree stress wave target areas
- Interwhorls = shorter flight-paths (< 1 meter), more clear wood
- Across whorls = longer flight-paths (~ 1 meter), spans branch whorls

Phase 1: Materials and methods

5 – *Operational plantations*

4 – *Standing-tree tools*

3 – *Measurement areas*
- Interwhorl 1, interwhorl 2, whorl 1,2

2 – *Measurement techniques*
- Probes same-face or opposite-face

1 – *Log-based tool*
Young tree phenotypic study

5 plantations spanning ages 6 – 15 years

Table 1: Operational plantations

<table>
<thead>
<tr>
<th>Plantations</th>
<th>Years planted (tree age)</th>
<th>DBH (cm)</th>
<th>No. of Douglas-fir</th>
<th>No. of Western hemlock</th>
</tr>
</thead>
<tbody>
<tr>
<td>Peeler Greene</td>
<td>2004-05 (7)</td>
<td>4.5</td>
<td>12</td>
<td>13</td>
</tr>
<tr>
<td>Rhubarb 2</td>
<td>2002-03 (9)</td>
<td>6.9</td>
<td>13</td>
<td>12</td>
</tr>
<tr>
<td>Ellmaker Parkview</td>
<td>2001-02 (10)</td>
<td>6.2</td>
<td>12</td>
<td>13</td>
</tr>
<tr>
<td>Edward Spring</td>
<td>1998-99 (13)</td>
<td>13.4</td>
<td>12</td>
<td>9</td>
</tr>
<tr>
<td>Elephant Foot</td>
<td>1996-1997 (15)</td>
<td>14.4</td>
<td>13</td>
<td>14</td>
</tr>
</tbody>
</table>

Phase 1: Materials and methods

5 plantations ages 6 – 15 years

**Time-of-flight measurements per tree:**
- 4 tools x 3 locations x 2 sensor placements x 3 TOFs = 72 TOFs / tree

**Calculate alternative flight paths**
- Sensor distance and tree diameter

**Resonance acoustic velocities taken using the HM200**
- Minimum log length 2 m
**Which tools are best?**

**Objective:** Evaluate standing-tree tools for measuring AV in young trees. Effective tools have high correlations with other tools.

**Method:** Compare correlations among tools (using the same-face and opposite-face methods).

- **Same-face** = Average $r_{1,2} \& r_{4,5}$
- **Opposite-face** = Average $r_{1,3} \& r_{4,6}$

---

<table>
<thead>
<tr>
<th>Objective.</th>
<th>Evaluate standing-tree tools for measuring AV. Effective tools have high correlations with other tools.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Method.</td>
<td>Compare tool correlations within (1) same-face method and (2) opposite-face method.</td>
</tr>
</tbody>
</table>
| Results. | - **Ultra Timer** = some poor correlations
- **MicroTimer, TreeSonic 1, and TreeSonic 2** = no clear differences |
| Conclusions. | - No need to consider TreeSonic 2 (sliding hammer is awkward and physically demanding)
- Drop the UltraSonic Timer |

---

**Table 2. Correlations among acoustic tools and sensor placements for Douglas-fir and western hemlock pooled across five sites. Douglas-fir correlations are below the diagonal and western hemlock are above the diagonal.**

<table>
<thead>
<tr>
<th>Acoustic tool</th>
<th>Micro Timer</th>
<th>Tree Sonic 1</th>
<th>Tree Sonic 2</th>
<th>Ultra Timer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Micro Timer</td>
<td>-</td>
<td>0.76</td>
<td>0.44</td>
<td>0.36</td>
</tr>
<tr>
<td>Tree Sonic 1</td>
<td>0.34</td>
<td>-</td>
<td>0.52</td>
<td>0.25</td>
</tr>
<tr>
<td>Tree Sonic 2</td>
<td>0.42</td>
<td>0.39</td>
<td>-</td>
<td>0.10</td>
</tr>
<tr>
<td>Ultra Timer</td>
<td>0.04</td>
<td>-0.07</td>
<td>-0.04</td>
<td>-</td>
</tr>
</tbody>
</table>

**Table 2**

- TreeSonic 1 = TreeSonic + SD02 sensor
- TreeSonic 2 = TreeSonic + sliding hammer sensor
**Which probe placement is best?**

**Which tools?**
- TreeSonic
- Microsecond timer
- UltraSonic timer

**Whorls a problem?**

**Which methods?**
- Same-face method
- Opposite-face method

---

**Objective.** Evaluate the same-face method of probe placement versus the opposite-face method

**Method.** Which tool correlations are higher (1) same-face method or (2) opposite-face method?

**Results**
- Same-face correlations are slightly higher than opposite-face
- But...only one flight path examined

**Conclusions**
- Test same-face and opposite-face methods in progeny tests

---

**Table 2. Correlations among acoustic tools and sensor placements for Douglas-fir and western hemlock pooled across five sites. Douglas-fir correlations are below the diagonal and western hemlock are above the diagonal.**

<table>
<thead>
<tr>
<th>Sensor Placement</th>
<th>Opposite face sensors</th>
<th>Same face sensors</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Micro Tree Sonic 1</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>Tree Sonic 2</td>
<td>0.42</td>
</tr>
<tr>
<td></td>
<td>Ultra Timer</td>
<td>0.46</td>
</tr>
</tbody>
</table>

**Correlation coefficients (*) are among averages for interwhorls 1 and 2.**

TreeSonic 1 = TreeSonic + SD02 sensor
TreeSonic 2 = TreeSonic + sliding hammer sensor

---

**Figure 1.** Hypothesized stress wave flight paths for the same-face and distance adjusted values (Mohan et al 2008)

**Tree measurement diagram**
**Objective.** Test the effects of whorls

If whorls affect AV, then correlations between two interwhorl measurements will be larger than correlations involving across-whorl measurements

**Method.** Do these two types of correlations differ?
- Interwhorl #1 versus Interwhorl #2
- Across-whorl versus interwhorl*

*average of interwhorls 1 and 2

**Conclusion.** No adverse effect of measuring across whorls in either Douglas-fir or western hemlock
Phenotype study conclusions (preliminary)

- **We dropped the UltraSonic Timer.** UltraSonic correlations are weak, and measurement distances between sensors are short.

- **We dropped the TreeSonic with ‘standard’ sliding hammers.** The TreeSonic or Microsecond Timer with SD02 sensors have good correlations and are easier to use.

- **Measuring across whorls isn’t a problem.**

- **We will continue to study sensor placement.** We don’t have adequate information to judge effectiveness, so we will study sensor placement in progeny tests.

Genetics of wood stiffness

Oguz Urhan – Master’s candidate

Figure 1: TreeSonic 1 (SD02 sensor)  
Figure 2: TreeSonic 2 (TS sensor)
Phase-2 - Genetic improvement of wood stiffness in young Douglas-fir and western hemlock

**Goals and objectives**

**Long-term goal**
- Genetically improve juvenile wood stiffness in 6- to 12-year-old Douglas-fir and western hemlock trees

**Objectives**
- Determine optimal approaches (tools and methods) for measuring and selecting for juvenile wood stiffness at young ages
- Estimate genetic gains for wood stiffness for 6- to 12-year-old Douglas-fir and western hemlock trees using the most promising standing-tree acoustic tools

**Remaining questions**

**Tool and sensors**
- Microsecond timer?
- TreeSonic (with SD-02 sensors)?

**Method**
- Same-face method?
- Opposite-face method?

**Measurement production**

**Genetic parameters**
- Heritabilities
- Potential genetic gains
Methods and tools

Which tools?
- Microsecond Timer
- TreeSonic

Advantages/disadvantages of tools?

<table>
<thead>
<tr>
<th>Advantage</th>
<th>Disadvantage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Smaller and more practical</td>
<td>On/off switch and reset button</td>
</tr>
<tr>
<td>Faster</td>
<td>Reset last reading each time</td>
</tr>
<tr>
<td>Automatically switch on/off</td>
<td>SD-02 probe bending</td>
</tr>
<tr>
<td>No button on the unit</td>
<td>SD-02 sensor more practical than original TreeSonic</td>
</tr>
<tr>
<td>Bigger and heavier</td>
<td></td>
</tr>
</tbody>
</table>

Which methods?
- Same-face method
- Opposite-face method

Young tree genetic study

<table>
<thead>
<tr>
<th>Program</th>
<th>Site</th>
<th>Species</th>
<th>Age</th>
<th># of families</th>
<th>Mating design</th>
</tr>
</thead>
<tbody>
<tr>
<td>Noctic (Pruned)</td>
<td>Roaring river</td>
<td>Douglas-fir</td>
<td>12</td>
<td>78</td>
<td>Nested</td>
</tr>
<tr>
<td>Hemic (Not pruned)</td>
<td>Toledo</td>
<td>Western hemlock</td>
<td>10</td>
<td>80</td>
<td>Nested</td>
</tr>
<tr>
<td>Track inland</td>
<td>Fir grove</td>
<td>Douglas-fir</td>
<td>8</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

Table 3 Measurement production

<table>
<thead>
<tr>
<th>Same-face &amp;</th>
<th>Same-face (Estimated)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Opposite-face</td>
<td>Pruned site</td>
</tr>
<tr>
<td>Microsecond Timer</td>
<td>27 trees/h</td>
</tr>
<tr>
<td>TreeSonic</td>
<td>32 trees/h</td>
</tr>
</tbody>
</table>

Males nested in females
Females nested in males
Application of probes and measurements

**Placement of probes and penetration depth**
- Always on the same aspect
- 45 +/- 15 degree angle
- 20 – 25 mm penetration depth

**Distance**
- No fixed distance

**Diameter**

Preliminary results and conclusions

---

**Table 4: Approximate individual-tree narrow-sense heritabilities**

<table>
<thead>
<tr>
<th></th>
<th>Same-face</th>
<th>Opposite-face</th>
</tr>
</thead>
<tbody>
<tr>
<td>Microsecond timer</td>
<td>0.507</td>
<td>0.418</td>
</tr>
<tr>
<td>TreeSonic</td>
<td>0.525</td>
<td>0.445</td>
</tr>
</tbody>
</table>

**Preliminary conclusions**
- Standing-tree acoustic velocity measurements in juvenile trees are heritable
- Same-face is better than opposite-face. No difference between tools

**Opposite-side method**
- I used circumferential opposite-face method
- Test other approaches

---

**Figure 1. Hypothesized stress wave flight paths for the same-face and opposite face methods (Mohan et al 2008)**
Progress

- Completed measurements of the Roaring River progeny test site. Measured 12-year-old Douglas-fir with the Microsecond Timer and TreeSonic – analyses are underway
- Now measuring the Toledo progeny test site. Measurements of 10-year-old western hemlock are completed for the Microsecond Timer and are underway for the TreeSonic
- Fir Grove progeny test site is the next step (8-year-old Douglas-fir)

Acknowledgements

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Ron Rhatigan, OSU
Cameron Muir, Starker Forests
Western Conifer Climate Change Consortium (WCCCC)
USDA Coordinated Agricultural Project

Western Conifer Forest Systems: Strategies for Climate Change Adaptation and Mitigation

WCCCC (WC4)
Western Conifer Climate Change Consortium

http://racc.forestry.oregonstate.edu/
Regional CAP for 2011 – delayed?

Regional approaches to Climate Change: CAP

- Application deadline – July 16, 2011?
- $4,000,000 per year ($20 million total) for up to 5 years
- Anticipates making 5 to 8 awards in FY 2011?
- Regional integrated CAP focusing on mitigation and adaptation, involving research, education, and outreach in:
  - Cropping systems: Legume or forage production systems
  - Animal systems: Ruminant livestock and dairy
  - Forest systems: Western conifers
  - Grassland, pastureland, and rangeland systems

Long-term goal

Synthesize existing knowledge and develop new knowledge on the impacts of climate change on western forest production systems, and then design, convey, and implement management strategies that maximize forest health, forest productivity, and greenhouse gas mitigation under changing climates
Stakeholders are critical

- “Demonstrate the adoption of approaches and practices across the region…”

- **Stakeholders are** seed orchard managers, nursery managers, silviculturists, managers of forest operations, wood products manufacturers, managers of carbon offsets programs, policy makers, teachers, and students

- **Organizations are** forest industry, governmental agencies, tribes, small private landowners, NGOs, and universities

- Included in project **advisory groups**

PNW regional meeting

<table>
<thead>
<tr>
<th>Rank</th>
<th>Stakeholders “Very important” or “top priority” topics</th>
<th>Potential Project Partners “Very important” or “top priority” topics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Effects on fire, insects, pests 82.3 %</td>
<td>Effects on fire, insects, pests 88.9 %</td>
</tr>
<tr>
<td>2</td>
<td>Monitoring</td>
<td>Forest modeling 63.3</td>
</tr>
<tr>
<td>3</td>
<td>Silviculture</td>
<td>Monitoring 76.5</td>
</tr>
<tr>
<td>4</td>
<td>Economics</td>
<td>Regional climate science 76.4</td>
</tr>
<tr>
<td>5</td>
<td>Forest genetics &amp; tree improvement 58.8</td>
<td>Effects on tree physiology 76.4</td>
</tr>
<tr>
<td>6</td>
<td>Regional climate science 52.9</td>
<td>Silviculture 65.7</td>
</tr>
<tr>
<td>7</td>
<td>Extension 52.5</td>
<td>Forest genetics &amp; tree improvement 66.6</td>
</tr>
<tr>
<td>8</td>
<td>Forest modeling</td>
<td>Social science 61.1</td>
</tr>
<tr>
<td>9</td>
<td>Social science</td>
<td>Forest carbon 58.8</td>
</tr>
<tr>
<td>10</td>
<td>Non-forest carbon</td>
<td>Economics 55.5</td>
</tr>
<tr>
<td>11</td>
<td>Effects on tree physiology 41.1</td>
<td>Non-forest carbon 50.0</td>
</tr>
<tr>
<td>12</td>
<td>Forest carbon</td>
<td>Extension 38.9</td>
</tr>
<tr>
<td>13</td>
<td>Education 29.4</td>
<td>Education 38.9</td>
</tr>
</tbody>
</table>
### Inland Empire regional meeting

**Table 1. Rankings of Topic Importance by Stakeholders and Potential Project Partners**

<table>
<thead>
<tr>
<th>Rank</th>
<th>Stakeholders</th>
<th>&quot;Very important&quot; or &quot;top priority&quot; topics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Effects on fire, insects, pests</td>
<td>85.7 %</td>
</tr>
<tr>
<td>2</td>
<td>Extension</td>
<td>85.7</td>
</tr>
<tr>
<td>3</td>
<td>Water Resources</td>
<td>85.7</td>
</tr>
<tr>
<td>4</td>
<td>Economics</td>
<td>78.8</td>
</tr>
<tr>
<td>5</td>
<td>Effects on tree physiology</td>
<td>78.8</td>
</tr>
<tr>
<td>6</td>
<td>Regional climate science</td>
<td>64.3</td>
</tr>
<tr>
<td>7</td>
<td>Monitoring</td>
<td>64.3</td>
</tr>
<tr>
<td>8</td>
<td>Social science</td>
<td>57.1</td>
</tr>
<tr>
<td>9</td>
<td>Education</td>
<td>46.2</td>
</tr>
<tr>
<td>10</td>
<td>Forest genetics &amp; tree improvement</td>
<td>42.9</td>
</tr>
<tr>
<td>11</td>
<td>Silviculture</td>
<td>42.8</td>
</tr>
<tr>
<td>12</td>
<td>Forest carbon</td>
<td>30.6</td>
</tr>
<tr>
<td>13</td>
<td>Forest modeling</td>
<td>28.6</td>
</tr>
<tr>
<td>14</td>
<td>Non-forest carbon</td>
<td>14.3</td>
</tr>
</tbody>
</table>

### Southwest regional meeting

**Table 1. Rankings of Topic Importance by Stakeholders and Potential Project Partners**

<table>
<thead>
<tr>
<th>Rank</th>
<th>Stakeholders</th>
<th>&quot;Very important&quot; or &quot;top priority&quot; topics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
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<td>Extension</td>
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</tr>
<tr>
<td>3</td>
<td>Water Resources</td>
<td>85.7</td>
</tr>
<tr>
<td>4</td>
<td>Economics</td>
<td>78.8</td>
</tr>
<tr>
<td>5</td>
<td>Effects on tree physiology</td>
<td>78.8</td>
</tr>
<tr>
<td>6</td>
<td>Regional climate science</td>
<td>64.3</td>
</tr>
<tr>
<td>7</td>
<td>Monitoring</td>
<td>64.3</td>
</tr>
<tr>
<td>8</td>
<td>Social science</td>
<td>57.1</td>
</tr>
<tr>
<td>9</td>
<td>Education</td>
<td>46.2</td>
</tr>
<tr>
<td>10</td>
<td>Forest genetics &amp; tree improvement</td>
<td>42.9</td>
</tr>
<tr>
<td>11</td>
<td>Silviculture</td>
<td>42.8</td>
</tr>
<tr>
<td>12</td>
<td>Forest carbon</td>
<td>30.6</td>
</tr>
<tr>
<td>13</td>
<td>Forest modeling</td>
<td>28.6</td>
</tr>
<tr>
<td>14</td>
<td>Non-forest carbon</td>
<td>14.3</td>
</tr>
</tbody>
</table>
Seed source adaptability is critical

- Large climatic transfer distances can result in maladapted plantations
- Transfer limits can be determined directly from provenance tests
- Sufficiently large provenance tests are rare
- Sufficiently large transfer distances are rarely tested

Superior adaptability of a Douglas-fir seed source from California growing in Spain (Hernández et al. 1993)

Finnish Forest Research Institute

Lodgepole pine provenance test in New Zealand (Wright 1976)

Lodgepole pine provenances from maritime areas are not adapted to the winters of eastern Finland.
Seedlot Selection Tool
Step by step example

Ronald Beloin\(^1\), J. Bradley St.Clair\(^2\), and Glenn T. Howe\(^1\)

\(^1\)Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR
\(^2\)USDA Forest Service Pacific Northwest Research Station, Corvallis, Oregon
Seedlot Selection Tool (SST)

Why develop a dynamic tool?

- New genetic research can be incorporated easily
- Climate change models and emissions scenarios can be updated easily
- Results can reflect the user’s assumptions about climate change and their risk tolerance
- The tool can be used to map any climate that is defined by temperature and precipitation (e.g., risk of Swiss Needle Cast disease)
- Many, many scenarios can be studied because the analyses are conducted by a large community
**Types of zones**

### Traditional zones
- Defined ‘circles on a map’
- Transfers in different geographic directions may be limited at different climatic distances

### Focal point zones
- Zones ‘float’
- Centered on your focal point
- Transfers are always limited at the same climatic distance

---

**Climate space and transfer limit**

Transfer limit = radius

On the standardized scale, the transfer limit = 1.0

Transfer distance = $d = \sqrt{(y_1^2 + y_2^2)}$
Euclidian climate distance is calculated from the focal point, normalized to a score of 0 to 100, and represented as color intensity.

Normalized scores that are greater than zero are mapped in the region, creating a focal point seed zone.

How the tool works

- Select your goal
- Login
- Enter location
- Select species
- Determine transfer limit
- Select climate models
- Apply constraints
- Map your results
Planting Healthy Forests

The seedlot selection tool (SST) is a GIS mapping program designed to help forest managers match seedlots with planting sites based on climatic information. The tool can be used to map current climates, or future climates based on selected climate change scenarios. Although it is tailored for matching seedlots and planting sites, it can be used by anyone interested in mapping present or future climates defined by temperature and precipitation.

Purpose

Forest managers can use this tool to help choose seedlots that are appropriate for planting on a particular site, or planting sites that are appropriate for a particular seedlot. This can be done using current climate scenarios, or ignoring potential climate change or by choosing climate change-related emissions scenarios and future target years. Because of the uncertainty in climate change projections, the tool is intended as a planning and educational tool that can help users explore alternative future conditions, access risk, and plan preemptively, but current the user should always consult the operations manual.

Current regions

Choose a Region Below to Start

[sst.forestry.oregonstate.edu]
Seedlot Selection Tool (SST)

Given a specific planting site …

**Which seedlot is well adapted today?…**

And in the future given a climate change scenario?

sst.forestry.oregonstate.edu

Seedlot Selection Tool (SST)

Given a specific seedlot …

**Where is it expected to be well adapted today?…**

And in the future given a climate change scenario?

sst.forestry.oregonstate.edu
**Data inputs: location**

Welcome!

Logged in as [username]  Logout

Your stored input sets:  prw_zone14_mapmap (planting)  

Current input set:  prw_zone14_mapmap

Rename  Duplicate  Change goal of this input set  Delete this input set

**Location of Planting Site**

You can use Google Maps or coordinates to show the location of your site.

- N. Latitude: 43.66092
- W. Longitude: 122.38083
- Elevation at these coordinates: 2718 feet

**Data inputs: species**

**Select Species** (optional)

You can use species-specific or generic zones and transfer limits.

- `Common`  `Scientific`
- Unspecified (Unspecified)
- Douglas fir (Pseudotsuga menziesii)
- Lodgepole pine (Pinus contorta)
- Noble fir (Abies procera)
- Pacific silver fir (Abies amabilis)
- Ponderosa pine (Pinus ponderosa)
- Western hemlock (Tsuga heterophylla)
- Western larch (Larix occidentalis)
- Western red cedar (Thuja plicata)
- Western white pine (Pinus monticola)
Data inputs: transfer limit

Transfer Limit
Use a recommended list, enter your own limit, or use an existing zone to calculate a limit.

Select a recommended transfer model and limit | Select my own climate variables and limits | Use a zone to calculate a limit

Mean annual Precip (MAP) [mm]
Description: mean annual precipitation millimeters

Climate Variables Table  Method for determining transfer limit. Select my own climate variables and limits

<table>
<thead>
<tr>
<th>Name of climate variable</th>
<th>Present climate value</th>
<th>Climate value in target year</th>
<th>Target year</th>
<th>Transfer limit</th>
<th>Ready to Map?</th>
</tr>
</thead>
<tbody>
<tr>
<td>Edit Delete</td>
<td>Mean annual Temp (MAT)</td>
<td>103</td>
<td>103</td>
<td>Present</td>
<td></td>
</tr>
<tr>
<td>Edit Delete</td>
<td>Mean annual Precip (MAP)</td>
<td>1360</td>
<td>1360</td>
<td>Present</td>
<td></td>
</tr>
</tbody>
</table>

Data inputs: transfer limit

Select a recommended transfer model and limit | Select my own climate variables and limits | Use a zone to calculate a limit

Mean annual Temp (MAT) [°C/°F]

Select the zone to use for calculating the transfer limit

Name                      | Feature | Low elevation | High elevation |
---------------------------|---------|---------------|----------------|
Select Basic CR modified (1996) | 9       | 2001          | 3000           |
Select Original ORAVX (1973) | 482     | 2001          | 3000           |
Select NWTC ROSETIC 2ndGen Breeding | ROSEBURG | 2501          | 4000           |

Choose the center of the zone to be mapped
- Use your location coordinates
- Use the climate center of your input zone
Calculate transfer limit
**Data inputs: transfer limit**

Select the zone to use for calculating the transfer limit.

<table>
<thead>
<tr>
<th>Name</th>
<th>Feature</th>
<th>Low elevation</th>
<th>High elevation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Basic OR modified (1996)</td>
<td>9</td>
<td>2001</td>
<td>3000</td>
</tr>
<tr>
<td>Original ORWA (1973)</td>
<td>482</td>
<td>2001</td>
<td>3000</td>
</tr>
<tr>
<td>NVTIC ROSETIC 2nd Gen Breeding</td>
<td>ROSEBURG</td>
<td>2501</td>
<td>4000</td>
</tr>
</tbody>
</table>

Choose the center of the zone to be mapped:
- Use your location coordinates
- Use the climatic center of your input zone

**Climate Variables Table**

Method for determining transfer limit. Zone location coordinates used as the climatic center of output map.

<table>
<thead>
<tr>
<th>Name of climate variable</th>
<th>Present climate value</th>
<th>Climate value in target year</th>
<th>Target year</th>
<th>Transfer limit</th>
<th>Ready to Map?</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean annual Temp (MAT)</td>
<td>115</td>
<td>125</td>
<td>2010</td>
<td>20</td>
<td>✓</td>
</tr>
<tr>
<td>Mean annual Precip (MAP)</td>
<td>3202</td>
<td>3202</td>
<td>Present</td>
<td>150</td>
<td>✓</td>
</tr>
</tbody>
</table>

**Goal:** Find planting sites. Climate space is defined for seedlot in present climate. Map can be produced for present or future climates.

**Goal:** Find seedlots. Climate space is defined for planting site in future climate. Map can be produced only for present climates.

---

62
Data inputs: climate models

Climate Models
You may use present climate only, or present and future climates by selecting an emission scenario, future climate model, and year.

Future Climate Model

<table>
<thead>
<tr>
<th>Choose a present climate model</th>
</tr>
</thead>
<tbody>
<tr>
<td>Interpolation Model</td>
</tr>
<tr>
<td>Climate Normals</td>
</tr>
<tr>
<td>1961-1990 normals</td>
</tr>
<tr>
<td>Show Details</td>
</tr>
</tbody>
</table>

Add a future climate model to study climate change (Optional)

<table>
<thead>
<tr>
<th>Emission Scenarios</th>
</tr>
</thead>
<tbody>
<tr>
<td>SRES A2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Climate Change Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>3rd Gen Coupled GCM T63 run1</td>
</tr>
</tbody>
</table>

Target Year: 2050

Show Details of Climate Data Source

Data inputs: constraints

Constraints
You can limit the extent of your map based on constraints such as species range, photoperiod, latitude, longitude, elevation, and distance.

<table>
<thead>
<tr>
<th>Species Range Map</th>
</tr>
</thead>
<tbody>
<tr>
<td>Douglas fir</td>
</tr>
</tbody>
</table>

Add

No area constraints are in effect

<table>
<thead>
<tr>
<th>Constraint</th>
<th>Description</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Photoperiod</td>
<td>Difference in minutes</td>
<td>30</td>
<td>January</td>
</tr>
</tbody>
</table>

| Latitude         | Degrees N. Latitude          | 35      | 53      |
| Longitude        | Degrees W. Longitude         | -121.7  | -111    |
| Elevation        | Elevation in feet            | 0       | 0       |
| Distance         | Decimal degrees              | 0       | 0       |
Map results

Map results
Data inputs: transfer limit

Transfer Limit

Select a recommended transfer model and limit

- Mean annual Temp (MAT) [°C/°F]
- Mean Temp warmest month (MMMT) [°C/°F]
- Mean Temp coolest month (MCMT) [°C/°F]
- Continentality (C) = MMMT - MCMT [°C/°F]
- Mean annual Precip (MAP) [mm]
- Mean summer Precip (BSP) [mm]
- Annual heat moisture index (AHM) [°C/°F]
- Summer heat moisture index (SHM) [°C/°F]
- Degree-days below 0°C [°C/°F]
- Degree-days below 10°C [°C/°F]
- Degree-days above 10°C [°C/°F]
- Degree-days above 18°C [°C/°F]
- Frost-free days (NFFD) [days]
- Frost-free period (FFP) [days]
- Date FFP begins (SFFP) [Julian day]
- Date FFP ends (EFP) [Julian day]
- Precip as snow (PAS) [mm]
- Extreme min Temp (EMT) [°C/°F]

Select my own climate variables and limits

- Climate value
- Climate value in target year
- Target year
- Transfer limit
- Ready to map?

Use a zone to calculate a limit

- GIS

Transfer limits from seedling tests

Collect seed from many trees

Grow families in a common environment

Measure many adaptive traits

Traits vs source environ.
Data inputs: transfer limit

Trait 1 = \( f \) (minimum temperature for Winter, Fall, Summer, and Summer precipitation)

Trait 2 = \( f \) (Summer precipitation and maximum temperature for Spring, Summer, Winter)
Find seedlots (2050)

Mean annual temperature & mean annual precipitation

Trait 1 and Trait 2

Next steps

- Add seed, breeding zones for other species
- Add more present and future climate models, especially regional models for the PNW
- Continue analyses needed to develop transfer limit recommendations
- Add multivariate models
- Develop analogous web tools for other regions
- Enhance map data layers
Acknowledgements

- Lauren Magalska - GIS assistance
- Tongli Wang - ClimateWNA climate data
- Nick Crookston – ANUSPLIN climate data
- Paul Berrang – Eastern regions tester
- Greg DeVeer - web designer
Center for Forest Provenance Data

Objectives

1. Archive data from long-term provenance tests and seedling genecology tests
2. Make datasets available to researchers through the web

Web site: http://cenforgen.forestry.oregonstate.edu/index.php

Denise Cooper, Brad St.Clair, Glenn Howe, Jessica Wright, Greg DeVeer
Funded by USFS Climate Change Research Program

Current Status

- 19 studies in system
  - 11 Douglas-fir
  - 1 Whitebark Pine
  - 2 Sugar Pine
  - 3 Ponderosa Pine
  - 1 White Fir / California Red Fir
  - 1 Ponderosa Pine / Jeffery Pine

- 3 studies to process, add to database/web

- Some studies provide data for all categories; others require contacting PI for response data
### Budget and Other Business

**Glenn Howe**  
Pacific Northwest Tree Improvement Research Cooperative  
Department of Forest Ecosystems and Society  
Oregon State University

---

**Budget 2010-11**

**Main points**

- 2010-11 income = $110K
- Rayonier = new member
- 2011-12 income = $110K
- Indirect = 13%
- Income exceeded expenses (see next slide)
- Have substantial carryover – this year only (see next slide)

#### Budget 2010-11

<table>
<thead>
<tr>
<th>Organization</th>
<th>Financial Support</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Regular Members</strong></td>
<td></td>
</tr>
<tr>
<td>Cascade Timber Consulting</td>
<td>8,000</td>
</tr>
<tr>
<td>Bureau of Land Management</td>
<td>8,000</td>
</tr>
<tr>
<td>Forest Capital Partners</td>
<td>8,000</td>
</tr>
<tr>
<td>Green Diamond Resource Company</td>
<td>8,000</td>
</tr>
<tr>
<td>Longview Timber Company</td>
<td>8,000</td>
</tr>
<tr>
<td>Olympic Resource Management</td>
<td>8,000</td>
</tr>
<tr>
<td>Oregon Department of Forestry</td>
<td>8,000</td>
</tr>
<tr>
<td>Plum Creek Timber Company</td>
<td>8,000</td>
</tr>
<tr>
<td>Port Blakely Tree Farms</td>
<td>8,000</td>
</tr>
<tr>
<td>Rayonier</td>
<td>8,000</td>
</tr>
<tr>
<td>Roseburg Forest Products</td>
<td>8,000</td>
</tr>
<tr>
<td>Stimson Lumber Company</td>
<td>8,000</td>
</tr>
<tr>
<td>Washington State Dept. of Natural Resources</td>
<td>8,000</td>
</tr>
<tr>
<td><strong>Associate Members</strong></td>
<td></td>
</tr>
<tr>
<td>Starker Forests</td>
<td>4,000</td>
</tr>
<tr>
<td><strong>Contractual Members</strong></td>
<td></td>
</tr>
<tr>
<td>Lone Rock Timber Company</td>
<td>2,000</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>110,000</strong></td>
</tr>
</tbody>
</table>

---

---

---
### Budget 2010-11

**Main points**

- Summarizes costs of personnel
- Personnel costs were covered by PNWTIRC members and OSU (Director)
- Expenses were less than income because CAFS and CTGN funds were used to pay some salaries
- Carryover increased
- Budget could change after we learn which CAFS proposals are funded – but probably not

<table>
<thead>
<tr>
<th>Income and Expenditures</th>
<th>OSU</th>
<th>Members</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>OSU Forest Research Laboratory</td>
<td>121,387</td>
<td>0</td>
<td>121,387</td>
</tr>
<tr>
<td>Membership fees and contracts</td>
<td>0</td>
<td>110,000</td>
<td>110,000</td>
</tr>
<tr>
<td>Carryover from previous year</td>
<td>0</td>
<td>25,576</td>
<td>25,576</td>
</tr>
<tr>
<td><strong>Total income</strong></td>
<td><strong>121,387</strong></td>
<td><strong>110,000</strong></td>
<td><strong>231,387</strong></td>
</tr>
</tbody>
</table>
| Salaries and CAR**  
  Director (0.5 FTE funded by OSU) | 68,080 | 68,080 |
  Program Manager (0.5 FTE) | 7,420 | 7,420 |
  Research Coordinator (0.1 FTE) | 13,665 | 13,665 |
  Graduate students (0.50 FTE) | 29,169 | 29,169 |
  Student employees | 6,699 | 6,699 |
  Contracts | 0 | 0 |
  Supplies and services | 4,066 | 4,066 |
  Travel | 3,925 | 3,925 |
| **Total direct costs (TDC)** | **68,080** | **6,699** | **134,779** |
| Indirect costs** | 53,302 | 5,988 | 61,290 |
| **Direct + Indirect Costs** | **121,387** | **74,088** | **195,475** |

*Notes:
**OPE = other personnel expenses
**TDC indirect costs = 40.5% of TDC
**Group indirect costs = 13% of Group TDC

### Budget 2010-11

**Main points**

- Summarizes costs by project
- Most project costs reflect allocation of personnel costs to different projects
- Overall, expenditures were less than projected because CAFS and CTGN funds were used to pay some salaries
- We did not undertake additional CTGN wood stiffness field work this year
- The CAFS DF provenance test proposal was not funded

<table>
<thead>
<tr>
<th>Income and Expenditures</th>
<th>Proposed (T10)</th>
<th>Actual (T11)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Members fees and contracts</td>
<td>102,000</td>
<td>110,000</td>
</tr>
<tr>
<td>Carryover from previous year</td>
<td>22,402</td>
<td>25,576</td>
</tr>
<tr>
<td><strong>Total income</strong></td>
<td><strong>124,402</strong></td>
<td><strong>135,576</strong></td>
</tr>
</tbody>
</table>
| Salaries and CAR**  
  Minirized Seed Orchards | 8,785 | 9,595 |
  Site Characterization (CAFS) | 20,230 | 24,817 |
  Wood Quality (CTGN) | 16,939 | 0 |
  Wood Quality (CAFS) | 20,110 | 17,085 |
  CFS provenance tests (CAFS) | 12,924 | 0 |
  Technology Transfer | 4,983 | 0 |
  Administration | 11,645 | 14,365 |
| **Total direct costs (TDC)** | **109,666** | **68,532** |
| Indirect costs** | 14,119 | 6,589 |
| **Direct + Indirect costs** | **123,785** | **75,121** |

*Notes:
**Cooperator funds only
**Direct costs are 13% of TDC
Budget details for 2010-2011

Attachment #4
Expenditures of Cooperator Funds for Fiscal Year 2010-2011 by Project and Activity

<table>
<thead>
<tr>
<th>Expense*</th>
<th>Min Orchards</th>
<th>Site Chair (CAFIS)</th>
<th>WQ (CTGN)</th>
<th>WQ (CAFIS)</th>
<th>Technology Transfer</th>
<th>Admin</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Director (funded by OSU) (approx. FTE)</td>
<td>0.10</td>
<td>0.15</td>
<td>0.00</td>
<td>0.15</td>
<td>0.00</td>
<td>0.10</td>
<td>0.00</td>
</tr>
<tr>
<td>Program Manager (approx. FTE)</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.10</td>
<td>0.10</td>
</tr>
<tr>
<td>Research Coordinator (approx. FTE)</td>
<td>4.096</td>
<td>0.00</td>
<td>0.00</td>
<td>0.11</td>
<td>0.00</td>
<td>0.02</td>
<td>13.635</td>
</tr>
<tr>
<td>Graduate students (approx. FTE**</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Student employees</td>
<td>5.099</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Personnel sub-total</td>
<td>9.196</td>
<td>24.642</td>
<td>0.00</td>
<td>13.710</td>
<td>0.00</td>
<td>9.374</td>
<td>56.912</td>
</tr>
<tr>
<td>Contracts</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Supplies &amp; Services</td>
<td>61.00</td>
<td>0.00</td>
<td>0.00</td>
<td>867</td>
<td>0.00</td>
<td>4.097</td>
<td>4.097</td>
</tr>
<tr>
<td>Travel</td>
<td>398</td>
<td>175</td>
<td>0.00</td>
<td>2.487</td>
<td>0.00</td>
<td>624</td>
<td>3.925</td>
</tr>
<tr>
<td>Non-personnel sub-total</td>
<td>400</td>
<td>175</td>
<td>0.00</td>
<td>3.355</td>
<td>0.00</td>
<td>4.99</td>
<td>8.920</td>
</tr>
<tr>
<td>Total direct costs (TDC)</td>
<td>9.596</td>
<td>24.817</td>
<td>0.00</td>
<td>17.065</td>
<td>0.00</td>
<td>14.365</td>
<td>65.832</td>
</tr>
<tr>
<td>Indirect costs (13% of TDC)</td>
<td>1.294</td>
<td>3.228</td>
<td>0.00</td>
<td>2.216</td>
<td>0.00</td>
<td>1.967</td>
<td>8.556</td>
</tr>
<tr>
<td>Total costs</td>
<td>10.890</td>
<td>28.045</td>
<td>0.00</td>
<td>19.281</td>
<td>0.00</td>
<td>16.332</td>
<td>74.388</td>
</tr>
</tbody>
</table>

*Personnel expenses include salary plus other personnel expenses (OPE)  
**Full-time graduate student assistantship = 0.49 FTE

Budget 2011-12

Main points

- Summarizes proposed costs of personnel for 2011-2012
- Part-time Program Manager (shared with CAFS and Strauss)
- Change to full-time Research Coordinator this year
- Increase in expenditures  
  - No CTGN funds to augment
- Partial support of graduate student (Oguz Urban)
- Contracts = proposed SNP genotyping

Attachment #5
Proposed Expenditures of Cooperator Funds for Fiscal Year 2011-2012

<table>
<thead>
<tr>
<th>Income and Expenditures</th>
<th>FY 2011-12</th>
<th>FY 2011-12</th>
</tr>
</thead>
<tbody>
<tr>
<td>Income from Cooperators</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Membership fees and contracts</td>
<td>110,000</td>
<td>110,000</td>
</tr>
<tr>
<td>Carryover from previous year</td>
<td>25,595</td>
<td>61,196</td>
</tr>
<tr>
<td>Total income</td>
<td>135,595</td>
<td>171,196</td>
</tr>
<tr>
<td>Expenditures</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Salaries and OPE</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Director (0.3 FTE) funded by OSU</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Program Manager (0.10 FTE)</td>
<td>7,420</td>
<td>7,420</td>
</tr>
<tr>
<td>Research Coordinator</td>
<td>13,655</td>
<td>73,746</td>
</tr>
<tr>
<td>Graduate students (0.50 FTE)</td>
<td>20,168</td>
<td>7,000</td>
</tr>
<tr>
<td>Student employees</td>
<td>5,099</td>
<td>7,000</td>
</tr>
<tr>
<td>Contracts</td>
<td>0</td>
<td>15,000</td>
</tr>
<tr>
<td>Supplies and Services</td>
<td>4,965</td>
<td>6,900</td>
</tr>
<tr>
<td>Travel</td>
<td>3,925</td>
<td>4,900</td>
</tr>
<tr>
<td>Total direct costs (TDC)</td>
<td>65,832</td>
<td>123,046</td>
</tr>
<tr>
<td>Indirect costs**</td>
<td>8,558</td>
<td>15,966</td>
</tr>
<tr>
<td>Direct + Indirect Costs</td>
<td>74,388</td>
<td>137,112</td>
</tr>
<tr>
<td>Carryover to next year</td>
<td>61,196</td>
<td>33,274</td>
</tr>
</tbody>
</table>

*OPE = other personnel expenses  
**Gross indirect costs = 13% of Gross TDC
Main points

- Summarizes proposed costs by project.
- We expect that site characterization research will be augmented by CAFS.
- We expect that WQ research will be augmented by CAFS.
- I propose to transition into a new PNWTRC project on SNP-based marker-assisted selection.

### Budget details for 2011-2012

#### Attachment #7

<table>
<thead>
<tr>
<th>Expense*</th>
<th>Mini Orchards</th>
<th>Site Char. (CAFS)</th>
<th>SNP MAS</th>
<th>WQ Tech (CAFS)</th>
<th>Transfer</th>
<th>Admin.</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Director (funded by OSU)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>(approx. FTE)</td>
<td>0.05</td>
<td>0.10</td>
<td>0.15</td>
<td>0.10</td>
<td>0.00</td>
<td>0.10</td>
<td>0.50</td>
</tr>
<tr>
<td>Program manager</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>7,500</td>
<td>7,500</td>
</tr>
<tr>
<td>(approx. FTE)</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.10</td>
<td>0.10</td>
</tr>
<tr>
<td>Research Coordinator</td>
<td>22.124</td>
<td>7.375</td>
<td>7.375</td>
<td>29.498</td>
<td>0</td>
<td>7.375</td>
<td>73,746</td>
</tr>
<tr>
<td>(approx. FTE)</td>
<td>0.30</td>
<td>0.10</td>
<td>0.10</td>
<td>0.40</td>
<td>0.00</td>
<td>0.10</td>
<td>1.00</td>
</tr>
<tr>
<td>FRA/Graduate students</td>
<td>0</td>
<td>7,500</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>7,500</td>
<td></td>
</tr>
<tr>
<td>(approx. FTE)</td>
<td>0.00</td>
<td>0.13</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.13</td>
<td></td>
</tr>
<tr>
<td>Student employees (proportion of expense)</td>
<td>2,000</td>
<td>0</td>
<td>2,000</td>
<td>1,000</td>
<td>0</td>
<td>1,000</td>
<td>7,000</td>
</tr>
<tr>
<td></td>
<td>0.43</td>
<td>0.00</td>
<td>0.29</td>
<td>0.14</td>
<td>0.00</td>
<td>0.14</td>
<td>1.00</td>
</tr>
<tr>
<td>Personnel sub-total</td>
<td>25,124</td>
<td>14,875</td>
<td>9,375</td>
<td>30,498</td>
<td>0</td>
<td>15,875</td>
<td>95,746</td>
</tr>
<tr>
<td>Contracts</td>
<td>0</td>
<td>0</td>
<td>15,000</td>
<td>0</td>
<td>0</td>
<td>15,000</td>
<td></td>
</tr>
<tr>
<td>Supplies &amp; Services</td>
<td>250</td>
<td>250</td>
<td>1,500</td>
<td>1,500</td>
<td>0</td>
<td>3,000</td>
<td>6,500</td>
</tr>
<tr>
<td>Travel</td>
<td>300</td>
<td>250</td>
<td>250</td>
<td>2,000</td>
<td>0</td>
<td>1,000</td>
<td>4,800</td>
</tr>
<tr>
<td>Non-personnel sub-total</td>
<td>550</td>
<td>500</td>
<td>10,750</td>
<td>4,800</td>
<td>0</td>
<td>6,000</td>
<td>26,300</td>
</tr>
<tr>
<td>Total direct costs (TDC)</td>
<td>25,674</td>
<td>15,375</td>
<td>26,125</td>
<td>34,998</td>
<td>0</td>
<td>19,875</td>
<td>137,912</td>
</tr>
<tr>
<td>Indirect costs (13% of TDC)</td>
<td>3,338</td>
<td>1,999</td>
<td>3,396</td>
<td>4,550</td>
<td>0</td>
<td>2,584</td>
<td>15,998</td>
</tr>
<tr>
<td>Total costs</td>
<td>29,011</td>
<td>17,373</td>
<td>29,521</td>
<td>39,548</td>
<td>0</td>
<td>22,458</td>
<td>153,912</td>
</tr>
</tbody>
</table>

*Personnel expenses include salary plus other personnel expenses (OPE)
**Full (half-time) graduate student assistantship = 0.49 FTE
Conifer Translational Genomics Network
Coordinated Agricultural Project

Douglas-fir SNP chip
Future of Douglas-fir genomics research and application

Glenn Howe, Jianbin Yu, and Scott Kolpak

www.pinegenome.org/ctgn

The Conifer Translational Genomics Network Coordinated Agricultural Project is a multi-state, multi-institution project, funded by USDA/CSREES/NRI and the USDA Forest Service. CTGN will deliver genomic assisted breeding by linking laboratory and field research with education and extension. Assertive and comprehensive education and extension programs will provide widespread training for post-doctoral researchers, graduate and undergraduate students, tree breeders, managers, stakeholders, and the general public.

What is CTGN CAP?
Overview

- What are SNPs? How do we find them?
- Transcriptome sequencing
- SNP discovery
- Marker-assisted selection – Genomic selection
- A Douglas-fir SNP chip is coming!
- Conclusions and future
What are SNPs?
How do we find them?

Single nucleotide polymorphism (SNP)

Tree 1

<table>
<thead>
<tr>
<th>Maternal chrom.</th>
<th>Paternal chrom.</th>
</tr>
</thead>
<tbody>
<tr>
<td>A C G T G T C G</td>
<td>A C G T G T C A</td>
</tr>
<tr>
<td>G T C T T A G</td>
<td>G T C T T A G</td>
</tr>
</tbody>
</table>

Tree 2

<table>
<thead>
<tr>
<th>Maternal chrom.</th>
<th>Paternal chrom.</th>
</tr>
</thead>
<tbody>
<tr>
<td>A C G T G T C G</td>
<td>A C G T G T C A</td>
</tr>
<tr>
<td>G T C T T A G</td>
<td>G T C T T A G</td>
</tr>
</tbody>
</table>

Tree 3

<table>
<thead>
<tr>
<th>Maternal chrom.</th>
<th>Paternal chrom.</th>
</tr>
</thead>
<tbody>
<tr>
<td>A C G T G T C G</td>
<td>A C G T G T C A</td>
</tr>
<tr>
<td>G T C T T A G</td>
<td>G T C T T A G</td>
</tr>
</tbody>
</table>

Tree 1 is **heterozygous**
Trees 2 and 3 are **homozygous**
A genome from many short sequences

Next-generation sequencing

Find SNP markers
Focus of Douglas-fir CTGN program

Need more SNP markers for Douglas-fir

- Available resources at the start of the CTGN project
  - 18,000 ESTs (Sanger) and 384 SNP chip (121 genes)

We added next-generation transcriptome sequencing for SNP discovery

- DOE Joint Genome Institute 454 sequencing project (Dean et al)
- New CTGN sequencing (454 and Illumina)
- Collaboration with Rich Cronn, USFS (Illumina sequencing)

Use of CTGN information and resources

- Incorporate phenotypes from the NWTIC program (relevant to breeders)
- A valuable goal would be to genotype all second-cycle parents
- Measure new phenotypes where possible
Transcriptome sequencing and SNP discovery

- mRNA isolation from diverse tissues
- cDNA Library preparation
- 454 and Illumina sequencing
- Sequence assembly and annotation
- SNP detection and SNP chip design

Transcriptome sequencing strategy

**Sanger sequences have lower error rates**
- 18K previous Sanger sequences from Dana Howe project
- Used with 454 sequences for transcriptome reference

**Roche 454 GS-FLX Titanium provides longer reads**
- DOE JGI collaboration (single-genotype sample)
- Univ Illinois Carver Biotechnology Center (multi-genotype sample)
  - Transcriptome reference and SNP discovery
  - Diverse tissues from trees of 79 seed sources throughout the year

**Illumina Genome Analyzer IIx provides greater depth**
- Greater sequence depth than 454 sequencing
- Multi-genotype samples for SNP discovery
Table 1. Characteristics of Douglas-fir cDNA libraries and numbers of sequences (reads) filtered using the snoWhite pipeline.

<table>
<thead>
<tr>
<th>Plant materials (dataset ID)</th>
<th>Collection information</th>
<th>Sequencing method*</th>
<th>Total reads in dataset (% of library total)</th>
<th>Number of reads filtered from the input dataset (% of library total)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Multi-genotype #1 (MG1_S)</td>
<td>Cold season Greenhouse</td>
<td>Sanger Normalized</td>
<td>12157 (100)</td>
<td>57 (0.47) 0 (0.00) 2 (0.02) 2 (0.02) 0 (0.00) 1 (0.01)</td>
</tr>
<tr>
<td>Multi-genotype #2 (MG2_R)</td>
<td>Cold and warm seasons</td>
<td>GS-FLX Titanium Normalized</td>
<td>1709211 (100)</td>
<td>6649 (0.39) 1893 (0.11) 8570 (0.50) 5519 (0.32) 7264 (0.42) 11114 (0.65)</td>
</tr>
<tr>
<td>Single-genotype (SG_R)</td>
<td>July 8, 2008</td>
<td>GS-FLX Titanium Non-normalized</td>
<td>1241260 (100)</td>
<td>6882 (0.53) 1826 (0.15) 11070 (0.89) 10463 (0.84) 86828 (0.70) 21849 (1.76)</td>
</tr>
<tr>
<td>All libraries</td>
<td></td>
<td></td>
<td>2962628 (100)</td>
<td>13288 (0.45) 3719 (0.13) 16442 (0.66) 15984 (0.54) 94092 (3.18) 32964 (1.11)</td>
</tr>
</tbody>
</table>

*GS-FLX Titanium is the Roche 454 sequencing platform.

New 454 sequences (reads) after cleaning

<table>
<thead>
<tr>
<th>Source</th>
<th>No. reads</th>
<th>Min length</th>
<th>Max length</th>
<th>Mean length</th>
<th>Bases</th>
</tr>
</thead>
<tbody>
<tr>
<td>SG-JGI</td>
<td>1100843</td>
<td>50</td>
<td>706</td>
<td>343</td>
<td>3780207441</td>
</tr>
<tr>
<td>MG-UIC</td>
<td>1657805</td>
<td>50</td>
<td>955</td>
<td>382</td>
<td>632655354</td>
</tr>
</tbody>
</table>

JGI mean=343

UIUC mean=382
## DF transcriptome assembly

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total reads</td>
<td>2764549</td>
</tr>
<tr>
<td>Assembled reads</td>
<td>2544087</td>
</tr>
<tr>
<td>Total assembled</td>
<td>2741911</td>
</tr>
<tr>
<td>Singletons</td>
<td>102623</td>
</tr>
<tr>
<td>Isogroups (genes)</td>
<td>25002</td>
</tr>
<tr>
<td>Isotigs</td>
<td>38589</td>
</tr>
<tr>
<td>One isotig/isogroup</td>
<td>18774</td>
</tr>
<tr>
<td>Mean length of isotig</td>
<td>1390</td>
</tr>
<tr>
<td>N50</td>
<td>1883</td>
</tr>
<tr>
<td>Total consensus nucleotides</td>
<td>72302278</td>
</tr>
</tbody>
</table>

### DF isotigs vs WS unigenes

<table>
<thead>
<tr>
<th>Type</th>
<th>No. of WS hits</th>
<th>Diff DF hits same WS?</th>
<th>Do other DF overlap?</th>
<th>No. of WS hits</th>
<th>Isotig Confid.</th>
<th>Number of isotigs</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>1</td>
<td>No</td>
<td>_</td>
<td>5140</td>
<td>Highest</td>
<td>261</td>
</tr>
<tr>
<td>II</td>
<td>2+</td>
<td>No</td>
<td>_</td>
<td>894</td>
<td>Highest</td>
<td>86</td>
</tr>
<tr>
<td>III</td>
<td>1</td>
<td>Yes</td>
<td>No</td>
<td>1767</td>
<td>Medium</td>
<td>577</td>
</tr>
<tr>
<td>IV</td>
<td>1</td>
<td>Yes</td>
<td>Yes</td>
<td>1736</td>
<td>Medium</td>
<td>6974</td>
</tr>
<tr>
<td>V</td>
<td>2+</td>
<td>Yes</td>
<td>No</td>
<td>587</td>
<td>Medium</td>
<td>161</td>
</tr>
<tr>
<td>VI</td>
<td>2+</td>
<td>Yes</td>
<td>Yes</td>
<td>3406</td>
<td>Lower</td>
<td>7040</td>
</tr>
<tr>
<td>VII</td>
<td>No hits</td>
<td>_</td>
<td>_</td>
<td>13530</td>
<td>_</td>
<td>15099</td>
</tr>
</tbody>
</table>

I. Total hits _
II. _
III. _
IV. _
V. _
VI. _
VII. _

---

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We can infer the functions of many genes

Table 2. Numbers and percents of Douglas-fir cDNA sequences with matches to sequences in three protein databases (BlastX e-value < 10^{-5}).

<table>
<thead>
<tr>
<th>Database</th>
<th>Unigenes (25002)</th>
<th>Singletons (102623)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number</td>
<td>Percent</td>
</tr>
<tr>
<td>Uniref50</td>
<td>15054</td>
<td>80.2</td>
</tr>
<tr>
<td>TAIR9</td>
<td>13747</td>
<td>73.2</td>
</tr>
<tr>
<td>Annot8r</td>
<td>11733</td>
<td>62.5</td>
</tr>
</tbody>
</table>

1 Unigenes are Newbler v2.3 isogroups. For the isogroups with more than 1 isotig, a hit was counted only if all isotigs matched the same protein in the database.

† Singletons are 454 reads that did not assemble with any other reads.

Table 3. Numbers of Douglas-fir cDNA sequences with matches to sequences in the Uniref50 protein database. Matches are grouped by taxonomic affiliation and percentages are relative to the total number of matches (BlastX e-value < 10^{-5}). Numbers of input Douglas-fir sequences are in parentheses.

<table>
<thead>
<tr>
<th>Taxonomic category</th>
<th>Unigenes (25002)</th>
<th>Singletons (102623)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number</td>
<td>Percent</td>
</tr>
<tr>
<td>Conifers</td>
<td>4088</td>
<td>27.16</td>
</tr>
<tr>
<td>Other plants</td>
<td>9713</td>
<td>64.52</td>
</tr>
<tr>
<td>Fungi</td>
<td>6</td>
<td>0.04</td>
</tr>
<tr>
<td>Invertebrates</td>
<td>487</td>
<td>3.24</td>
</tr>
<tr>
<td>Vertebrates</td>
<td>17</td>
<td>0.11</td>
</tr>
<tr>
<td>Other Eukaryotes</td>
<td>582</td>
<td>3.87</td>
</tr>
<tr>
<td>Bacteria</td>
<td>123</td>
<td>0.82</td>
</tr>
<tr>
<td>Viruses</td>
<td>4</td>
<td>0.03</td>
</tr>
<tr>
<td>Environmental samples</td>
<td>21</td>
<td>0.14</td>
</tr>
<tr>
<td>Unassigned</td>
<td>13</td>
<td>0.09</td>
</tr>
<tr>
<td>Total matches</td>
<td>15054</td>
<td>100</td>
</tr>
</tbody>
</table>
We can infer the functions of many genes

<table>
<thead>
<tr>
<th>Annotation</th>
<th>Accession</th>
<th>Species</th>
<th>BIC</th>
<th>E-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enhanced disease susceptibility 1</td>
<td>P40697</td>
<td>Anabalon thalas</td>
<td>268</td>
<td>2.00E-53</td>
</tr>
<tr>
<td>Putative uncharacterized protein</td>
<td>P40696</td>
<td>Macraequorus</td>
<td>55.5</td>
<td>2.00E-36</td>
</tr>
<tr>
<td>Disease resistance protein CPR3</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>834</td>
<td>2.00E-39</td>
</tr>
<tr>
<td>Non-specific lipid transfer protein 1</td>
<td>P41637</td>
<td>Anabalon thalas</td>
<td>728</td>
<td>2.00E-12</td>
</tr>
<tr>
<td>Ceramide fatty alcohol lyase</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>210</td>
<td>5.00E-10</td>
</tr>
<tr>
<td>Probable disease resistance protein AAG79380</td>
<td>P40697</td>
<td>Anabalon thalas</td>
<td>407</td>
<td>e-55</td>
</tr>
<tr>
<td>Probable uncharacterized protein</td>
<td>P40694</td>
<td>Anabalon thalas</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Cell cycle-related protein</td>
<td>P40697</td>
<td>Anabalon thalas</td>
<td>244</td>
<td>2.00E-19</td>
</tr>
<tr>
<td>Leucine</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>1.6</td>
<td>3.00E-36</td>
</tr>
<tr>
<td>Aquaporin</td>
<td>P40697</td>
<td>Anabalon thalas</td>
<td>261</td>
<td>2.00E-54</td>
</tr>
<tr>
<td>Leucine-rich repeat transduction-like protein kinase (Frq, OB6914)</td>
<td>Anabalon thalas</td>
<td>107</td>
<td>e-125</td>
<td></td>
</tr>
<tr>
<td>Leucine-rich repeat transduction-like protein kinase (Frq, OB6914)</td>
<td>Anabalon thalas</td>
<td>107</td>
<td>e-125</td>
<td></td>
</tr>
<tr>
<td>Ceratophyllum digiti fruticosum 1</td>
<td>P40692</td>
<td>Anabalon thalas</td>
<td>228</td>
<td>3.00E-19</td>
</tr>
<tr>
<td>Purine nucleoside phosphorylase 1, yeast (Pur, OB691)</td>
<td>Anabalon thalas</td>
<td>275</td>
<td>e-123</td>
<td></td>
</tr>
<tr>
<td>Monomeric glycoside hydrolase 16</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>275</td>
<td>3.00E-19</td>
</tr>
<tr>
<td>179 kDa low molecular weight protein</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>1.6</td>
<td>e-125</td>
</tr>
<tr>
<td>179 kDa low molecular weight protein</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>1.6</td>
<td>e-125</td>
</tr>
<tr>
<td>Disease resistance protein CPR2</td>
<td>P40694</td>
<td>Anabalon thalas</td>
<td>137</td>
<td>2.00E-44</td>
</tr>
<tr>
<td>Xanthin dehydrogenase</td>
<td>P40694</td>
<td>Anabalon thalas</td>
<td>264</td>
<td>3.00E-26</td>
</tr>
<tr>
<td>Dehydration responsive element binding protein 2A, OB69122</td>
<td>Anabalon thalas</td>
<td>117</td>
<td>2.00E-25</td>
<td></td>
</tr>
<tr>
<td>Argonaute (AGO3), like protein</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>137</td>
<td>0</td>
</tr>
<tr>
<td>Argonaute (AGO3), like protein</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>137</td>
<td>0</td>
</tr>
<tr>
<td>Gamma subunit of ATP synthase</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>137</td>
<td>5.00E-13</td>
</tr>
<tr>
<td>Putative gly4</td>
<td>P40694</td>
<td>Anabalon thalas</td>
<td>137</td>
<td>5.00E-13</td>
</tr>
<tr>
<td>Disease resistance protein like</td>
<td>P40694</td>
<td>Anabalon thalas</td>
<td>137</td>
<td>5.00E-13</td>
</tr>
<tr>
<td>Leucine-rich repeat transduction-like protein</td>
<td>P40693</td>
<td>Anabalon thalas</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
Illumina short-read sequencing
Multi-genotype sample

Goal was to increase sequence depth and confidence of SNP calls

- Genome Analyzer IIx
- Illumina paired-end sequencing
  - 100-bp reads
  - 64.0 million reads (32.0 million pairs)
- Same multi-genotype sample as 454 sequencing
- Accomplishments
  - We mapped the reads to our reference transcriptome and detected 206,026 potential SNPs (all isotigs)

---

Illumina short-read sequencing
Gene expression samples

Primary goal is to compare gene expression among provenances, sites, and seasons (Cronn, Knaus, Dolan)

- Collaboration with ongoing USDA AFRI project
- Illumina single-read sequencing
  - 80 bp single-end reads
  - We used 22.4 million reads
  - Will generate ~20 Gbp of transcriptome sequence
- Coos Bay (coastal DF) and Yakima (interior?) seed sources
- Accomplishments
  - We mapped the reads to our reference transcriptome and detected a total of 170,629 SNPs summed over two seed sources (all isotigs)
Extension to interior Douglas-fir

**Goal was to develop SNP markers for interior Douglas-fir (var. glauca)**

- Collaboration with Sam Cushman, USFS Rocky Mountain Station
- Include ‘interior’ SNPs on the SNP chip
- Multi-genotype sample = 80.4 million reads (40.2 million pairs)
  - Trees in BCMoF provenance test and N. Idaho
  - Marc Rust, Director, Inland Empire Tree Improvement Cooperative
  - Needles, stems, and buds
- Accomplishments
  - We mapped the reads to our reference transcriptome and detected 203,714 potentially unique and shared SNPs with coastal Douglas-fir (all isotigs)

Potential SNP markers in Douglas-fir

**SNPs detected in our most confident genes**

(1 isotig/isogroup)

<table>
<thead>
<tr>
<th>Douglas-fir variety</th>
<th>No. of SNPs</th>
<th>No. of genes with SNPs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coastal</td>
<td>238,760</td>
<td>17,556</td>
</tr>
<tr>
<td>Interior</td>
<td>151,918</td>
<td>16,580</td>
</tr>
<tr>
<td>Both (in common)</td>
<td>71,376</td>
<td>13,759</td>
</tr>
</tbody>
</table>

**Conclusion = lots of SNP markers to choose from!**
The promise of genomic selection

Paradigm shift in perspective

- Forget about finding individual markers associated with desirable traits
- Explain desirable traits by using many, many markers at the same time
- Now possible because we can genotype many SNP markers at modest cost
  - SNP, single nucleotide polymorphism, = changes between A, G, C, T
- Why might it be useful?
The promise of genomic selection

Genotype, then use existing phenotypes to train GEBV model

**Model training step**

- Phenotypic selection (select on BLUP BV)
- Genomic selection (select on GEBV)

- Phenotype progeny (field tests)
- Make crosses
- Genotype progeny (SNP markers)

GEBV = genomic estimated breeding value
Tree Genome Simulator

Five modules
- QTL allele pool
- Genetic map
- Parents
- Progeny
- SNP haplotypes

A Douglas-fir SNP chip is coming!
SNP chip

**SNP choices are based on...**

- Confidence in the assembled gene
  - 1 isotig/isogroup versus 2+ isotig/isogroup
  - White spruce comparisons (highest, higher, medium, lower confidences)

- Inferred functions (annotations)
  - Growth, wood properties, adaptation to environmental stresses
  - Genes targeted by loblolly pine SNP chip

- SNP quality based on SAMTools statistics
  - Primarily consensus quality, SNP quality, number of covering reads

- SNPs detected in multiple datasets (including interior Douglas-fir)

- Illumina Infinium SNP design scores

Douglas-fir SNP chip (Illumina Infinium)

**Douglas-fir SNP chip from will soon become available**

- Recently ordered - now working with Illumina to finalize SNP choices

- Up to 9000 SNPs (9000 ‘attempted bead types’)

- Cost of the chip is covered by CTGN

- Additional cost of genotyping ~10$/sample
Proposed PNWTIRC research

*Use SNP chip to genotype NWTIC second cycle parents*

- Test the SNP chip on coastal and interior Douglas-fir
- Genotype NWTIC second-cycle parents
- Leverage CTGN information and investment in SNP chip
- Total cost for PNWTIRC genotyping may be $15K
- Develop a longer-term proposal for PNWTIRC research on genomic selection
  - *New PNWTIRC graduate student?*
- Use as a foundation for other competitive grant proposals

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Conclusions and future

www.pinegenome.org/ctgn
Future

**SNP verification is the highest priority for Douglas-fir**

- Goal is to maximize the number of SNPs assayed (versus genotypes) to be able to test genomic selection
- Our CTGN goal was to construct the largest SNP chip possible
  - 1536 SNP chip was originally proposed
  - We recently ordered an Infinium SNP chip for Douglas-fir
  - Potentially 9000 SNPs with CTGN funds
- Test the SNP chip on the highest priority genotypes
- Make the SNP chip available to tree breeders so that in-kind support can expand the number of genotypes analyzed

Douglas-fir CTGN accomplishments

**New phenotypes and breeding values**

- BVs for wood stiffness, fall cold hardiness, vegetative phenology, or reproductive phenology were estimated for about 1300 genotypes
- BVs for growth and stem form are already available for these same genotypes

**Reference transcriptome for Douglas-fir**

- A reference transcriptome based on 2.8M Roche 454 and 12K Sanger sequences has 25,002 isogroups (gene models) and 102,623 singletons

**SNP chip for coastal and interior Douglas-fir**

- As many as 9000 SNPs (ABTs) and 1152 samples
- Costs of the SNP chip (but not genotyping) are covered by CTGN

**Tree Genome Simulator**

- Software can be used to design and evaluate marker-assisted selection schemes
Acknowledgements

Genomic resources from CTGN can be used by Douglas-fir breeders

- Pacific Northwest Tree Improvement Research Cooperative (PNWTIRC)
- Northwest Tree Improvement Cooperative (NWTIC)
- Inland Empire Tree Improvement Cooperative (IETIC)

Collaborators are...

- PNWTIRC, NWTIC (Keith Jayawickrama), and IETIC (Marc Rust)
- USFS Pacific Northwest Research Station (Cronn)
- University of GA and Joint Genome Institute (Dean)
- USFS Rocky Mountain Research Station (Cushman)

Thank You.

Conifer Translational Genomics Network
Coordinated Agricultural Project
Background

Miniaturized Seed Orchards (MSO) *

- Increased per hectare seed yields through higher stocking of orchards and crown management (e.g., fruit trees, Pinus radiata)
- Shift to earlier production of operational quantities of seed
- Increased genetic gains by facilitating pollination techniques (CMP, SMP) and reducing pollen contamination (bloom delay)
- Reduced costs of CMP, SMP, and cone harvest

Orchards were mostly grafted in 2003 and 2004

Flower stimulation began in 2009

Table 1: MSO research goals and progress (Anekonda and Adams 1999)

<table>
<thead>
<tr>
<th>Original objectives</th>
<th>Location</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>1) Compare three orchard types for seed production and management efficiency</td>
<td>Plum Creek MSO</td>
<td>Ongoing</td>
</tr>
<tr>
<td>2) Define the best age to begin floral stimulation in MSOs</td>
<td>Roseburg Resources Vaughn &amp; PNWCTA orchards</td>
<td>Completed - Cherry et al. 2007</td>
</tr>
<tr>
<td>3) Evaluate crown control techniques</td>
<td>Roseburg Resources Vaughn orchard</td>
<td>Completed - Pruning study</td>
</tr>
<tr>
<td>4) Compare pollination methods (CP, SMP)</td>
<td></td>
<td>Drop objective</td>
</tr>
<tr>
<td>5) Evaluate the clonal response to MSO management regimes</td>
<td>Plum Creek MSO</td>
<td>Ongoing</td>
</tr>
</tbody>
</table>

Table 2: MSO spacing, no. of trees, and crown height.

<table>
<thead>
<tr>
<th>Spacing (m)</th>
<th>No. of trees</th>
<th>Stems / ha</th>
<th>Crown height (m)</th>
</tr>
</thead>
<tbody>
<tr>
<td>4x6</td>
<td>640</td>
<td>416</td>
<td>4</td>
</tr>
<tr>
<td>2x4</td>
<td>640</td>
<td>1,250</td>
<td>3</td>
</tr>
<tr>
<td>1x3</td>
<td>768</td>
<td>3,333</td>
<td>2</td>
</tr>
</tbody>
</table>

3 orchard spacings
- 4x6 m, 2x4 m, 1x3 m

4 block-pairs / spacing
- 8 total replications

5-tree to 6-tree row-plots
**MSO design and layout**

**Table 3: Clone composition**

<table>
<thead>
<tr>
<th>Clone category</th>
<th>Age of ortet at grafting</th>
<th>No. clones</th>
</tr>
</thead>
<tbody>
<tr>
<td>Forward</td>
<td>10</td>
<td>12</td>
</tr>
<tr>
<td>Forward</td>
<td>30</td>
<td>4</td>
</tr>
<tr>
<td>Backward</td>
<td>60-100</td>
<td>8</td>
</tr>
</tbody>
</table>

**Orchard activities 2010 - 2011**

**Flower stimulation**
- Half the blocks in the 2x4 and 4x6 m orchards, all of the 1x3 m orchard block were stimulated in the spring of 2010 (girdling and calcium nitrate)

**Data collected**
- **2010 crop** – crown size, cone counts, seed counts
- **2011 crop** – cone counts
Talk outline

**Talk goal:** Discuss cone production differences among orchard spacings and age of ortets

- What factors influenced cone production in 2010 and 2011?

**Talk outline**

- **Crown volume** – 2010 crop, background and results
- **Cone production** – 2010 and 2011 crops by spacing, ortet age, and crown volume
- **Flower production** – 2010, background, comparisons with cone production
- **Future directions**

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Crown measurements

**Observations**

- Crown shapes are different between clone ages
Crown volume measurements

**Observations**
- Crown shapes are different between clone ages

**4x6 orchard (2010)**
- Backward
- Forward

Observations
- Pruning altered crown shape, but effects on crown volume are less known

**1x3 orchard (2010)**
- Backward
- Forward
Crown volume goals

Learn how orchard differences in crown volume affect cone production

1x3 orchard (2010)

Crown volume measurements

**Direct measurements**
- Crown height = total tree height - live crown height
- Crown shape
- Maximum crown radius (west side)

**Indirect measurements**
- Basal diameter – stem diameter at the middle of the first internode above the graft union
Crown volume by spacing and ortet age

Crows larger in 4x6 orchard
- Never pruned
- Wider spacing

Crows larger in forward clones
- Particularly in the 4x6 orchard
- Developmentally younger scions
- Management levels-the-playing-field (e.g., 1x3 & 2x4 orchards)

Cone production by spacing: 2011 crop

- Stimulation increases cone production
- Cones / tree = 4x6 m orchard is best
- Cones / hectare = 2x4 m orchard is best
Cone production by spacing
2010 vs. 2011 cone crops

- Tradeoff between managing for more cones/tree vs cones/hectare
- Consider smaller trees at higher planting densities

Cone production per hectare by spacing

Twice the cones in 2011
- Larger and older trees
- Flower stimulation differed
  - 2010 = girdling + calcium nitrate + GA
  - 2011 = girdling + GA
- Good cone year in 2011
Miniaturized seed orchards

2x4 orchard

4x6 orchard

Crown volume & cone production by spacing

- 2010 cone crop – 4x6 orchard trees are twice as large, but still support the same number of cones per unit crown volume
- 2011 cone crop – measure this fall
Cone production by ortet age

- Higher cone production in young clones
- Mostly influenced by trees in the 4x6 orchard

PACIFIC NORTHWEST TREE IMPROVEMENT RESEARCH COOPERATIVE
Cone production by ortet age

- Higher cone production in young clones
- Mostly influenced by trees in the 4x6 orchard
- Likely a consequence of the larger crowns on the forward selections

2010 cone crop: Data collection

**Flower data**
- Flower counts
  - Female flowers were counted (to the nearest 10 flowers)
  - Numbers of male flowers were estimated and placed into 5 classes
- Floral developmental stages
  - Rated using a 5-point scale

**Vegetative bud development ("bud burst")**
- Rated using a 5-point scale

**Frost flower damage survey**
- Damaged female flowers: Yes or no
- Percent damaged female flowers
- Floral developmental stage when damage occurred
2010 cone crop
Flowering by spacing and ortet age

Female flowers

Male flowers

More male and female flowers from developmentally younger trees

2010 cone crop: Flowers and cones

Moderate flower to cone relationship because of frost damage, liberal scoring
Acknowledgements

Field work help

Annie Simmonds
Elaine Blampied
Oguz Urhan
Liz Etherington

Jim Smith – orchard management, project management

Future measurement activities 2011-2012

<table>
<thead>
<tr>
<th>Activity</th>
<th>Scope</th>
<th>Date</th>
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</thead>
<tbody>
<tr>
<td>Crown measurements</td>
<td>2011 crop - cones / crown volume</td>
<td>October</td>
</tr>
<tr>
<td>Flower counts</td>
<td>2012 crop – flwr. to cone relationship</td>
<td>April</td>
</tr>
<tr>
<td>Flower &amp; bud phenology</td>
<td>2012 crop – diff. between orchards</td>
<td>April</td>
</tr>
<tr>
<td>Flower stimulation</td>
<td>2013 crop – stim. method or methods</td>
<td>March</td>
</tr>
<tr>
<td>Cone counts</td>
<td>2012 crop – cones by orchard spacing</td>
<td>August</td>
</tr>
<tr>
<td>Seed measurements</td>
<td>2012 cone – filled seed consequences</td>
<td>November</td>
</tr>
</tbody>
</table>

- 2011 Cone crop = half of the 2x4 and 4x6 m orchards replications
- 2012 Cone crop = half of the 2x4 and 4x6 m orchards, all 1x3 replications
- 2013 Cone crop = same replications as 2011
Future management activities 2011-2012

**Flower stimulation**

- **Plan is to stimulate half of the 2x4 and 4x6 orchards in the spring of 2012**
- **Plan is to use calcium nitrate fertilizer and girdling**
- **Discuss the value of testing GA x N treatments**
  - Results will only be available after the PNWTIRC report is completed
  - Advantage – may shed light on alternative methods
  - Disadvantage – may compromise future comparisons of orchards

**Bloom delay**

- **Plan is not to use bloom delay**
- **Discuss the value of testing bloom delay treatments**
  - Results will only be available after the PNWTIRC report is completed
  - Advantage – learn something?
  - Disadvantage – published results on bloom delay are already available, this research does not seem to be MSO-specific, and treatments may compromise future comparisons of orchards
Future management activities 2011-2012

Pruning

- Plum Creek’s long-term recommendation is to leave the trees unpruned, so no pruning is planned for this year
- Our plan is to complete MSO research over the next year, so lack of pruning will not impact these plans

Future management activities 2011-2012

Thinning

- Plum Creek’s recommendation is to thin the 1x3 and 2x4 orchards after the 2012 cone harvest
- Our plan is to complete MSO research over the next year, so thinning will not impact our plans
- Discuss thinning strategies
  - 1x3 spacing has formed a closed canopy, mechanized management not possible now, cone collection will be difficult, remove alternate rows
  - 2x4 spacing – crowns are starting to compete, mechanized management becoming difficult, maximal cone production might start declining