

Pacific Northwest Tree Improvement
Research Cooperative
Annual Report
2014-2015

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

Glenn Howe, Oguz Urhan, Scott Kolpak,
Erda Çeler, Keith Jayawickrama, Dominique Bachelet,
Brad St.Clair, Anna Magnuson



Don Paulson

PACIFIC NORTHWEST TREE IMPROVEMENT RESEARCH COOPERATIVE

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Report authors and editors

Glenn Howe Keith Jayawickrama

Oguz Urhan Dominique Bachelet

Scott Kolpak Brad St.Clair

Erda Çeler Anna Magnuson

Cover photo by Don Paulson, www.donpaulson.com

For information

Glenn.Howe@oregonstate.edu

phone 541-737-9001, fax 541-737-1393

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Pacific Northwest Tree Improvement Research Cooperative

Annual Report 2014-2015

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

Bureau of Land Management
Cascade Timber Consulting
Green Diamond Resource Company
Hancock Forest Management
Olympic Resource Management
Oregon Department of Forestry
Oregon State University
Plum Creek Timber Company
Port Blakely Tree Farms
Rayonier Forest Products
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

HIGHLIGHTS OF 2014-2015

- We obtained our first data from the 50K SNP chip (Affymetrix Axiom genotyping array). Analyses of our first set of 1,536 trees indicates that we will be able to reliably assay about 20K SNPs. During 2015-2016, we will analyze the rest of the 1,920 trees in the study, and begin analyses of genomic selection. This is a collaboration with Keith Jayawickrama and the Northwest Advanced Renewables Alliance.

- Oguz Urhan continued his work on developing classical and molecular breeding strategies for western white pine. This project is being funded by the Center for Advanced Forestry Systems (CAFS) in collaboration with the Inland Empire Tree Improvement Cooperative, US Forest Service, and British Columbia Ministry of Forests. Oguz Urhan is being supported by a scholarship from the Turkish government.

- We began work on the drought hardiness study, a collaboration with the Bureau of Land Management, Northwest Tree Improvement Cooperative, Plum Creek Timber Company, and Silver Butte Timber Company. Erda Çeler is undertaking this study as part of her Master's thesis project. She and others began taking measurements on three genetic test plantations in southern Oregon in September 2015. Erda is being supported by a scholarship from the Turkish government.

- We have begun a re-design of the Seedlot Selection Tool (SST). This is a collaborative project between the PNWTIRC, USFS Pacific Northwest Research Station, and the Conservation Biology Institute.

- We began working on analyses of data from the Douglas-fir Heredity Study, a provenance test established in 1915. This is a collaborative project between the PNWTIRC (Glenn Howe) and USFS Pacific Northwest Research Station (Brad St.Clair)

- We launched the PNWTIRC newsletter, which will be used to keep members informed about key events and accomplishments during the year.

MESSAGE FROM THE DIRECTOR

We lost a good friend and colleague this year. Randall Greggs passed away on May 11, 2015, after battling cancer for a year and a half. Throughout much of that time, he remained as active as ever with the PNWTIRC and other forestry activities. Randall obtained a master's degree in silviculture and forestry from the University of Washington, 1981. He worked for Plum Creek for nine years, but was working for Simpson Timber Company when I first met him in 2001. Simpson was reorganized in 2006, so Randall eventually became a forestry operations manager with the Green Diamond Resource Company, which was created to manage Simpson's forest lands.

Randall was passionate about his work, and known for freely sharing his ideas. He was a great supporter of the PNWTIRC, both intellectually, and by serving numerous stints as the Policy/Technical Committee Chair and industry representative to the NSF Center for Advanced Forestry Systems. I met him at the Portland airport at the start one of our trips to the annual CAFS meeting. We sat down for an early morning coffee while waiting for the plane to board, and became so engrossed in our conversation that we barely noticed as our plane lifted-off to the east coast. Randall had lots to say, much to contribute, and will be greatly missed.



Glenn Howe, PNWTIRC Director

AGENDA – THURSDAY OCTOBER 22, 2015
– ANNUAL MEETING –
PACIFIC NORTHWEST TREE IMPROVEMENT RESEARCH
COOPERATIVE (PNWTIRC)

START TIME: 8:30 AM for coffee; 9:00 AM for presentations
LOCATION: David Douglas Room; World Forestry Center, Portland, OR
LUNCH: Lunch provided

Time	Topic	Responsibility
8:30-9:00	Coffee	
9:00-9:15	Welcome and Introductions	Sara Lipow
9:15-9:30	Overview <ul style="list-style-type: none"> • <i>PNWTIRC accomplishments for 2014-15</i> • <i>PNWTIRC plans for 2015-16</i> 	Glenn Howe
9:30-10:00	Phenotypic and molecular breeding in western white pine <ul style="list-style-type: none"> • <i>Update on CAFS/STDP projects</i> 	Oguz Urhan Scott Kolpak
10:00-10:15	Effects of genetics and site on Douglas-fir drought hardiness	Erda Celer
10:15-10:45	Break	
10:45-11:15	Next-generation SNP chip and genomic selection in Douglas-fir	Glenn Howe
11:15-12:00	Five-year plan – Progress report	Glenn Howe
12:00-1:00	Lunch	
1:00-1:20	Budget and other business <ul style="list-style-type: none"> • <i>Budget presentation and vote</i> • <i>Elect new Policy/Technical Committee Chair</i> 	Glenn Howe Sara Lipow
1:20-1:40	Conservation Biology Institute – Data Basin <ul style="list-style-type: none"> • <i>A science-based mapping and analysis platform</i> 	Dominique Bachelet
1:40-2:00	Break	
2:00-2:20	Decision support tools for forest management <ul style="list-style-type: none"> • <i>Reinvention of the Seedlot Selection Tool</i> • <i>Visions of other tools for forest managers</i> 	Glenn Howe
2:20-2:50	100-year results from the Douglas-fir heredity study <ul style="list-style-type: none"> • <i>Results from the latest analyses and historical perspective</i> 	Brad St.Clair
2:50-3:00	<ul style="list-style-type: none"> • Wrap-up and adjourn 	Glenn Howe

ABSTRACT: Overview of PNWTIRC Activities for 2015

Glenn Howe

PNWTIRC Director, Glenn Howe, presented an overview of activities for 2015. Glenn described the current PNWTIRC staff, which consists of Scott Kolpak, Kori Ault, Lauren Magalska, Oguz Urhan, and Erda Çeler. Sara Lipow of Roseburg Forest Products is currently serving as the Policy/Technical Committee Chair. Key activities over the past year included the development and testing of the 50K SNP chip (Affymetrix Axiom genotyping array), the continued development of classical and molecular breeding strategies for western white pine (a CAFS project), and the initiation of a project on the genetics of drought hardiness in Douglas-fir. Glenn also described two collaborative projects between the PNWTIRC and the USFS Pacific Northwest Research Station (Brad St.Clair). The first is a reanalysis of 100 years of data from the USFS Douglas-fir Heredity Study, and the second is a redesign of the Seedlot Selection Tool, a web application that can be used to match seedlots and planting sites based on climate. Glenn also described the initiation of the PNWTIRC Newsletter, recent presentations by PNWTIRC personnel, and current collaborations and grants.

PNWTIRC Annual Meeting 2015

October 22, 2015

Glenn Howe

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

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PNWTIRC personnel

2014-2015

- Director – **Glenn Howe**
- Research Coordinator – **Scott Kolpak**
- Program Manager – **Kori Ault**
- Graduate students – **Oguz Urhan, Erda Çeler**
- Faculty Research Assistant – **Lauren Magalska**
- Policy/Technical Committee Chair – **Sara Lipow**

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PNWTIRC highlights for 2014-2015

- **Promising results from the 50K SNP chip (Affymetrix Axiom)**
 - Collaboration with Keith Jayawickrama and the Northwest Advanced Renewables Alliance (NARA)
- **Continued to develop breeding strategies for WWP**
 - Collaboration with Marc Rust, Richard Sniezko, and others
 - Oguz Urhan is being supported by a scholarship from the Turkish government
- **We began work on the drought hardiness study**
 - Collaboration with Keith Jayawickrama, BLM, Plum Creek, Silver Butte
 - Erda Çeler is being supported by a scholarship from the Turkish government
 - Scott Kolpak and Kori Ault have been instrumental in providing guidance
- **Began working with Brad St.Clair on the DF Heredity Study**
- **Launched the PNWTIRC newsletter**

Breeding western white pine
Oguz Urhan and Scott Kolpak

Phenotypic and molecular breeding in western white pine
Oguz Urhan
Scott Kolpak

Douglas-fir drought hardiness
Erda Çeler

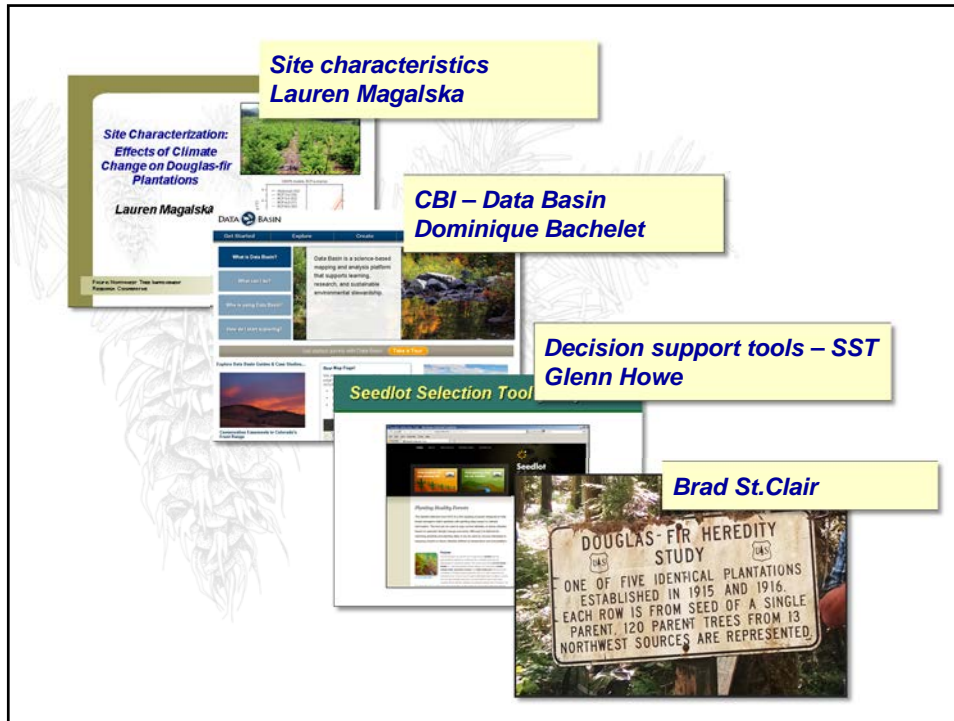
Effects of Genetics and Site on Douglas-fir Drought Hardiness
Erda Çeler

Next-generation SNP chip for Douglas-fir
Glenn Howe
Stephanie Guide
Sanjuro Jogdeo
Rich Cronn
Keith Jayawickrama
Callum Bell

Next-generation SNP chip
Glenn Howe

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New directions in western white pine research

Toward genomic selection in western white pine

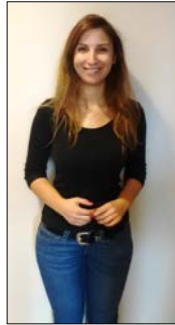
Axiom 96-format and 384-format Arrays

Regional analyses of WWP tests (IETIC, USFS, BCMoF)

Table 1. Western white pine breeding programs and tests in the Pacific Northwest, Inland Empire, and British Columbia.

Breeding program	Test type	Tests	Number of			Mating design	Age	Traits	Measurement	Age
			Plantations	Families						
USFS Dorena	Progeny	2	12	80 - 81		Half-diallel, OP	9 - 16	HT, DBH, RUST traits, SURV, Damage		7,12
	Nursery screening	3	4	60 - 240		Half-diallel, OP	5 - 16	HT, DBH, RUST traits, SURV, Damage		1,2,3,4,5,6
USFS/IETIC	Progeny	5	8	200 - 325		OP	32 - 37	HT, DBH, RUST traits, SURV, Damage		3,5,7,10,15
	Farm-field	5	5	105 - 600		OP	19 - 32	HT, DBH, RUST traits, SURV, Damage		
	Nursery screening	17	17	100 - 318		OP	5 - 32	HT, DBH, RUST traits, SURV, Damage		
	Realized gain	3	6	422 - 462		OP	3 - 10	HT, DBH, RUST traits, SURV, Damage		
	Performance	22	27	7 - 262		OP	2 - 28	HT, DBH, RUST traits, SURV, Damage		
BC Ministry of Forests	Progeny	5	14	49+		Half-diallel, OP	9 - 14	HT, DBH, RUST traits, SURV, Damage		7,10,13

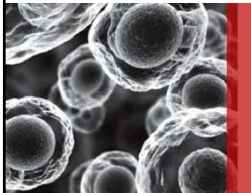
Effects of genetics and site on Douglas-fir drought hardiness



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Axiom 50K Douglas-fir SNP chip



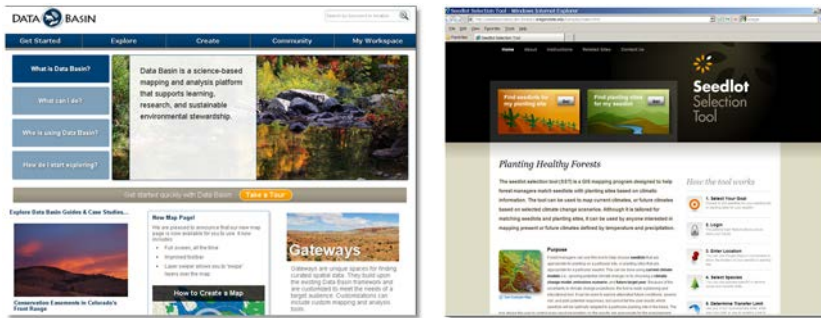
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Affymetrix

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Rebirth of the Seedlot Selection Tool



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100 Years of Douglas-fir genetics



Highlights of 2014-2015

Oguz represented OSU at the CAFS annual meeting

- Rust, M.L., Davis, A., Howe, G.T., Hipkins, V. 2015. Development of genetic markers for western white pine and Douglas-fir. *Presentation in:* Center for Advanced Forestry Systems Annual Meeting, May 19-21, Asheville, North Carolina.
- Klocko, A., Ma, C., Robertson, S., and Strauss, S.H. 2015. *FT* genes for accelerating flowering in *Eucalyptus*. *Presentation in:* Center for Advanced Forestry Systems Annual Meeting, May 19-21, Asheville, North Carolina.
- Klocko, A., and Strauss, S.H. 2015. Production and analysis of flowering-modified eucalypts. *Presentation in:* Center for Advanced Forestry Systems Annual Meeting, May 19-21, Asheville, North Carolina.

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Current collaborations and grants

- **CAFS. Center for Advanced Forestry Systems – Phase II.** Howe, G.T., Maguire, D.A. and Strauss, S.H. National Science Foundation Industry/University Cooperative Research Center Program, 2012-2017, \$300,000 (OSU).
- **USFS Forest Health Protection, Special Technology Development Program. Genetic markers for western white pine (WWP): Enabling molecular breeding for resistance to white pine blister rust.** Howe, G.T., Davis, A., Hipkins, V., Liu, J.-J., Mahalovich, M.F., Rust, M., and Sniezko, R., 2014-2016, \$99,685. Funding for 2014 (\$16,000) was received.
- **University of Idaho and the Inland Empire Tree Improvement Cooperative. Genetic markers for western white pine (WWP): Enabling molecular breeding for resistance to white pine blister rust.** Howe, G.T., 2013-2015, \$30,000.

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Current collaborations and grants

- **USFS Rocky Mountain Research Station. *Developing a SNP panel for interior Douglas fir.*** Howe, G.T. and Cushman, S. USDA-Forest Service Joint Venture Agreement, 2011-2015, \$28,755.
- **U.S. Endowment for Forestry and Communities. *Forest health biotechnologies: What are the drivers of public acceptance?*** Needham, M.D. and Howe, G.T. 2013-2015, \$100,000.
- **USFS Pacific Northwest Research Station. *Meta-analysis of Douglas-fir provenance tests to estimate responses to seed transfer and climate change.*** Howe, G.T. and St.Clair, J.B. USDA-Forest Service Joint Venture Agreement, 2013-2018, \$100,000.

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Current collaborations and grants

- **USFS Pacific Northwest Research Station. *Evaluating assisted migration options for adapting to climate change.*** Howe, G.T. and St.Clair, J.B. USDA-Forest Service Joint Venture Agreement, 2013-2019, \$40,000.

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ABSTRACT: Phenotypic and Molecular Breeding in Western White Pine

Oguz Urhan, Glenn Howe, Marc Rust, Richard Sniezko, Scott Kolpak

Oguz Urhan, a PhD candidate, is working on quantitative genetic and genomic approaches to enhance resistance to the non-native fungal pathogen, *Cronartium ribicola*, in western white pine (WWP). Recent advances in genomics may provide important technologies that could be used alongside the classical approaches to either enhance disease resistance in selected populations, or shorten the time for developing improved varieties. We are collaborating with Marc Rust of the Inland Empire Tree Improvement Cooperative (IETIC, ID), Mary Mahalovich (USFS Region 1, ID), Richard Sniezko (USFS Dorena Genetic Resource Center, OR), Jun-Jun Liu of the Canadian Forest Service (BC), and Nicholas Ukrainetz and John King of the BC Ministry of Forests. The objectives of this project are to (1) review and synthesize breeding program strategies for improving genetic resistance in the three main programs (BC, OR, ID); (2) conduct quantitative genetic analyses of blister rust resistance; (3) evaluate advanced genomic techniques to improve resistance breeding including 'breeding-without-breeding' (BWB) and 'genomic selection' (GS); and (4) position ourselves to implement GS in WWP by developing single nucleotide polymorphic (SNP) genetic markers and conducting simulation studies of GS.

We conducted simulation analyses to test how many SNP markers are needed to accurately assign seed orchard progeny to parents in the Bingham Seed Orchard, which is the key step in implementing BWB. We wrote software that uses the genetic composition of the seed orchard (e.g., breeding program pedigree) to simulate SNP genotypes for the trees in the seed orchard and their open-pollinated progeny. Second, we used the SOLOMON program (Christie *et al.*, 2013) to test whether we could use the SNP genotypes of the progeny to infer their parents. We did this using various number of SNPs (100, 200, 300, and 400). Overall, the results indicate that as many as 200 SNPs will be needed to practice BWB in the Bingham orchard, and this number may be higher for orchards where pollen contamination is an issue. At least for seed orchards with similarly complex pedigrees, these results indicate that it may be challenging to practice BWB in a cost-effective manner.

Phenotypic and Molecular Breeding in Western White Pine

Oguz Urhan
 Glenn Howe
 Marc Rust
 Richard Sniezko
 Scott Kolpak



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Western white pine (WWP) breeding programs

- WWP is an economically and ecologically important conifer
- White pine blister rust (WPBR) causes heavy mortality
- Three main resistance breeding programs in North America
 - USFS Dorena Genetic Resource Center (DGRC)
 - USFS and Inland Empire Tree Improvement Cooperative (IETIC)
 - BC Ministry of Forests

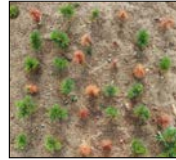


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Resistance breeding programs

- Focus on improving resistance using recurrent selection
- The main goal is to incorporate disease resistance into improved genotypes and seed orchards
 - *Nursery inoculation trials*
 - *Field performance tests*
 - *Field progeny tests*
- Measurements focus on survival, infection rates, resistance mechanisms, and growth



Susceptible family



Resistant family



Seed orchard



Plantation

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Thesis goals and chapters

- Review existing knowledge about the genetics of resistance to white pine blister rust
- Evaluate breeding strategies for improving resistance to white pine blister rust
- Thesis chapters are:
 - *A review of breeding programs and strategies designed to enhance resistance to white pine blister rust*
 - *Quantitative genetics of resistance to white pine blister rust*
 - *Molecular breeding strategies for western white pine*
 - *Options for breeding western white pine for resistance to white pine blister rust*

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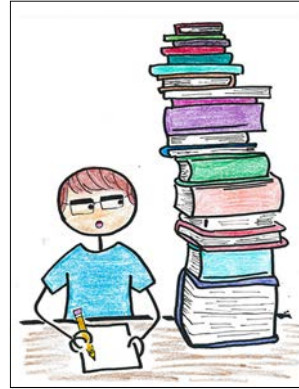
A review of breeding programs and strategies designed to enhance resistance to white pine blister rust

Research questions

- What have we learned about the genetics of resistance to white pine blister rust?
- What resources are available for future breeding?
- How might recent developments in quantitative genetics and genomics affect future breeding strategies?

Objectives

- Review breeding programs and strategies for improving genetic resistance to white pine blister rust
- Summarize available breeding materials, genetic tests, seed orchards, and genomic resources



<https://uscmataadvising.files.wordpress.com>

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Quantitative genetics of resistance to WPBR

Research questions

- Which levels of disease incidence are best for identifying disease resistant genotypes?
- How strong are genotype by environment interactions for disease resistance?
- Is recurrent selection for additive genetic value optimal?
- How well do inoculation trials predict field performance?



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Quantitative genetics of resistance to WPBR

Research questions

- What are the time-trends in heritability?
- What are the genetic correlations between disease resistance and growth traits?
- Do spatial analyses improve the identification of disease resistance genotypes?
- **Results from quantitative genetics chapter will be used in later simulation studies**



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Quantitative genetics of resistance to WPBR

Objectives

- Select genetic tests from three breeding programs to estimate genetic parameters for resistance to white pine blister rust
- Understand how quantitative resistance can be studied in the presence of major gene resistance (MGR)
- Select genetic tests that have different levels of infection to investigate the relationship between heritability and disease incidence
- Select diallel tests to estimate additive and non-additive genetic variation for resistance to white pine blister rust
- Investigate genetic correlations among traits (e.g., DBH and height)

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WWP breeding programs and tests

Table 1. Western white pine breeding programs and tests in the Pacific Northwest, Inland Empire, and British Columbia.

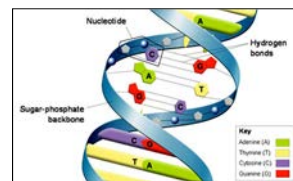
Breeding program	Test type	Number of			Mating design	Current age	Traits	Measurement	
		Tests	Plantations	Families				Age	
USFS Dorena	Progeny	2	12	80 - 81	Half-diallel, OP	9 - 16	HT, DBH, RUST traits, SURV, Damage	7,12	
	Nursery screening	3	4	60 - 240	Half-diallel, OP	5 - 16	HT, DBH, RUST traits, SURV, Damage	1,2,3,4,5,6	
USFS/IETIC	Progeny	5	8	200 - 325	OP	32 - 37	HT, DBH, RUST traits, SURV, Damage	3,5,7,10,15	
	Farm-field	5	5	105 - 600	OP	19 - 32	HT, DBH, RUST traits, SURV, Damage		
	Nursery screening	17	17	100 - 318	OP	5 - 32	HT, DBH, RUST traits, SURV, Damage		
	Realized gain	3	6	422 - 462	OP	3 - 10	HT, DBH, RUST traits, SURV, Damage		
	Performance	22	27	7 - 262	OP	2 - 28	HT, DBH, RUST traits, SURV, Damage		
BC Ministry of Forests	Progeny	5	14	49+	Half-diallel, OP	9 - 14	HT, DBH, RUST traits, SURV, Damage	7,10,13	

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Molecular breeding strategies for WWP

- The costs of genotyping are declining
 - *New genetic markers*
 - *New genotyping platforms*
- Advanced genomic technologies may revolutionize tree breeding
 - *Genomic Selection (GS)*
 - *Breeding-Without-Breeding (BWB)*
- New developments may accelerate resistance breeding in WWP



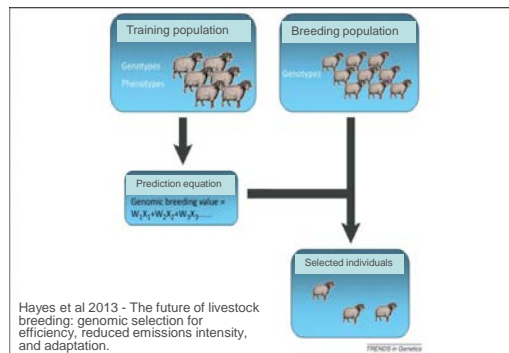
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Molecular breeding strategies for WWP

Genomic selection (Meuwissen et al 2001)

Genomic selection is a form of marker-assisted selection that uses markers to cover the whole genome



Success of GS depends on:

- Size and structure of the training population
- Heritability
- Marker density
- Effective population size (N_e) of the breeding population
- Relatedness between the training population and the breeding population
- Statistical methods

Hayes et al 2013

Molecular breeding strategies for WWP

Genomic selection research question

- How do training population size, heritability, choice of breeding population, and marker density affect the success of genomic selection?

Objective

- Use existing WWP pedigrees, **quantitative genetic information**, and a simulation approach to evaluate the potential success of genomic selection in WWP



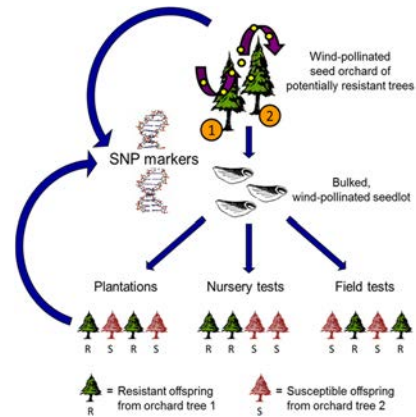
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Breeding-Without-Breeding

How to implement BWB

- Wind-pollinated seeds can be collected from 'resistant' trees from seed orchards
- Seeds planted in many operational plantations, nursery screening trials, and field evaluation tests
- SNP/SSR markers can be used to determine the parents of the resistant (R) and susceptible (S) trees
- Field "tested" resistant trees can be used in the next cycle of breeding



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Molecular breeding strategies for WWP

'Breeding-Without-Breeding' (El-Kassaby et al 2007)

Potential benefits

- May be valuable for identifying parents of blister rust resistant trees in operational plantations, nursery tests, or field genetic tests
- May save time and the cost of controlled crossing
- May increase genetic gain

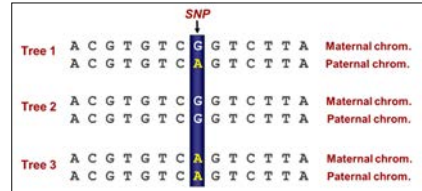
Success of BWB depends on:

- Number of SNP markers
- Seed orchard mating dynamics (e.g., pollen contamination)
- Seed orchard composition
 - Relatedness
 - Number of clones, ramets, or trees
- Genetic variation in disease resistance
- Trait heritability (h^2)

Molecular breeding strategies for WWP

Breeding-without-breeding research questions

- Is Breeding-Without-Breeding feasible for white pine breeding programs?
- How do seed orchard dynamics, composition and heritability affect the genetic gain?
- How many SNP markers are required to have substantial genetic gain using BWB?



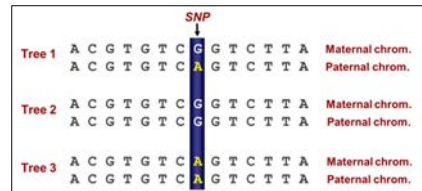
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Molecular breeding strategies for WWP

Objectives

- Implement a parentage assignment technique
 - *Complex mating system*
- Determine to accuracy of assigning progeny to parents
- Conduct simulation studies to see the factors that affect the success
 - *Heritability*
 - *Genetic markers*
 - *Seed orchard composition*
 - *Seed orchard mating dynamics*



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Options for breeding western white pine for resistance to white pine blister rust

Research questions

- How might white pine breeding programs be structured in the future?
- How might new genotyping technologies affect white pine breeding activities?

Objectives

- Evaluate approaches to enhance resistance to white pine blister rust and describe options for future breeding activities



<http://blogs.cisco.com>

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Recent progress
on BWB simulations

Simulating BWB in western white pine

How many SNPs are needed?

- How many SNPs are needed to assign progeny to parents?
- Examined the WWP Bingham seed orchard – a clonal/seedling orchard with many related genotypes in Idaho
- Simulate the SNP genotypes of seed orchard parents
- Simulate the SNP genotypes of wind-pollinated offspring
- Use a parentage reconstruction program (SOLOMON) to determine how many SNP markers are needed

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Data analysis pipeline

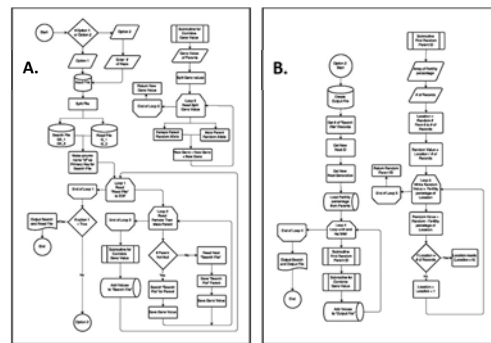
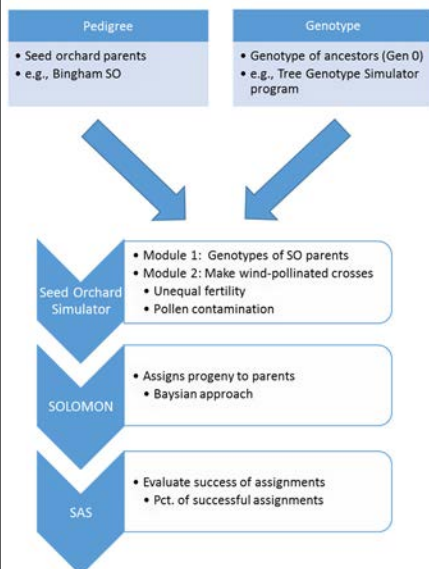
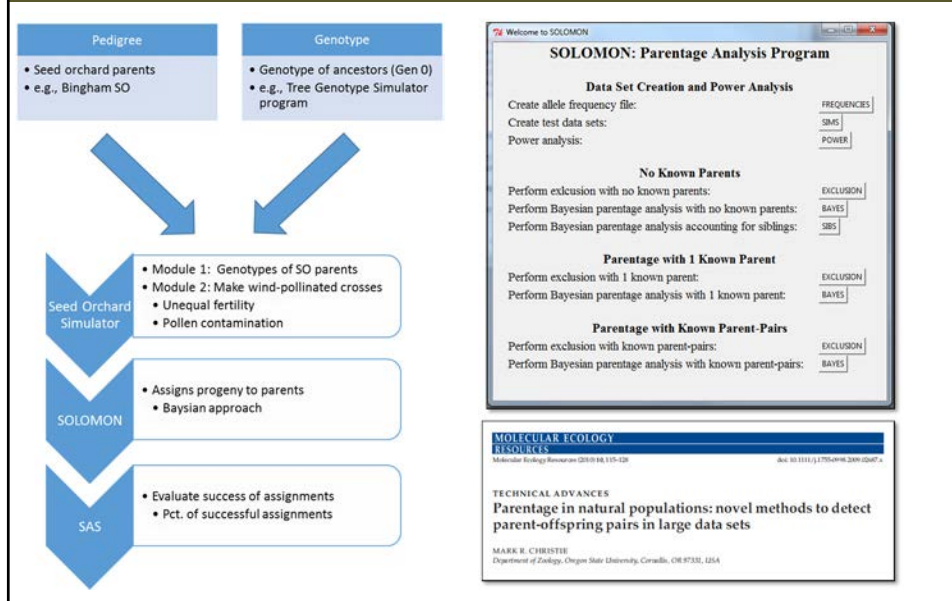


Figure 1. Seed Orchard Simulator*. **A.** Module 1: The program uses a breeding program pedigree and simulated SNP genotypes of the base population to simulate the SNP genotypes for all seed orchard trees. **B.** Module 2: Using the simulated genotypes of the seed orchard trees, the relative fertilities of the seed orchard trees and level of pollen contamination as inputs, the program simulates an open-pollinated orchard seedlots (i.e., simulated SNP genotypes for the desired number of seed or seedlings).

* Program code developed by Hao Truong

Data analysis pipeline



SOLOMON results - Bingham Seed Orchard

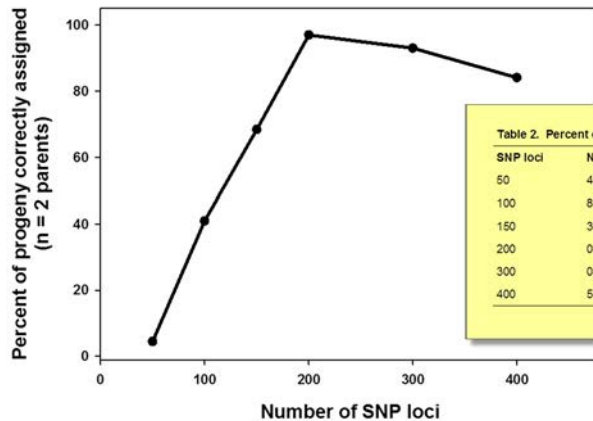


Table 2. Percent of progeny correctly assigned to n=0, 1, or 2 parents.

SNP loci	N = 0 parents	N = 1 parents	N = 2 parents
50	49.7	45.8	4.5
100	8.6	50.4	41.0
150	3.6	28	68.4
200	0.1	2.9	97.0
300	0.9	6.1	93.0
400	5.6	10.3	84.1

200 SNPs needed to assign offspring to parents

SOLOMON conclusions

Bingham orchard

- The highest percentage of correct parent assignments (both parents) occurred with 200 SNP loci (97%)
- This is a higher number of loci than expected because:
 - *A high number of half-sibs were grafted into the orchard (often three seedlings per family)*
 - *There is a high degree of relatedness among seed orchard trees (e.g., full-sibs, half-sibs, parent/progeny, parent/grand kids)*

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Future directions

- Continue with seed orchard simulations and parentage analysis
 - *Examine random mating vs variable fertility*
 - *Incorporate pollen contamination*
 - *Include a range of orchards differing in complexity*
 - *BLM's Horning Seed Orchard (clonal, fewer genotypes, low relatedness)*
 - *Bingham Seed Orchard (clonal/seedling, more genotypes, higher relatedness)*
- Examine heritability effects on genetic gain

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Acknowledgements

Thanks to....

- *Lauren Magalska, Oregon State University*
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- *Mary F. Mahalovich, USFS, Northern, Rocky Mountain, Southwestern, and Intermountain Regions*
- *Angelia Kegley, USFS, Dorena Genetic Resource Center*
- *Douglas Savin, USFS, Dorena Genetic Resource Center*
- *John King, British Columbia Ministry of Forests and Range*
- *Nicholas Ukrainetz, British Columbia Ministry of Forests and Range*
- *Colleen Ramsower, University of Arizona Genetics Core*
- *USDA Forest Service Health Protection–Special Technology Development Program (STDP)*

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ABSTRACT: Effects of Genetics and Site on Douglas-fir Drought Hardiness

Erda Çeler and Glenn Howe

Breeding programs for Douglas-fir aim to increase growth and wood quality, while maintaining adaptability for frost and drought hardiness. However, populations that grow faster are also typically less tolerant of drought and other stresses. To better understand the genetics of drought hardiness in Douglas-fir, a study was initiated by Jeannette Griese of the BLM in 2008-2009, and later implemented cooperatively by the Northwest Tree Improvement Cooperative, Bureau of Land management, Plum Creek Timber Company, and Silver Butte Timber Company.

In 2015, Erda Çeler, began using this experiment for her M.S. thesis research. The objectives of her research are to (1) identify the impacts of drought on seedling growth and survival; (2) develop recommendations for practicing assisted migration; (3) characterize genetic variation in drought hardiness; (4) study the adaptability of families to climate conditions in southern Oregon using ClimateNA models; and (5) obtain baseline measurements to help in the analysis and interpretation of future measurements in the drought hardiness study.

The complete experiment contains more than 18,000 Douglas-fir seedlings from more than 400 parents from western Oregon and Washington that were planted at three sites in southern Oregon. Measurements that are being recorded in 2015 and 2016 include 2014 height, 2015 height, second flushing, spring bud flush, sunscald stem damage, foliage damage, leader damage, and mortality. This study will provide useful information to enhance drought hardiness by breeding and appropriately deploying genotypes from Douglas-fir breeding programs.

Effects of Genetics and Site on Douglas-fir Drought Hardiness

Erda Çeler and Glenn T. Howe

*Department of Forest Ecosystems and Society
Oregon State University*

In collaboration with the Bureau of Land Management,
Plum Creek Timber Company, and Silver Butte Timber
Company

**PNWTIRC Annual Meeting
October 22, 2015**

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Introduction

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Overview

- Drought adversely affects natural and artificial regeneration of Douglas-fir (Spittlehouse 1985)
- Drought diminishes the ability of seedlings to resist damage from herbicides, pathogens, and frost (Hobbs et al 1980)
- Climate change is expected to exacerbate drought stress in the PNW

It is important to incorporate drought hardiness into Douglas-fir breeding programs

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Previous drought hardiness research by the PNWTIRC

Genetic variation in drought hardiness of coastal Douglas-fir seedlings from British Columbia¹

T.S. Anekonda, M.C. Lomas, W.T. Adams, K.L. Kavanagh, and S.N. Aitken

- 39 full-sib families from British Columbia measured in raised nursery beds
- Foliage damage and xylem cavitation increased, and xylem hydraulic conductivity decreased, under drought stress
- Lots of environmental variability - heritabilities averaged only 0.19
- Growth in moist conditions nearly uncorrelated with drought hardiness
- Did not study the effects of seedling origin on drought hardiness

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Previous drought hardiness research by the PNWTIRC (Cont'd)

Response of annual growth ring components to soil moisture deficit in young, plantation-grown Douglas-fir in coastal British Columbia

Andrew D. Bower, W. Thomas Adams, David Birkes, and Darek Nalle

- Can growth ring components be used to evaluate the genetics of drought hardiness?
- 10 growth ring variables measured in 6 progeny tests (X-ray densitometry)
- Drought response coefficient (DRC) may be useful for identifying drought hardy genotypes
- Growth ring approach is challenging – substantial drought is needed – new studies should be designed to impose substantial drought stress

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About this experiment

- The project was initiated by Jeannette Griese at the BLM in 2008-2009
- Currently managed as a collaboration among...
 - Northwest Tree Improvement Cooperative (Keith Jayawickrama)
 - Bureau of Land Management (Mike Crawford, Jeannette Griese, and George McFadden)
 - Plum Creek Timber Company (Jim Smith)
 - Silver Butte Timber Company (Darin McMichael)

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About this experiment (Cont'd)

- Seedlots
 - Most are *OP* seed from first-generation parents in orchards
 - Some are second-generation full-sib crosses
 - Two are woods-run seedlots from southern OR

- Seedlings were grown in the BLM Sprague greenhouse

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Goals and Objectives

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Main goals

- Understand the impacts of drought on growth and survival of Douglas-fir seedlings
- Enhance approaches for genetically improving drought hardiness and deploying genotypes from breeding programs
- Understand the potential effects of climate change and provide information for practicing effective assisted migration

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Specific objectives

- Determine drought impacts on seedling growth and survival
- Develop recommendations for practicing assisted migration
- Characterize genetic variation in drought hardiness
- Use ClimateNA models to determine adaptability of families to climate conditions in southern Oregon
- Obtain baseline measurements to help in the analysis and interpretation of future observations

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Research Questions

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Research questions

- Is there genetic variation in first-year survival and growth among the Douglas-fir families?
- Is variation in drought hardiness associated with the climatic origin of the parents?
- Is there an association between drought hardiness and seedling characteristics at the time of planting?
- Is early bud flush associated with drought hardiness?

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Experimental Plan

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Description of the study

- Focus on the morphological, physiological, and genetics aspects of drought hardiness
- Collect data on growth traits and damage from drought and herbicides
- > 18,000 seedlings from the PNW
- > 400 families
 - *Most parents from western Oregon*
 - *Some parents from western Washington*

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Sites

Seedlings planted in 2015 on 3 sites in southern Oregon

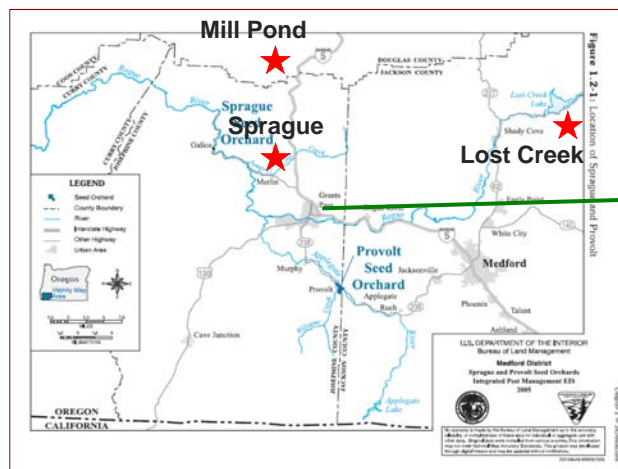
- Lost Creek (Plum Creek)
- Mill Pond (Silver Butte)
- Sprague (BLM)

A weather station at each site is recording detailed weather data

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Locations

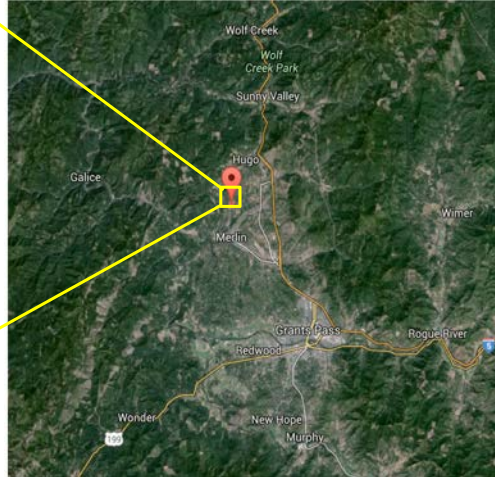
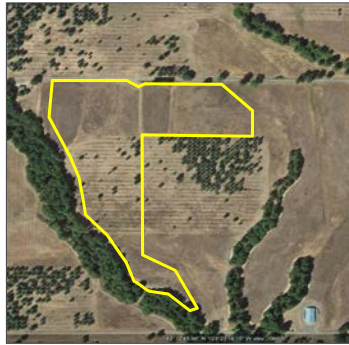


Grants
Pass

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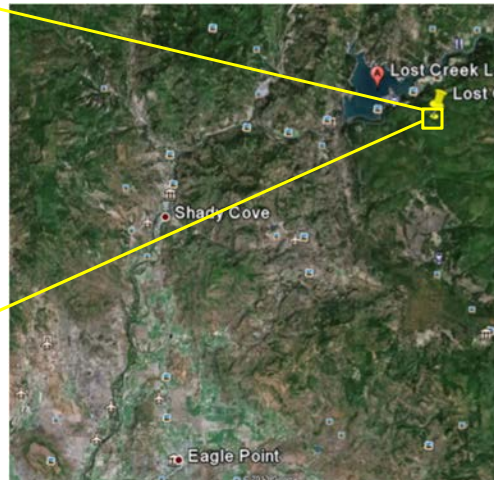
Sprague site



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Lost Creek site



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Mill Pond site



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Methodology

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Trait measurements

- **Height**
 - In two different seasons (2014 and 2015)

- **Second flushing**
 - Presence/absence



Height measurements

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Trait measurements (Cont'd)

- **Herbicide damage (Mill Pond)**
 - Four categories to classify severity of the damage
 - Chlorosis
 - Needle curl
 - Shoot curl
 - Dead leader

- **Bud flush**
 - Yes/No?
 - Bud stage?



Seedling with herbicide damage

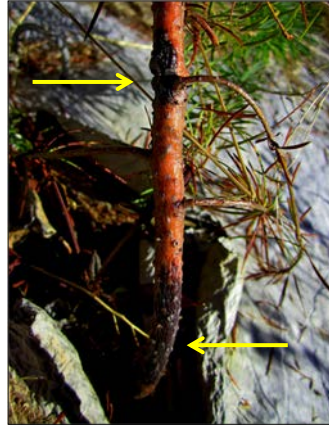
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Trait measurements (Cont'd)

- **Sunscald**
 - *Percentage of stem damage by sunscald*

- **Mortality**
 - *Dead/alive*



Stem with sun-scald

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Timeline

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Timeline

- Fall 2015
 - *Height, second flushing, mortality, drought-induced foliage damage, sunscald, and herbicide damage*
- Spring 2016
 - *Bud flush*
- Spring-Fall 2016
 - *Data analysis and results*

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Acknowledgements

- Keith Jayawickrama (NWTIC)
- Mike Crawford, Jeannette Griese, and George McFadden (BLM)
- Jim Smith (Plum Creek)
- Darin McMichael (Silver Butte)

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Thank you!!

Erda.Celer@oregonstate.edu



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ABSTRACT: Next-generation SNP Chip and Genomic Selection in Douglas-fir

Glenn Howe, Keith Jayawickrama, Scott Kolpak, Stephanie Guida, Sanjuro Jogdeo, Rich Cronn, and Callum Bell

Genomic selection (GS) may transform tree breeding by allowing breeders to shorten the breeding cycle, reduce the costs of progeny testing, increase heritabilities, and select for mature traits, such as wood properties at the seedling stage. The objective of GS is to predict breeding values using a genome-wide set of markers, typically tens of thousands of single nucleotide polymorphic markers (SNPs). Unlike candidate gene approaches (e.g., association genetics), genomic selection will work for any measured trait (e.g., growth, stem form, physiology). GS has been highly effective in livestock breeding, and is beginning to be used operationally on *Eucalyptus* in Brazil.

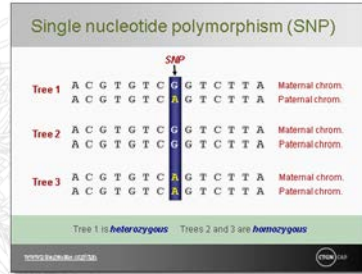
To practice GS, we need to be able to assay thousands of SNPs on many trees. The 'first-generation' Illumina Infinium SNP array for Douglas-fir allows us to assay 7,256 SNPs. However, we used the more affordable Affymetrix Axiom SNP array for our operational test of GS. This high-density array was used to test 55,776 potential SNPs in Douglas-fir. Because the SNPs were derived from transcriptome sequencing, the array targets SNPs in the expressed genes in the Douglas-fir genome.

We are in the process of testing the array on 1,920 Douglas-fir trees, and data from our first set of 1,420 genotyped trees are very promising. We found that ~20K SNPs could be reliably genotyped. For 19,822 SNPs that had a call frequency greater than 85%, the median call rate was 99.3% and the median minor allele frequency was 0.215. This array will serve as an excellent foundation for testing genomic selection in Douglas-fir breeding programs. Future work will focus on developing analytical approaches for 'rescuing' SNPs that do not meet Affymetrix default quality control thresholds. This should allow us to increase the number of available SNPs. We will then evaluate GS using our sampled breeding materials, including evaluation of alternative breeding strategies.

This abstract contains text from the manuscript entitled "A SNP resource for Douglas-fir: de novo transcriptome assembly and SNP detection and validation" by Howe, G.T., Yu, J., Knaus, B., Cronn, R., Kolpak, S., Dolan, P., Lorenz, W.W., Dean, J.F.D. BMC Genomics 14:137 (2013).

Next-generation SNP chip for Douglas-fir

Glenn Howe
 Keith Jayawickrama
 Scott Kolpak
 Stephanie Guida
 Sanjuro Jogdeo
 Rich Cronn
 Callum Bell

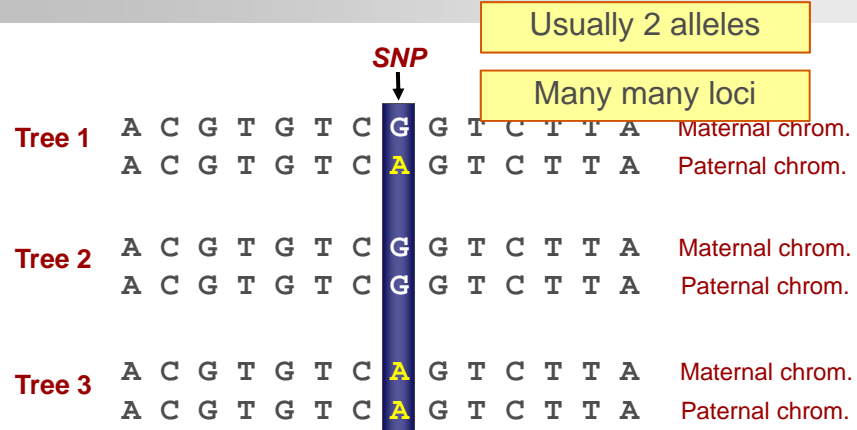


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What are SNPs?
 What are they good for?

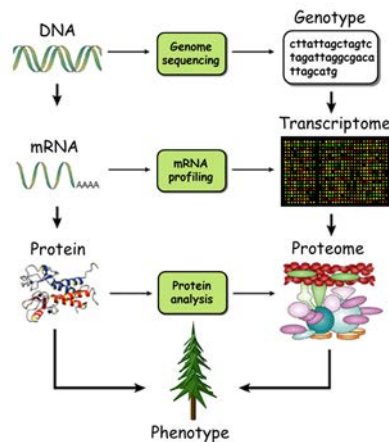
Single nucleotide polymorphism (SNP)



Tree 1 is *heterozygous* Trees 2 and 3 are *homozygous*

**SNPs may be in genes (transcriptome)
or
not in genes (rest of genome)**

DNA → mRNA → Protein



Genomic selection

Genomic selection

Unlike candidate gene approaches, genomic selection markers will work for any measured trait

Wood chemistry (including the traits important to NARA)

Growth

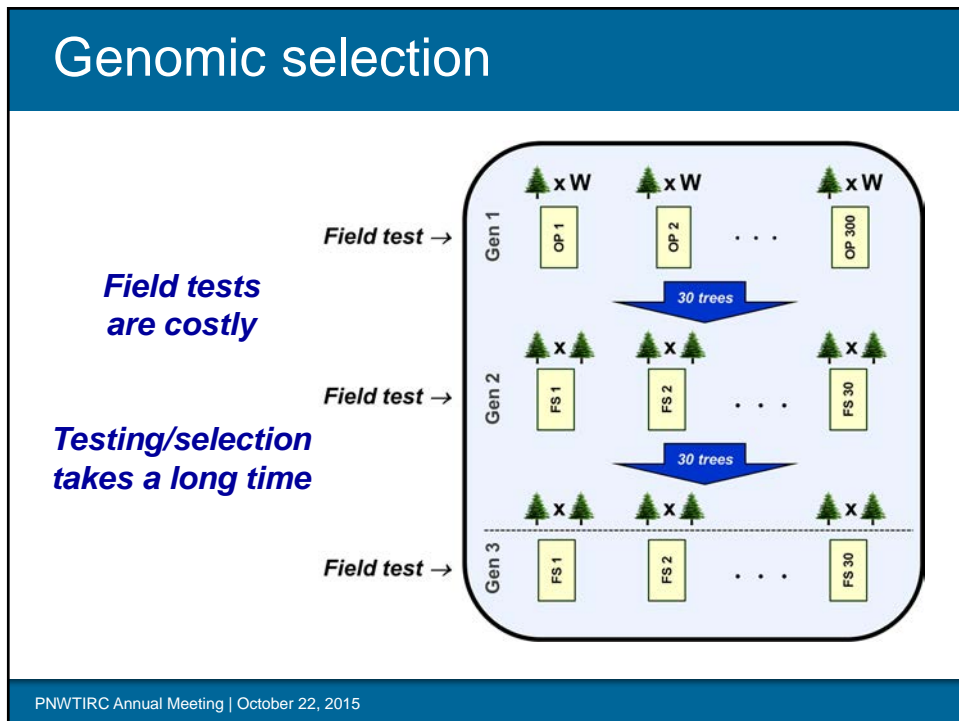
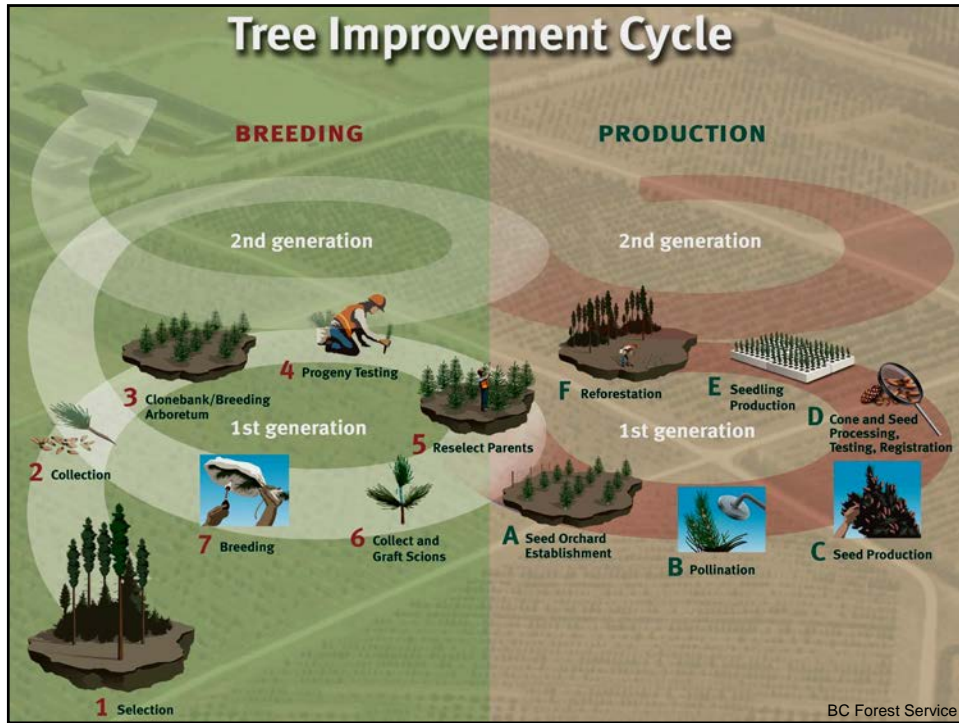
- Height*
- Diameter*
- Volume*

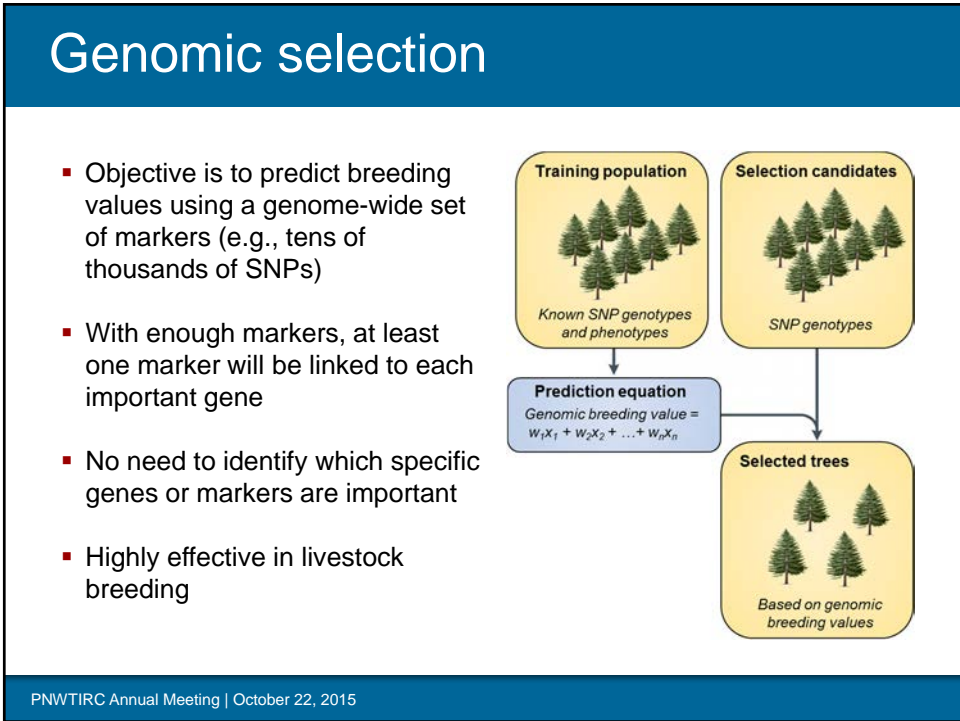
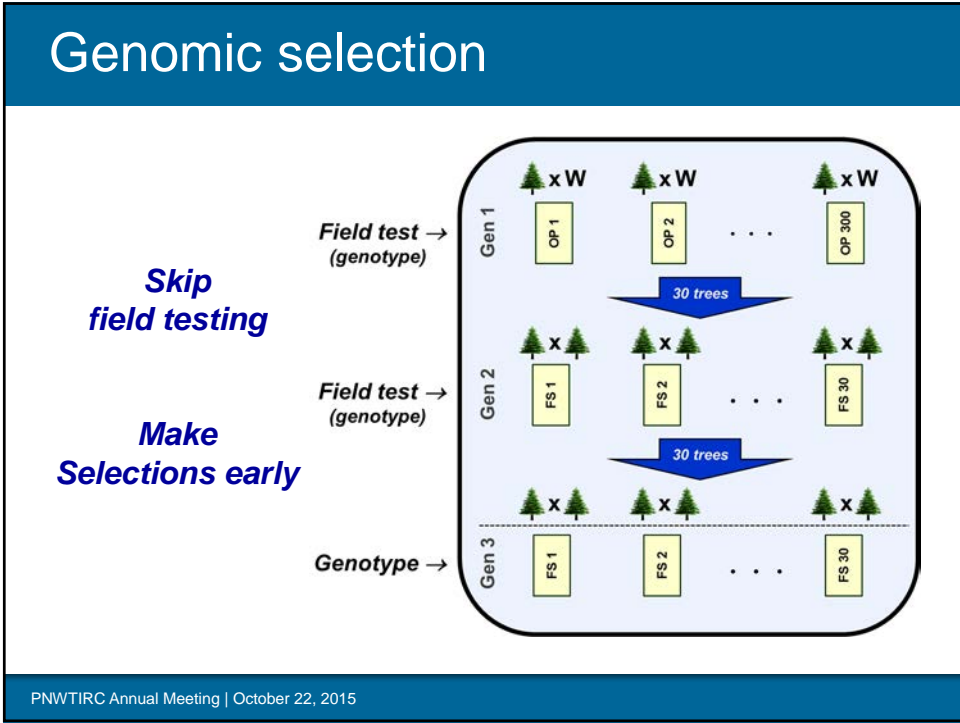
Stem form

- Ramicorn branches and forks*
- Sinuosity*

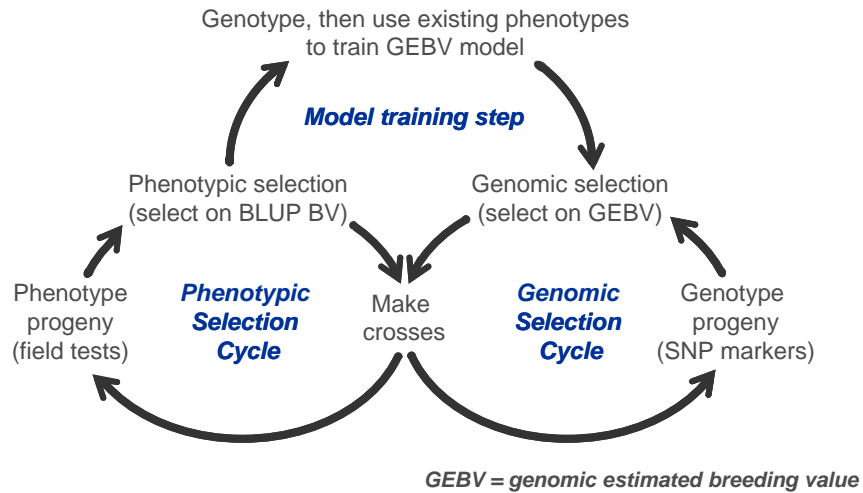
Physiology

- Cold hardiness*
- Spring bud flush*



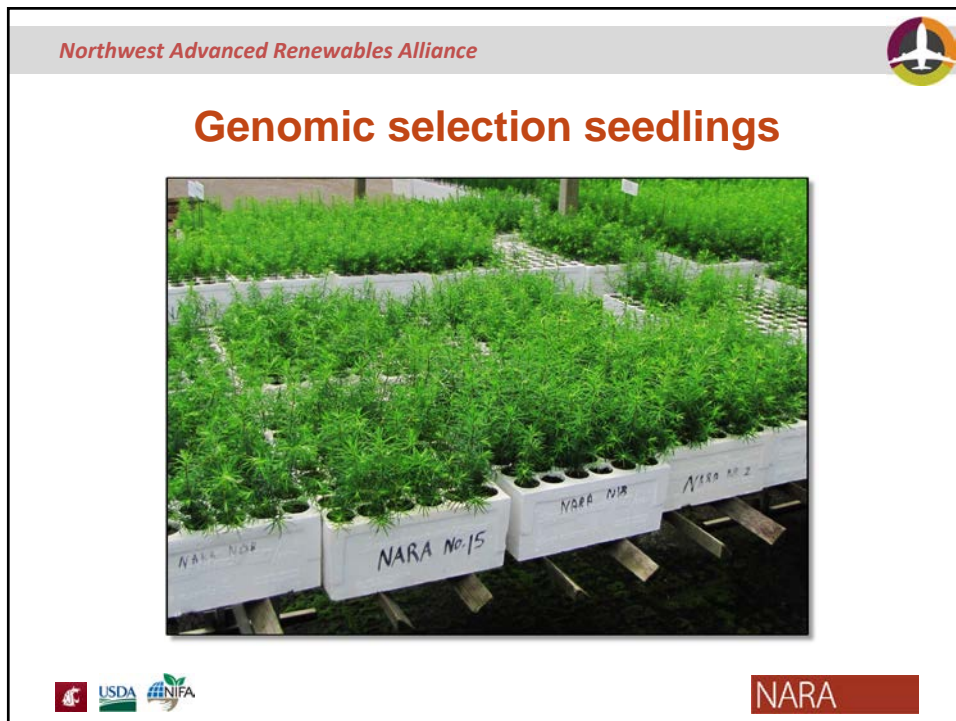
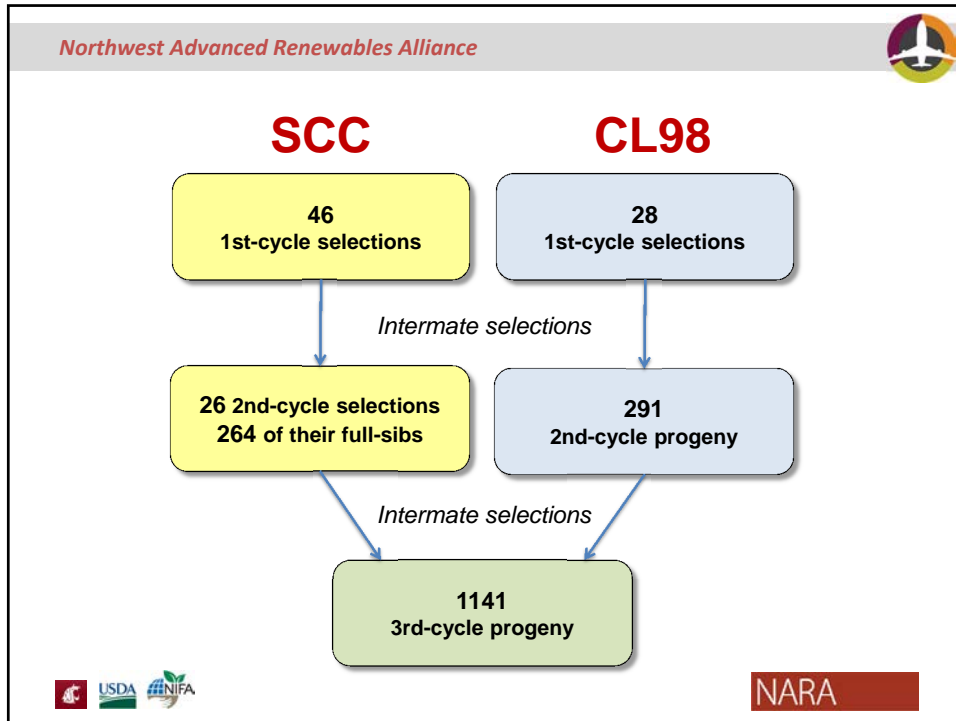


The promise of genomic selection




Population design


Population size (N_e)
Number of generations
Quality of field tests
Measurement traits and ages



Northwest Advanced Renewables Alliance



Genomic selection study site




USDA NIFA

NARA

A Douglas-fir SNP chip

www.pinegenome.org/ctgn



Douglas-fir SNP chip (Illumina Infinium)

Douglas-fir SNP chip is available

- 7256 SNPs can be assessed
- Many more potential SNPs are available



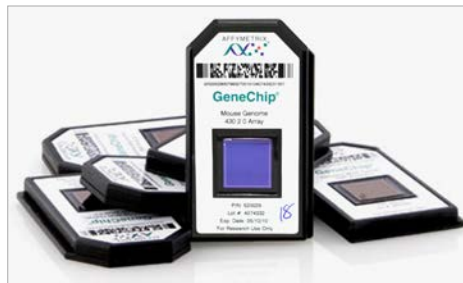
Numbers and percentages of putative Douglas-fir SNPs attempted and assayed with an Illumina Infinium SNP array (n = 260 trees).

SNPs attempted	8769
SNPs assayed by Illumina	8067
Percent of SNPs (assayed/attempted)	92.0
SNPs assayed by Illumina	8067
SNPs called (call frequency ≥ 0.85)	7256
Percent of SNPs (called/assayed)	82.7
SNPs called (call frequency ≥ 0.85)	7256
SNPs called that are polymorphic (MAF ≥ 0)	5847
Percent SNPs (called MAF > 0/called)	80.6
SNPs attempted	8769
SNPs called that are polymorphic (MAF ≥ 0)	5847
Percent SNPs (called MAF > 0/attempted)	66.7

MAF = minor allele frequency. MAF > 0 means there's more than 1 allele

Affymetrix Axiom array is cheaper

Large-scale genotyping service from GeneSeek



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Axiom genotyping array

NARA

Genomic selection in Douglas-fir NARA update

Keith Jayawickrama
Matt Trappe
Glenn Howe

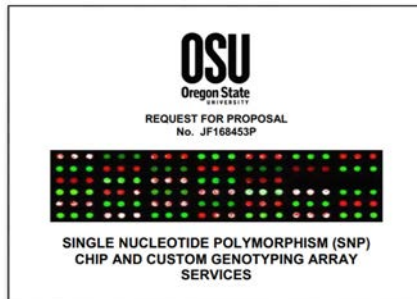
Northwest Advanced Renewables Alliance





NARA Douglas-fir marker plan

- We genotyped ~1,900 trees
- We attempted to genotype > 50,000 SNPs
- Affymetrix Axiom platform



Resources for genomic selection

Heard et al. BMC Genomics 2013, 14:137
<http://www.biomedcentral.com/14712/216814137>

RESEARCH ARTICLE Open Access

A SNP resource for Douglas-fir: *de novo* transcriptome assembly and SNP detection and validation

Glenn T Howe^{1*}, Jianbin Yu^{2*}, Brian Anka³, Richard Cronn⁴, Scott Kolpak⁵, Peter Dolan⁶, W Walter Lorenz² and Jeffrey D Dwan⁷

“Our SNP database may contain as many as ~200,000 true SNPs, and as many as ~69,000 SNPs that could be genotyped at ~20,000 gene loci”

Walter et al. BMC Genomics 2012, 13:671
<http://www.biomedcentral.com/14712/216814137>

RESEARCH ARTICLE Open Access

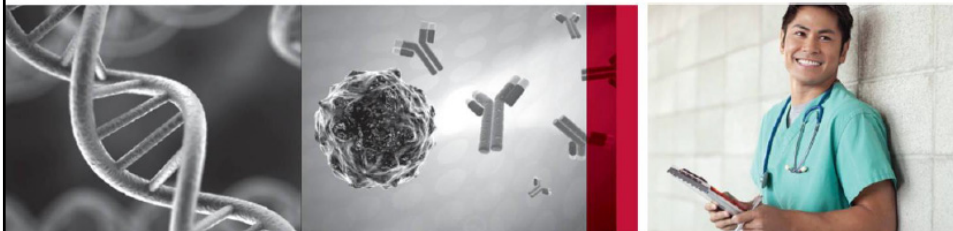
A catalogue of putative unique transcripts from Douglas-fir (*Pseudotsuga menziesii*) based on 454 transcriptome sequencing of genetically diverse, drought stressed seedlings

Thomas Müller¹, Ingo Ensminger^{1,2*} and Kell J Schmidt^{1*}

“A total number of 187,653 single nucleotide polymorphisms (SNPs) were detected by three SNP detection tools”



Analytical procedures needed for conifers



OSU_DouglasFir

Advanced Filters

eBioscience

GeneChip

USB

Final Advanced Workflow (Conifers)

Execute default Best Practice Workflow

→

Keep recommended probesets.

Combine 'CallRateBelowThreshold' and 'Other' probeset lists

→

Keep these results (after inspection). Use calls from adjusted calls table.

Execute Ps_CallAdjust (threshold=0.1) on combined list

→

Many more probesets are expected in 'MonoHighResolution'.

Rescue lower resolution 3-cluster probesets from Above:

- nClus = 3
- nObs (intersect all 3 clusters) ≥ 2
- HomRO > 0
- HetSO > 0
- CallRate ≥ 80

Remove rescued probesets from original 'Other' probeset list:

- Execute AxiomGT1 calling on remaining 'Other' probesets using Inbred Penalty = 4
- Execute Ps_Metrics and Ps_Classification with HomRO1 = -10 on these results

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eBioscience
GeneChip
USB

Results – 3 cluster rescue

- Performing the probeset rescue operation on the combined 'Other' and 'CallRateBelowThreshold' probesets results in **5802** probesets passing the advanced filter thresholds.
 - These probesets are lower resolution (clusters are closer together)
 - SNPs are still likely polymorphic and probesets are providing accurate calls
 - Must use Ps_CallAdjust-ed calls table to increase stringency on call confidence

AX-117400028
Intensity: called genotypes

AX-118136670
Intensity: called genotypes

AX-118136293
Intensity: called genotypes

AX-117400024
called genotypes

AX-118136670
called genotypes

AX-118136293
called genotypes

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USB

Example R code (You will need to change paths) 1 of 3

```
## read in Ps.performance.txt table from default Best Practice Workflow
perf <- read.table("../results/step2/SNPolisher/Ps.performance.txt", sep="\t", header=T, stringsAsFactors=F)

## Create combined PS list with Other and CRBT
perf.other <- perf[perf$ConversionType == "Other",]
perf.crbt <- perf[perf$ConversionType == "CallRateBelowThreshold",]
ps.other.crbt <- append(perf.other[1,], perf.crbt[1,])

write.table(ps.other.crbt, "/Final_Workflow/other_crbt.ps", sep="\t", quote=F, row.names=F, col.names="probeset_id")





## Execute Ps_CallAdjust and Ps_Metrics

library("SNPolisher")

Ps_CallAdjust(
  pidFile="/Final_Workflow/other_crbt.ps",
  callFile="/results/step2/AxiomGT1.calls.txt",
  confidenceFile="/results/step2/AxiomGT1.confidences.txt",
  threshold=0.1,
  outputFile="/Final_Workflow/CallAdjust_0.1_other_crbt.txt"
)

Ps_Metrics(
  pidFile="/Final_Workflow/other_crbt.ps",
  posteriorFile="/results/step2/AxiomGT1.snp-posteriors.txt",
  callFile="/Final_Workflow/CallAdjust_0.1_other_crbt.txt",
  output.metricsFile="/Final_Workflow/metrics_CallAdjust_0.1_other_crbt.txt"
)
```

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Results from first set of trees

About 20K SNPs available

Classification	No. of SNPs with call rate (CR) of:	
	97%	85%
Polymorphic high resolution	14,959	19,822
No minor homozygote	6,140	6,140
Monomorphic high resolution	12,807	12,814
Converted	33,906	38,776
Off-target variant	423	423
Other	16,493	16,493
Call rate below threshold	4,944	74
Not converted	21,860	16,990
Total	55,766	55,776

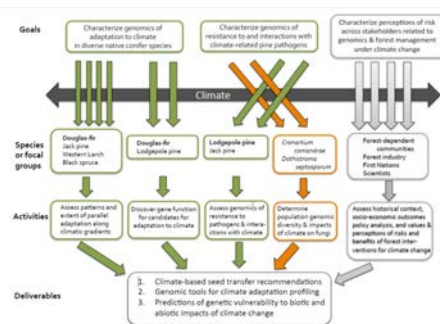
Next steps

Priorities and implementation addressed by subcommittee

- Test genomic selection using current data
- Evaluate alternative breeding strategies using simulations
 - Combine with early testing?
 - Reduce sizes of progeny tests?
 - Skip a cycle of progeny testing?
 - Incorporate financial analyses?
- Quantitative genetics expertise needed
- How to cover the costs of new SNP genotyping?
 - Grant support?
 - Collaborations?
 - Operating funds from PNWTIRC?
 - Special projects (e.g., leveraged support from metacooperatives)?

Potential collaborations

Genome Canada LSARP Proposal: CoAdapTree: Healthy Trees for New Climates
 Project Leaders: Sally Atken, UBC; Sam Yeaman, University of Calgary;
 and Richard Hamelin, Laval University and UBC



Multi-species genotyping arrays

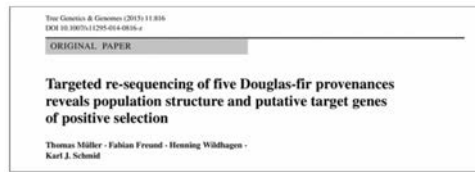
PACIFIC NORTHWEST TREE IMPROVEMENT
 RESEARCH COOPERATIVE



Third-generation SNP chip?

Other SNP resources are becoming available

- Transcriptome and genomic sequencing projects in Europe
- Douglas-fir genome sequence



Any new genotyping should include new SNP candidates

PACIFIC NORTHWEST TREE IMPROVEMENT
RESEARCH COOPERATIVE



ABSTRACT: Five-year Plan Discussion

Glenn Howe

Glenn Howe led a discussion on developing plans for the next five years. Key topics that were addressed were the goals of the planning process and the best way to involve PNWTIRC members. Glenn emphasized the potentially transformative nature of research on genomics in general, and research on genomic selection, in particular. Although we have been focusing on these topics recently, important questions remain. Should we continue to plan for heavy attention on genomic selection over the next 5 years, or so? If so, how fast do we want to move on this? Do we want to devote more resources to speed progress, or are we happy with the current pace?

Before we commit to taking the next steps in genomic research, we need to test that our SNP genotyping array is suitable for future genomic selection in Douglas-fir—and completing this step could take a good portion of 2015-2016. New genomic selection research and implementation will require funds for research personnel and SNP genotyping, so we will need to integrate research needs with future funding. Changes in funding through the Center for Advanced Forestry Systems (CAFS) will affect future available funding.

We also discussed the other things we should be doing. What are the other research topics we just cannot ignore? Should we return to an emphasis on workshops and training? Finally, Glenn presented an overview of PNWTIRC dues and funding history, emphasizing that dues have been kept low for many years because of external grant funding. However, particularly with CAFS funding, that situation will not continue indefinitely. A planning subcommittee was formed, consisting of Sara Lipow, Jeff DeBell, Josh Sherrill, Margaret Banks, Dan Cress, and Michael Crawford.

Five-year Plan Discussion

Glenn Howe

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

PACIFIC NORTHWEST TREE IMPROVEMENT
RESEARCH COOPERATIVE



Planning process

Planning subcommittee

Sara Lipow

Josh Sherrill

Dan Cress

Jeff DeBell

Margaret Banks

Michael Crawford

Subcommittee meeting scheduled for November 16

What should be the goals of the planning process?

What's the best way to survey member's views?

PACIFIC NORTHWEST TREE IMPROVEMENT
RESEARCH COOPERATIVE



Background and discussion

Genomics research on Douglas-fir is increasing dramatically worldwide – this is a great foundation for molecular breeding

Should we continue to plan for heavy attention on genomic selection over the next 5 years, or so?

If so, how fast do we want to move on this ? Do we want to devote more resources to speed progress, or are we happy with the current pace?

PACIFIC NORTHWEST TREE IMPROVEMENT
RESEARCH COOPERATIVE



Discussion

Before we commit, we need to make sure that the SNP chip is suitable for genomic selection in Douglas-fir

Genomic selection research and implementation will require funds for (1) research personnel and (2) genotyping

Research personnel fits nicely with normal PNWTIRC model—but genotyping benefits some members more than others...different funding model?

PACIFIC NORTHWEST TREE IMPROVEMENT
RESEARCH COOPERATIVE



What else should we be doing?

Other research topics we just can't ignore?

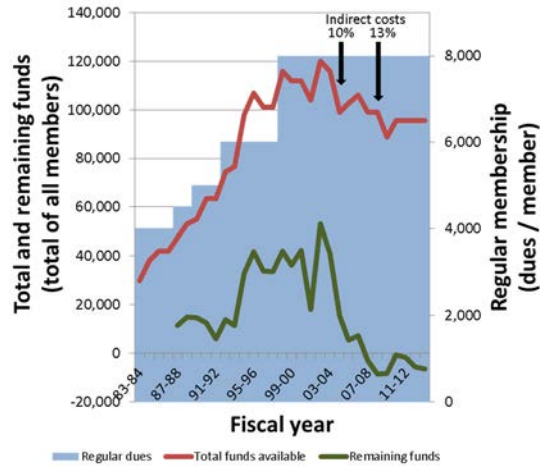
Workshops or other training?

PACIFIC NORTHWEST TREE IMPROVEMENT
RESEARCH COOPERATIVE



PNWTIRC dues history


- Regular dues = dues for a single 'regular' member
- Total funds available = total of all dues minus indirect costs
- Indirect costs (10%) started in FY04-05, increased to 13% in FY09-10
- Remaining funds = total funds available minus personnel costs for 1 staff position and 1 graduate student
- First 15 years = 4 dues increases
- Last 16 years = no dues increases



ABSTRACT: Conservation Biology Institute and Data Basin: A science-based mapping and analysis platform

Dominique Bachelet

The Conservation Biology Institute (CBI) is a non-profit center that provides scientific expertise to support the conservation and recovery of biological diversity through applied research, education, planning, and community service. CBI develops innovative conservation tools, techniques, and analyses to help organizations, agencies, and companies utilize the best available conservation evidence. Major accomplishments include publishing the first national protected areas database for the United States ([PAD-US CBI Edition](#)), and CBI partnered to produce the first national conservation easement database ([NCED](#)), spearheading climate change adaptation through practical applications of forecasting models, and the development of a successful web-based conservation data sharing system called Data Basin (<https://databasin.org>). We have developed 21 customized public Gateways that are powered by Data Basin that highlight curated spatial information for a particular geography, topic, project, or organization. Dominique Bachelet (CBI), Brad St.Clair (USFS), and Glenn Howe (OSU, PNWTIRC) are collaborating to develop a new version of the Seedlot Selection Tool that will be delivered through Data Basin.



THE ALL-PURPOSE COOKBOOK

joy


OF COMMUNICATING SCIENCE EFFECTIVELY

by LUCKY SCIENTISTS


Conservation Biology Institute and Data Basin

A science-based mapping and analysis platform


Dr. Dominique Bachelet
senior climate change scientist,
CBI
& assoc. prof.
Biol. & Ecol. Eng.
Oregon State University




Dr. Barry Baker



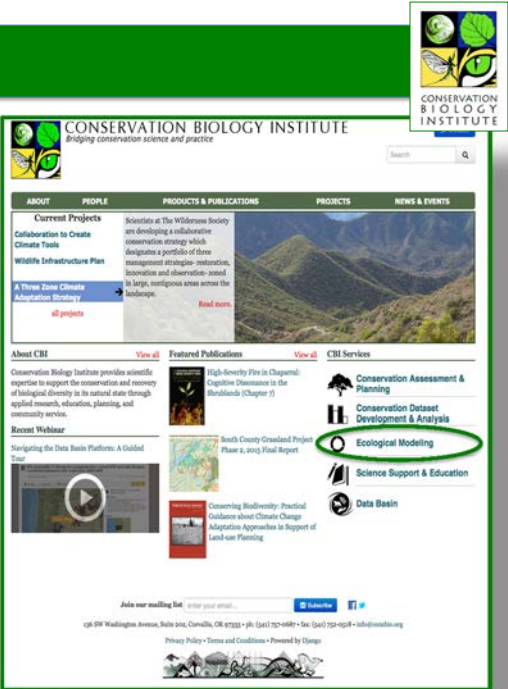
Dr. Alex Syphard



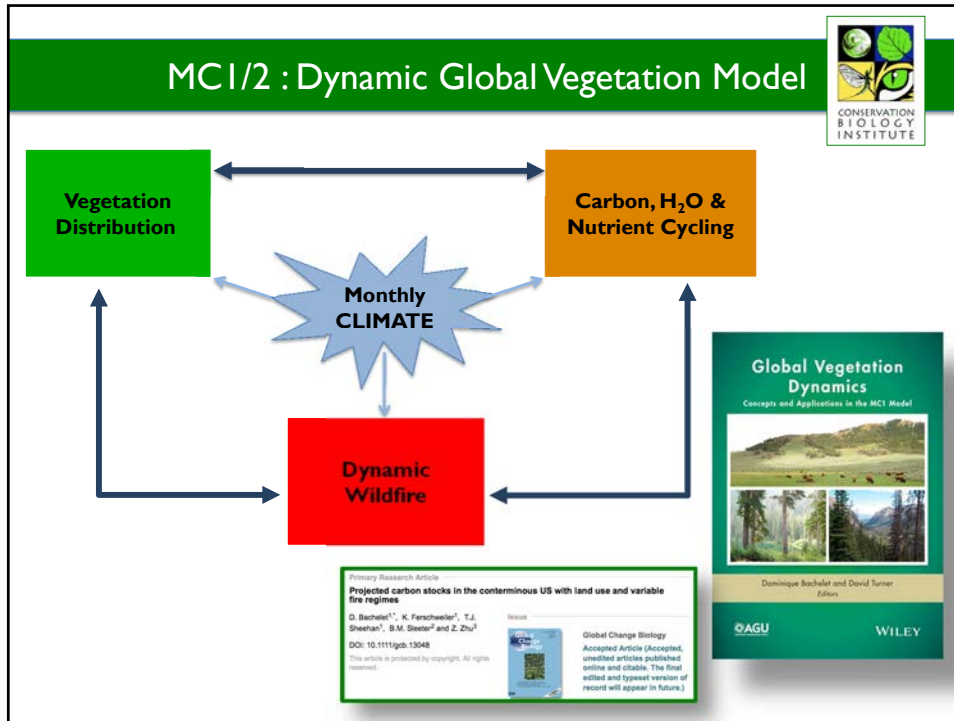
Ken Ferschweiler



Tim Sheehan

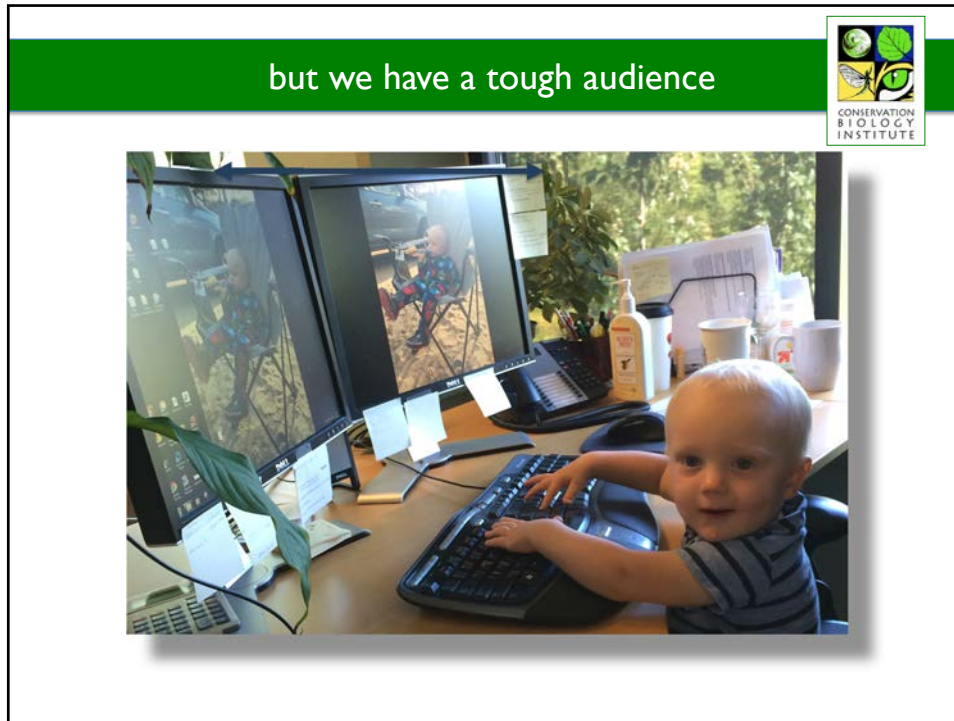


The screenshot shows the Conservation Biology Institute website with a green header and navigation menu. The main content area features 'Current Projects' with links to 'Collaboration to Create Climate Tools', 'Wildlife Infrastructure Plan', and 'A Three Zone Climate Adaptation Strategy'. A 'Featured Publications' section highlights 'High-Severity Fire in Chaparral: Cognitive Dissonance in the Herblands (Chapter 7)' and 'South County Grassland Project: Phase 2, 2013 Final Report'. A 'CBI Services' sidebar lists 'Conservation Assessment & Planning', 'Conservation Dataset Development & Analysis', 'Ecological Modeling' (circled in green), 'Science Support & Education', and 'Data Basin'. The footer includes contact information for 194 SW Washington Avenue, Suite 200, Corvallis, OR 97331.




Communicating Results – Custom Web Pages


The screenshot shows a custom web page for communicating climate scenarios. At the top left is a photo of Mike Gough. The main header is "US FOREST SERVICE" with the tagline "The Research Center for the Land and the People". Below this is "PACIFIC NORTHWEST ECOSYSTEM RESILIENCE". The page features a navigation menu with "Home", "Workshops", "ACT Table", "Climate Projections", "Data & Maps", and "About us". The central content area is titled "INTEGRATED CLIMATE SCENARIOS (NORTHWEST)" and includes a map of the Northwest with a "Select Ecoregion" dropdown. Below the map are three charts: "Maximum Temperature", "Precipitation", and "Consumed". The "Maximum Temperature" chart shows "RCP 4.5 MRSIC ESM-CM3 Mean Max Temperature (Blue Mountains)" from 2000 to 2050. The "Precipitation" chart shows "Rcp45 MRSIC ESM-CM3 2011-2050 (Blue Mountains)". The "Consumed" chart shows "Rcp45 MRSIC ESM-CM3 with Fire Sup. Carbon Consumed (Blue Mountains)". The page footer includes the URL <http://consbio.webfactional.com/pnw/projections.html> and another URL <http://consbio.webfactional.com/integratedscenarios/rcp85.html>.




Hot Shot Team to Communicate the Science




Mike Lundin




Nik Molnar



Brendan Ward



Dan Harvey




Visualizing and Sharing Spatial Data - databasin.org

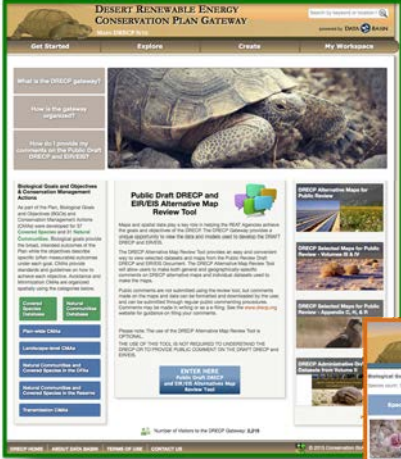
The screenshot displays the databasin.org web application. At the top, there is a navigation bar with 'Get Started', 'Explore', 'Create', 'Community', and 'My Workspaces'. The main content area is divided into several sections: a 'What to Do Next?' sidebar, a central map of the western United States showing 'Fraction of Area Burned Per Decade under the A2 Emission Scenario, 800 meter, Scenario (with landuse), 800 meter', and a 'Create' sidebar on the right with options like 'Create a Map', 'Import a Dataset', 'Create Group', 'Create Gallery', and 'Create a Guide/Case study'. A 'Conservation Priority Working Group' window is also visible. The bottom of the page features the 'DATA BASIN' logo and a 'Map Details' sidebar.


Comparing/Testing/Sharing Model results

This screenshot provides a closer look at the map interface. The 'Map Details' sidebar on the left lists several data layers, with the third layer, 'Fraction of Area Burned per Decade under the A2 Emission Scenario (with landuse), 800 meter', circled in red. The top toolbar contains various map controls, with the 'Layers' and 'Legend' icons also circled in red. The map itself shows the same western US region with a color-coded overlay representing the fraction of area burned. The legend on the right indicates a scale from 0 to >1. The bottom of the interface shows a 'Use Time Info From' dropdown set to '1/1/2011', which is also circled in red.

Gateways – Focused, Customized









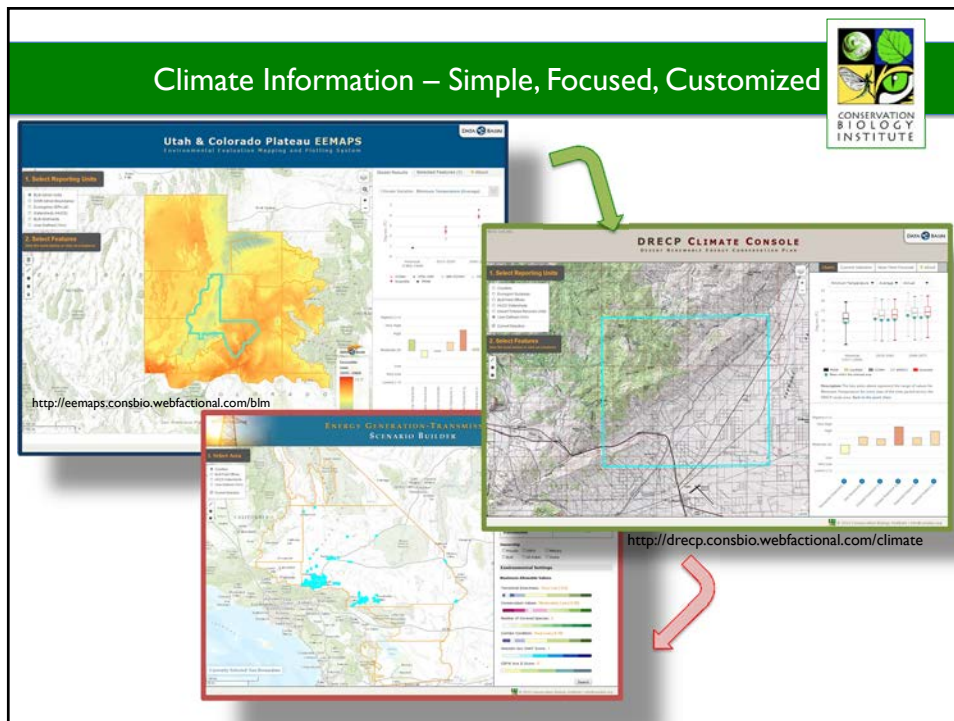
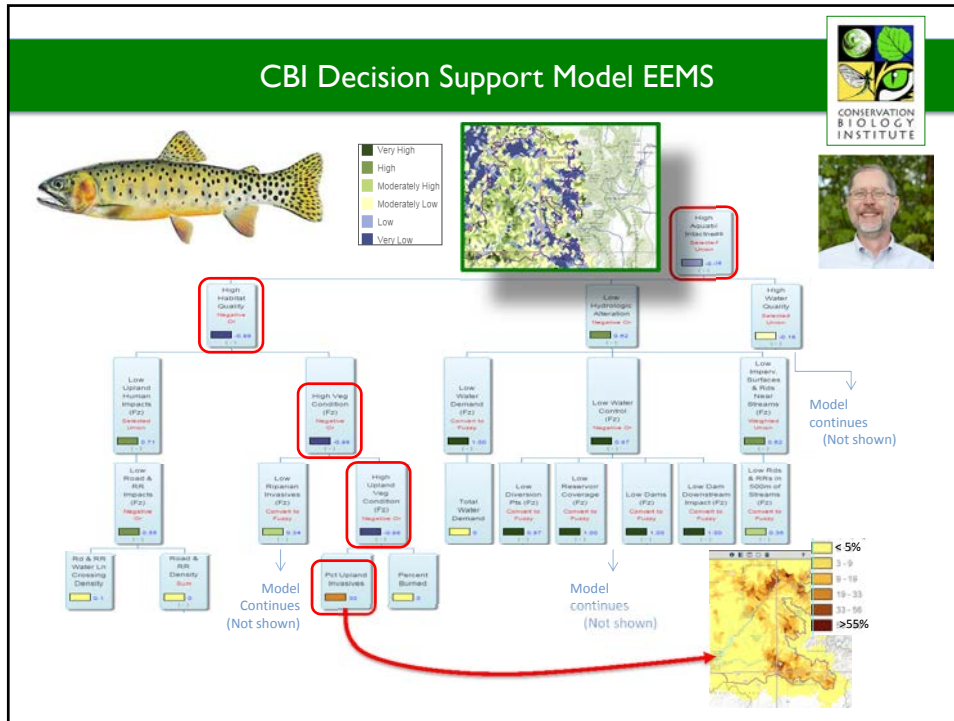
<http://drecp.databasin.org/>

11


Example of Custom Tool









Feedback to Deliver More Usable Climate Tools





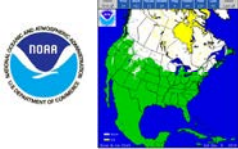
- . Testing existing tools (NOAA, USGS, CBI)
- . Working with developer to design new tool
- . Provide feedback for improvement

Funding sources:

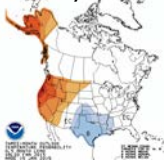


& GB-LCC


Snowcover




90 day forecast




Regional Climate Extremes



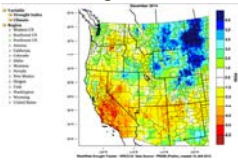
Climate at a glance



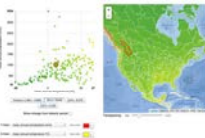
USGS National Climate Change Viewer




Drought Tracker




AdaptWest



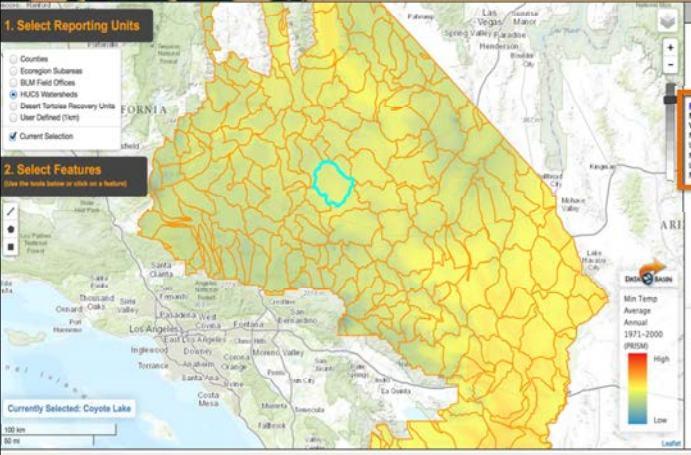
Integrated Scenarios



Getting Feedback on Climate Console – California



DRECP CLIMATE CONSOLE
DESERT RENEWABLE ENERGY CONSERVATION PLAN



Minimum Temperature | Average | Annual

25

PRISM, historical (1971-2000)
Mean within the selected area: 11.28°C
Variability across the DRECP study area:
Maximum: 19.6°C
Upper quartile: 14.1°C
Median: 11.3°C
Lower quartile: 6.3°C
Minimum: -1.6°C

UNCERTAINTY

Historical (1971-2000) | 2019-2045 | 2046-2075


PRISM | CasDM2 | CCSM4 | MRDC3 | Ensemble

Min Temp | Average | Annual | PRISM

Highest (+): Very High | High | Moderate (0) | Low | Very Low

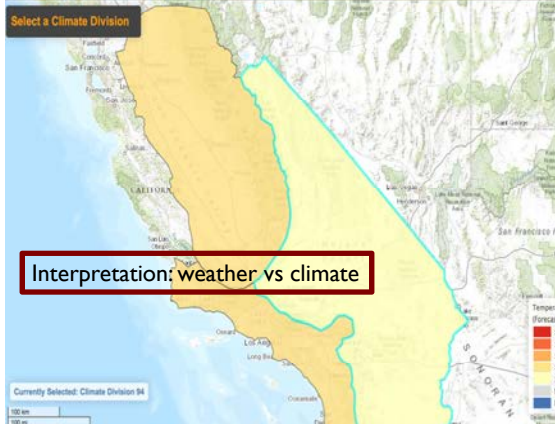
© 2015 Conservation Biology Institute | info@combio.org

Request for short term forecast but ...



DRECP CLIMATE CONSOLE
DESERT RENEWABLE ENERGY CONSERVATION PLAN

Select a Climate Division





Currently Selected: Climate Division 94

Climate Division 94

Time Frame: Temperature | Precipitation

Oct-Nov-Dec 2015
 Nov-Dec-Jan 15-16
 Dec-Jan-Feb 15-16
 Jan-Feb-Mar 2016
 Feb-Mar-Apr 2016
 Mar-Apr-May 2016
 Apr-May-Jun 2016
 May-Jun-Jul 2016
 Jun-Jul-Aug 2016
 Jul-Aug-Sep 2016
 Aug-Sep-Oct 2016
 Sep-Oct-Nov 2016
 Oct-Nov-Dec 2016

Change from the Historical Mean: ↑ 0.10°F | ↑ 0.44 in.

Show on Map


	Temperature	Precipitation
Historical Mean	56.87°F	1.49 in.
Forecast Mean	57.02°F	1.93 in.
90% Confidence Interval	54.54°F - 59.57°F	0.30 in. - 4.89 in.

Reference: Beniston et al., 2000, *Int. J. Appl. Meteor. Soc.* 41:1271-1279
 Source: <http://www.drc.org/forecast>

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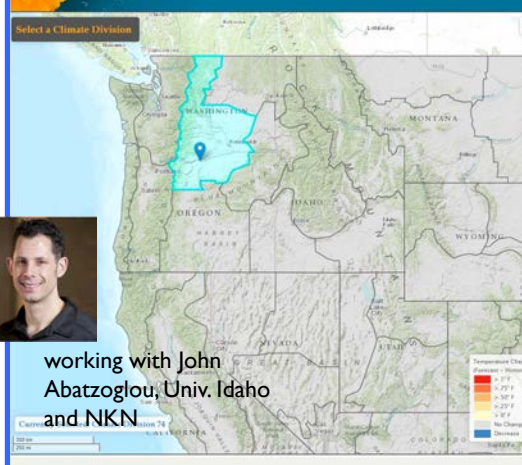
Interpretation: weather vs climate

Scale Issue (climate divisions, downscaling)



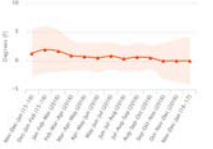
CALIFORNIA CLIMATE CONSOLE
CLIMATE PROJECTIONS FOR THE STATE OF CALIFORNIA

Select a Climate Division





Currently Selected: Climate Division 78

Temperature Forecast



Precipitation Forecast





working with John
Abatzoglou, Univ. Idaho
and NKN

Working on a carbon tool ...



Creating new blueprints, testing feasibility ...

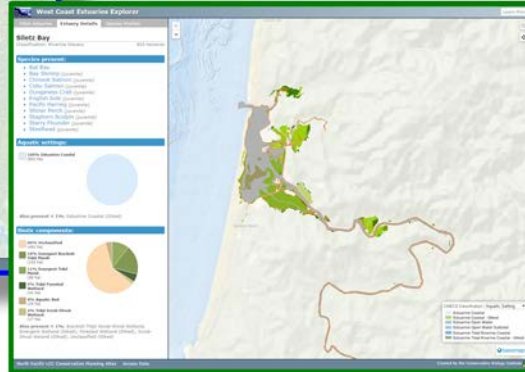
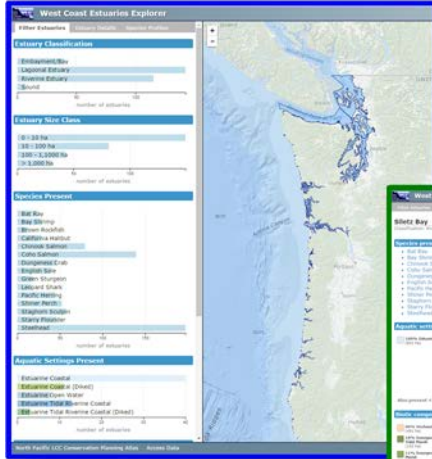


Choose the representative concentration path (RCP) to use in the projection. (Different RCPs project different levels of future carbon emissions.) When completed, the tool will interactively provide information about each of the RCPs in an information box.

Other tools in the works ...



for example ...



Thank you for your attention



Feedback or interest in collaboration
 Email: dominique@consbio.org

ABSTRACT: Decision Support Tools for Forest Management

Glenn Howe, Brad St.Clair, Dominique Bachelet

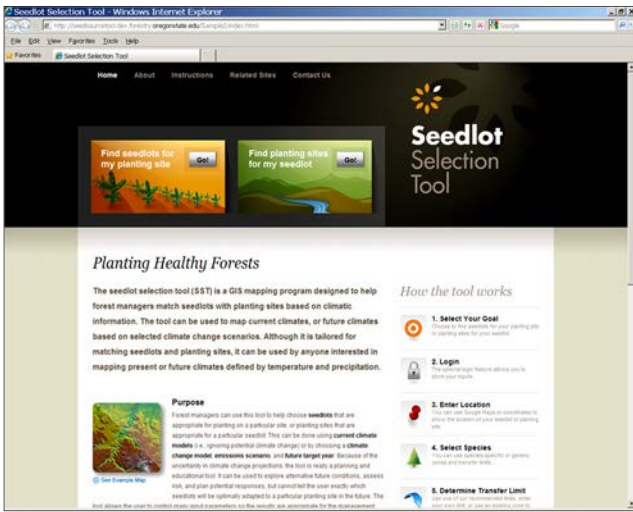
The original version of the Seedlot Selection Tool (SST) was developed through a collaboration between Glenn Howe (OSU, PNWTIRC) and Brad St.Clair (US Forest Service, Pacific Northwest Research Station). The SST is a GIS mapping tool designed to help forest managers match seedlots with planting sites based on climatic information. The climates of the planting sites can be chosen to represent current climates, or future climates based on selected climate change scenarios. To provide better long-term maintenance and integration of the latest climate information, the SST will soon be made available to the public through the Conservation Biology Institute's Data Basin (<https://databasin.org>). The Data Basin provides free access to spatial data and non-technical tools that allow users to explore data sets and create maps on topics related to climate change and conservation.



Decision Support Tools for Forest Management

Glenn Howe, Brad St.Clair, Dominique Bachelet

Seedlot Selection Tool (SST)



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.

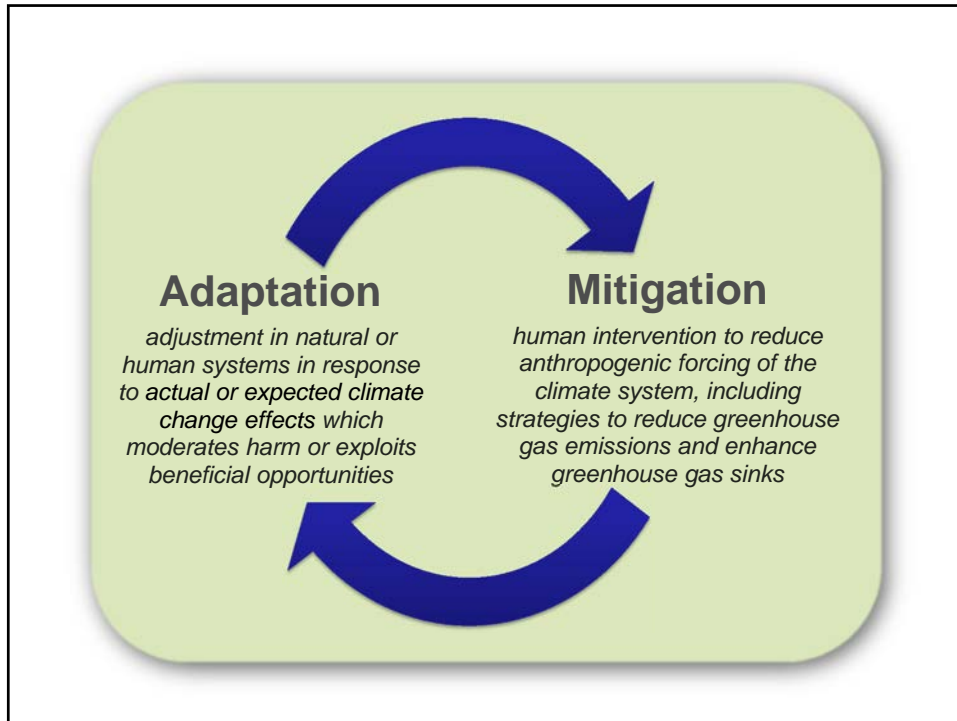
Purpose

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 models (i.e., ignoring potential climate changes) or by choosing a climate change model, emissions scenario, and future target year. Because of the uncertainty in climate change projections, the tool is really a screening and educational tool. It can be used to explore alternative future conditions, assess risk, and gain potential responses, but it cannot tell the user exactly which seedlots will be optimally adapted to a particular planting site in the future. The tool allows the user to create and save seedlot preferences in the results log, accessible to the user at any time.

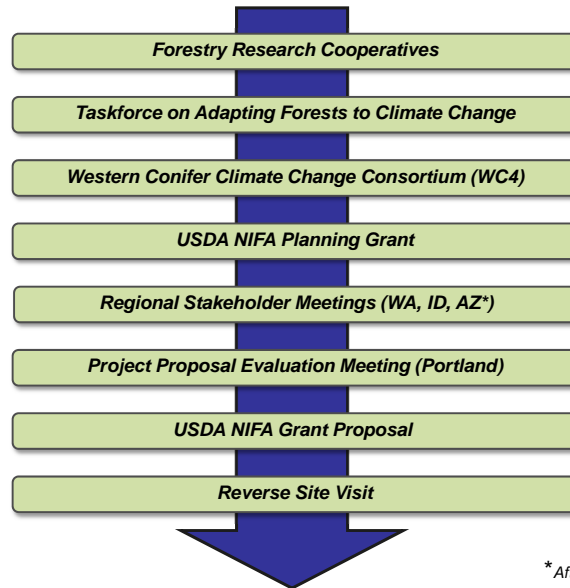
How the tool works

- 1. Select Your Goal**
Choosing a goal determines your planting site.
- 2. Login**
The online registration allows you to save your results.
- 3. Enter Location**
You can use Google Maps or coordinates to enter the location of your seedlot or planting site.
- 4. Select Species**
Choose one or more species (by its generic name and transfer limit).

4. Determine Transfer Limit
You set your own transfer limit, which will allow you to save or transfer seedlots.



History of the idea...



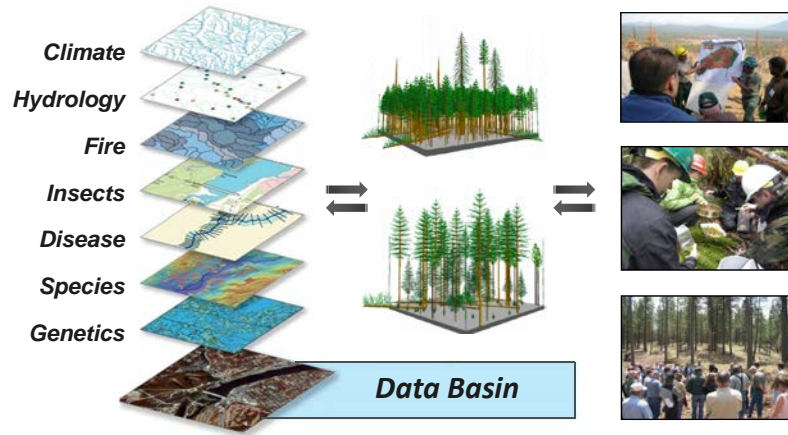
* After the Portland meeting

Details

How can forest managers respond?

1. *Climate*
2. *Vulnerability*
3. *Species selection*
4. *Genetics - seedlot selection*
5. *Stand management*

Concept - Putting it all together



1. Climate

What climate changes are projected for my lands?

Can choose time frame

Continuously updated as new information becomes available

ClimateNA

Home People Research Teaching Publications Data Miscellaneous

[Other climate data](#) | [Species range maps](#) | [Other data](#)

Historical and projected climate data for North America (ClimateNA)

The software, downloadable from this web page, can be used to estimate more than 50 monthly, seasonal, and annual variables, including many economically or biologically relevant variables such as growing and chilling degree days, heating and cooling degree days, Hargrave's moisture deficit and reference evaporation, beginning and end of the frost-free period, etc.

Click on the thumbnails below and use the zoom tool  to see high resolution images of mean annual temperature (MAT), mean winter temperature with inversions in northern mountain valleys (MWT), mean annual precipitation with leeward rainsadows (MAP), and a climate moisture index (CMI):



MAT



MWT



MAP



CMI

2. Vulnerability

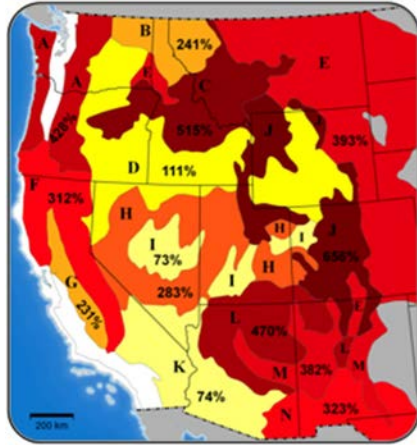
Which sites are most vulnerable to climate change?

Where should I prioritize my adaptation and mitigation strategies?

Integrate all threats

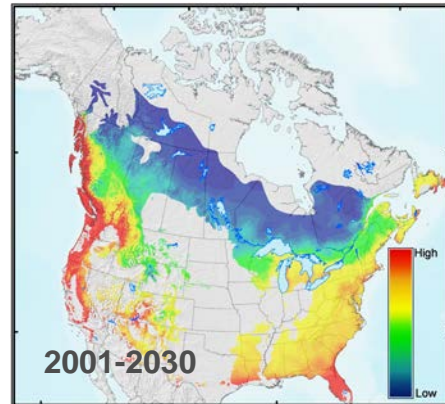
Key components of vulnerability

Wildfire change per 1°C global warming



Littell

Probability of mountain pine beetle cold tolerance



Bentz

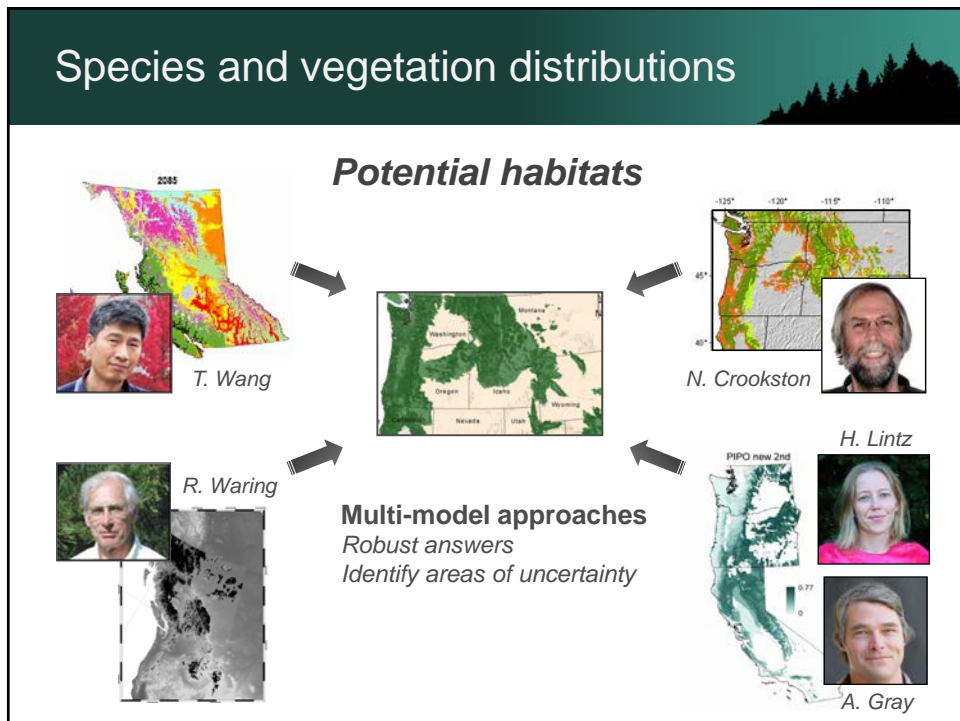
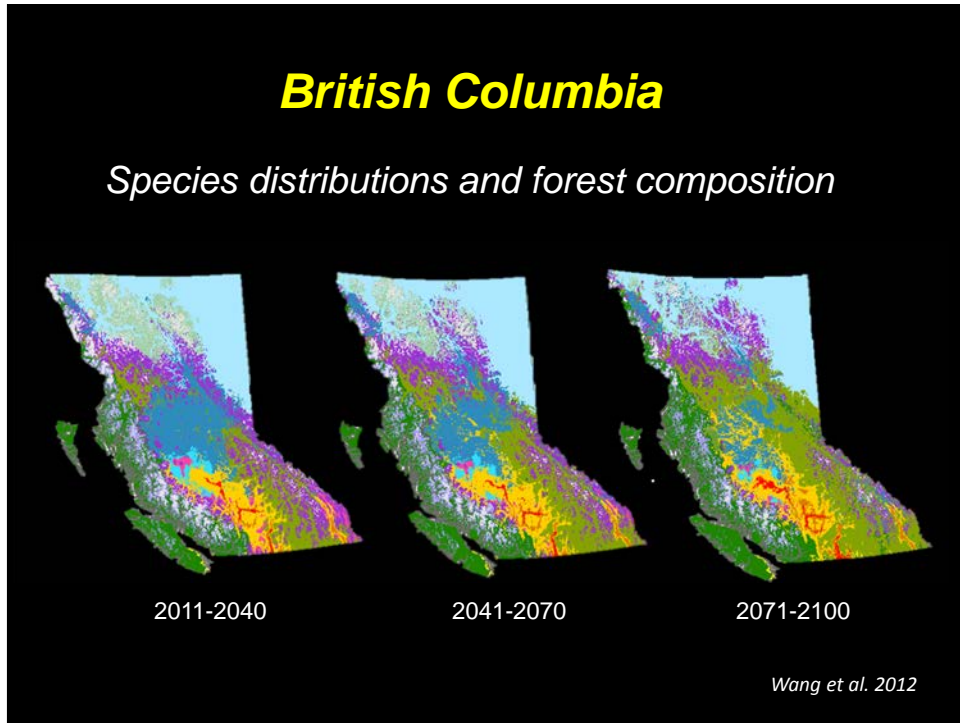
Normals, CRCM v. 4.2.0, IPCC A2 scenario.
Régnière and St-Amant. 2007, Bentz et al. 2010

3. Species

Which species should I favor in the future?

Which species are not good choices for the future?

Deliver scientific results using a multi-model approach



Objectives

4. Genetics

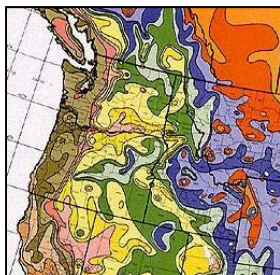
Which seedlots should I plant on my site?

Where will I get my seed in the future?

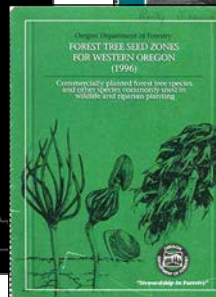
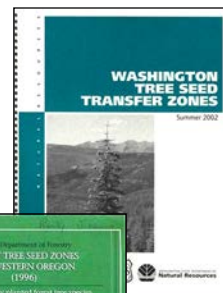
Where can trees from my seed orchard be planted?



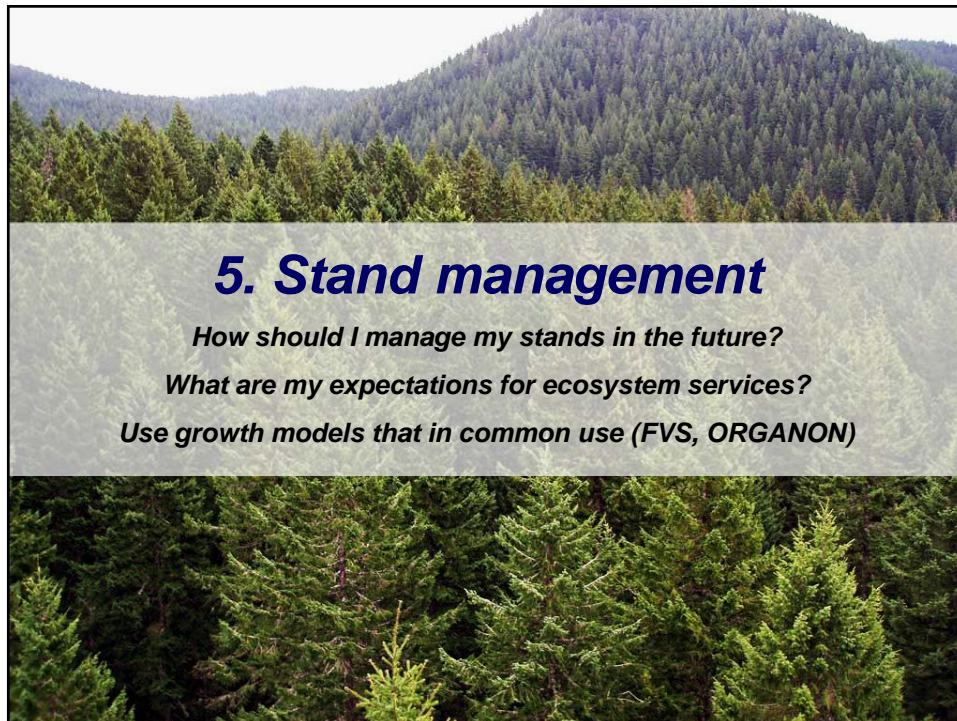
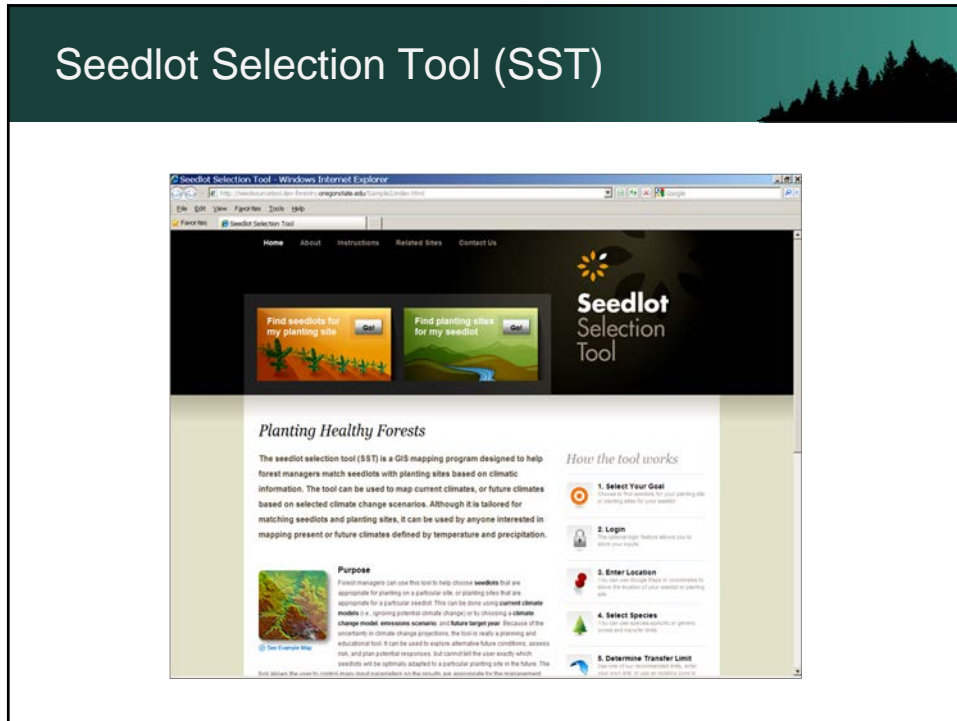
Plant trees genetically adapted to the future climate



Seed zones and breeding zones are largely delineated based on climate



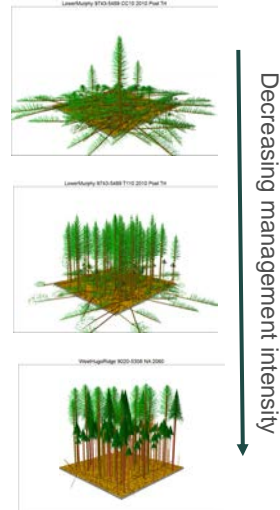
Seedlot Selection Tool (SST)



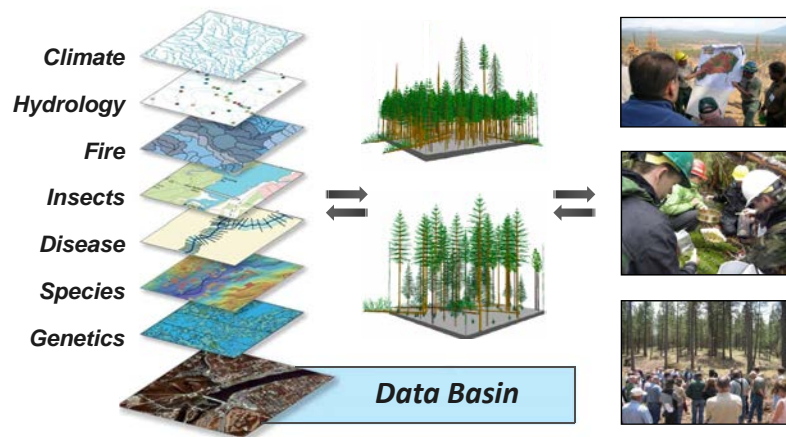
Silvicultural adaptation and mitigation options

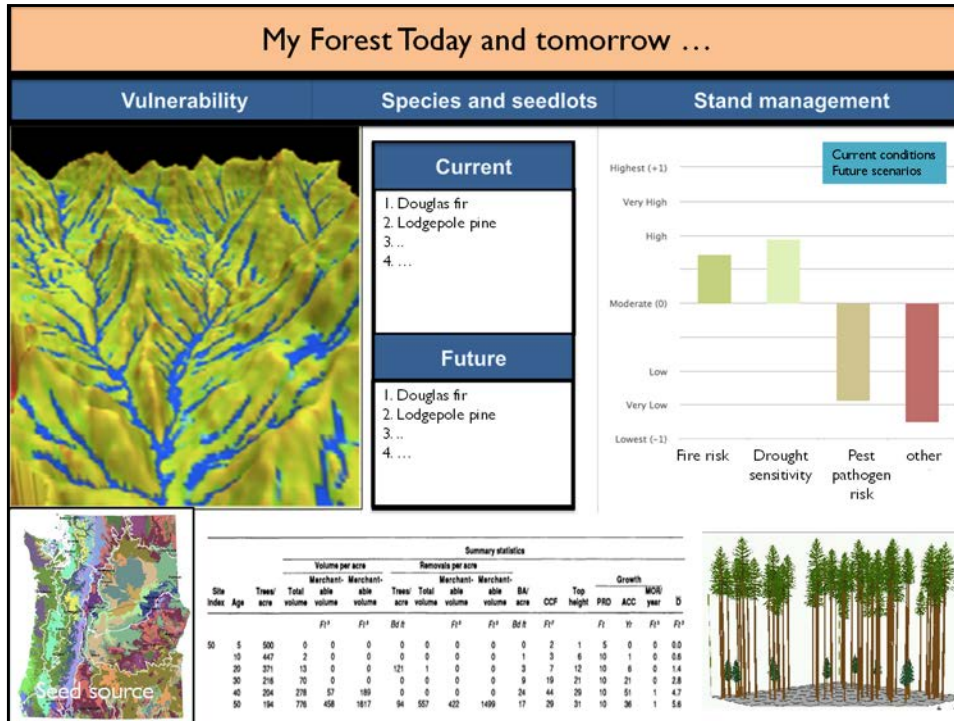
- **Rotation**
 - Shorten to reduce risk
 - Lengthen to increase C storage
- **Regeneration**
 - Increase control of competing vegetation
 - Use more stress-resistant stock types
 - Anticipate seed zone, species shifts
- **Thinning**
 - Lower tree density and leaf area
 - Change species composition
 - Biomass for energy or biochar
- **Directly control site resources**
 - Spray for insects and disease
 - Manage for 'fire-resistant' landscapes
 - Increase fertilization and irrigation

FVS Outputs



Concept - Putting it all together

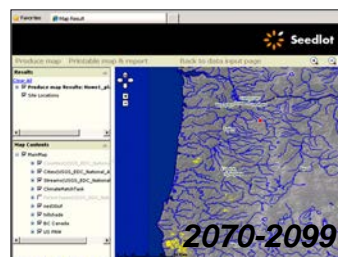
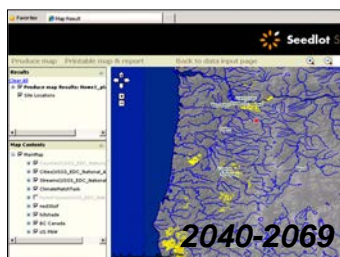
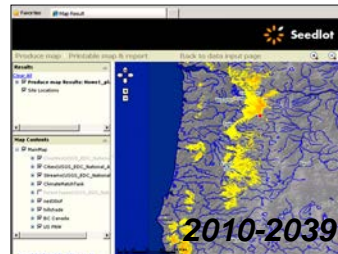




Seedlot Selection Tool (SST)

22

Find seedlots for my planting site

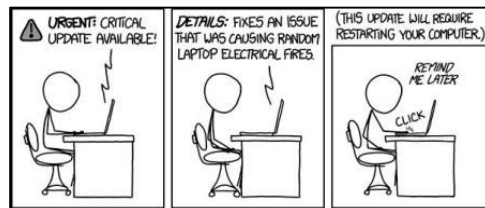


Seedlot selection tool

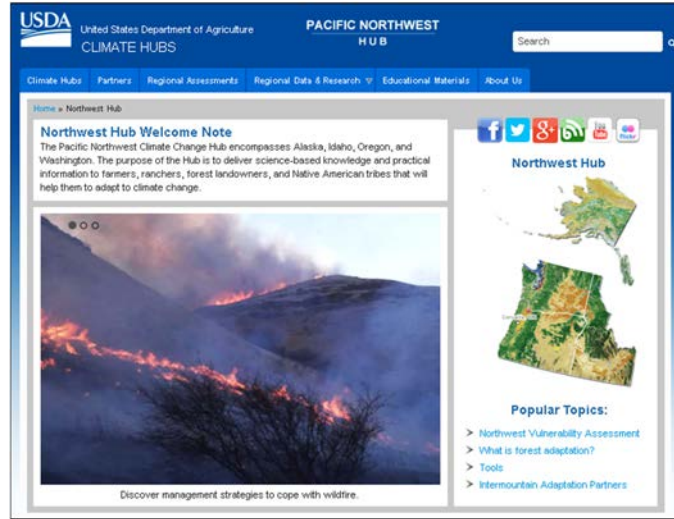
SST worked great...

But not forever...

Must be maintained by skilled programmers



Pacific Northwest Climate Hub



Data Basin distributes spatial data

- Spatial data delivery
- Interpretation tools
- Project description
- Networking tools



Conservation Biology Institute
www.databasin.org

ABSTRACT: 1915 Douglas-Fir Heredity Study

Brad St.Clair and Glenn Howe

The Douglas-fir Heredity Study was planted beginning in 1915, over 100-years ago. The objective was to determine the best type of ‘seed tree’ to use for collecting seed for artificial reforestation in the Pacific Northwest. Brad St.Clair (US Forest Service, Pacific Northwest Research Station) and Glenn Howe (OSU, PNWTIRC) are collaborating to analyze this historic study on the genetics of Douglas-fir.

Six test sites were planted with 120 families from 13 provenances. Because this study was initiated before modern concepts of experimental design were developed, it was planted without the normal randomization or blocking that would typically be used today. Instead, family row plots were planted together by provenance, with each site having the same layout.

The sites were measured for height and/or diameter every 10 years. Current analyses are focusing on characterizing variation among provenances at each site for survival, height, and diameter at 10-year increments. Models relating the performance of the provenances to their climate of origin (e.g., mean annual temperature) will be developed to understand the effects of seed transfer and climate change. Early results suggest that provenance variation within sites is low for height and diameter. Survival is variable at most sites, and generally unrelated to the seed source climate or climatic transfer distance. Observing mortality over time made a significant impression on Pacific Northwest land managers—resulting in a conservative approach to seed transfer and small zones in the Pacific Northwest. The study suggests that natural selection has occurred within provenances, potentially leading to the formation of land races.

1915 Douglas-Fir Heredity Study

Brad St.Clair

USFS Pacific Northwest Research Station, Corvallis, OR

Glenn Howe

Oregon State University, Corvallis, OR



Pacific Northwest Tree Improvement Research Cooperative Annual Meeting, October 22, 2015, Portland, OR

Background



Douglas-Fir Heredity Study

Original objective: determine the best type of tree for seed collections for artificial reforestation and for seed trees

Study Design

- 120 families from 13 provenances
- Planted at 6 test sites (5 left) in 1915 and 1916
- Family row plots of variable length with families blocked together by provenances
- Same layout at every site; no randomization; no blocks

Measured heights and/or diameters approx.
every 10 years to age 80, then again at age 100



Analysis

- Variation among provenances at each site for survival, height, and diameter at different ages
 - Progeny from different parent trees (families) serve as replicates for provenances
- Response functions at each site
 - Performance relative to climate of seed sources
 - Expressed as transfer distances (MAT)
- Transfer function over all sites
 - Performance as a function of climatic transfer distance (MAT)

Test Site Means

- Four mild test sites with temperate climates and plenty rain
- One higher elevation test site with slow growth
- Overall low survival

Table 1. Location, elevation, climate, and overall means for survival, height and DBH after 100 years (2013) for five test sites of DFHS

Plantation	Latitude	Longitude	Elevation (ft)	Mean annual temp (-C)	Coldest Month temp (-C)	Mean annual precip (in)	Survival (%)	Height (ft)	DBH (in)
Hebo	45.148	123.756	2,100	8.3	2.5	2,670	14	109	18.7
Wind River	45.792	121.927	1,160	9.0	0.3	2,630	19	129	16.7
Stillaguamish	48.064	121.548	1,880	7.4	-1.0	3,460	11	123	21.5
Lower Mt Hood	45.268	121.821	2,800	6.9	-0.8	2,010	31	84	11.5
Upper Mt Hood	45.263	121.774	4,500	5.4	-2.0	1,910	25	63	13.2

Provenance Means

- Overall provenance means: range of about 4°C
 - Most from sources warmer than the test sites (typical of population movements in the early 20th century)
 - Some movements to higher elevation test site as much as 5-6°C
- Overall, not large differences in growth or survival among provenances

Table 2. Location, elevation, climate, and overall means after 100 years (2013)

Provenance	Latitude	Longitude	Elevation (ft)	Mean annual temp (-C)	Coldest Month temp (-C)	Mean annual precip (mm)	Survival (%)	Rank	Height (m)	Rank	DBH (cm)	Rank
Lakeview	47.176	122.592	100	10.7	3.8	1,060	16	13	105	5	17.3	4
Benton	44.642	123.580	700	10.5	3.8	1,720	16	12	100	12	15.5	12
Portland	45.489	122.730	300	11.0	3.5	1,150	19	5	100	13	15.2	13
Gates	44.750	122.417	950	9.9	2.8	1,750	18	9	107	2	17.3	5
Granite Falls	48.104	121.916	400	9.6	2.3	1,940	18	10	107	1	17.6	1
Carson	45.718	121.825	400	10.4	1.7	1,720	17	11	102	11	16.9	11
Hazel	48.263	121.844	900	8.9	1.6	2,340	18	8	104	8	17.0	9
Fortson	48.267	121.725	500	8.5	0.9	2,690	20	4	104	9	17.0	10
Darrington	48.254	121.592	500	8.9	0.8	2,420	20	1	107	3	17.5	2
Wind River	45.823	121.958	1,350	8.9	0.2	2,440	20	2	104	10	17.1	8
Santiam	44.661	121.907	3,200	7.1	-0.6	2,040	19	6	105	7	17.1	7
Race Track	45.897	121.850	2,600	7.2	-0.7	2,630	19	7	105	6	17.2	6
Palmer	45.559	122.001	2,500	6.8	-0.7	3,370	20	3	106	4	17.4	3

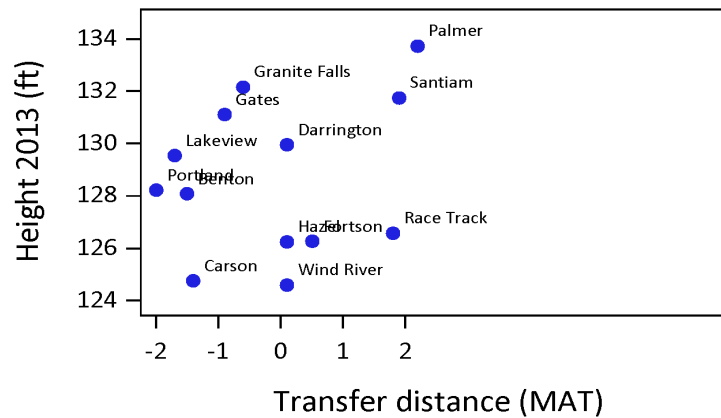
Provenance Variation Within Sites

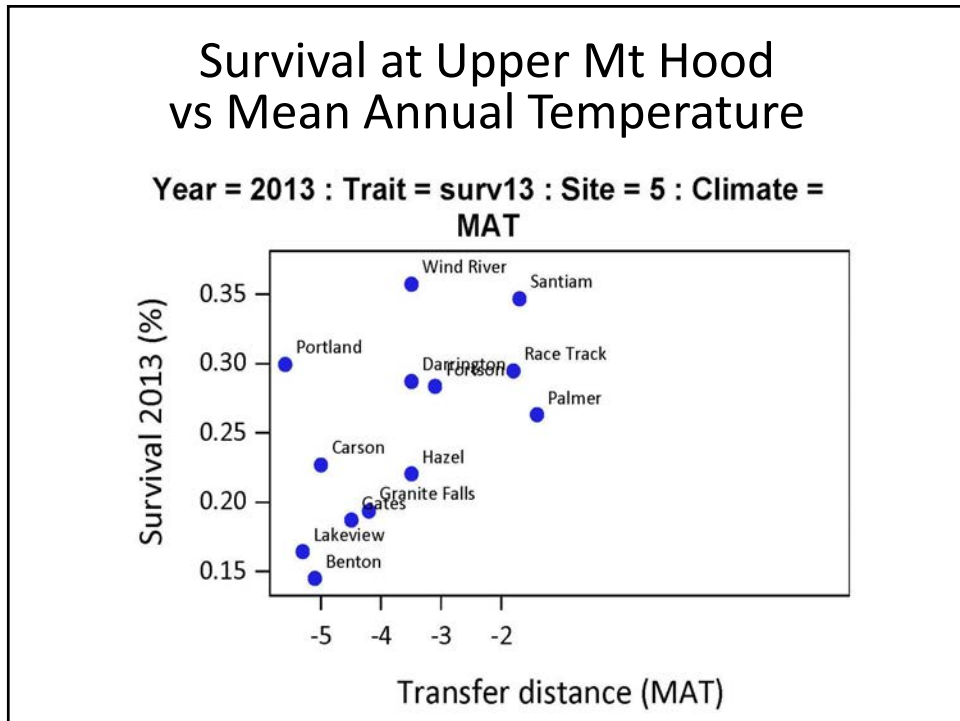
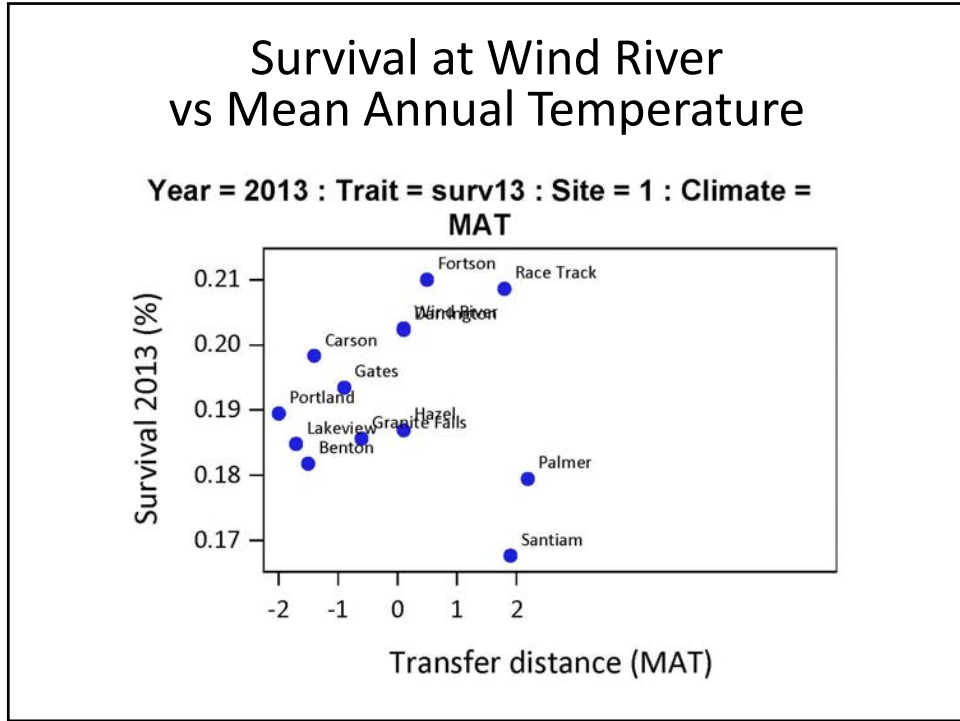


- Little provenance variation in heights and diameters
 - Possible that smaller trees died, reducing variation (land race formation?)
- Survival variable at most sites
 - Generally unrelated to climate of seed source or transfer distance
- Except:
 - Related to transfer distance at colder, high elevation site with lower survival from low elevation sources (15%) compared to higher elevation sources (36%)
- Considerable variation within provenances

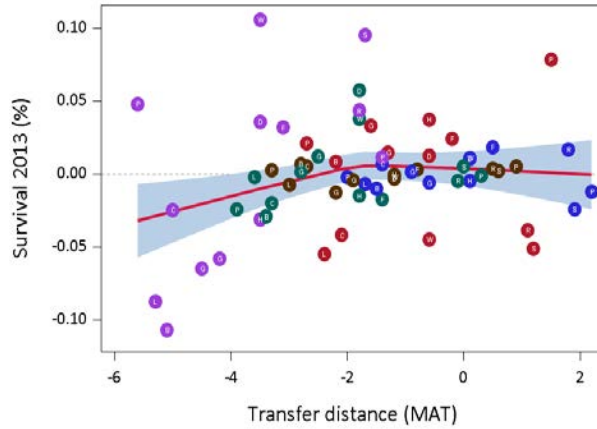
Height Age 100 at Wind River vs Mean Annual Temperature

Year = 2013 : Trait = HT2013 : Site = 1 : Climate = MAT

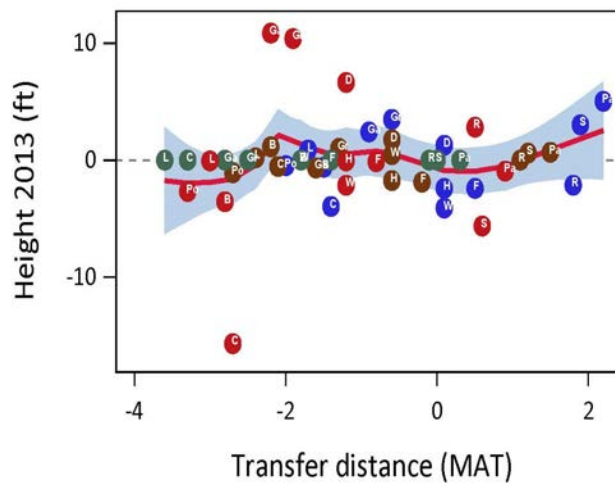




Survival At All Sites vs Transfer Distance in Mean Annual Temperature

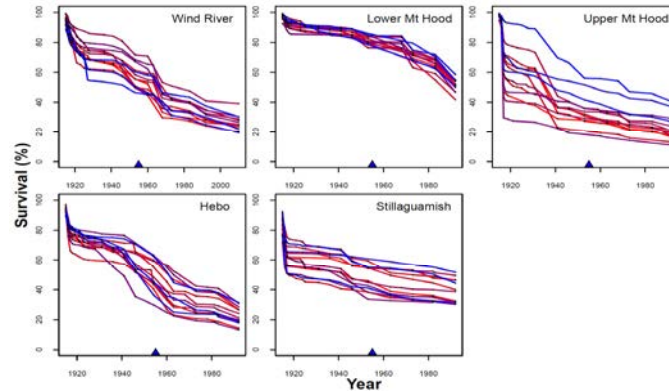


Height at All Sites vs Transfer Distance in Mean Annual Temperature



Some evidence for pulses of mortality associated with extreme climate events such as 1955 November 'Deep Freeze', particularly at warmer sites.

Figure 9: Survival over time. Blue triangle indicates 1955, the year of the November "Deep Freeze." Old arboretum reports indicate that there was also a severe winter in 1949-1950 and a severe drought in 1951.



Lessons Learned

- Observing mortality over time made a significant impression on Roy Silen, resulting in a conservative approach to seed zones and tree improvement in the Pacific Northwest (including observations at Wind River Arboretum).
- Considerable variation within provenances; can be exploited for tree improvement.
- Population movement guidelines restricting movements between 1,000 ft elevation bands probably resulted in improved survival and productivity of plantations.
- Study indicates a possibility for natural selection within provenances, potentially leading to the formation of land races.
- Implications for assisted migration strategies in response to climate change:
 - Okay to begin moving populations to warmer climates up to at least 2°C, but may not want to make overly large movements, particularly if climate variability increases (e.g., observations at milder sites of frost damage due to 1955 freeze).
 - Recommend mixtures of provenances to allow for some natural selection and human selection by thinning.

APPENDIX I

Presentations

by PNWTIRC personnel 2014-2015

Rust, M.L., Davis, A., Howe, G.T., Hipkins, V. 2015. Development of genetic markers for western white pine and Douglas-fir. Presentation in: Center for Advanced Forestry Systems Annual Meeting, May 19-21, Asheville, North Carolina.

Klocko, A., Ma, C., Robertson, S., and Strauss, S.H. 2015. *FT* genes for accelerating flowering in *Eucalyptus*. Presentation in: Center for Advanced Forestry Systems Annual Meeting, May 19-21, Asheville, North Carolina (Presented by Oguz Urhan).

Klocko, A., and Strauss, S.H. 2015. Production and analysis of flowering-modified eucalypts. Presentation in: Center for Advanced Forestry Systems Annual Meeting, May 19-21, Asheville, North Carolina (Presented by Oguz Urhan).

APPENDIX II

Collaborations and Grants

2014-2015

CAFS Center for Advanced Forestry Systems – Phase II. Howe, G.T., Maguire, D.A., and Strauss, S.H. National Science Foundation Industry/University Cooperative Research Center Program, 2012-2017, \$300,000 (OSU).

USFS Forest Health Protection, Special Technology Development Program. Genetic markers for western white pine (WWP): Enabling molecular breeding for resistance to white pine blister rust. Howe, G.T., Davis, A., Hipkins, V., Liu, J.-J., Mahalovich, M.F., Rust, M., and Sniezko, R., 2014-2016, \$99,685. Funding for 2014 (\$16,000) was received.

University of Idaho and the Inland Empire Tree Improvement Cooperative. Genetic markers for western white pine (WWP): Enabling molecular breeding for resistance to white pine blister rust. Howe, G.T., 2013-2015, \$30,000.

USFS Rocky Mountain Research Station. Developing a SNP panel for interior Douglas fir. Howe, G.T. and Cushman, S. USDA-Forest Service Joint Venture Agreement, 2011-2015, \$28,755.

U.S. Endowment for Forestry and Communities. Forest health biotechnologies: What are the drivers of public acceptance? Needham, M.D. and Howe, G.T. 2013-2015, \$100,000.

USFS Pacific Northwest Research Station. Meta-analysis of Douglas-fir provenance tests to estimate responses to seed transfer and climate change. Howe, G.T. and St.Clair, J.B. USDA-Forest Service Joint Venture Agreement, 2013-2018, \$100,000.

USFS Pacific Northwest Research Station. Evaluating assisted migration options for adapting to climate change. Howe, G.T. and St.Clair, J.B. USDA-Forest Service Joint Venture Agreement, 2013-2019, \$40,000.

APPENDIX III

Annual Meeting Minutes

October 22, 2015, Portland, OR

I. ATTENDEES

Kori Ault, PNWTIRC, OSU	Sara Lipow, Roseburg Forest Products
Dominique Bachelet, CBI	Lauren Magalska, PNWTIRC, OSU
Margaret Banks, Stimson Lumber Co.	Josh Misenar, Sierra Pacific Industries
Candace Cahill, Rayonier	Fred Pfund, Starker
Erda Celer, PNWTIRC, OSU	Bruce Ripley, Hancock
Mike Crawford, BLM	Jim Smith, Plum Creek Timberlands
Dan Cress, Olympic Resource Management	Brad St.Clair, Forest Service, PNWRS
Glenn Howe, PNWTIRC, OSU	Hao Truong, PNWTIRC, OSU
Keith Jayawickrama, NWTIC, OSU	Oguz Urhan, PNWTIRC, OSU
Don Kaczmarek, ODF	Mike Warjone, Port Blakely Tree Farms
Andrea Kelsey, USFS	Andrew Wodnik, ORM
Scott Kolpak, PNWTIRC, OSU	Terrance Ye, NWTIC, OSU

II. WELCOME

Sara Lipow, PNWTIRC Policy/Technical Chair, called the meeting to order at 9:00 am.

III. PNWTIRC HIGHLIGHTS FOR 2014-15

Glenn Howe presented an overview of major accomplishments for 2014-15.

1. PNWTIRC administration
 - Director – Glenn Howe
 - Research Coordinator – Scott Kolpak
 - Program Managers – Kori Ault
 - Graduate students – Oguz Urhan, Erda Çeler
 - Faculty Research Assistant – Lauren Magalska
 - Policy/Technical Committee Chair – Sara Lipow
2. Research
3. Presentations by PNWTIRC personnel during 2014-15
4. Collaborations and grants during 2014-15

IV. PNWTIRC RESEARCH PRESENTATIONS

V. FIVE-YEAR PLAN DISCUSSION

Members offered suggestions for topics to be included in the five-year plan, including (1) developing new collaborations (particularly in the area of genomics), (2) consideration of new workshops and training, (3) appropriate balance of applied versus more basic research, and (4) planning and communication. Members also suggested important research topics that should be considered including genomic selection, breeding-without-breeding, disease resistance, abiotic stress resistance, Seedlot Selection Tool, relative economic value (economic weights) of traits, gene conservation, and climate change.

VI. BUDGET AND OTHER BUSINESS

Glenn Howe presented the budget for FY 2014-2015, and the proposed budget for FY 2015-16. Income was \$102K for 2014-15, and the 2015-16 income is expected to be the same. CAFS funds were used to pay some salaries. A motion to approve the budget for 2014-15 and the proposed budget for 2015-16 was offered, seconded, and approved by unanimous voice vote.

VII. POLICY/TECHNICAL COMMITTEE CHAIR

Sara Lipow was nominated as the new Policy/Technical Committee Chair and elected by unanimous voice vote. Mike Warjone was nominated PNWTIRC representative to CAFS and elected by unanimous voice vote.

VIII. MEETING ADJOURNED

The meeting adjourned about 3 pm.

APPENDIX IV

Financial Statement 2014-2015

PNWTIRC Financial Support for Fiscal Year 2014-2015

Regular members ¹	\$96,000
Associate members ¹	4,000
Contracts	2,000
Forest Research Laboratory, Oregon State University ²	124,118
Total	226,118

¹ Each Regular Member contributed \$8,000 and each Associate Member contributed \$4,000 excluding in-kind contributions of labor, supplies, etc.

² The contribution from Oregon State University includes salaries, facility costs, and administrative support.