

Background for Today's Meeting

- ✓ Species distribution models do not take into account standing genetic diversity and adaptive genetic potential
- ✓ Baseline databases are needed of the current genetic diversity and adaptive potential for large numbers of tree species
- ✓ The basic research is well underway and the technology platforms exist to develop baseline databases





EGFHN

Ecosystem Genomics and Forest Health Network

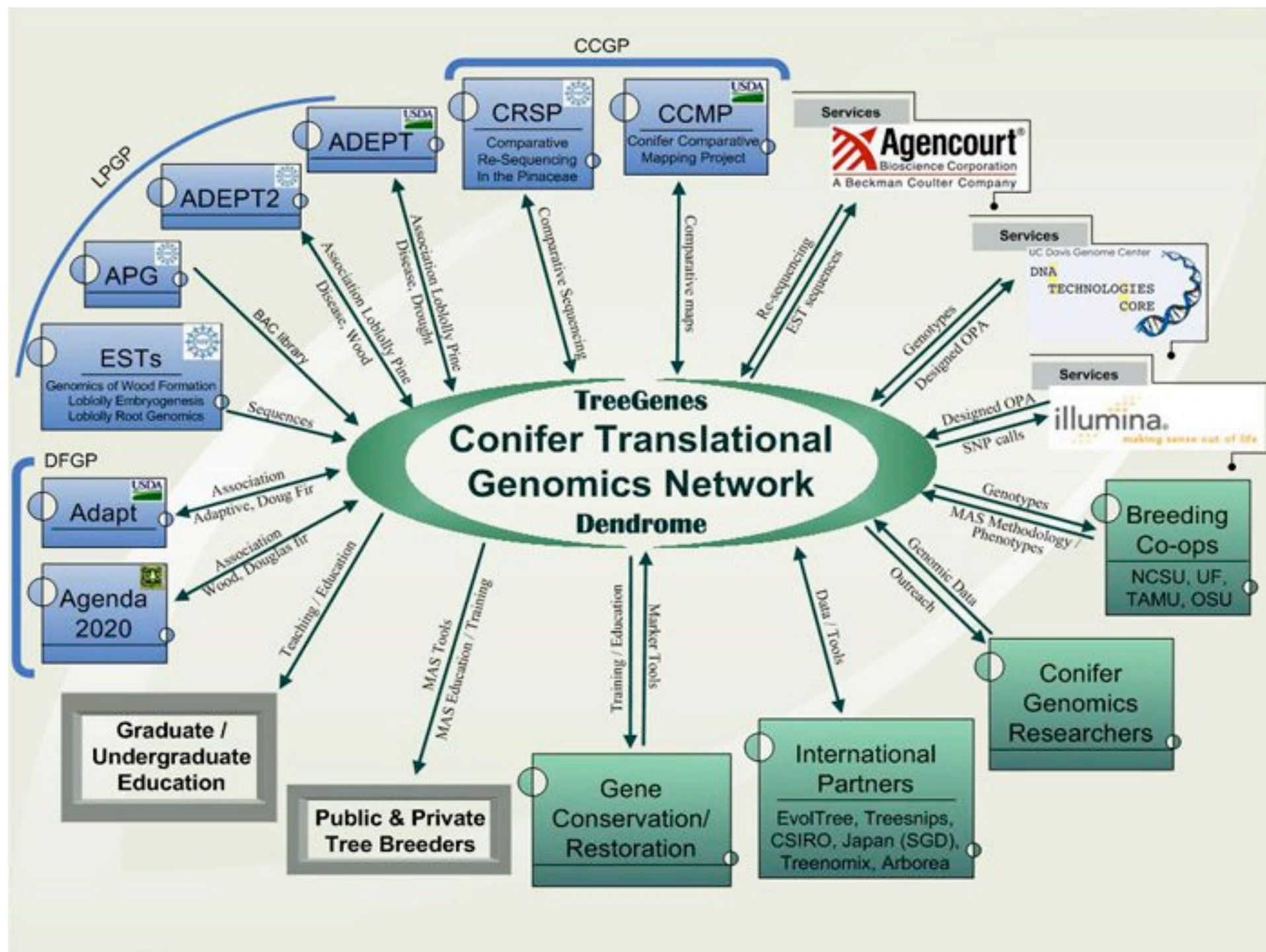


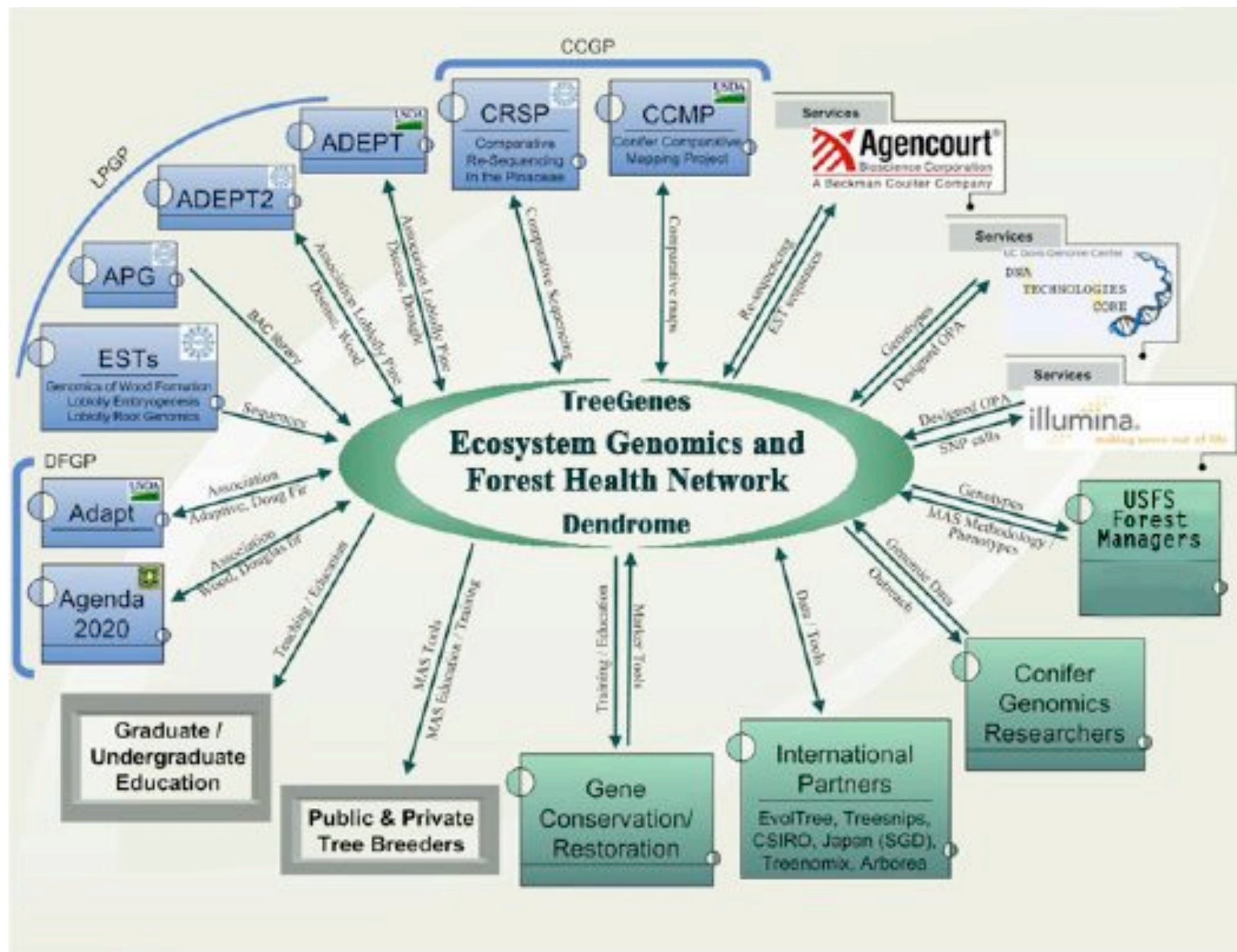


CTGN

Conifer Translational Genomics Network









CTGN

CTGN: Who's Involved?

- UC Davis
 - David Neale
 - Jennifer Lee
 - Jill Wegrzyn
- Oregon State
 - Glenn Howe
 - Dave Harry
 - Nick Wheeler
- NC State
 - Steve McKeand
 - Ross Whetten
- Texas A&M
 - Tom Byram
- Univ Florida
 - Dudley Huber
- Univ Georgia
 - Jeff Dean
- US Forest Service
 - Brad St. Clair
 - Dana Nelson

EGFHN: Who Should Be Involved?

- US Forest Service
- Other Federal Law Land Management Agencies (BLM, NPS)
- State Forestry
- NGOs
- Universities

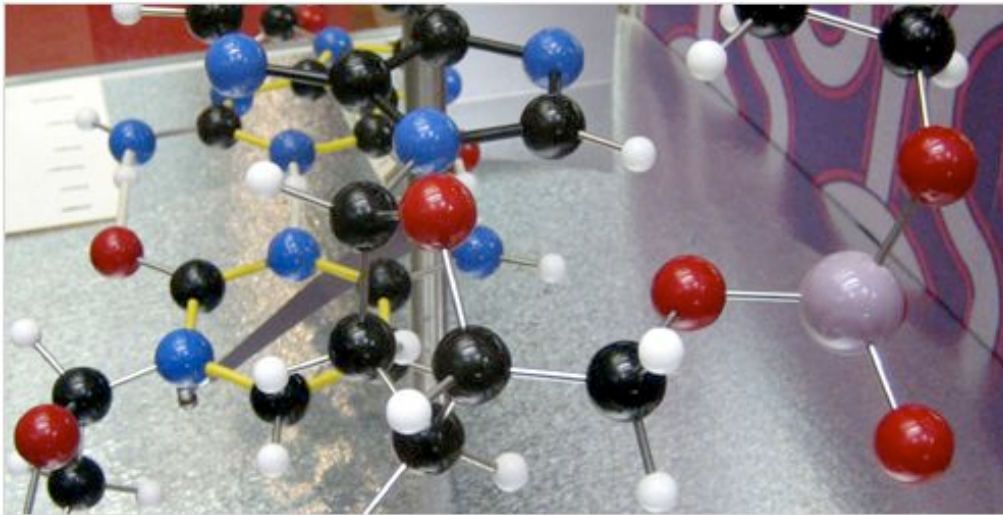
Ecosystem Genomics and Forest Health Network

- ✓ Need for forest health diagnostic tools
- ✓ How such tools are being developed
- ✓ How to create the EGFHN

Traits that are Controlled by Single Genes

Mapping / Positional Cloning Disease Resistance Genes

Eye on DNA | How will it change your life?

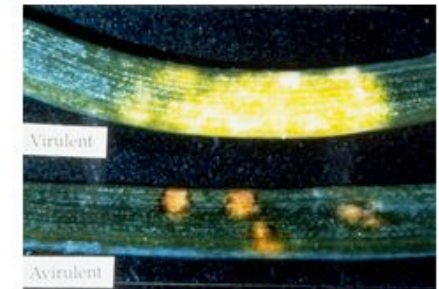
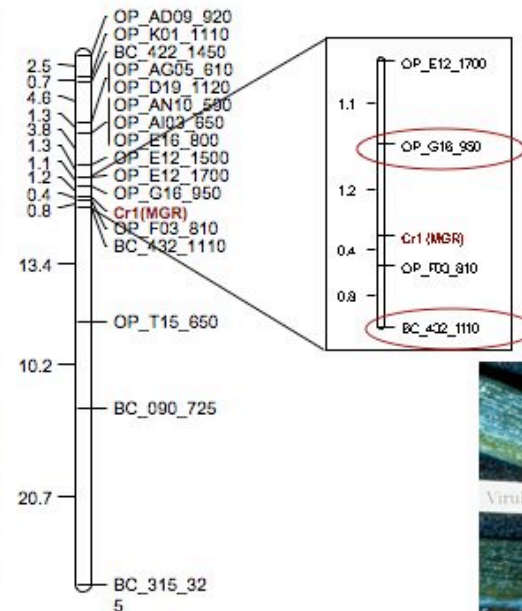


What happens after a positive breast and ovarian cancer (BRCA) genetic test?

by Dr. Hsien-Hsien Lei

Posted August 15, 2007 in [DNA Testing](#), [DNA and Disease](#)

SP_5701



CTGN

Overall Goal: *Implement marker-assisted breeding for three conifer species:*



Pinus taeda
(loblolly pine)

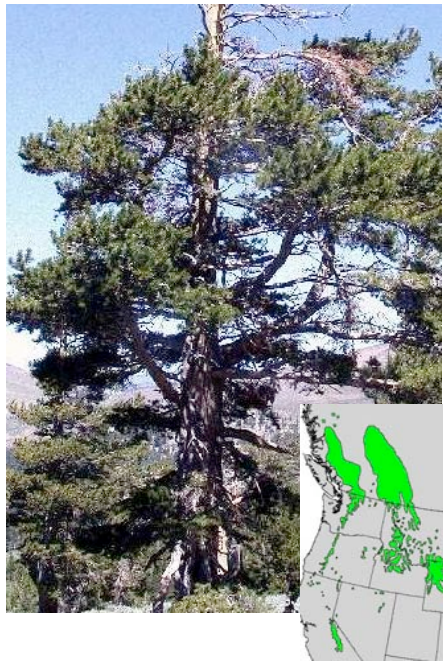


Pinus elliottii
(slash pine)

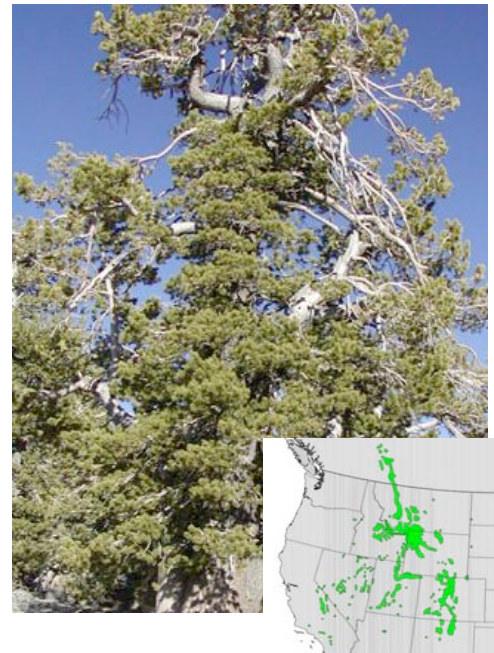


Pseudotsuga menziesii
(Douglas-fir)

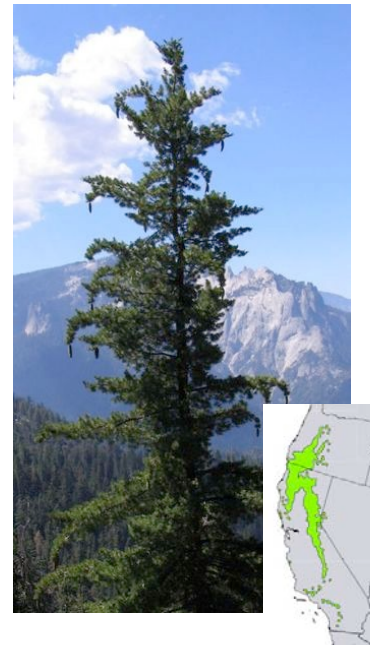
Overall Goal: *Develop and Apply Forest Health Diagnostic Tools:*



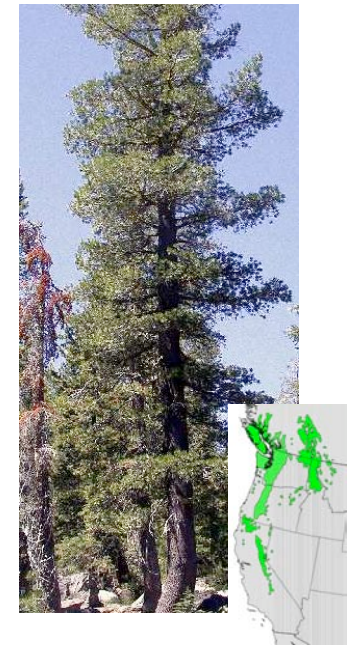
Pinus albicaulis
(Whitebark pine)



Pinus flexilis
(Limber pine)



Pinus lambertiana
(Sugar Pine)

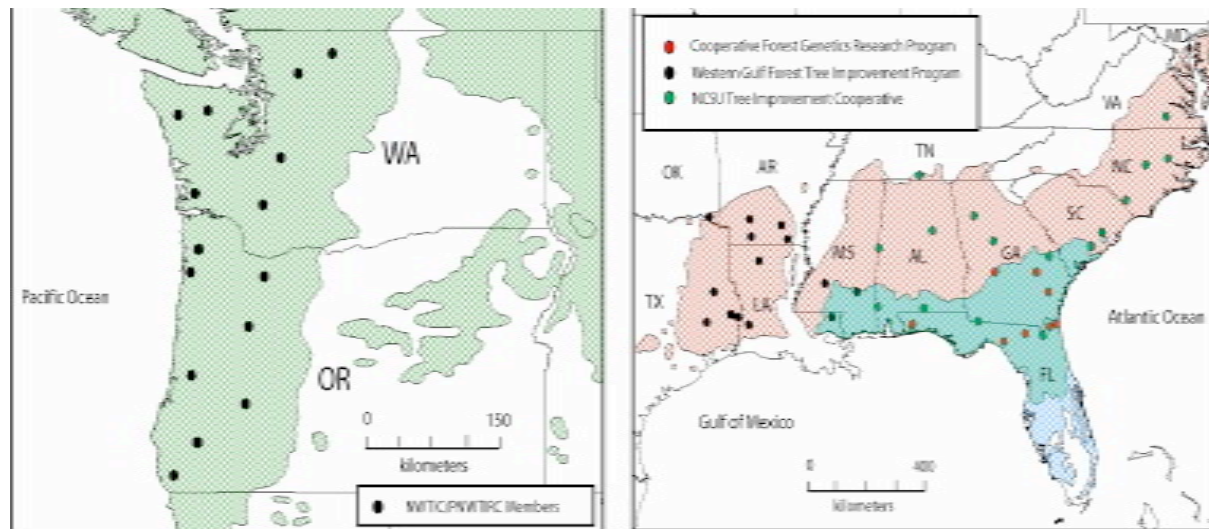


Pinus monticola
(Western White Pine)

CTGN

Tree Improvement Infrastructure

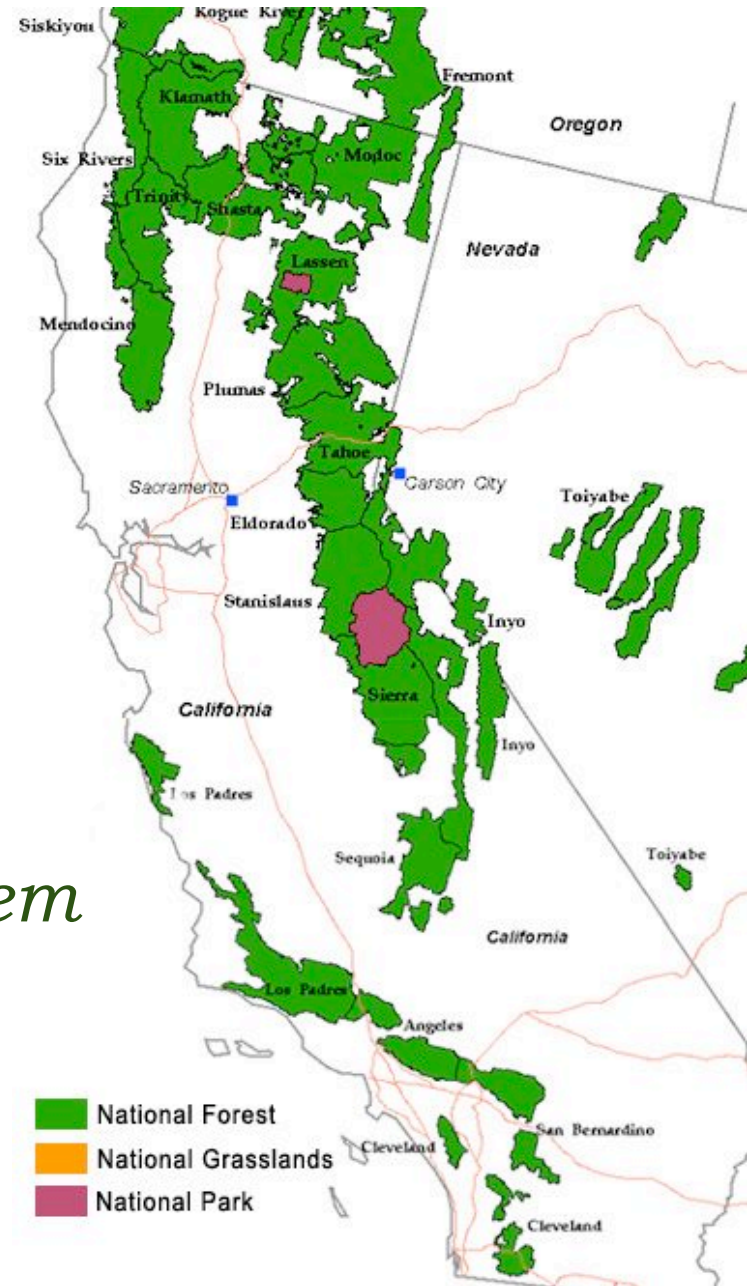
- **Tree Improvement Cooperatives:** Long-term collaborations with public, private, & academic partners
- Distributed ownership & responsibilities
- Goal: to support regeneration activities and decision tools





EGFHN

National Forest System



Progeny Tests

	1 st Gen	2 nd Gen	3 rd Gen	Special	Total	Parents	Progeny ¹
U Florida	628	39	24	156	847	4,030	1,694,000
NCSU	792	1,578	153	100	2,623	6,097	5,246,000
TAMU	1,062	78		213	1,353	4,524	2,706,000
OSU	895	78			973	27,000	1,946,000
Total					5,796	41,651	11,592,000

¹Estimated using an average of 2,000 trees per progeny test planting.

PSW Heritage Plantations (1)

- Cannon (SP), 1984, El Dorado Co., CA
- Fitch-Rantz (SP), 1984, El Dorado Co., CA
- Sundown (SP), 1988, Curry Co., CA
- Burnt Timber (SP), 1988, Josephine Co., OR
- Harrel (SP), 1992, El Dorado Co., CA
- IFG1 (RF,WF), 1976, El Dorado Co., CA
- Iron Mtn. (RF,WF), 1976, El Dorado Co., CA
- Swain Mtn. (RF,WF), 1976, Lassen Co., CA

EGFHN

Long Term Genetic Test Resources



CTGN

In-Kind Support from Coop Members

- Selected populations
- Germplasm
- Breeding orchards
- Test sites
- Database
- Expertise



EGFHN

In-Kind Support from EGFHN Members

- Land Management Expertise
- Basic Forest Biology, Genetics, Ecology, Pathology, Entomology, Silviculture



Marker Breeding of Conifers

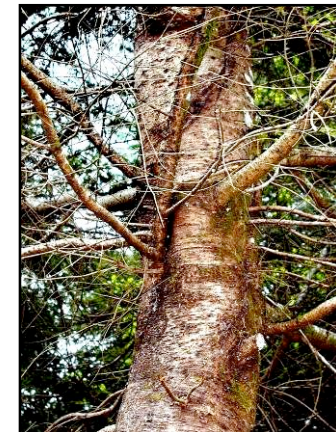
Growth



Adaptability



Straightness



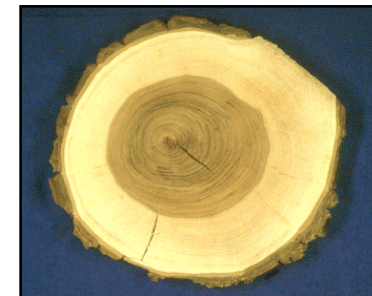
Disease resistance



Insect resistance



Wood quality



Forest Health Diagnostics

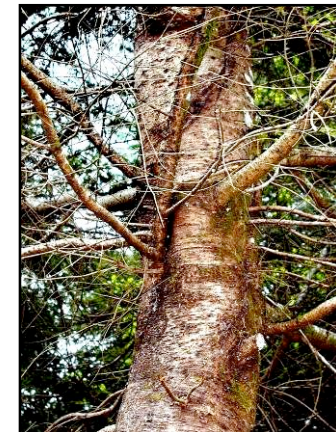
Growth



Adaptability



Straightness



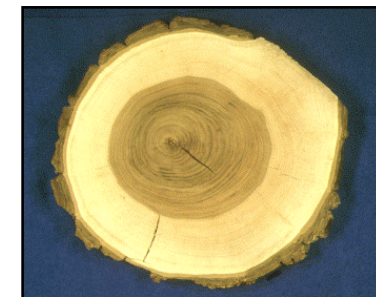
Disease resistance



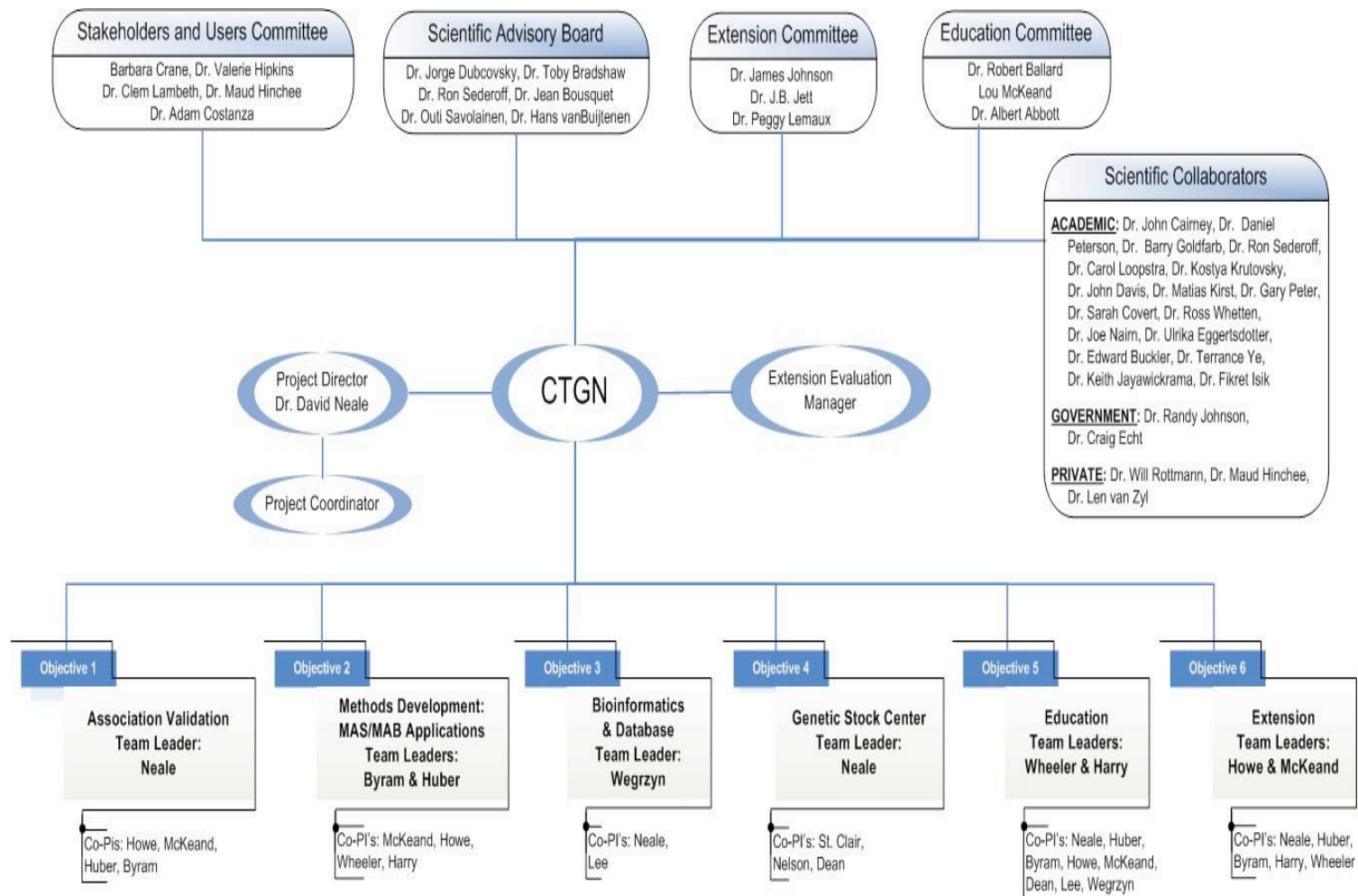
Insect resistance



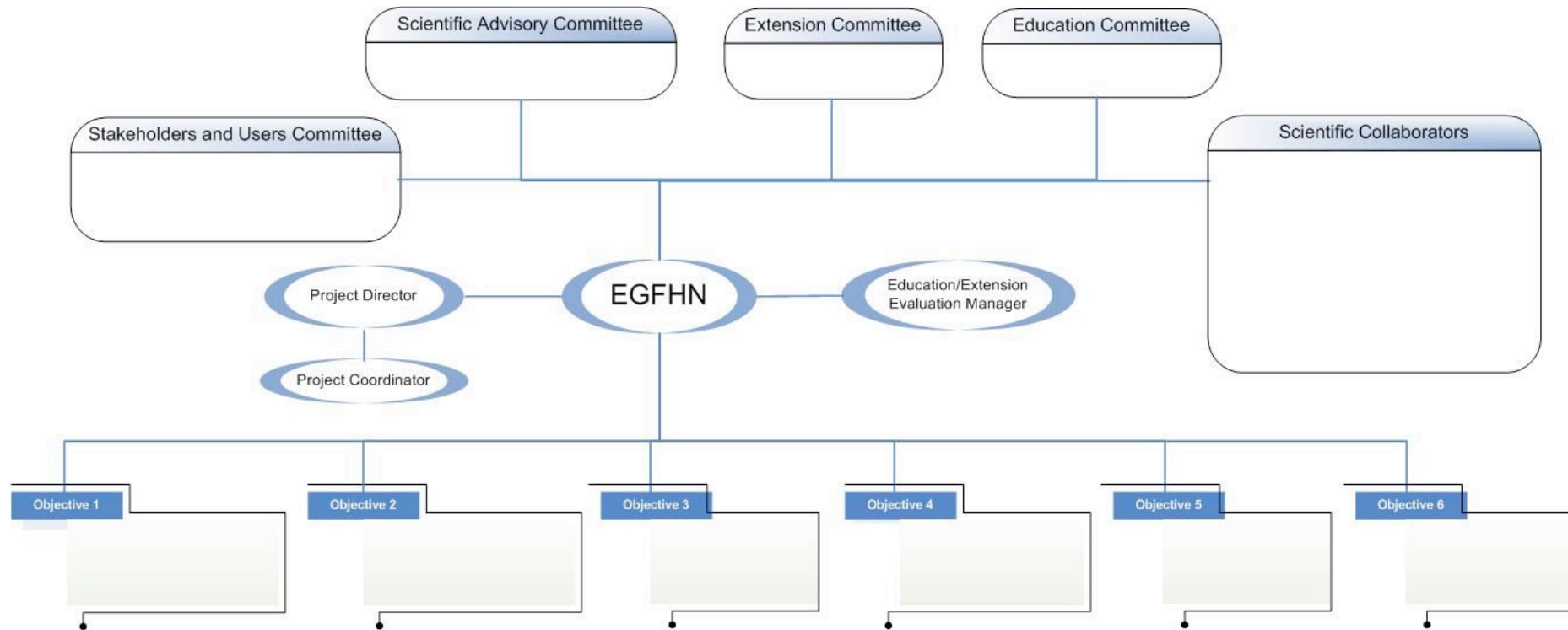
Wood quality



CTGN



EGFHN



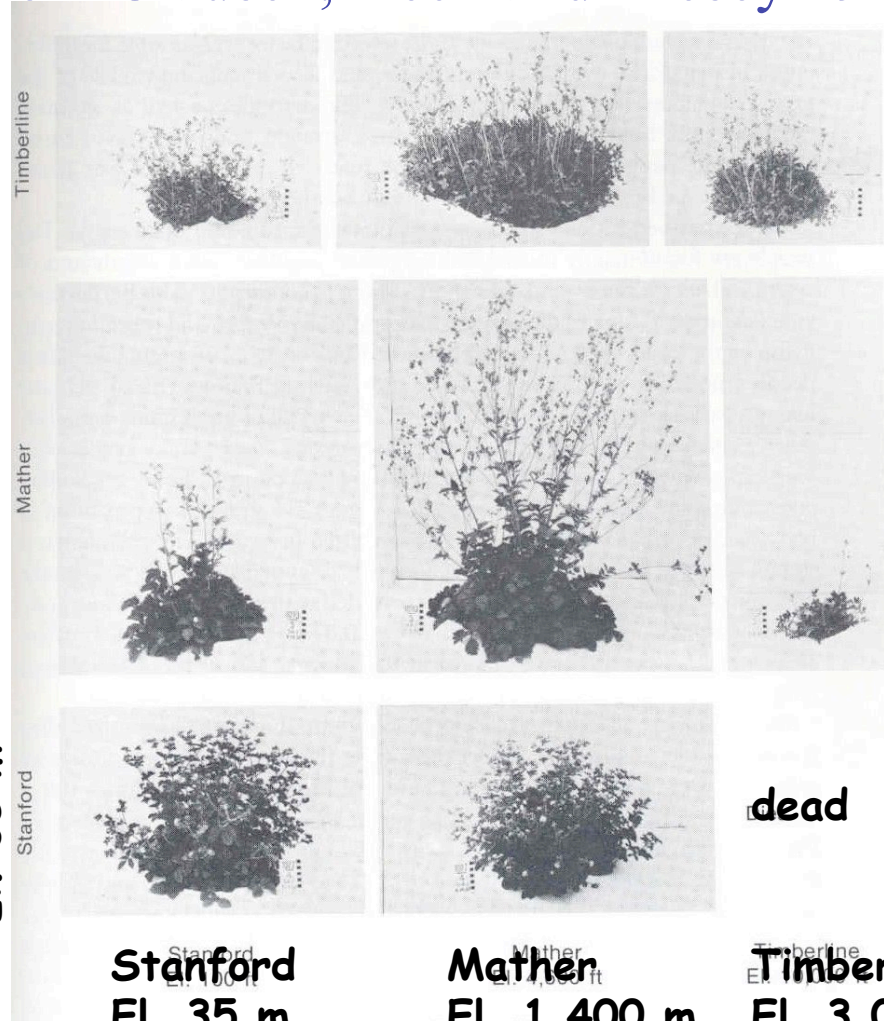
Potentilla glandulosa from three different elevations planted
at three different elevations
(from Clausen, Keck and Hiesey 1940)

Native to

Timberline
El. 3,030 m

Mather
El. 1,400 m

Stanford
El. 35 m



Stanford
El. 35 m

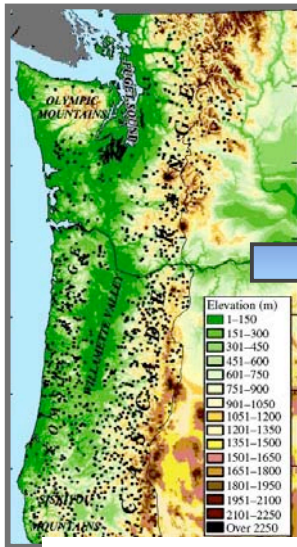
Mather
El. 1,400 m

Timberline
El. 3,030 m

Grown at

Douglas-fir common garden study

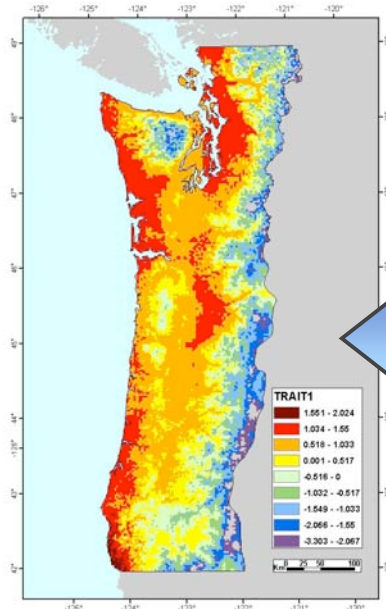
**Collect
seed
from
many
trees**



**Grow families in a
common environment**

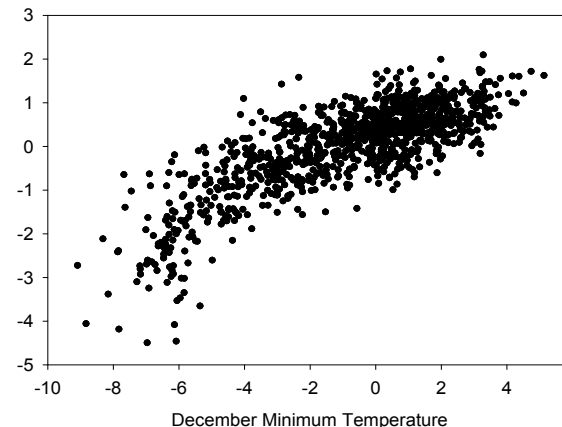


**Measure many
adaptive traits**



GIS

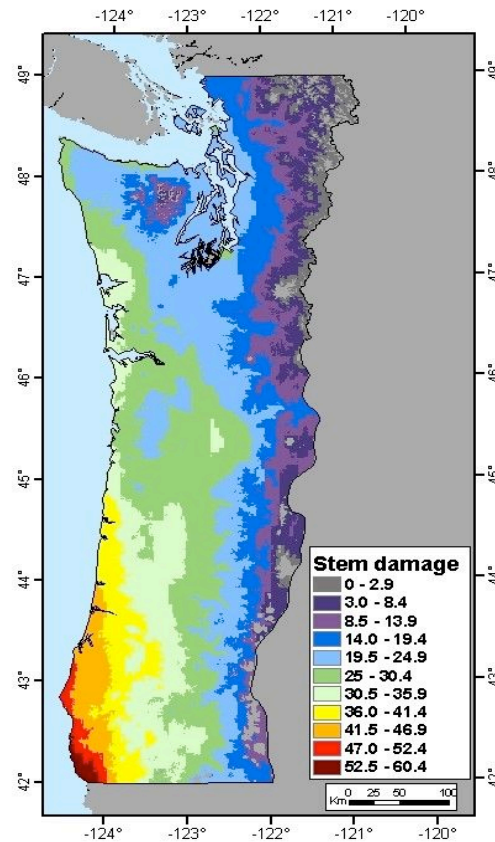
Douglas-Fir of Western OR and WA



**Traits vs
source
environment**

St. Clair, J.B., Mandel, N.L., and Vance-Borland, K.W. 2005. Genecology of Douglas-fir in western Oregon and Washington. *Anal. Bot.* 96:1199-1214.

Fall cold damage



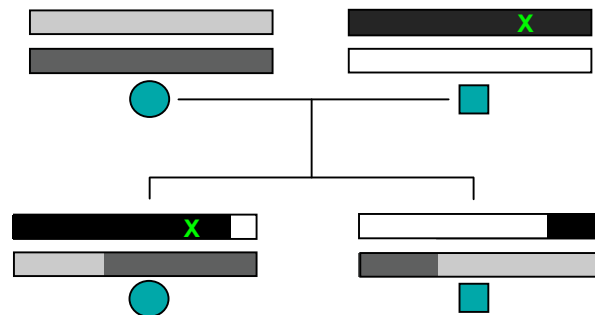
$$r = 0.79$$

$$Q_{st} = 0.68$$

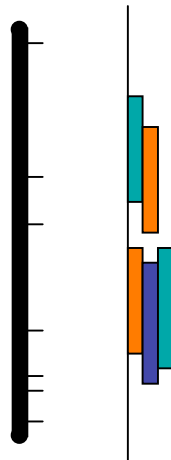
Related to winter temperature, frost dates, latitude, and to a lesser extent elevation and summer aridity.

Linkage *versus* Association

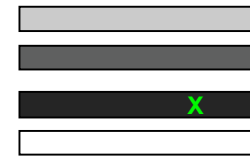
A favourable mutation



LG



Mapping pedigree



several generations



Natural population
(= multiple genetic
backgrounds)

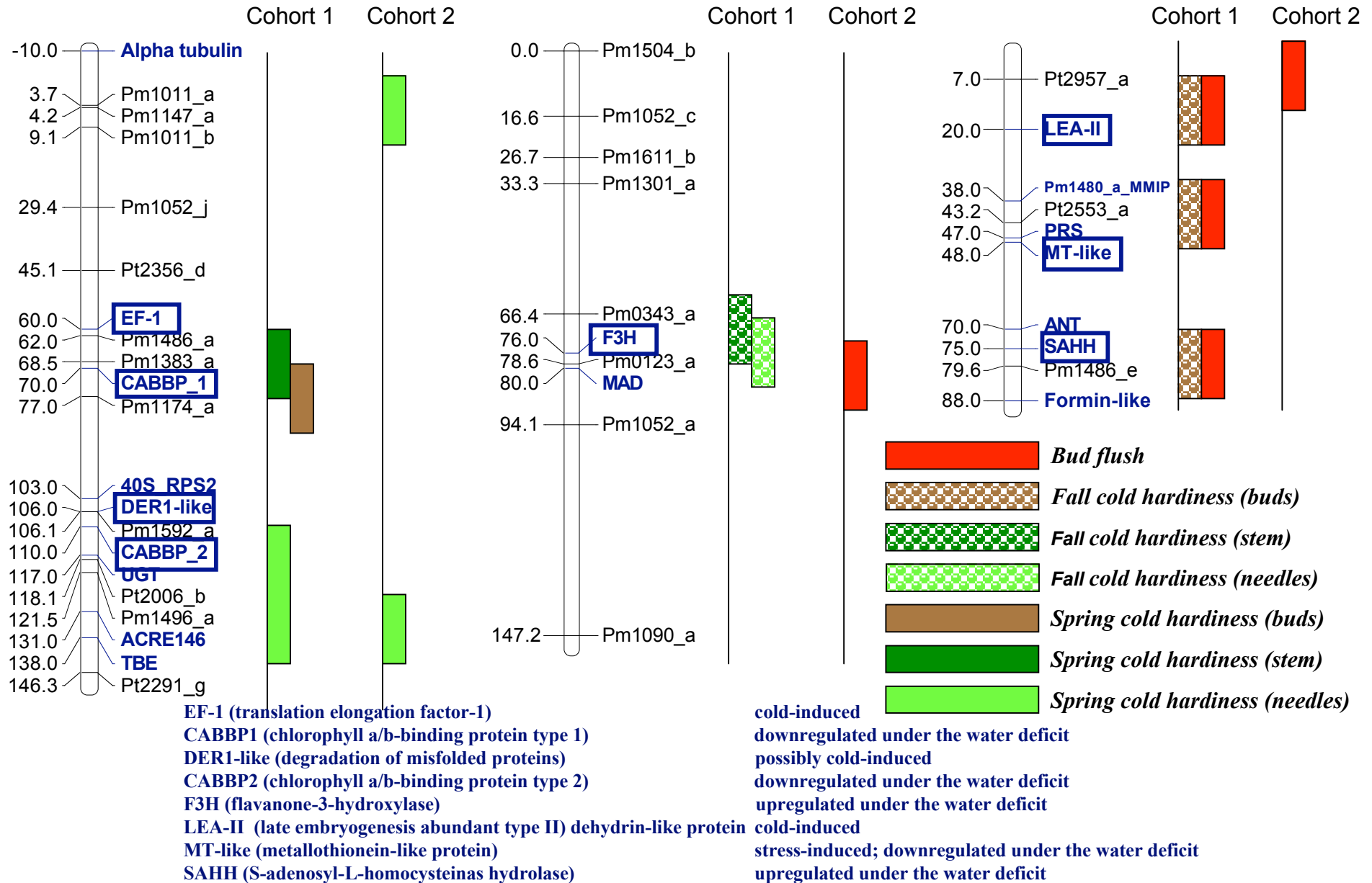
QTL mapping and positional candidate genes

LG1

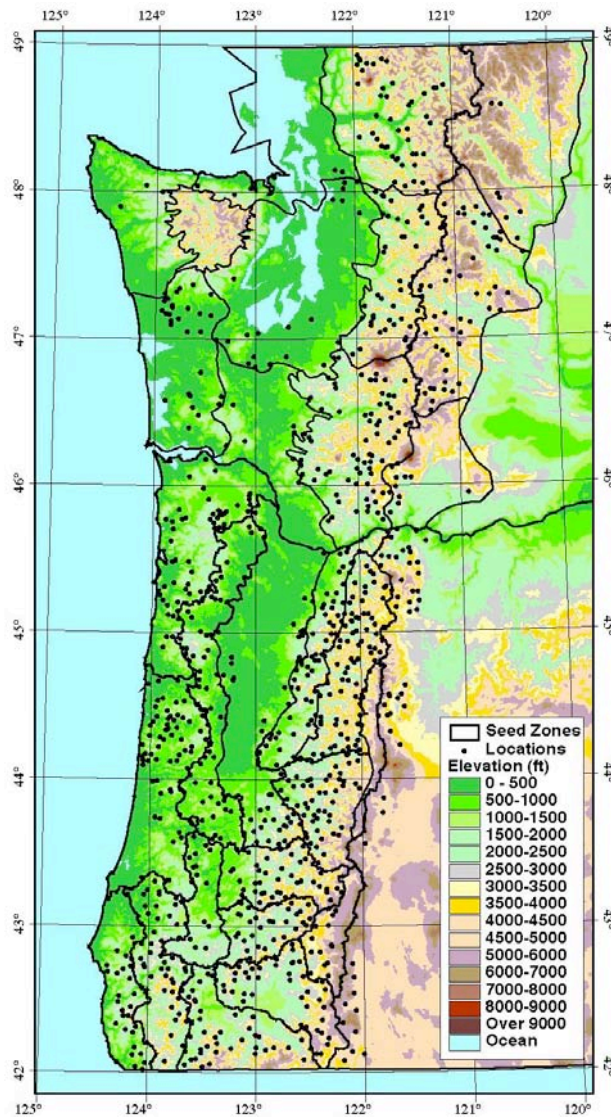
LG2

LG4

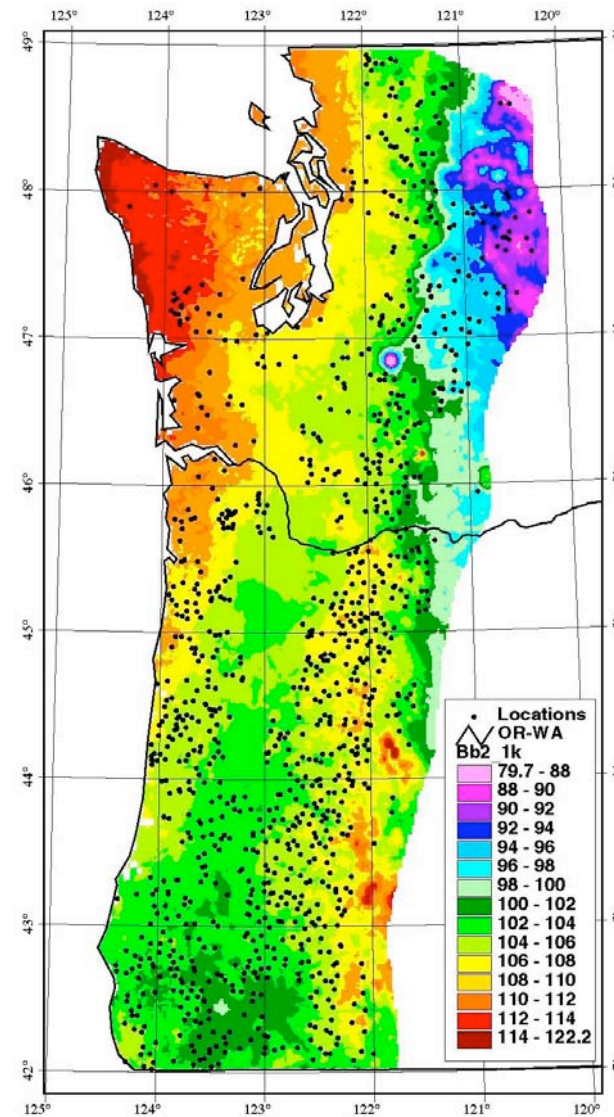
Jermstad et al. 2001a,b, 2003
Wheeler et al. 2004



GIS derived maps of parent trees in the common-garden population

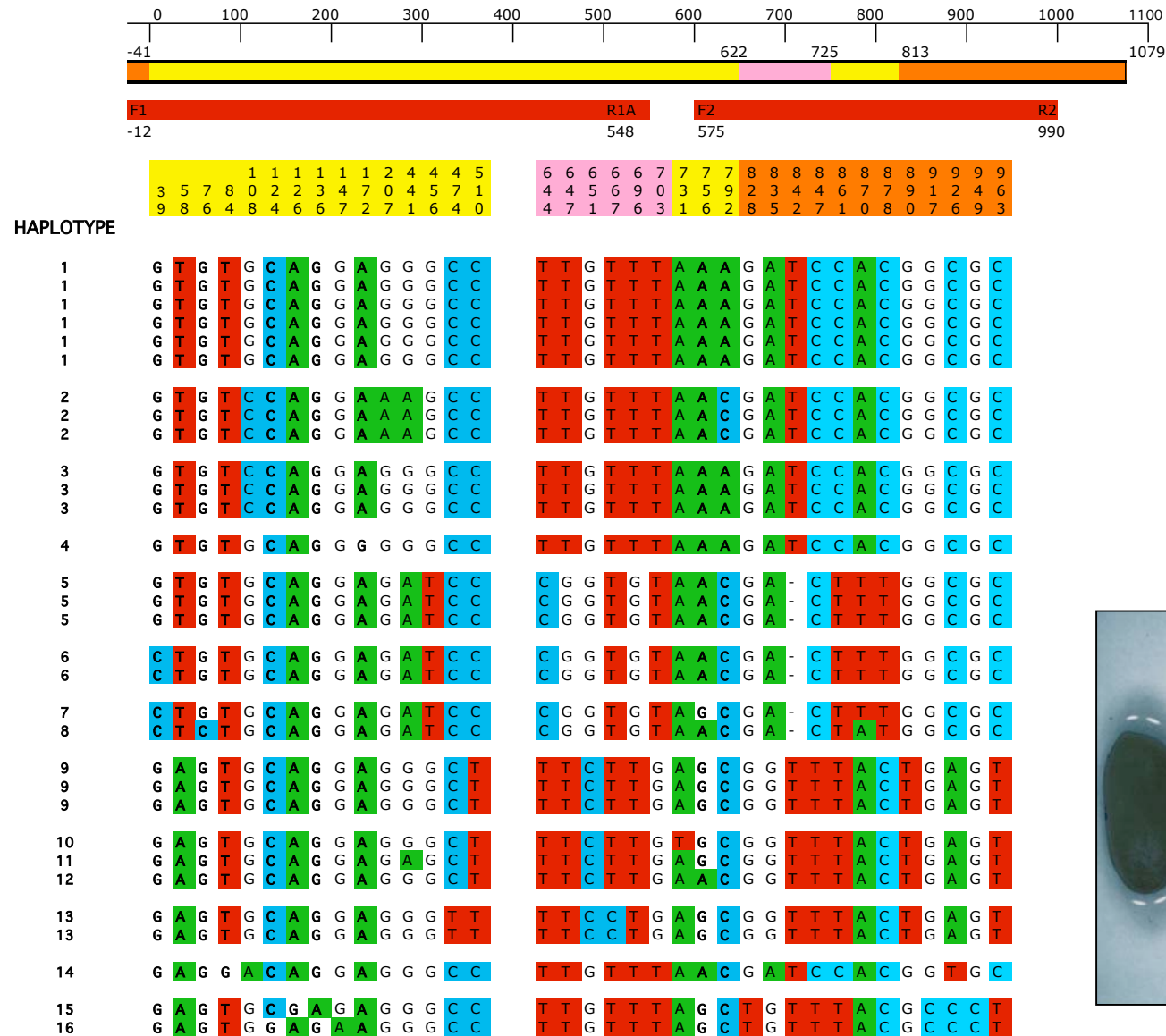


Elevation and seed zones



Julian day for family mean bud flush

Direct determination of haplotypes - AGP6



Diversity at Candidate Genes

104 candidate genes:

5.6 ± 5.3 SNPs per gene (range: 0 - 34)

SNP frequency:

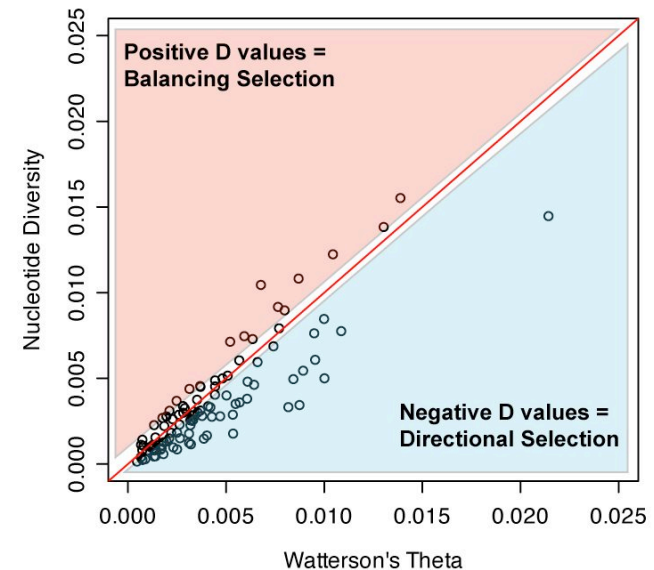
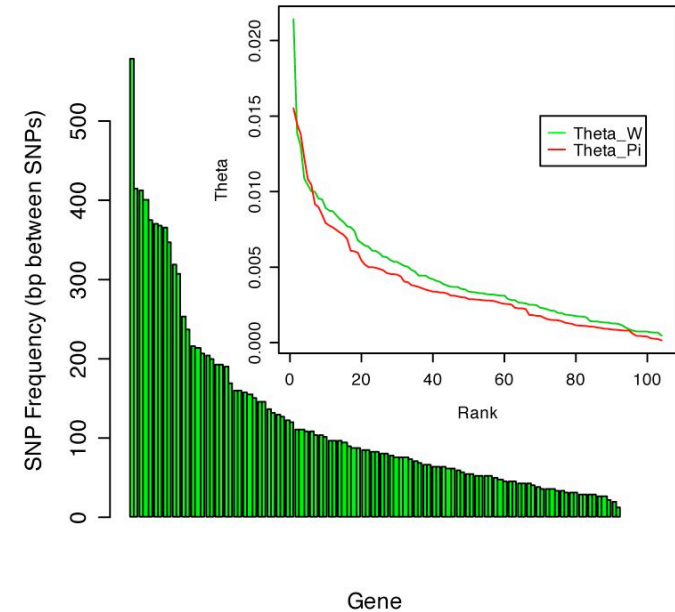
1 in 27 to 1 in 578

Average: 1 in 121

Nucleotide diversity

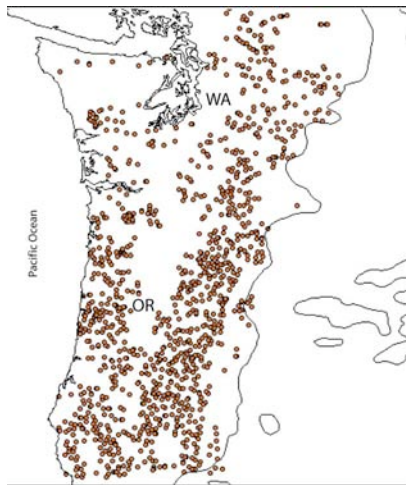
$$\theta_W = 0.00426 \pm 0.00339$$

$$\theta_\pi = 0.00362 \pm 0.00319$$



Douglas-Fir Association Genetics

Association Population:



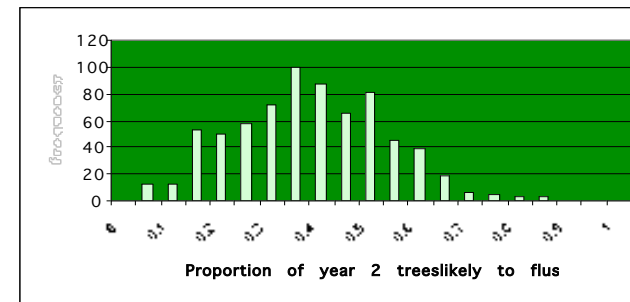
756 individuals

Rangewide in OR and WA

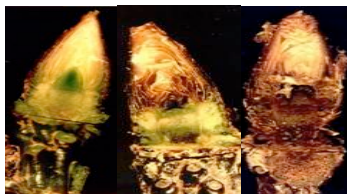
Representative of several phenotypic and environmental gradients



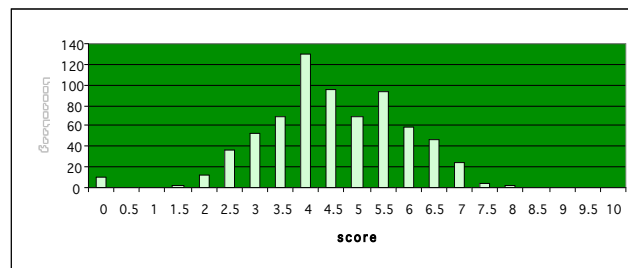
Bud set



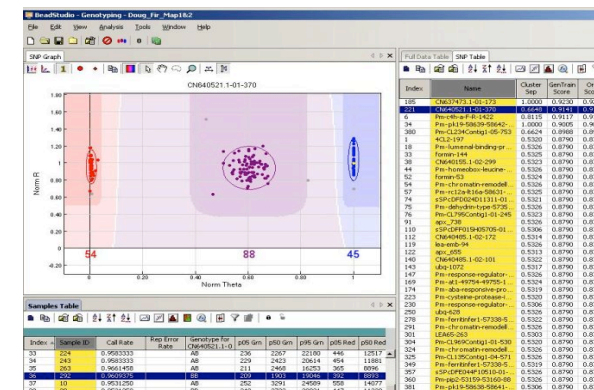
Phenotypes: 21 related to cold acclimation



Bud damage

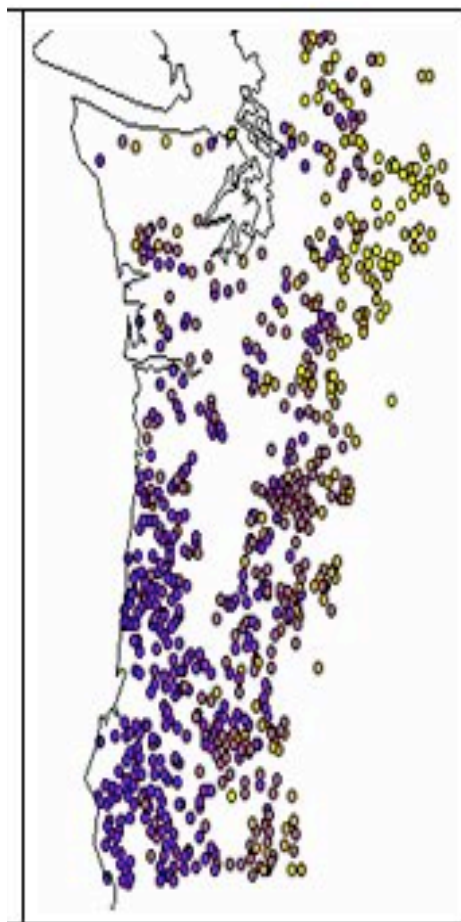


Genotypes: 384 SNPs from 104 candidate genes



Illumina GoldenGate® 384 OPA

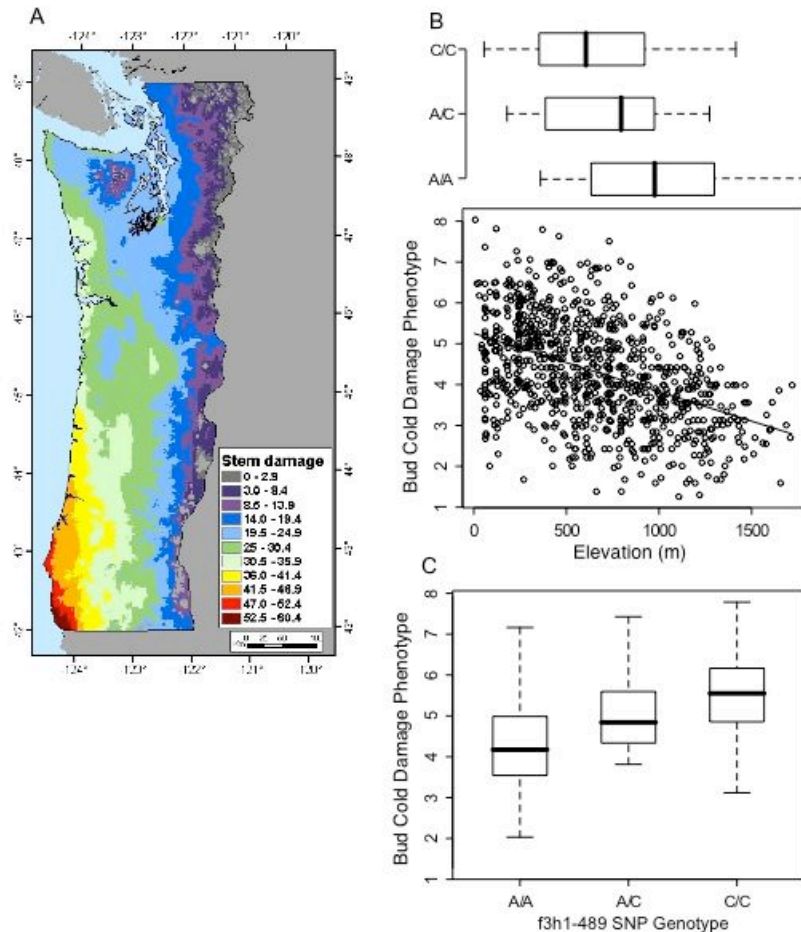
Significant Associations



Geographic variation in bud cold damage phenotype

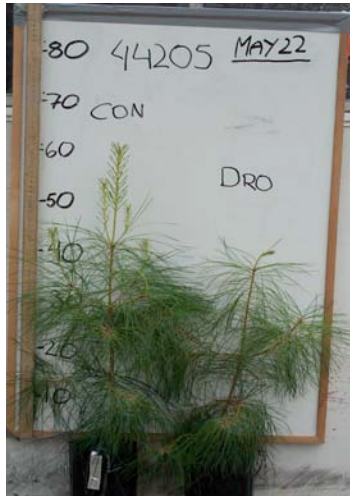
Gene (No. SNPs)	PVE	Traits (No. Traits)
Cyclosporin (1)	0.20-5.48	Bud cold (13)
Helicase (1)	0.09-5.40	Bud cold (7)
Cysteine protease (1)	0.15-3.04	Bud cold (4)
4cl (1)	0.12-2.40	Shoot weight (3)
Ca-dependent protein kinase (2)	1.54-1.65	Bud cold (1)
Heme-binding protein (1)	2.05	Bud cold (1)
Lumenal binding protein (1)	0.30	Bud set (1)
LRR receptor protein kinase (1)	1.51	Bud cold (1)
f3h (1)	0.94	Total weight (1)

Genotype-Phenotype Associations along Environmental Gradients



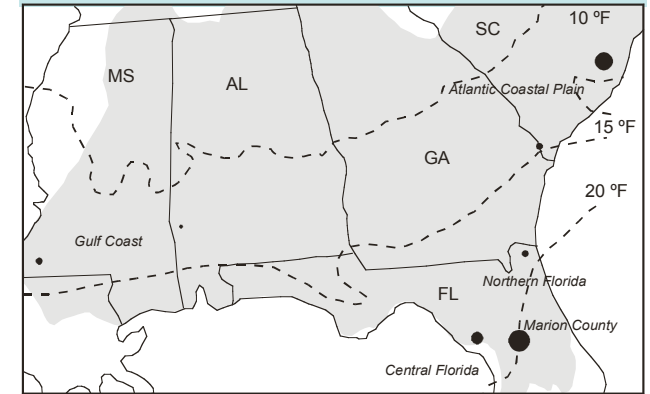
“Even apparently similar adaptations may be built from genetically different components.”

T. Dobzhansky (1960)



Partial diallel, 15-24 offspring from 61 families. Association with CID (Carbon Isotope Discrimination, related to Water Use Efficiency, in two sites: Cuthbert and Palatka). Analyses using the *Quantitative Transmission Disequilibrium Test (QTDT)*

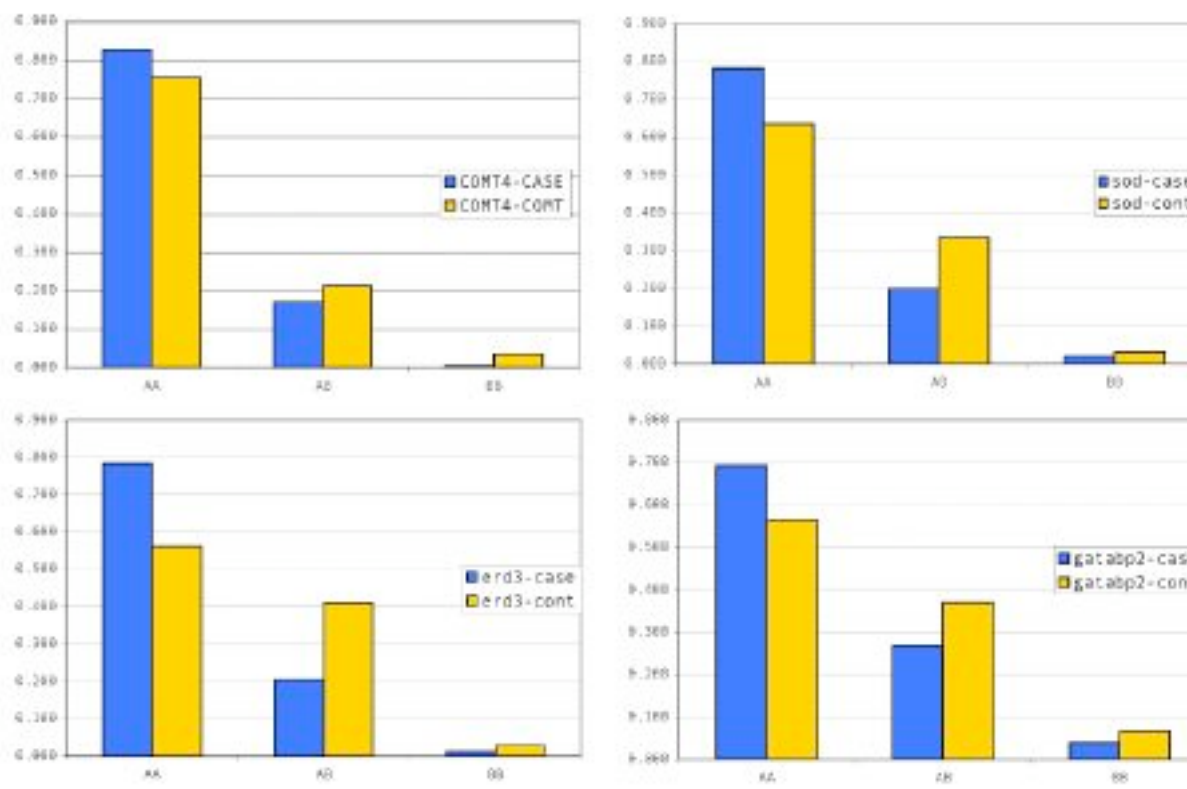
FBRC association population in loblolly pine



SNP	Gene	Cuthbert			Palatka		
		MAF	Within - family ¹	Total	MAF	Within - family ¹	Total
Q1	<i>Dehydrin 1</i>	0.26	0.003	0.04 0	0.27	ns	ns
C13	<i>Putative cell wall protein, similar to lp5 in Pinus taeda</i>	0.11	ns	ns	0.11	0.015	0.018
S9	<i>Cu/Zn superoxide dismutase, nuclear gene for chloroplast product</i>	0.16	0.087	PS	0.16	0.049	0.08 6
C22	<i>wrky-like transcription factor</i>	0.46	0.035	0.05 5	0.47	ns	ns

¹ *P*-values computed by permutation (1000 permutations)

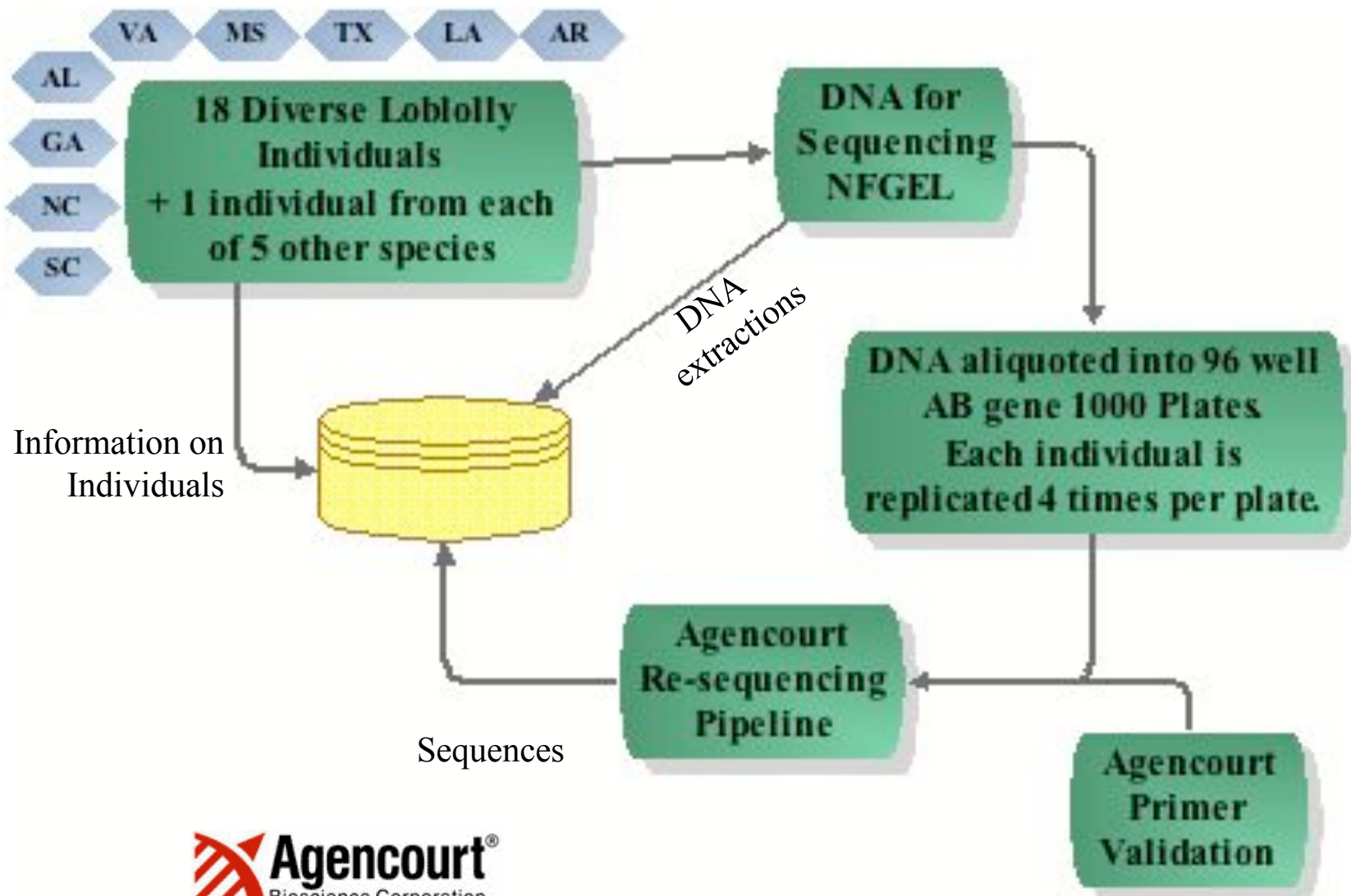
Fusiform Rust Allelic Frequency Distributions between Case(Gall+) and Control(Gall-) Groups



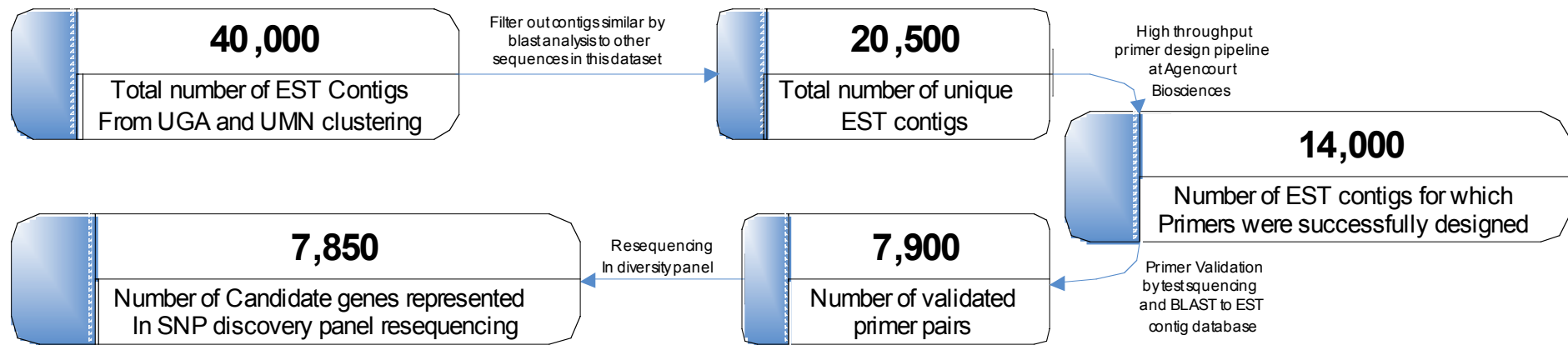
Locus	Case			Control			P	ODDS-RATIO	STD.ERR.	CI%95
	AA	AB	BB	AA	AB	BB				
COMT4	257	53	1	330	93	15	1.32×10^{-3}	10.993	1.050	9.943-12.043
erd3	250	65	4	271	198	14	3.72×10^{-10} ***	2.834	0.591	2.243-3.426
gatabp2	214	83	12	274	179	32	1.17×10^{-3} *	1.748	0.375	1.373-2.123
SOD-CHL	239	61	6	300	158	15	6.40×10^{-5} **	1.638	0.513	1.124-2.151

Bonferroni significance level *=0.05, **=0.01, ***=0.001

Re-sequencing 10K Genes



ADEPT2 Resequencing Status



7.5 SNPs/amplicon (based on ~2,200 amplicons) x 7,850 amplicons =

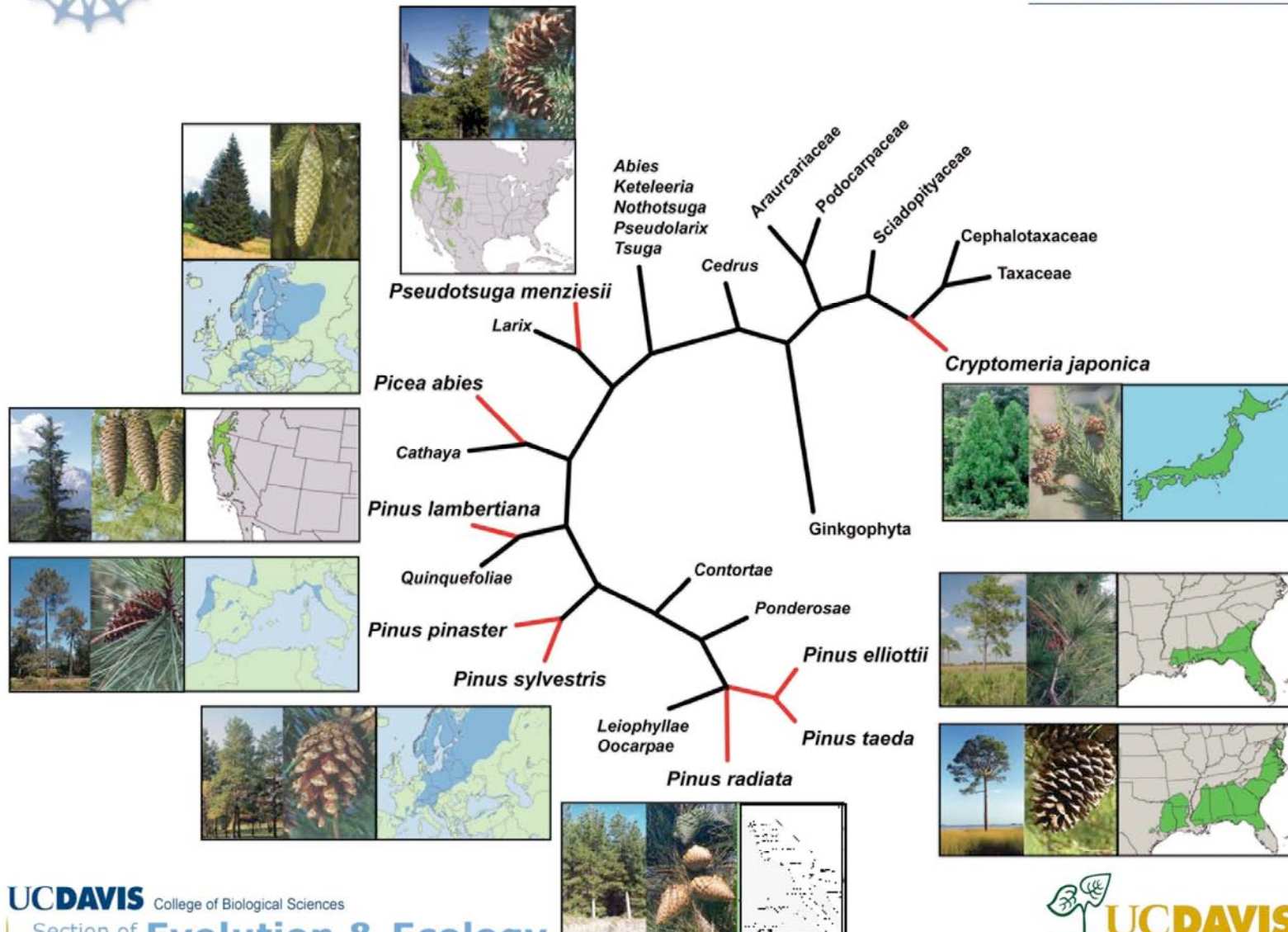
~ 40,000 SNPs



Comparative Re-Sequencing in the Pinaceae

<http://dendrome.ucdavis.edu/crsp/>

UC DAVIS
UNIVERSITY OF CALIFORNIA



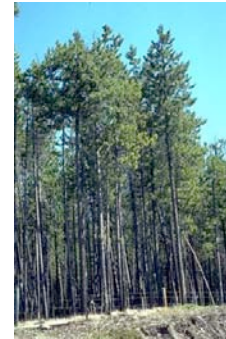
EGFHN

SNP Discovery Projects Currently Underway

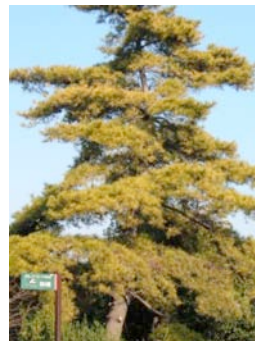
Coast redwood – Save the Redwoods League



Lodgepole pine – CSUS/UCD



California whites pines – ADEPT2/NSF



European pines – EU consortium



Black cottonwood – Chevron



Trentino Italy conifers – ACE/SAP

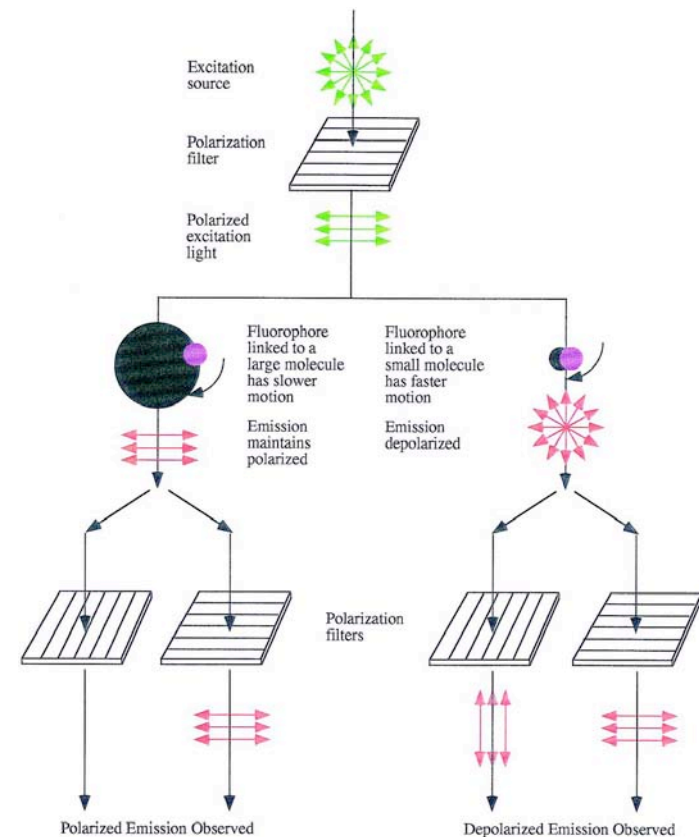


Island Radiata Pine - Csiro

Populus nigra – USDA/Greenwood Resources



Fluorescence Polarization with Terminator-Dye Incorporation (FP-TDI) - a method for SNP detection



DNA Technologies Core Facility

The mission of the DNA Technologies Core at the UC Davis Genome Center is to provide DNA analytical services to campus and other researchers. We are currently focused on single nucleotide polymorphism (SNP) genotyping. Our goal is to enable access to high throughput, genome-wide analyses at economical recharge rates, as a functional extension of your laboratory. The services offered by the Genome Center complement other UC Davis facilities in order to provide access to numerous technologies for molecular marker analysis.

UC Davis Genome Center

DNA
TECHNOLOGIES
CORE



Facility Services

Illumina Golden Gate SNP Genotyping

Luminex SNP Genotyping

DNA Quantification

PCR

Coming Soon! BeadXpress Genotyping & Ultra High Throughput Sequencing

Equipment & training

Analyst Plate Reader

Robotic Liquid Handlers

Find out more about getting trained

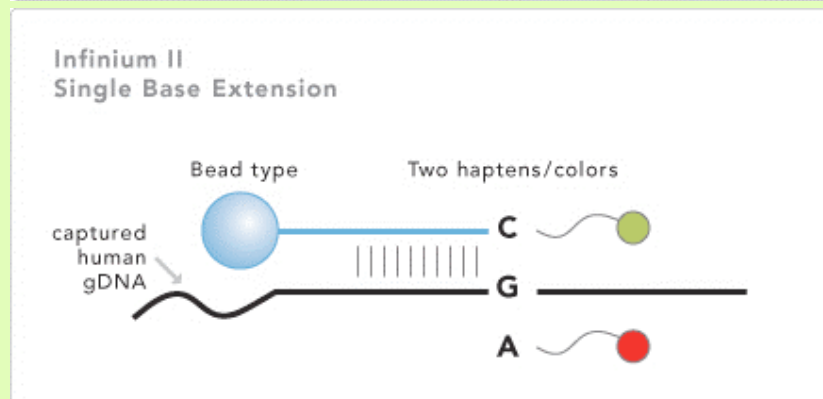
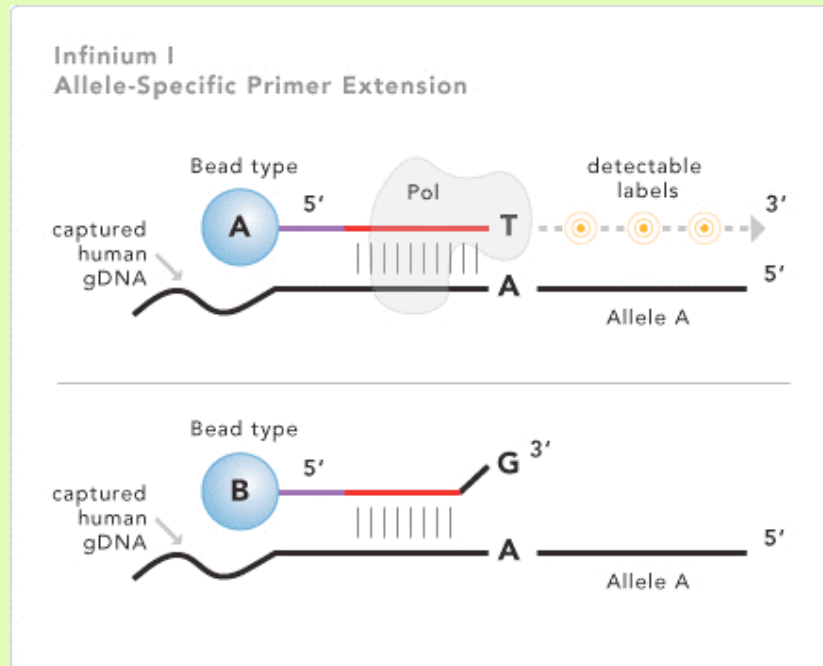
Illumina- BeadStation500G-BeadLab Platform



~150,000 data points per week at UCD Genome Center

Infinium Assay from Illumina

How it Works:



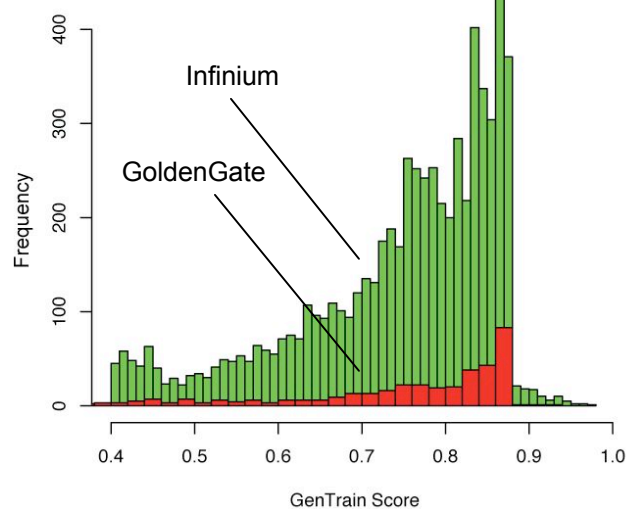
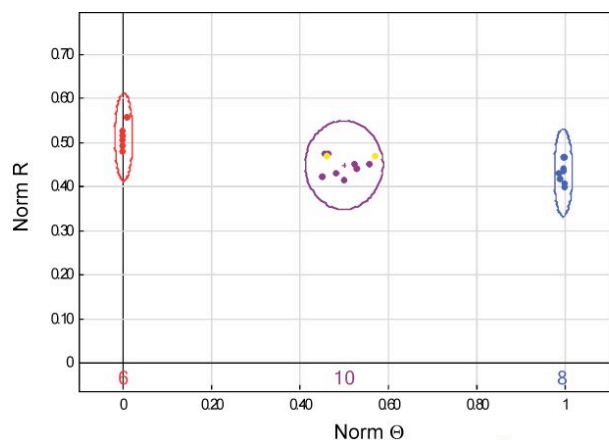
Specifics:

1. 7,600 to 60,000 bead types for 12 samples at a time
2. Moderate to high conversion from other assays (e.g., Golden Gate)
3. Available to non-model organisms (coming soon)

From: <http://www.illumina.com/home.ilmn>

CTGN

Infinium Pilot Study - Results



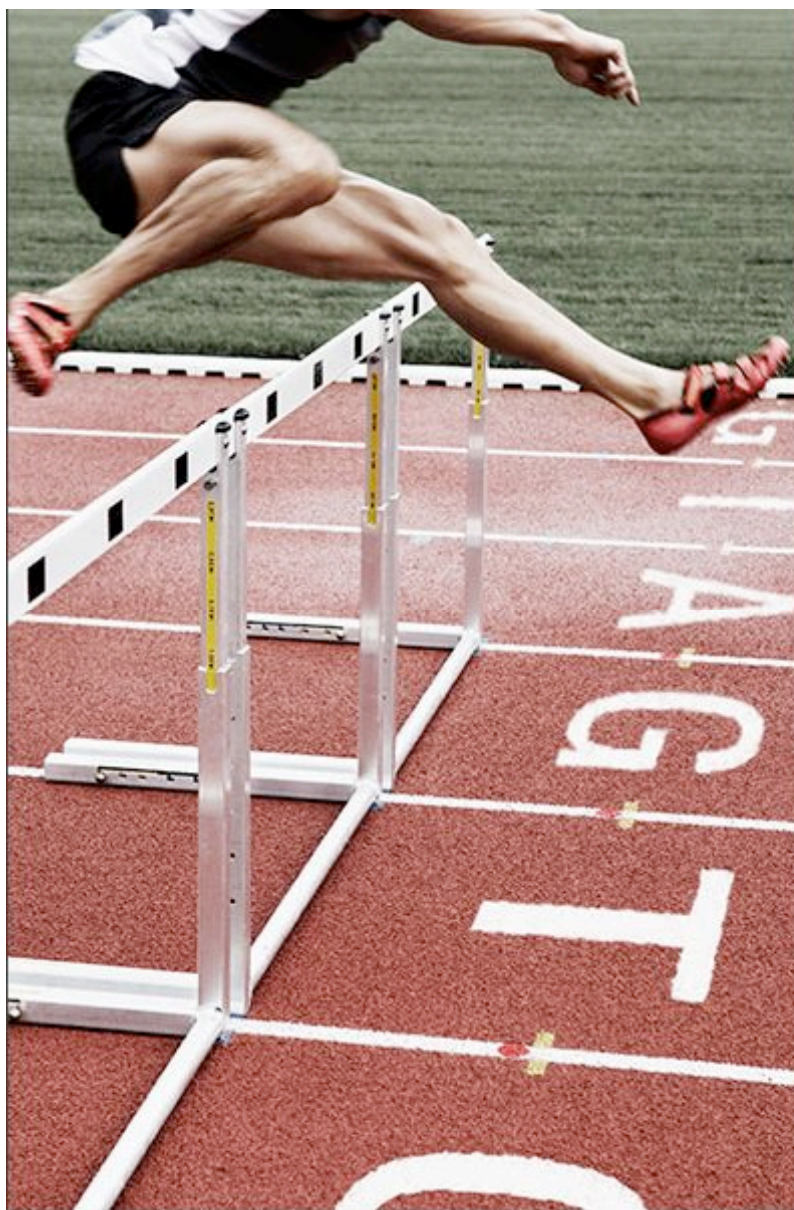
Out of the 7,600 SNPs queried:

~6500 SNPs produced data conducive to calling genotypes

Of those ~6500 SNPs, ~750 were difficult to cluster or at odds with heritability information

Of the remaining 5750 SNPs, ~4000 were monomorphic

This gives an overall conversion rate of 75% of which 30% were segregating within a single pedigree.



PACIFIC
BIOSCIENCES™

Search



Register for More Information

[ABOUT US](#)

[TECHNOLOGY](#)

[APPLICATIONS](#)

[NEWS & EVENTS](#)

[CAREERS](#)

[CONTACT US](#)

Ready to leap...

A **groundbreaking** DNA sequencing technology is going to redefine the field. Single molecule real time.

Pacific Biosciences is a bold company developing a transformative DNA sequencing platform. Our breakthrough single molecule, real time (SMRT™) technology delivers the ultimate combination of long reads, low costs, and fast cycle times. A new paradigm for whole genome analysis is about to emerge.

NEWS

- >> Pacific Biosciences Preparing the 15-Minute Genome by 2013
- >> California Company Claims Faster, Cheaper Gene Map

EVENTS

- >> PacBio presents SMRT™ DNA Sequencing Technology at AGBT Conference

SMRT™ TECHNOLOGY



View Our
4:05 minute
Technology
Demo

[SITE MAP](#) | [PRIVACY POLICY](#) | [TERMS OF USE](#)

©2008 Pacific Biosciences, Inc. All rights reserved.

XTRACTOR

X-tractor GeneTM

automated nucleic acid extraction



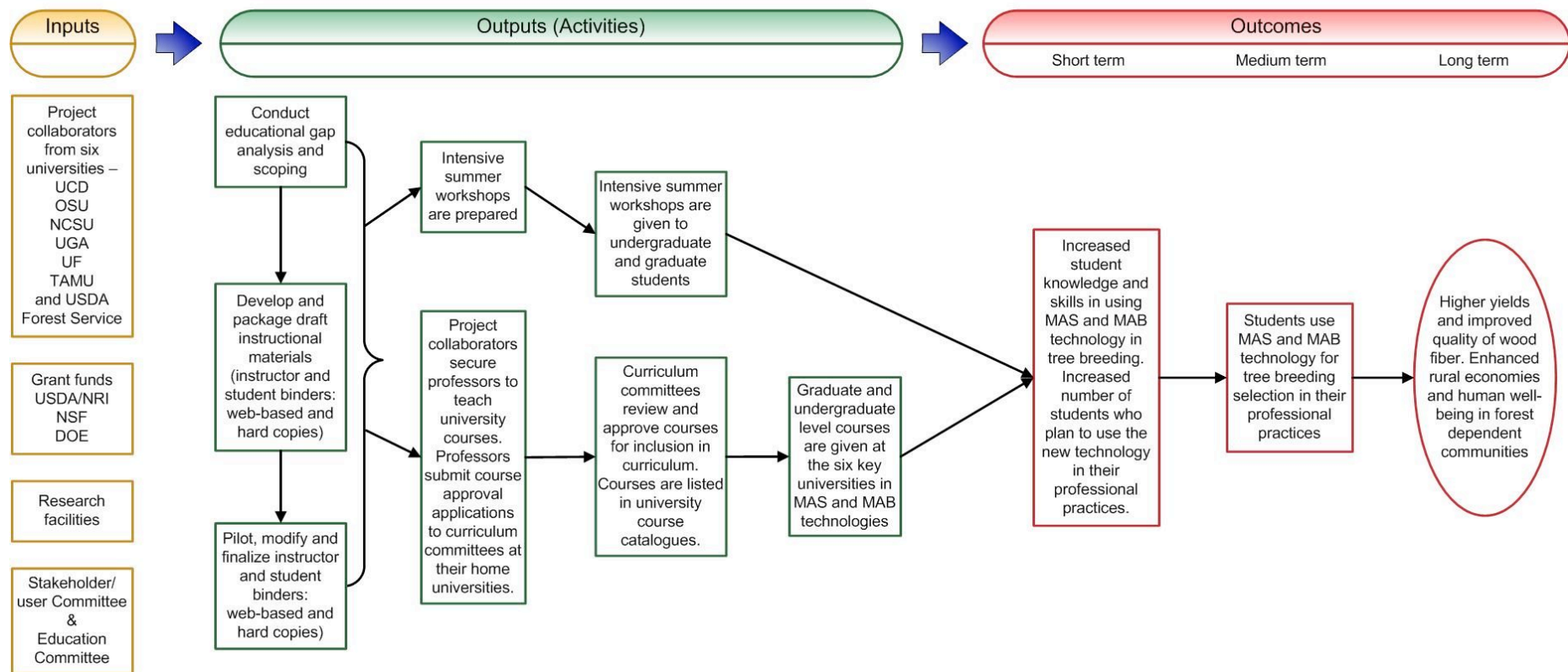
simple affordable complete

CTGN: Educational Activities



Team Leaders:
Dave Harry
Nick Wheeler

Education Logic Model

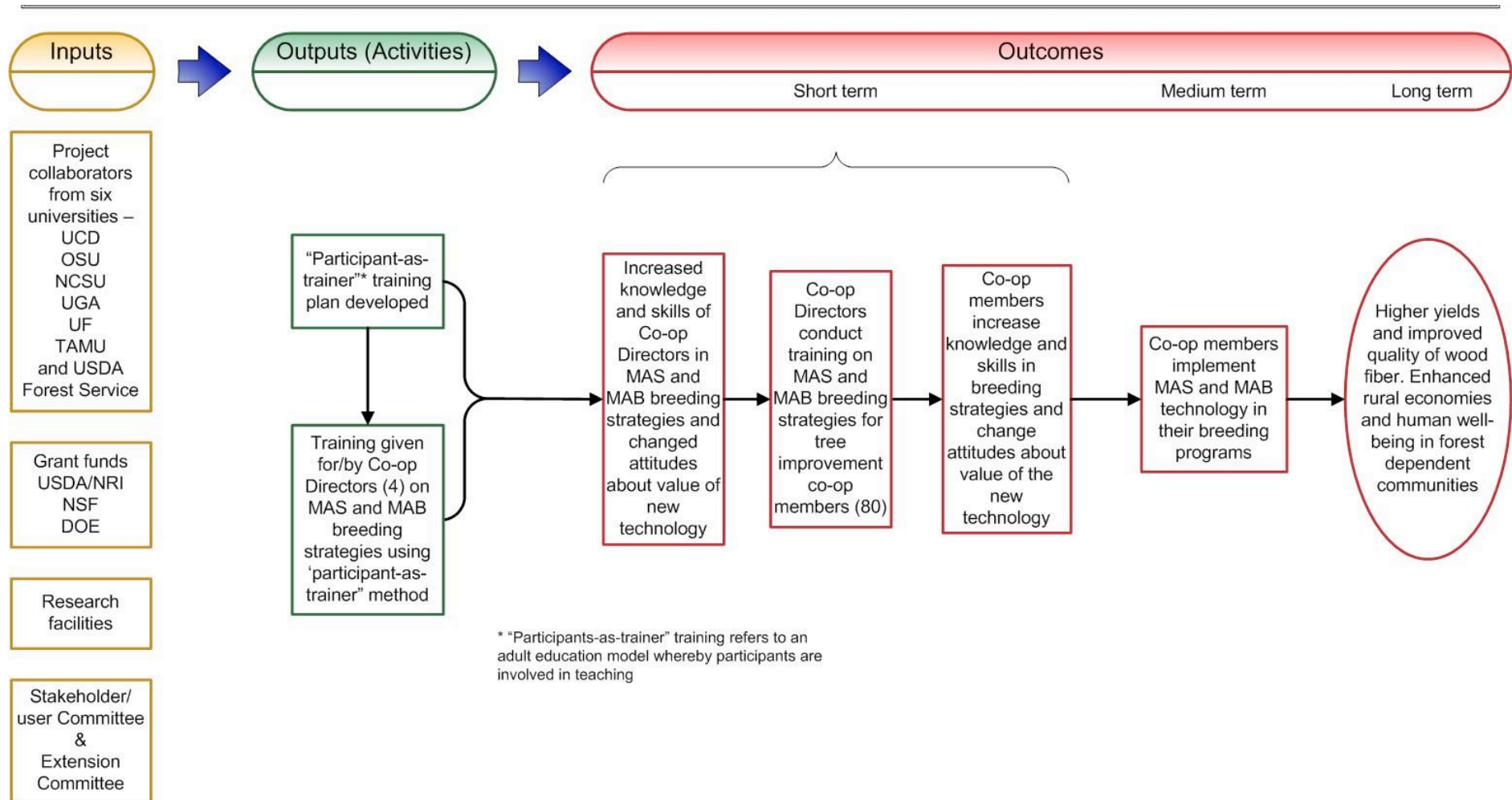


CTGN: Extension Objective 6

*Mission and Activities
Team Leaders: Wheeler and Harry*



Extension Logic Model





EGFHN

Ecosystem Genomics and Forest Health Network



Ecosystem Genomics and Forest Health Network:

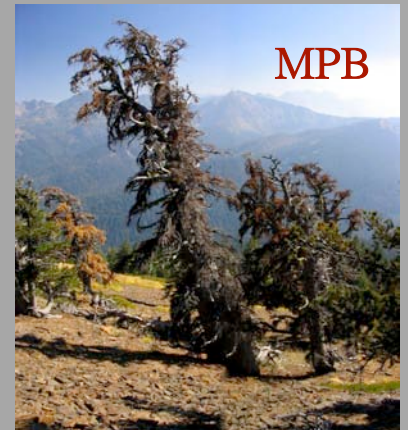
*A Case Study for an
Integrative Ecological
and Genomic Approach to
Address Forest
Ecosystem Health*

Natural and Anthropogenic Threats to High Elevation White Pine Ecosystems in California

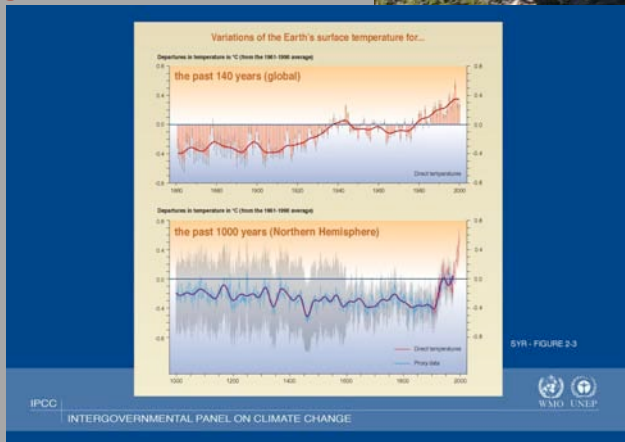
WPBR



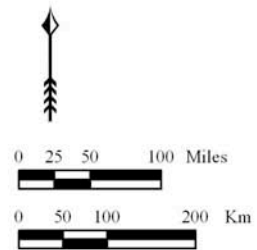
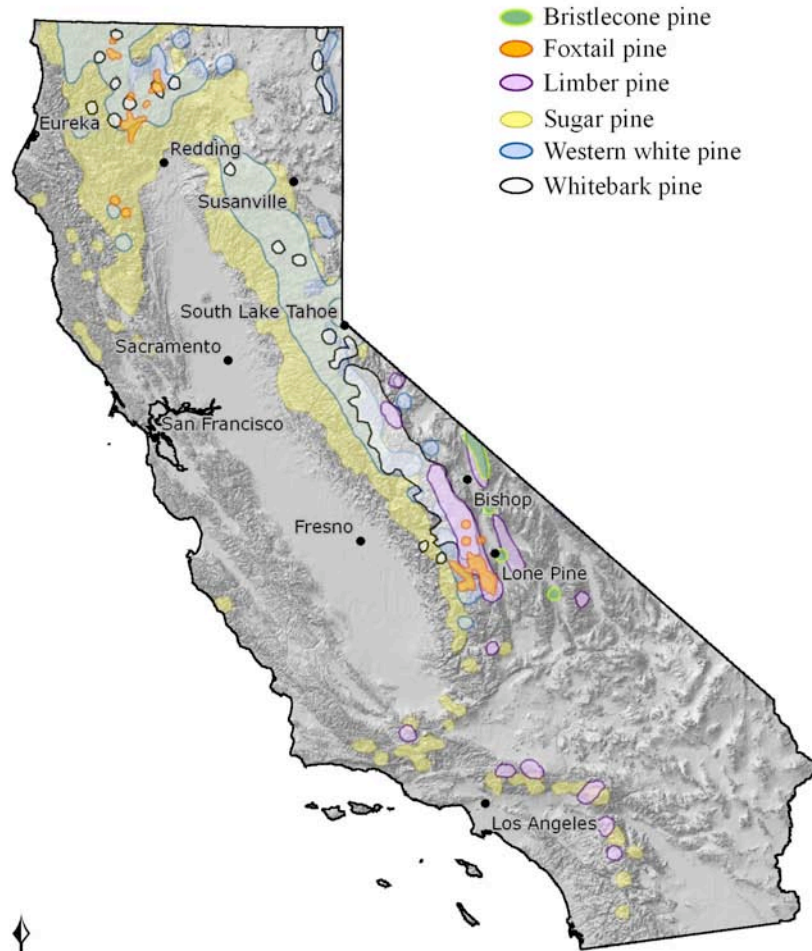
MPB



CLIMATE

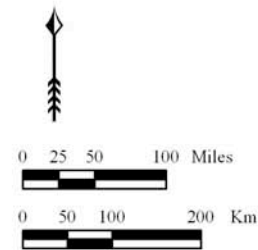
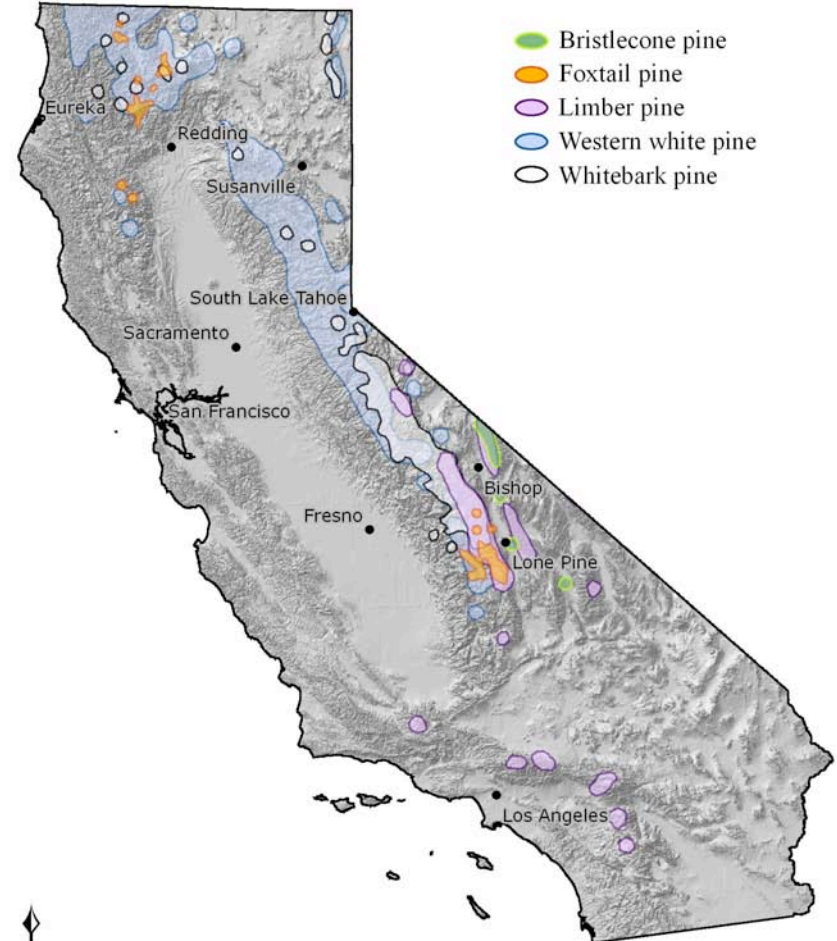


Geographic distribution of 5-needle pines in California



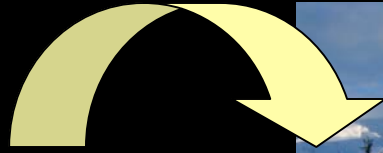
Source:
U.S. Geological Survey,
1999, Digital representation of
"Atlas of United States Trees"
by Elbert L. Little, Jr.

Geographic distribution of high elevation 5-needle pines in California



Source:
U.S. Geological Survey,
1999, Digital representation of
"Atlas of United States Trees"
by Elbert L. Little, Jr.

Hydrologic functions/
Watershed protection



Biological diversity



Photo: Deems Burton

Wildlife habitat



Photo by A. Wilson

Important food resource

I. Distribution of white pine blister rust in high elevation forests.

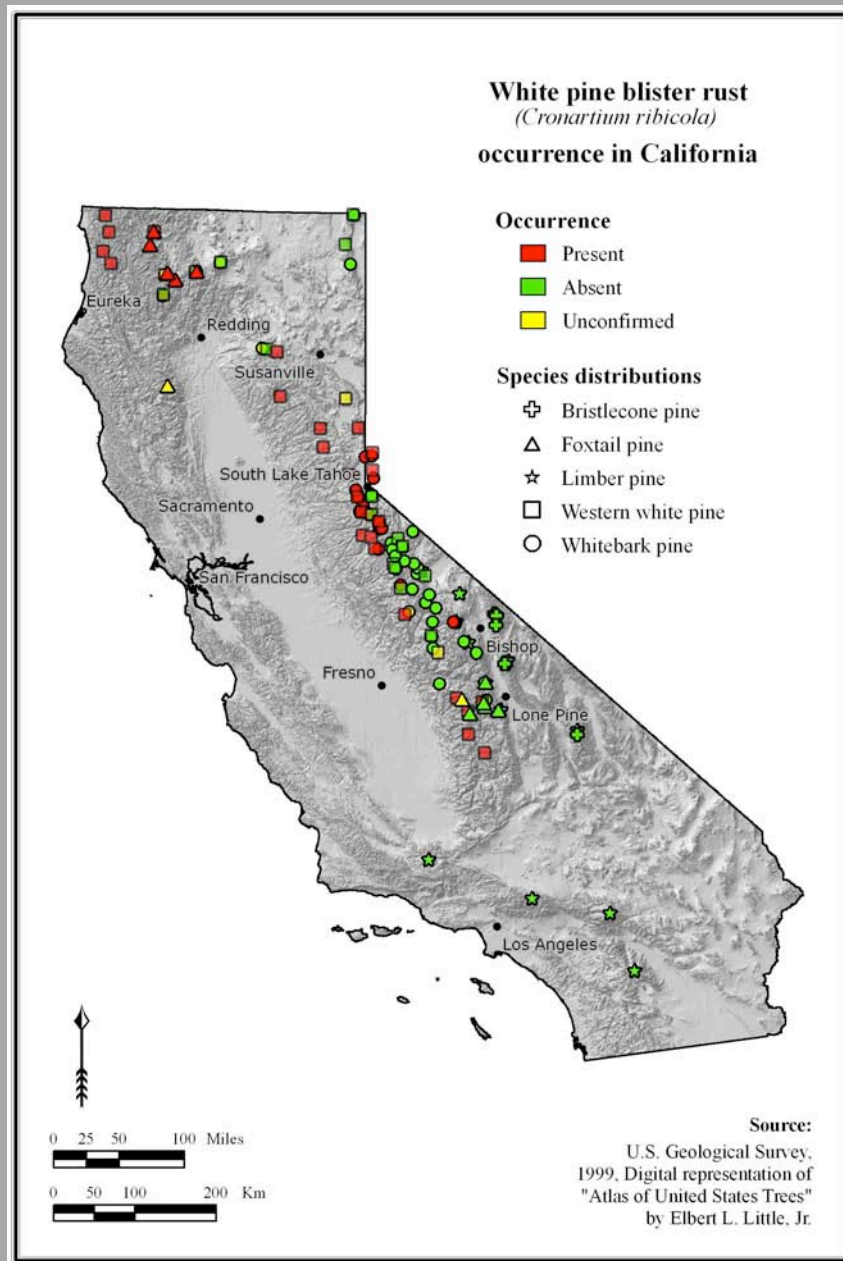


Photo: Det Vogler



Photo: Det Vogler



I. WPBR: Demographic effects

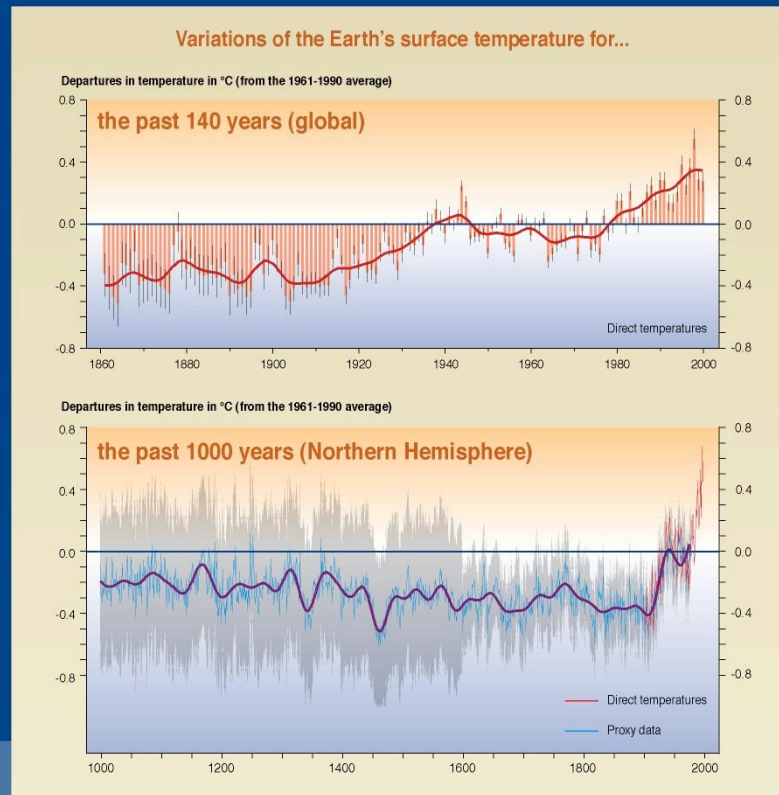
- Juvenile mortality
- Reduced fecundity
- Lower recruitment
- Reducing dispersal and establishment potential



X

X

Climate



SYR - FIGURE 2-3

Range shifts and forest tree responses.

III. Climate-driven outbreaks of native insects - MPB



- MPB preferentially attacks drought-stressed trees.
- In high elevation forests we see evidence of MPB and mortality but at low levels and often associated with protracted drought periods. Some exceptions.
- Lack continuous and extensive LPP/WP forests for large outbreaks to occur.



Photo: Sheri Smith

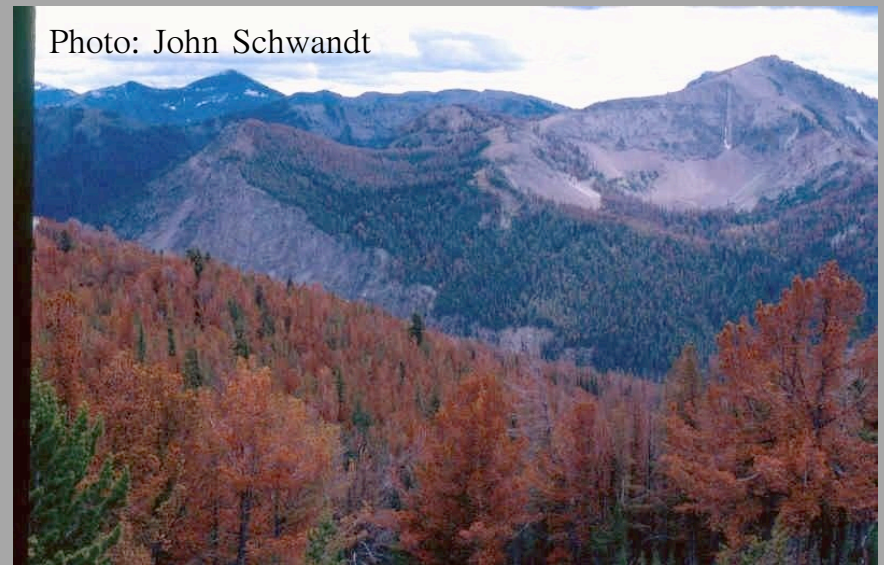


Photo: John Schwandt

THREE IMPORTANT TRAITS FOR PRESENT AND FUTURE BIOTIC AND ABIOTIC CONDITIONS

- DISEASE RESISTANCE
- PHENOLOGY
- WATER-USE EFFICIENCY

GENETIC BASIS OF DISEASE RESISTANCE

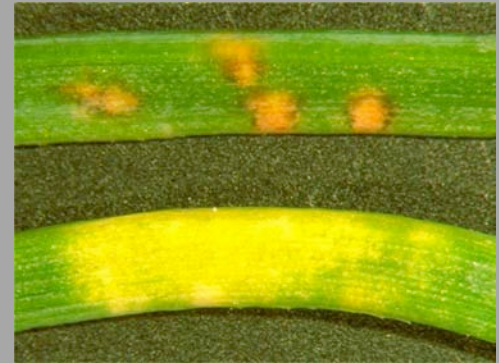


- Active Resistance - Interaction between host and pathogen.
- Passive Resistance - Disease avoidance (e.g., precocious germination, rapid hardening off, early or late flowering, etc.), tolerance, or escape.

(Burdon 1987 - Diseases and Plant Population Biology)

ACTIVE RESISTANCE

- Major Gene for Resistance (MGR)
- Partial Resistance, Slow Rusting Resistance (polygenic)



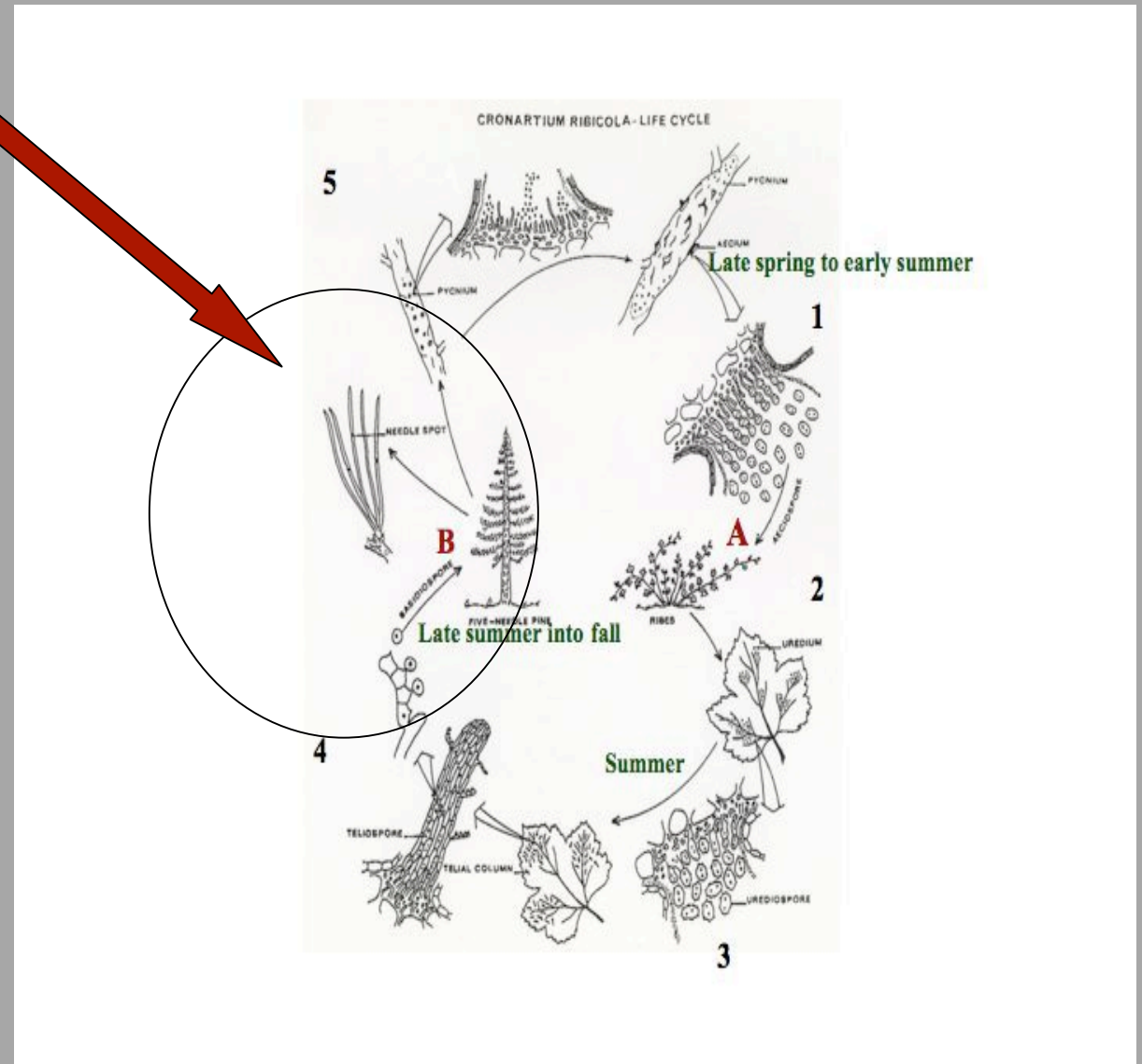
Passive Resistance

Phenology and Disease Avoidance

Phenological control: bud set and early onset of winter dormancy (A. Delfino-Mix, pers. obs.). Resulting in stomatal closure that inhibits pathogen entry.

Genetically controlled and influenced by: temperature, photoperiod, soil moisture, light quality, nutrients (Jermstad et al. 2003, Howe et al. 2003).

Cold, dry and high



Water-Use Efficiency and Host Suitability to Native Insects?

- California Mediterranean climatic regime and drought adaptation.
- Are water-use efficient/drought tolerant genotypes less susceptible to MPB?





Integrate ecological and genomic approaches to:

- Identify standing variation of complex adaptive traits across high-elevation montane landscapes in California.
- How does the variation and distribution of these traits (resistance, phenology, WUE) relate to patterns observed in disease occurrence, MPB and drought-mediated mortality.

Ecosystem genomics and forest health

Detlev R. Vogler

How do we think about forest health?

- I believe it's not so important **what** we think about forest health; what really matters is **how** we think about it.
- Thought is an active process of engaging with concepts and phenomena, and of recognizing that thoughts and ideas have history and context, and that they evolve in a social and philosophical environment.

The challenge we face

Hamlet, Act I, Scene V: Having seen the ghost.

Horatio: *O day and night, but this is wondrous strange!*

Hamlet: *And therefore as a stranger give it welcome.
There are more things in heaven and earth, Horatio,
Than are dreamt of in your philosophy.*

What is forest health?

- A condition wherein a **forest** has the **capacity** across the **landscape** for **renewal**, for **recovery** from a wide range of **disturbances**, and for the **retention** of its ecological **resiliency**, while meeting current and future **needs of people** for desired levels of values, uses, products, and services.
- Source: Forest Health Protection website, Oct 2003

Another definition (I)

- The ability of the forest to sustain itself **ecologically** and provide what **society** wants and needs is what defines a healthy forest. Maintaining the balance between forest sustainability and production of goods and services is the challenge for owners and managers....
- **Ecological:** A healthy forest maintains its unique species and processes, while maintaining its basic structure, composition, and function.

Another definition (2)

- ***Social***: A healthy forest has the ability to accommodate current and future needs of people for values, products, and service.
- These ***ecological*** and ***social*** components are inextricably linked. Forests cannot meet social needs without possessing the sustained capacity to grow, reproduce, recycle nutrients, and carry out other ecological functions.

Another definition (3)

- This definition of forest health is further expanded to accommodate changing conditions (climate change), exotic introductions, watershed health, wildland interface development, forest growth and yield, insects and disease, wildlife and fire management, and biological diversity.
- Source: Idaho Forest Products Commission

The challenge

- Managing ecosystems and landscapes so that they achieve ecological and social goals is a daunting challenge, and one we have barely begun to address.
- The tools we have used to date have been inadequate to the challenge, and our range of expertise poorly integrated.
- We need a new way to think about forests, and genomics may provide the impetus.