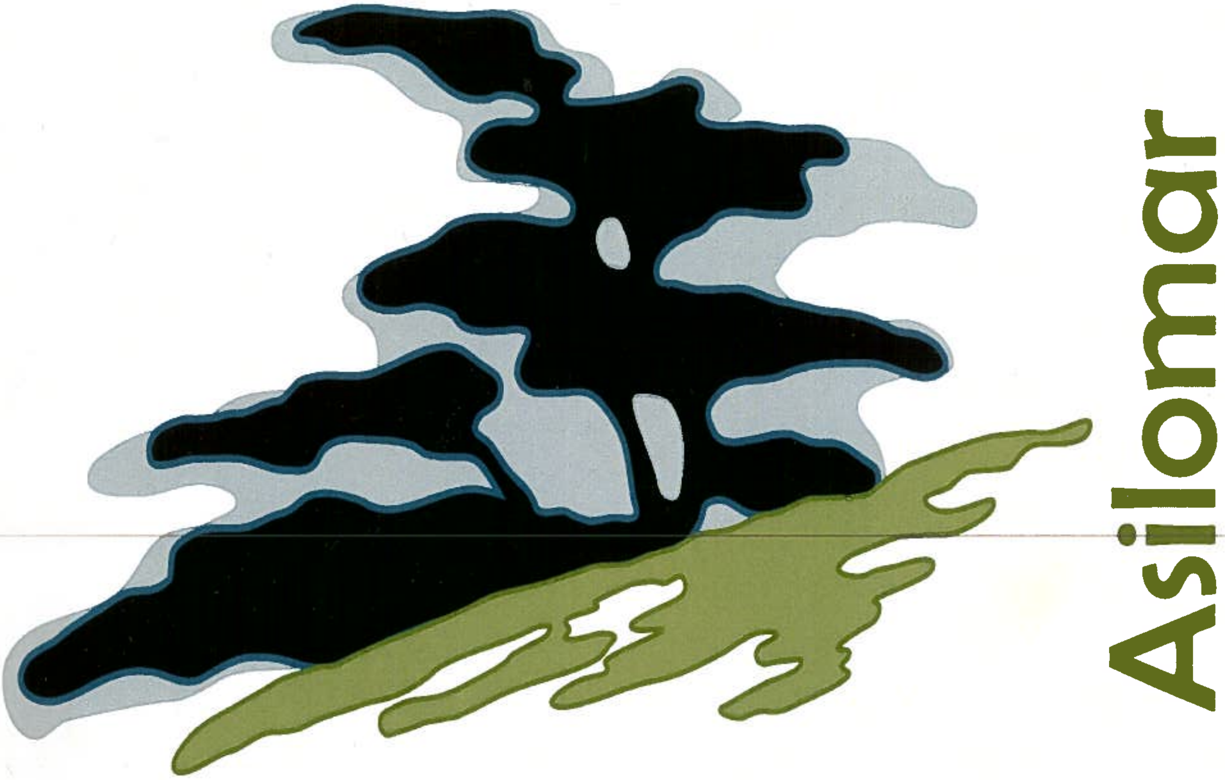

Adaptation of Trees to Changing Climates

Tom Adams Symposium

WFGA 2009 July 9-13, 2009

TABLE OF CONTENTS

WFGA GOALS

The Western Forest Genetics Association is an informal organization that has been dedicated for 54 years to the advancement of forest genetics through the interchange among workers in forest population, quantitative, and molecular genetics and tree breeding. Focus has been in the western North America and WFGA has sponsored meetings in Canada, Mexico, and the US. In this year's meeting in Asilomar State Park, CA, our theme in our plenary session is on the adaptation of forest trees and forest management systems to changing climates.

SPONSOR

Pacific Southwest Research Station, USDA Forest Service.

CONVENORS

Robert D Westfall (Chair), USDA Forest Service, PSW Research Stn, Albany, CA, USA
Tongli Wang (President WFGA), University of British Columbia, Vancouver, BC, Canada
Marilyn Cherry (VP WFGA), Oregon State University, Corvallis, OR, USA
Andrew Bower, USDA Forest Service, Corvallis, OR, USA
Jessica Wright, USDA Forest Service, PSW Research Stn, Davis, CA, USA
Andrew Eckert, University of California Davis, Davis, CA, USA

Special thanks to Christine Chourmouzis for designing the logo.

Adaptation of Trees to Changing Climates

Western Forest Genetics Association

2009 Biennial Meeting • August 9 -13, 2009, Asilomar, California

Sunday, Aug 9, 2009

3:00 PM Registration opens at the Asilomar Conference Center
6:00 Dinner

7:10 Invited speaker: **Jeremy Littell**, Climate Impacts Group, University of Washington, Seattle, WA.
"A Profound Lack of Wheeled Animals: Climate Change, Adaptation and Decision Making in Rugged Landscapes"

8:00 Reception and Social

Monday, Aug 10, 2009

7:00 AM Registration
7:30 Breakfast

8:45 **ADAMS SYMPOSIUM**:

- *The Molecular Basis of Adaptation in Forest Trees: Mount Moosilauke to the Sierra Nevada* — **David Neale**, University of California, Davis, CA

- *Association Studies of Wood Development and Stress-Related Genes in Loblolly Pine* — **Carol Loopstra**, Texas A&M University, College Station, TX

Break

- *New Tools and Approaches for Improving Wood Stiffness in Douglas-fir Breeding Programs* — **Glenn Howe**, Oregon State University, Corvallis, OR

- *The Adaptive Potential of Turkish Red Pine (Pinus brutia Ten.) to Expected Climatic Changes in the Mediterranean Region* — **Zeki Kaya**, Middle East Technical University, Ankara, Turkey

12:00 Lunch

- *Adapting to Climate Change: Running after the Red Queen* — **Brad St. Clair**, USDA Forest Service, Corvallis, OR

- *What can the Genetics and Genomics of Adaptation to Low Temperatures Tell Us about Life in a Warming World?* **Sally Aitken**, University of British Columbia, Vancouver, BC

Break

- *Assisting Assisted Migration* — **Greg O'Neill**, BC Ministry of Forests and Range, Kalamalka Research Station, Vernon, BC

- *Mating System and Gene Flow in Forest Trees: Picturing Population Dynamics* — **Jaroslaw Burczyk**, Kazimierz Wielki University, Bydgoszcz, Poland

- *Gene Flow in Forest Trees: Implications for Climatic Adaptation* — **Gancho Slavov**, West Virginia University, Morgantown, WV

6:00 Banquet

Tuesday, Aug 11, 2009

7:30 AM Breakfast
8:45 Greetings

9:00 Invited Talk: *Complex climate changes in mountainous regions and their ecological consequences;* **Jessica Lundquist**, University of Washington. "" (given by Bob Westfall)"

Session I: GENEOLOGY
Moderator: **Greg O'Neill**

9:40 Invited speaker: **Tongli Wang**, University of British Columbia. "*Applications of forest genecology in adapting to climate change*"

10:20 Break

10:40 Volunteer Presentations

10:40 **Sierra Curtis-McLane**: Can whitebark pine grow north of its current species range under climate change? A genetic analysis using common gardens
11:00 **Victoria Sork**: Climatically structured patterns of genetic variation in a California endemic oak, *Quercus lobata*
11:20 **John Major**: Light-energy processing and needle level related adaptive traits; and growth of Eastern White Pine (*Pinus strobes* L.) from large, central vs. small, isolated, marginal populations under three silvicultural treatments
11:40 **Charlie Cartwright**: Comparison of genetic variation in early height growth of Pacific silver fir and sub-alpine fir with consideration of implications for forest management

12:00 Lunch

Session II: ECOLOGICAL GENOMICS
Moderator: **Sally Aitken**

1:30 PM Invited speaker: **Andrew Eckert,** University of California, Davis. *"Genomic approaches to the identification of adaptive genetic diversity in forest trees"*

2:10 Volunteer Presentations

2:10 **Jason Holliday**: Association mapping of autumn cold hardiness and budset timing in Sitka spruce (*Picea sitchensis*)
2:30 **Kathie Jermstad**: Mapping loci in sugar pine associated with major gene resistance and partial resistance to White Pine Blister Rust
2:50 **Nick Wheeler**: Marker informed breeding in tree improvement: How does that work?

3:10 Break

Session III: ECOSYSTEMS AND TREE SPECIES MODELLING
Moderator: **Brad St. Clair**

3:40 Invited speaker: **Andreas Hamann,** University of Alberta. *"Dealing with uncertainty in model-based adaptation strategies to climate change"*

4:20 Volunteer Presentations

- 4:20 **David Roberts**: Do climate match and no-analogue climates represent a barrier to bioclimate envelope modeling of future ecosystem projections?
- 4:40 **Pei-yu Chen**: Developing seed transfer guidelines with multivariate regression tree analysis

6:00 Dinner
7:10 Poster Session (refreshments/cash bar)

Wednesday, Aug 12, 2009

7:30 AM Breakfast

Session IV: INSECTS AND DISEASES
Moderator: **Andy Bower**

8:40 Invited speaker: **Det Vogler**: US Forest Service. *"Resistance: What is it good for?"*

9:20 Volunteer Presentations

- 9:20 **Anna Schoettle**: Family variation in cankering following inoculation with *Cronartium ribicola* in *Pinus flexilis*
- 9:40 **Jessica Wright**: Tales from the trichomes- Population and family variation in early growth traits and resistance to *Phytophthora ramorum* in a common garden of tanoak
- 10:00 **John Major**: Weevil incidence, growth, phenology, and branch-level dynamics of *Pinus strobes* from large and small populations under three silvicultural treatments

10:20 Break

Session V: POLICY AND APPLICATIONS

Moderator: **Jack Woods**

10:50 Invited speaker: **Mike Landram,** US Forest Service. *"Adaptation of Silvicultural Policies to Climate Change"*

11:30 Volunteer Presentations

11:30 **Andy Bower**: USFS Genetic Resources Program strategies for adapting to climate change in the Pacific Northwest Region.

12:00 Lunch
12:45 PM **WFGA Business Meeting**

1:50 Invited speaker: **Bill Libby**: "Pines of the Monterey forest through time"

2:30 **Optional Field Tour**: Monterey pine forests and pitch canker
6:00 Dinner
8:00 Bonfire

Thursday, Aug 13, 2009

7:30 Breakfast
9:00 Volunteer presentations

9:00 **Denise Cooper:** Establishing a center for forest provenance data
9:20 **John Church:** Yearly Ponderosa Pine metabolism trends provide in-sight into adaptation to changing climate conditions

9:40 Presentation of Critchfield Memorial Scholarship award

10:00 Break
10:30 **WFGA Business Meeting**
12:00 PM Lunch
1:00 Conference adjourns

POSTER SESSION:

Aubry, Carol: USDA Forest Service Region 6 Whitebark Pine Program

Fins, Lauren: Blister Rust, Mountain Pine Beetle and Fuels in Whitebark Pine Populations in the Frank Church RONR Wilderness Area.

Gray, Laura, and **Andreas Hamann:** Predictive Species Range Maps and Distributions for Major Tree Species in Western North America Under Climate change

Hong, Yong-Pyo, et al: Outcrossing Rates of Korean Pines in Natural Population of Mt. Seorak in Korea Revealed by Allozyme and cpSSR Marker Analysis

Kegley, Angelia, et al.: Testing of Port-Orford-cedar for Resistance to *Phytophthora lateralis* Using Rooted Cuttings

Schreiber, Stefan: Drought Response of Aspen and Hybrid Poplars: A Comparison Based on Growth in Field Experiments and Physiological Traits

USDA Forest Service Genetic Resources Program: Keeping Forests Healthy

Wang, Hong-Fang, et al.: Ecological and Genetic Consequences of Fragmentation in an Urban Population of Chinese Pine (*Pinus tabulaeformis* Carr.)

USDA Forest Service Region 6 Whitebark Pine Program

Carol Aubry

Area Geneticist, Olympic National Forest, Olympia, WA

The USDA Forest Service, Pacific Northwest Region has developed a restoration strategy for whitebark pine in Oregon and Washington. The goal of the strategy is to restore and conserve a network of viable populations of whitebark pine and associated species across the Pacific Northwest. The restoration strategy is a comprehensive 5-year plan to be implemented from 2009-2013. The priority actions of this plan are:

A. Restore areas where whitebark pine habitat has been affected by fire, mountain pine beetle, or white pine blister rust by planting seed or seedlings, thinning competing trees, or pruning trees with infected limbs.

B. Collect whitebark pine seed samples across the Pacific Northwest and protect in long-term storage.

C. Increase levels of genetic resistance to blister rust infection in whitebark pine populations through tree selection, resistance screening, and wise use of seed from resistant trees.

D. Evaluate units where health, stand condition, and restoration needs are unknown.

E. Work collaboratively with research scientists and land managers in other agencies to increase understanding of the complex and synergistic impacts of blister rust, fire, mountain pine beetle and climate change on present and future health and distribution of whitebark pine plant communities.

USDA Forest Service Genetic Resources Program Strategies for Adapting to Climate Change in the Pacific Northwest Region

Andy Bower[1] and Vicky Erickson[2]

[1]Geneticist, USDA Forest Service, Corvallis, OR
[2]Regional Geneticist, USDA Forest Service, Pendleton, OR

The USDA Forest Service Genetic Resources Program for the Pacific Northwest Region (Region 6) is implementing restoration and conservation activities to adapt to climate change in national forests in Oregon and Washington. The goal of these activities is to ensure resilience in plant communities through the use of genetically appropriate material in restoration; gain a better understanding of current patterns of adaptive variation, especially of native plants, and how these species may respond to changing climate; and providing increased protection of rare/at-risk/high priority ecosystems, habitats, species, and genotypes both *in situ* and *ex situ*. A key element for the continued success of the program is the maintenance and improvement of existing infrastructure to support restoration activities. The US Forest Service is developing a proposal for a national Investment Strategy for Climate Change, which if enacted will provide support for Genetic Resources Programs nationwide.

Comparison of Genetic Variation in Early Height Growth of Pacific Silver Fir and Sub-alpine Fir with Consideration of Implications for Forest Management

Charlie Cartwright

Research Branch, Ministry of Forests, Cowichan Lake Research Station,
Mesachie Lake, BC

Similarities and differences in patterns of genetic variation in height age 5 years for Pacific silver fir (*Abies amabalis*) and sub-alpine fir (*A. lasiocarpa*) are reported based on 14 amabalis provenance test sites and 6 for sub-alpine fir. Implications of the results for management of the species are discussed in terms of seed transfer guidelines and potential for genetic gain. Ongoing genetic research efforts with these species are also described.

- Longpole pine dying - more abies planted
- good growth accross
  realized niche similar accross range

amabolis - won't tolerate frozen soils

Developing Seed Transfer Guidelines with Multivariate Regression Tree Analysis

Pei-yu Chen* and Andreas Hamann

Department of Renewable Resources, University of Alberta, Canada
peiyu@ualberta.ca

We present a new method to delineate seed zones and seed transfer guidelines using multivariate regression tree analysis. The approach can be applied to quantitative traits measured in provenance trials, physiological traits obtained in greenhouse or laboratory experiments, or gene frequencies from genetic marker studies. Data from multiple trials and/or a combination of different data types can be processed to arrive at seed transfer guidelines and seed zone delineations that are based on multiple criteria. The method works by partitioning variation in a dataset of dependent variables (growth, adaptive, and neutral marker traits), using a set predictor variables to explain the maximum amount of variation by a series of dichotomous splits of the genetic data set.

The predictor variables can be categorical (e.g. ecosystems), continuous (e.g. latitude or climate variables), or a combination of both. Different sets of predictor variable can be used for different purposes. In a case study for aspen we show how (1) latitude, longitude, and elevation of provenances can be used to develop simple seed transfer guidelines; (2) ecosystem classes and elevation as predictor variables can be used to delineate more sophisticated seed zones and breeding regions; (3) climate variables as predictors helps us to understand how genotypes are adapted to their environments, and how seed zones and breeding regions would need to be adjusted under climate change.

Yearly Ponderosa Pine Metabolism Trends Provide Insight Into Adaptation to Changing Climate Conditions

John N. Church[1], Lorraine Wiley[2], Richard S. Criddle, and Lee Hansen[3]

[1]GHH Engineering: johnnchurch@yahoo.com
[2]California State University, Fresno, Memoriam
[3]Department of Chemistry and Biochemistry, Brigham Young University, Emeritus
lee_hansen@byu.edu

The interaction of metabolism with environment is central to defining growth and distribution of plants. Respiratory and growth measurements of net metabolic energy were made for a year on three *Pinus ponderosa* planted in the University of California Davis arboretum, using the methods of Criddle et al. (1990). Slow metabolic energy accumulation to mean 30% of the final total occurred during bud development from July to October. Net energy loss occurred during November through January. Metabolic rates increased 1 to 4 weeks before elongation became visible. 80% or more of the total energy accumulated in February through May during rapid elongation. Metabolic rates had strong temperature dependence with highest rates approximating native range spring daily high temperatures (25C to 30C). To be site-adapted, metabolic temperature dependence must be coupled to ambient temperatures present when water is available. Current climate trends of relatively constant daily high temperatures and increasing night temperatures will dry sites earlier if precipitation patterns remain constant. This will uncouple metabolism of many trees from site conditions rendering them maladapted. Coupling tree metabolic temperature dependence, ambient temperature and timing of water availability to changing conditions will be critical to selecting adapted trees.

Can Whitebark Pine Grow North of its Current Species Range Under Climate Change? A Genetic Analysis Using Common Gardens

Sierra Curtis-McLane and Sally Aitken

Centre for Forest Conservation Genetics, University of British Columbia

Whitebark pine (*Pinus albicaulis*) is declining severely and is projected to lose much of its current climatic range by 2080 due to climate change. This study provides technical insight for decision makers concerned with facilitated migration by evaluating the biotic and abiotic limiting factors associated with recruitment of whitebark pine populations in areas north of the current species range that are predicted to be habitable under future climate scenarios.

In situ common gardens were established throughout western British Columbia using seeds from 7 whitebark pine populations. Nine thousand untreated seeds were planted in September 2008 while 7,000 seeds were x-rayed, stratified and clipped to maximize germination potential and then planted in June 2008. As of August 2008 germination in the common gardens varied significantly by seed treatment and population, but was not strongly affected by geographic location or microsite. Germination was strongly correlated with seed weight and with snow pack persistence at population origins, and weakly correlated with mean summer precipitation at the planting site.

Ex situ growth chamber experiments were also performed with five chambers representing a spectrum from current growing season temperatures to 10°C warming. In the first growing season all quantitative traits (percent emergence of seeds planted, percent emergence of total seeds, days to emergence, height, days to flush, days to second flush and days to final budset) varied significantly among temperature regimes, while only percent emergence, days to emergence and height varied significantly among populations as well as chambers.

Genomic Approaches to the Identification of Adaptive Genetic Diversity in Forest Trees

Andrew J. Eckert

Section of Evolution and Ecology and Center for Population Biology, University of California at Davis, Davis, CA 95616

Forest trees illustrate remarkable adaptations to their environments, ranging from latitudinal clines in phenological traits to growth habits across disparate soil types. Disentangling the genetic components that underlie these adaptations has had a long history in forest genetics, yet for many traits of interest only a handful of candidate loci have been identified. This is contrary to quantitative genetic predictions and decades of empirical research showing that most adaptive traits in forest trees are polygenic. Genomic tools offer promising insights into the detection and characterization of these components. Drawing from a multitude of molecular population and association genetic studies of North American conifers, the following points will be addressed: (1) genome-wide patterns of diversity and divergence; (2) the number, type and effect size of genes putatively under selection or associated with a phenotype; and (3) landscape patterns of genetic diversity at these loci. Themes emerging from this work illustrate the moderate levels of diversity and divergence and the often lineage and locus specific nature of these estimates, as well as the rarity of evidence for positive selection in conifer genomes, which may also be a function of the methods used to detect these patterns. These studies also highlight the need for further development and application, especially in natural populations, of high throughput marker technologies, functional studies of gene products identified as putatively adaptive and continued investigations into phylogeographic, eco-geographic and climatologic patterns across the distribution of forest trees.

Predictive Species Range Maps and Distributions for Major Tree Species in Western North America Under Climate change

Laura Gray and Andreas Hamann

Poster to be presented at the WFGA Annual General Meeting August 9-13th, 2009

In the wake of rising global temperatures, there is increasing demand to understand and quantify the potential biological and management implications of climate change, so that we can prevent, or at least prepare for, the potential impacts of varying temperatures and precipitation levels. Many studies suggest that there will be a significant biological response to climate change from a wide range of species and ecosystems. Due to North America's ecological and economic reliance on forests, predicting potential habitat of major tree species under a wide range of climate change scenarios can provide forest managers with a tool to address two major concerns in sustainable forestry: adequacy of forest reserves (protected areas), and species selection for reforestation under future climate change.

This study analyzed interpolated climate, soil and forest inventory data collected from western North America up to 100° longitude, excluding Alaska, and the Yukon and North West Territories.

Predictive niche modeling was used to identify a 'bioclimatic envelope' or environmental limits at which a species will persist, by correlating current species distributions with climate, soil and topography variables. Once the potential suitable habitats were classified for varying species frequencies, both a Random Forest and Discriminant Analysis model was used to classify the landscape under 20 climate change scenarios (5 international climate models x 4 standard emission scenarios) and for three future normal periods (2020s, 2050s and 2080s). Species frequencies were then applied to locations on the future landscape that were identified as suitable habitat, creating predictive species range maps.

It is widely accepted that climate limits species distribution, but it is unclear what influence climate has over species abundance. The resulting predictive habitat maps were analyzed to determine if similar or different climate factors are driving these processes.

The resulting predictive species range maps and the influential climate factors for determining species distribution and abundance will be presented for major tree species of North America.

Dealing With Uncertainty in Model-based Adaptation Strategies to Climate Change

Andreas Hamann

Department of Renewable Resources, University of Alberta, Canada
andreas.hamann@ualberta.ca

I review analytical and modeling approaches that have been used to infer climate change impacts on forest tree populations, making the case that that ecological niche models are fundamentally well suited to develop climate change adaptation strategies for management of forest genetic resources. An important concern that remains, however, is uncertainty in model projections due to a variety of factors. In a case study for western Canada, I show how this uncertainty may be dealt with through analysis of variance, where sources of uncertainty are represented as treatments in a complete factorial design. The treatments in this case study include (1) modeling methods, (2) baseline climate data, (3) choice of predictor variables, (4) general circulation models, and (5) emission scenarios. As dependent variables changes to species and ecosystem distributions under 144 treatment combinations were evaluated. Inclusion of topo-edaphic variables as predictors reduces projected habitat significantly, and general circulation models are by far the largest contributors to uncertainty. While modeling methods rarely had a notable main effect, they sometimes account for a very large proportion of uncertainty in modeling results through interaction terms with climate change predictions. This offers researchers the opportunity to filter out biologically and statistically unreasonable modeling results, and to provide practitioners with an improved range of predictions for climate-informed natural resource management.

Outcrossing Rates of Korean Pines in Natural Population of Mt. Seorak in Korea Revealed by Allozyme and cpSSR Marker Analysis

Yong-Pyo Hong*, Ji-Young Ahn, Young-Mi Kim, Byeong-Hoon Yang, and Seong-Doo Hur

Dept. of Forest Resources Development, Korea Forest Research Institute

To estimate the outcrossing rates and the number of pollen contributors (i.e., paternal parents) in a natural population of Korean pines in Mt. Seorak, allozyme and chloroplast DNA simple sequence repeats markers were analyzed. Multiple cones (3~4 cones per individual tree) were collected from 11 individual trees in 2007. Thirty seeds were randomly selected from each individual tree. After germination, DNA and protein was extracted from embryo and endosperm of the same seed, respectively. On the basis of allozyme markers observed in 11 polymorphic loci, estimate of multilocus outcrossing rates (tm) was 0.986 (S.D. 0.061). Estimates of correlated outcrossed paternity (rp = 0.528) and biparental inbreeding (tm - ts = 0.019) were obtained. These estimates resulted in neighborhood size (1/rp) of less than two individuals in the paternal mating pool. On the other hand, seeds having been generated via outcrossing were directly verified by comparing cpDNA haplotypes of embryos with those of mother trees, respectively. Relatively high outcrossing rate was observed (36.7~100%, average 83%). The number of unique haplotypes in embryos of a single mother tree, which represents the minimum number of pollen donors, was ranged from 6 to 20 with the average of 11.4, which suggests that relatively various paternal parents contributed to the gene pool of progeny population. Further data on the other mother trees will be presented and discussed on the poster.

New Tools and Approaches for Improving Wood Stiffness in Douglas-fir Breeding Programs

G.T. Howe*[1], M.L Cherry[1], V. Vikram[1], D.W. Cress[2], D. Briggs[3], T.Z. Ye[1], D.B. Neale[4], J. Yu[1], and K. Jayawickrama [1]

[1]Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR
[2]Olympic Resource Management, Port Gamble, WA
[3]School of Forest Resources, University of Washington, Seattle, WA
[4]Department of Plant Sciences, University of California, Davis, CA

Wood properties are becoming increasingly important in conifer breeding programs. Douglas-fir is largely used for structural wood products because its wood is strong, stiff, and dense. Therefore, wood stiffness has become a focus of genetic improvement. The Pacific Northwest Tree Improvement Research Cooperative has a long history of research on Douglas-fir wood properties. We will describe past work on the genetics of wood density, and recent work on the genetics of wood stiffness. Tools that can measure acoustic velocity in the wood of logs and standing trees look promising for improving stiffness in operational programs. We are also investigating the use of molecular markers (SNPs) as a way to increase the efficiency of wood stiffness improvement. Compared to using research populations, it may be challenging to incorporate genetic markers into Douglas-fir breeding programs because few SNP markers are currently available, pedigree founders may be unavailable for genotyping, and wood stiffness breeding values are available for only a modest number of parents. However, existing breeding values for growth and stem form, as well as the sheer size of the Northwest Tree Improvement Cooperative breeding program (30,000 tested parents and 4 million progeny in field tests), make the long-term prospects for testing and applying molecular markers seem promising. We will describe our studies on the use of acoustic tools for measuring wood stiffness, phenotypic evaluation of seed orchard parents as a way to estimate wood stiffness breeding values, trial application of SNP markers, and plans to develop an expanded SNP resource in Douglas-fir.

Mapping Loci in Sugar Pine Associated with Major Gene Resistance and Partial Resistance to White Pine Blister Rust

K. Jermstad[1], B. Kinloch[1], D. Burton[2], D. Davis[2], A. Mix[1], A. Eckert[3], J. Wegrzyn[3], and D. Neale[1,3]

[1]Institute of Forest Genetics, PSW, US Forest Service, Placerville, CA
[2]Happy Camp Outplant Site, Region 5 Genetics, US Forest Service, Happy Camp, CA
[3]Department of Plant Sciences, University of California, Davis, CA

Pines belonging to the *Pinus* subgenus *Strobus* are susceptible to a fungal pathogen (*Cronartium ribicola*) that was introduced to North America in the early 1900s. Two forms of resistance have been observed among the 5-needled pines: 1) simple and rapid resistance (a.k.a major gene resistance) which has been shown to segregate in progeny as a single dominant gene, and 2) partial resistance (a.k.a. slow-rusting resistance) which expresses a wide variety of disease phenotypes and lethality. The infinitesimal model for complex traits stipulates that multiple loci underpin the wide distribution of phenotypes observed, In sugar pine (*Pinus lambertiana*), we constructed a large mapping population segregating for partial resistance in order to map the quantitative trait loci (QTL) associated with this form of resistance. The QTL population and two open-pollinated single-tree populations heterozygous for monogenic resistance have been genotyped using a 1536 single nucleotide polymorphism OPA chip (Illumina Golden Gate Technologies) for construction of the first full-genome consensus map in the 5-needled pines.

The Adaptive Potential of Turkish Red Pine (*Pinus brutia Ten.*) to Expected Climatic Changes in the Mediterranean Region

Zeki Kaya

Department of Biological Sciences, Middle East Technical University, Ankara, Turkey

Turkish red pine (*Pinus brutia Ten.*) is naturally found mainly in the eastern Mediterranean Region and most widespread forest tree species in Turkey (15 % of the total forest land). The natural distribution of the species ranges from the sea level up to 1300 m in pure stands and to 1500 m as individuals. Since forest fires are frequent in the Mediterranean Region, Turkish red pine developed seed, cone and growth characteristics that help the species adapted to fire ecology. Artificial regeneration practice, which is a common practice, has increased the genetic diversity within population in coastal zones. This was evident from observation of no distinct pattern of genetic diversity according to the geography, elevation or breeding zones. The studies dealing with adaptive seedling characters and provenance tests indicated that this species shows high phenotypic plasticity and an opportunistic growth mode. According to the First National Communication on Climate Change of Turkey to UN Framework Convention on Climate Change (UNFCCC), by the end of this century average temperature will increase by 2-3°C along with substantial changes in precipitation patterns. Considering the genetic diversity pattern, ecology and physiological characters of species, while some portions of Turkish red pine's natural range will become inhospitable for this species, however, opportunities will emerge for deploying Turkish red pine into areas that are formerly out of its natural range.

Testing of Port-Orford-cedar for Resistance to *Phytophthora lateralis* Using Rooted Cuttings

Angelia Kegley[1*], Richard A. Sniezko[1], Paul Reeser[2], and Everett Hansen[2]

[1]USDA Forest Service, Dorena Genetic Resource Center, Cottage Grove, OR
[2]Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR

Port-Orford-cedar (*Chamaecyparis lawsoniana* (A. Murr.) Parl.) is susceptible to a root disease caused by *Phytophthora lateralis*, which has caused widespread mortality throughout its native range. A screening and breeding program was established to identify genetic resistance to the disease. One method of testing is a root dip inoculation, in which rooted cuttings are dipped briefly in a zoospore suspension of *P. lateralis* and monitored for mortality up to three years.

Testing of rooted cuttings from field selections began in 2000. Through 2007 a total of 911 selections (clones) have been tested. Generally, six rooted cuttings per clone were inoculated, and the mortality recorded periodically. The duration of the testing has increased from <1 year prior to 2003 to 2 or 3 years since. Although clones were expected to show either 0 or 100% mortality, the mortality in the trials spans the range. Clones showing 100% mortality are likely very susceptible (although the 'time to mortality' varies among these clones). Clones with intermediate mortalities (>0% and <100%) should undergo a second level of testing to confirm their level of resistance. Few clones (10 – 20%) show 0% mortality, and ~30-45% show 100%.

Adaptation of Silvicultural Policies to Climate Change

Michael Landram

Regional Silviculturalist, USDA Forest Service, Region 5, Vallejo, CA

Of the suite of currently applied silvicultural practices on national forests in California, tree planting offers the best opportunity to apply evolutionary adaptation knowledge, principles, and concepts to address climate change. Wildfires have created a maximum potential planting need on 245,000 acres so far this decade (2000-2008). The extent and severity of wildfire is expected to increase. The reforestation program has been restructured to rapidly respond to wildfire. The regional goal is to plant 2/3rds of the maximum potential need within 3 years after fire. Priority is given to "seedless" landscapes. Mixed species, mixed genotype plantings are encouraged. Natural regeneration is encouraged. Open canopied future conditions are encouraged. Seed plans are predicated accordingly with assumptions about wildfire occurrence. Our comfort level with site specific predicted future climate envelopes, especially in mountainous terrain, has not yet reached the point where sweeping modifications to seed transfer policies are indicated.

A Profound Lack of Wheeled Animals: Climate Change Adaptation and Decision Making in Rugged Landscapes

Jeremy Littell

JISAO CSES Climate Impacts Group, University of Washington, Seattle, WA

Projected climate change impacts on forest ecosystems will in many ways fundamentally alter Western landscapes and forest management. The "adaptation" we engage in to prepare for the impacts of climate change on forests and forest resources are analogous to some of the dilemmas and challenges a population would face on a "fitness" or "adaptive" landscape. Planning for the impacts of climate change - and at its logical extent, "pre-adapting" forest landscapes to the anticipated changes - requires strategies for navigating both the scientific and institutional barriers present in such a rugged adaptive landscape. While there are important scientific uncertainties about the impacts of climate change, it could be argued that clear paths forward exist to resolve these and the uncertainty associated with institutional barriers is as great or greater. There are, of course, important differences between genetic adaptive landscapes and those we might associate with planning for climate change, such as the potential for intent in the latter. However, if the general analogy of an adaptive landscape holds for any complex adaptive system, then there are some important adaptation principles that suggest general operational strategies for adapting to climate change in managed landscapes.

Complex Climatic Changes in Mountainous Environments and Associated Changes in Forest Vegetation

Jessica Lundquist[1], Robert D Westfall[2]*, Constance I Millar[2]

[1]Dept. Engineering, University of Washington, Seattle, WA, USA
[2]PSW Research Station, USDA Forest Service, Albany, CA, USA

Most analyses assume that mountain environmental responses will change linearly with climate. However, recent data suggests that spatiotemporal variation in temperature is complex in mountainous terrain, resulting in complex ecological responses. Previously, I (L) examined surface temperature variability using an array of 37 sensors within and in the vicinity of Yosemite National Park. I used empirical orthogonal functions (EOF) to identify dominant spatial patterns in temperature and their variation over time. The first EOF represented differences in surface temperatures from those in free air, driven by seasonal variation and by cyclonic/anticyclonic weather patterns. The second EOF represented west-east side differences in temperature, which were correlated with zonal wind flow, whereby strong west winds warm the west slope and cool the east. The third EOF indicates areas of cold air ponding. The fourth EOF shows spatial variation in lapse rates associated with north-south winds and rising/sinking air. Next, I present an automated algorithm to estimate areas of cold air pooling (CAP), based on DEMs, which were used to derive surfaces of local slope, curvature, and percentile elevation relative to surrounding terrain. Each pixel was classified as prone to CAP, not prone to CAP, or exhibiting no signal. Along-valley changes in the topographic amplification factor (TAF) were then calculated to determine whether the cold air in the valley was likely to pool. We (M&W) give examples from our work that show subalpine forest tree species expanding into unforested areas and moving up and down slope. We also show limber pine adapting to increases in temperature and increasing variability in precipitation.

HG-Andrews - cold drainage info

recruitement of Limber Pine
- similar at High lat. & low elevation
- episodic

PDO, Min temp - driving

Dead trees more sensitive to climate
- less water use efficient (Predawn moisture potential)
- genetic
- larger trees dead

Light-energy Processing and Needle Level Related Adaptive Traits; and Growth of Eastern White Pine (*Pinus strobus* L.) From Large, Central vs. Small, Isolated, Marginal Populations Under Three Silvicultural Treatments *

John E. Major, Alex Mosseler, Debby C. Barsi,
Britt Corriveau-Dupuis, and Moira Campbell

Natural Resources Canada, Canadian Forest Service - Atlantic Forestry Centre,
PO Box 4000, Fredericton, NB, Canada, E3B 5P7
Tel. (506) 452-3262, FAX: (506) 452-3525
jmajor@nrcan.gc.ca

Adaptive traits related to light-energy processing under different light levels have significant ecological implications for plant fitness. Our objective was to examine and compare light-energy processing, chloroplast pigment content, nitrogen economy, and needle level morphological adaptive traits; and growth of white pine (*Pinus strobus* L.) from large, central populations (central Ontario (ON)), in comparison with small, isolated populations (Newfoundland (NL)) under three silvicultural treatments (ST). Light levels were on average 100%, 42.0%, and 20.4% transmittance for the full sun, and intermediate and high shade ST, respectively, using a cleared or thinned 30-year-old red pine overstory to 2 levels. After 8-years, overall height growth was 4.10, 3.25 and 1.70 m for full sun, intermediate, and high shade ST, respectively ($P < 0.001$). Overall, ON populations had greater total height, diameter and current height growth than NL populations (all $P < 0.001$). At low light levels (10 and 25 μmol m^{-2}s^{-1}) high shade ST trees had higher photochemical quenching (*qP*), apparent photosynthesis (*APs*), and lower chlorophyll fluorescence (F_{pc}) compared to intermediate and full sun ST. There was an inflection in rankings at 50 μmol m^{-2}s^{-1}. At and beyond 100 μmol m^{-2}s^{-1}, full sun ST trees had higher *qP*, *APs*, lower F_{pc} , as compared to intermediate and high shade ST. There were no thermal dissipation efficiency (*qN*) differences among ST across all light levels. Light-energy processing traits had no regional effects. Average total chlorophyll concentration (CHL) and content (CHLC) increased in response to the intermediate shade ST but did not respond further or decreased to the high shade ST. Region was significant for CHL and CHLC with ON greater than NL. Chlorophyll a:b and CHL:carotenoid (CAR) ratios and needle level morphology responded significantly to all three ST. Needle N and C:N showed no regional effect and N showed a modest ST effect probably due to limited N availability in forested stands. Tree height and volume showed a curvilinear and linear relationship to light level, respectively. Tree height showed a positive linear relationship to *qP* ($r^2 = 0.668$), *APs* ($r^2 = 0.371$), chlorophyll a:b ratio ($r^2 = 0.598$), and needle N ($r^2 = 0.728$) (all $P < 0.001$). Tree height showed a negative linear relationship to F_{pc} ($r^2 = 0.539$), CHL:CAR ratio ($r^2 = 0.576$), C:N ratio ($r^2 = 0.706$), specific needle area ($r^2 = 0.680$), and needle area N^{-1} ($r^2 = 0.748$) (all $P < 0.001$).

---

*Full article, Major et al., 2009, Forest Ecology and Management, 257:168-181.

Weevil Incidence, Growth, Phenology, and Branch-level Dynamics of *Pinus strobus* From Large and Small Populations Under Three Silvicultural Treatments*

John E. Major, Alex Mosseler, Debby C. Barsi, Amanda Clouthier and Moira Campbell

Natural Resources Canada, Canadian Forest Service - Atlantic Forestry Centre,
PO Box 4000, Fredericton, NB, Canada, E3B 5P7
Tel. (506) 452-3262, FAX: (506) 452-3525
jmajor@nrcan.gc.ca

Our goal was to quantify the impact of three silvicultural treatments (STs) on weevil incidence, resulting tree growth effects, branch-level components of growth, and related adaptive trait information of white pine (*Pinus strobus* L.) from large, central populations in central Ontario (ON) versus small, isolated populations in Newfoundland (NL). Light levels were on average 100%, 42.0%, and 20.4% transmittance for the full-sun, intermediate-shade, and high-shade STs. After 8 years, overall incidence of weevil infestation was 42.1%, 23.4%, and 13.7% for the full-sun, intermediate-shade, and high-shade STs, respectively ($P < 0.001$). Weevil damage impact on total height and volume averaged -13.2% and -11.8%, respectively, and was largely consistent across STs and regions. Dominant lateral shoot length (which averaged 68% of leader length, $r^2 = 0.89$) analysis showed that ON populations had 32% longer shoot growth than the NL populations. There was no growth rate difference between NL and ON trees between Julian days 154 (near bud break) to 168 under the three STs. Bud set difference was a primary determinant of shoot-length growth differences between regions: Julian days 171 and 184 for the NL and ON populations, respectively, under all three STs. The primary determining factors related to shoot length were number of needle bundles and region, driven by light levels and day length, respectively, and internode length probably through inbreeding effects. Total height showed a positive curvilinear relationship to light level with a constant difference between regions, and diameter showed a curvilinear relationship to light level with no difference between regions at low light levels and progressively higher diameter for ON than NL populations as light levels increased. Shoot length and number of needle bundles showed a positive curvilinear relationship to light level, and specific needle area showed a negative curvilinear relationship to light level. Each day bud set was delayed resulted in an average of 2.5% or 0.5 cm more growth. To maximize fitness, conservation strategies should also now consider not only preservation but also examining and introducing adaptive trait variation in the context of anticipated environmental change.

---

*Full article Major et al., 2009, Can. J. For. Res. 39: 12-25.

Do Climate Match and No-analogue Climates Represent a Barrier to Bioclimate Envelope Modeling of Future Ecosystem Projections?

David R. Roberts[1] and Andreas Hamann[1]

[1]Department of Renewable Resources, University of Alberta, Edmonton, Alberta, Canada, drr3@ualberta.ca and Andreas.hamann@ales.ulaberta.ca

A variety of climate change models attempt to project species distributions for the coming century based on climatic projections. One potential criticism of these modelling studies is that future climates will be of novel arrangement (the interplay of climatic variables will be different) than any observed climate in the present day. Hence, if no analogous climate exists in the present with which to calibrate a model, the future model prediction outputs lack applicability. We have generated a bioclimate envelope model (BEM) based on machine learning for western North America, trained with ecological and climatic data from the present day, capable of reconstructing past ecosystems back to the Last Glacial Maximum as well as predicting future ecosystem patterns.
Comparing model back-predictions for the previous 21,000 years with palaeoecological data from the same period provides us with an effective method of BEM evaluation—providing the temporal (and corresponding climatic) limits of acceptable model extrapolation. Additionally, we have calculated the multivariate distances between the modern climate and the palaeoclimate values used for back-predictions and used these measures of climate dissimilarity to develop a quantitative threshold for model extrapolation. Future climate change projections were then examined for their climate dissimilarity from modern values. Our results indicate that the measures of climatic dissimilarity in future climate change projections are within ranges that can be accurately modelled with modern calibration data. We conclude that heterogeneity between modern climate and climate change projections should not present a significant barrier to bioclimate envelope modelling of near-future ecosystem distributions.

Imported *Phytophthora* Species in Finnish Nurseries and Their Detection

Anna Rytkönen[1], Arja Lilja[1], Jarkko Hantula[1]

[1]Finnish Forest Research Institute, PO Box 18, 01301 Vantaa, Finland

Phytophthora infestans has been the causal agent of potato late blight in Finland since the beginning of the last century. A more recently imported species, *P. cactorum*, has caused losses in strawberry and silver birch production since its discovery in the early 1990s. Since 2004, the Sudden Oak Death pathogen, *P. ramorum*, has been found annually by Finnish Food Safety Authority Evira in imported plants as well as in two domestic nurseries producing horticultural plants. Most common pathogens isolated from symptomatic Rhododendron plants are *Pestalotiopsis* sp., *P. inflata*, *Pl ramorum* and *P. cactorum*. In pathogenicity trial *P. inflata* was capable to infect most test plants including *Fragaria x ananassa*, *Betula pendula*, *Alnus glutinosa*, *Picea abies*, *Vaccinium myrtillus*, *V. uligonosum*, *V. vitis-idaea* and *V. angustifolium*. *P. ramorum* caused also stem lesions on *B. pendula*, *A. glutinosa* and *Vaccinium* spp. but was less pathogenic than *P. inflata*. *Pinus sylvestris* was resistant to both *P. ramorum* and *P. inflata*. Only *P. ramorum* was pathogenic to *Viburnum lentago*. Some strains of *P. ramorum* survived two weeks at -5°.

The classic methods of detection and identification of *Phytophthora* species require the isolation of the microbe, and include culturing for morphological character and growth measurements. We have developed a PCR-based tool for the detection and identification of *Phytophthora* directly from plant material.

DNA extraction from plant material was optimized using UltraClean Soil DNA Isolation Kit (Mo Bio Laboratories Inc.). DNA amplification with *Phytophthora*-specific primers designed for the Internal Transcribed Spacer (ITS) region combined with Denaturing Gradient Gel Electrophoresis (DGGE) allowed identification of all 16 tested *Phytophthora* species. The detection capability of the method was tested on different plant species infected with *Phytophthora sp.* The detection was successful from *Fragaria x ananassa*, *Betula pendula*, *Picea abies*, *Vaccinium myrtillus*, *V. uligonosum*, *Viburnum lentago*, *Malus domestica* Golden Delicious fruit, *Solanum lycopersicum* fruit, Rhododendron *Smirnowii* 'Hellikki', *R. Yakushimanum* 'Kullervo' and three cultivars of *R. Tigerstedtii* ('St Michel', 'Helsinki University', 'Axel Tigerstedt').

One of the most prominent advantages of the described identification method is that it is suitable for several *Phytophthora* species from the same sample, and regardless whether the species are previously know or not. Another advantage is that the detection is possible directly from plant material without subculturing.

Family Variation in Cankering Following Inoculation With *Cronartium ribicola* in *Pinus flexilis*

Anna W. Schoettle[1*], Richard A. Sniezko[2]; Angelia Kegley[2],
Kelly S. Burns[3], and Jerry Hill[2]

[1]USDA Forest Service, Rocky Mountain Research Station, Fort Collins, CO
[2]USDA Forest Service, Dorena Genetic Resources Center, Cottage Grove, OR
[3]USDA Forest Service, Forest Health Management, Lakewood, CO

Limber pine, *Pinus flexilis* James, is a 5-needle pine species with a broad latitudinal and elevational range in western North America. Limber pine populations in the Southern Rockies are currently being invaded by *Cronartium ribicola*, the fungus that causes white pine blister rust (WPBR) and proactive interventions to sustain their ecosystems are being developed (Schoettle and Sniezko 2007). Early WPBR resistance testing by Hoff et al. (1980) revealed resistance in the species and Kinloch and Dupper (2002) reported the occurrence of a hypersensitive reaction to WPBR in a bulk sample of limber pine from Colorado. Progeny from open pollinated seed from 112 individual trees across 11 locations in Colorado and southern Wyoming were tested for WPBR resistance at Dorena Genetic Resources Center (OR). Five of the 11 populations have been invaded by WPBR. Three month old limber pine seedlings were inoculated with *C. ribicola* and their phenotypic response followed for 2 years. Overall, 12% of the seedlings remained stem symptom-free. Frequency of the trait varied from 1 to 29% among sites and 0 to 100% among families. Other associated traits were also quantified. The data suggest a geographic pattern in the stem symptom-free trait and is being explored further. Application of our current research to the design of on-going *in situ* and *ex situ* conservation strategies for this species in the Southern Rockies will also be discussed.

Drought Response of Aspen and Hybrid Poplars: A Comparison Based on Growth in Field Experiments and Physiological Traits

Stefan Schreiber, Barb Thomas, Andreas Hamann and Uwe Hacke

Department of Renewable Resources, University of Alberta, Canada
stefan.schreiber@ales.ualberta.ca

Aspen (*Populus tremuloides*) and hybrid poplars (*Populus deltoids x*) are an important forest resource in Alberta, primarily for pulp and oriented strandboard production. Intensive selection and breeding programs are carried out for both aspen and hybrid poplar by private companies or cooperatives in Alberta. Prior to large scale employment of material from tree improvement programs, it is important to better understand the ecological genetics and phenotypic plasticity of these species, particularly in the context of changing climate. Alberta has experienced warming of approximately 0.7°C and a reduction of precipitation by 20% over the last 25 years. Is the planting stock from these breeding programs adapted for these new climate realities? Is there a difference between native aspen and hybrid poplar genotypes with respect to drought resistance?

This research project builds on plant material and data from aspen and hybrid poplar test plantations established over the last decade by the forest industry (Alberta-Pacific Forest Industries, Ainsworth Engineered Canada LP, Daishowa-Marubeni International Ltd., Western Boreal Aspen Corporation, Weyerhaeuser Company Ltd.). The analysed plantations are located at the Alberta-Pacific Forest Industries pulp mill site about 30 km west of Athabasca, Alberta, Canada. Additionally, an aspen provenance trail that has been replicated 6 times across Western Canada provides an outstanding opportunity to study genetic variation and phenotypic plasticity under different climate conditions. We report preliminary results in growth and adaptive traits and outline future research questions that are addressed in this project.

Gene Flow in Forest Trees: Implications for Climatic Adaptation

G. T. Slavov[1*], G. T. Howe[2], S. P. DiFazio[1], W. T. Adams[2]

[1]Department of Biology, West Virginia University, Morgantown, WV 26506-6057
[2]Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR

Local adaptation, the fitness advantage of genotypes residing in a given habitat compared to immigrant genotypes, is one possible outcome of the complex interactions between gene flow and natural selection. Two lines of evidence suggest that populations of tree species with wide geographic ranges are locally adapted. First, tree populations are strongly differentiated for traits that confer climatic adaptation. Second, genetic clines in adaptive traits are associated with corresponding gradients in climatic or location variables. These clines are repeated in different portions of a species' range and in different species, providing strong evidence that these patterns have been forged by natural selection. At the same time, however, both direct and indirect studies indicate that levels of pollen-mediated gene flow among tree populations are high. How is local adaptation maintained in the face of extensive gene flow? Phenology probably plays a pivotal role because the timing of dormancy release and bud flush simultaneously affects reproductive isolation and adaptation to climate. More specifically, we hypothesize that clinal phenological variation along climatic gradients reinforces local adaptation by (1) directly restricting pollen-mediated gene flow and (2) resulting in immigrants with reduced fitness. We review some of the empirical evidence that supports this hypothesis, outline an approach to elucidating the relative roles of gene flow and divergent selection in shaping patterns of local adaptation, and discuss the anticipated technical and conceptual challenges. Finally, we summarize the implications of this research for predicting the response of forest tree populations to climate change.

Climatically Structured Patterns of Genetic Variation in a California Endemic Oak, *Quercus lobata*

Victoria L. Sork[1], Frank Davis[2] , Delphine Grivet[3], and Hongfang Wang[4]

[1]Department of Ecology & Evolutionary Biology and
Institute of the Environment, UCLA
[2]Bren School of the Environment, UC Santa Barbara
[3]INIA, Dept. Forest Systems and Resources, Spain
[4]UCLA and Center of Landscape Ecology and Sustainability Science,
Beijing Normal University

The ability of tree populations to respond to climate change will be influenced by the underlying structure of genetic variation. Historical gene flow creates patterns of genetic differentiation that may allow some populations to be more predisposed to respond to climate change than others. In this paper, we examine geographic patterns of genetic variation in populations of valley oak (*Quercus lobata* Née), an endemic whose distribution has been more reduced by habitat conversion than any other major tree oak species in California. We have sampled valley oak at localities throughout its species range. Using chloroplast microsatellite genetic markers, we first document the historical genetic structure of the species using the program STRUCTURE. Using nuclear microsatellite genetic markers, we examine the spatial location of multilocus genotypes. Our findings indicate that the major genetic divergences are associated with populations on the foothills of the western Sierra Nevada range versus those along the eastern foothills of the Coastal ranges. We correlate the multilocus genotypes with climatic variables and find that the genotypes correlate with temperature seasonality and maximum Temperature. These findings demonstrate that the existing genetic structure of valley oak is already associated with climatic variables that will be affected by future climate change. Work is underway to identify candidate genes associated with plant response to climate change and then assess the geographic distribution of adaptive genetic variation. As we consider the response of valley oak to future climate change and existing patterns of genetic variation, it is likely that not all populations will respond similarly.

Ecological and Genetic Consequences of Fragmentation in an Urban Population of Chinese Pine (*Pinus tabulaeformis* Carr.)

Hongfang Wang[1,2], Jianping Ge[1], Victoria Sork[2], and Jianguo Wu[1,3]

[1]Center of Landscape Ecology and Sustainability Science,
Beijing Normal University, Beijing, China
[2]Department of Ecology and Evolution Biology and Institute of the Environment,
University of California, Los Angeles, CA
[3]School of Life Sciences and Global Institute of Sustainability,
Arizona State University, Tempe, AZ

Fragmentation is a critical issue for tree populations because patch size and isolation can promote inbreeding and loss of genetic diversity. In this study, we investigated an urban population Chinese Pine (*Pinus tabulaeformis* Carr.) planted in patches around Beijing to test the hypothesis that patch size and isolation affect mating pattern and or early fitness measures. Our design includes 28 urban patches, with patch size ranging from 1 to 2000 adult trees and isolation (edge distance index) from 35 to 243. To examine mating patterns, we collected 20-60 seeds from 1-2 adult tree(s) of each patch and then genotyped each embryo using seven paternally-inherited chloroplast microsatellites. For patches smaller than 40, we genotyped all adult trees within patch (26 patches). We estimated the selfing rate and immigration rate for each patch. Using 13-122 cones of each patch, we estimated average number of seeds each cone and filled seeds ratio each cone per tree per patch as measures of early fitness. Using a model selection approach, we found a strong inverse relationship between mating patterns, proportion filled seeds and patch size, and only a marginal contribution of isolation. We found that patch size was negatively associated with amount of selfing, immigration, and positively associated with seeds per cone, and proportion filled seeds. For this urban population, large patches minimize selfing and immigration and enhance seed production. Results from this analysis suggest that patch size may be more critical to the maintenance of genetic variation and inbreeding avoidance than connectedness to other patches.

Keeping Forests Healthy

USDA Forest Service Genetic Resources Program

America's forests face the stresses of severe weather, catastrophic fires, and global climate change. Invasive insects and diseases threaten entire populations of plants. Forest Service geneticists are uniquely positioned to help land managers address these challenges by: 1) Developing tree populations that are genetically resistant to nonnative pathogens or insects, 2) Maintaining seed inventories to support reforestation and restoration, 3) Developing seed movement guidelines, 4) Collecting seed and germplasm of species at risk, 5) Establishing seed production areas in native stands, 6) Leading training sessions and workshops on genetics, 7) Promoting genetic diversity of forest and rangeland plant species. National Forest geneticists are helping develop forests that tolerate changes in climate. Predictions indicate some species will not survive without assistance. Geneticists can establish these species in new areas by recommending the most appropriate seed sources.

Applications of Forest Genecology in Adapting to Climate Change

Tongli Wang[1], Sally N. Aitken[1] and Gregory A. O'Neill[2]

[1]Centre for Forest Conservation Genetics, Department of Forest Sciences,
University of British Columbia
[2]Research Branch, BC Ministry of Forests and Range

Genecology is the study of genetic variations in relation to the environment. Climate is a major environmental factor affecting the phenotype of trees, and is also a critical agent of natural selection that has molded among-population genetic variation. Population response functions describe the environmental effect of planting site climates on the performance of a single population, whereas transfer functions describe among-population genetic variation molded by natural selection for climate. Although these approaches are widely used to predict the responses of trees to climate change, both have limitations. We will review these limitation and present a novel approach that integrates both genetic and environmental effects into a single "universal response function" (URF) to better predict the influence of climate on phenotypes. Using a large lodgepole pine (*Pinus contorta* Dougl. ex Loud.) field transplant experiment comprising 140 populations planted on 62 sites to demonstrate the methodology, we show that the URF makes full use of data from provenance trials to: 1) improve predictions of climate change impacts on phenotypes; 2) reduce the size and cost of future provenance trials without compromising predictive power; 3) more fully exploit existing, less comprehensive provenance tests; 4) quantify and compare environmental and genetic effects of climate on population performance; and 5) predict the performance of any population growing in any climate. Finally, we will discuss how the URF to be used as a mechanistic model to predict population and species ranges for the future, and to guide assisted migration of seed for reforestation, restoration, or afforestation and genetic conservation in a changing climate.

Marker Informed Breeding in Tree Improvement: How Does That Work?

Nicholas Wheeler[1] and Tom Byram[2]

[1]Oregon State University
[2]Texas Forest Service and Texas A&M University

For many years (~20) tree breeders have been enticed with the promise that molecular markers may be used to enhance, complement or even replace their traditional selection methods. While markers have many applications in tree improvement program management today (e.g. quality control), their use as selection tools remains largely a promise. Rapid development of genomic scale technologies, including high throughput sequencing, gene and allele (SNPs) discovery, and genotyping platforms, coupled with advances in association genetics, once again provides promise of markers as indirect selection tools. These tools are as useful for adaptive traits as they are for purely commercial traits. The challenge to geneticists is to find and verify real trait / marker associations. The challenge to tree breeders is to determine how to use those associations. This talk outlines some of the approaches tree breeders may consider to use associations.

Tales From the Trichomes -Population and Family Variation in Early Growth Traits and Resistance to *Phytophthora ramorum* in a Common Garden of Tanoak

Jessica Wright[1], Katy Hayden[2], Matteo Garbelotto[2], Richard Dodd[2],
and Richard Sniezko[3]

[1]Institute of Forest Genetics, Pacific Southwest Research Station, USDA Forest Service
[2]University of California, Berkeley
[3]Dorena Genetic Resource Center, USDA Forest Service

Sudden Oak Death (SOD) is a non-native invasive pathogen, responsible for killing millions of trees, many in the California Coast Range. One of the hardest hit species is tanoak (*Lithocarpus densiflora*, but see Manos et al. 2008 for a possible taxonomic revision). For example, in the Big Sur area, near to 100% mortality has been observed in some populations. Moreover, tanoak is one of the few species that the pathogen responsible for SOD, *Phytophthora ramorum* can produce spores on. Tanoak is generally not considered an economically important tree species, and as such has historically received relatively little research attention. Our work has revealed very basic questions that are currently unanswered in tanoaks. Here we discuss research that has taken place over the last 3 years in a common garden environment to understand the levels of quantitative genetic variation in tanoak populations. By comparing estimates for early growth and trichome density to estimates of disease resistance using 3 inoculation techniques, we can gain an understanding of the association and potential costs of disease resistance.

EVENT PARTICIPANT LIST

Western Forest Genetics Association 2009 Meetng
August 9, 2009 - August 13, 2009

1. Tom Adams
   Oregon State University
   Dept. of Forest Ecosytems &Society
   321 Richardson Hall
   Corvallis, OR 97331
   541-937-6583
   w.t.adams@oregonstate.edu

2. Sally Aitken
   University of British Columbia
   Dept. of Forest Sciences
   3041-2424 Main Mall
   Vancouver, BC V6T 1Z4
   604-822-6020
   Sally.Aitken@ubc.ca

3. Andrew Bower
   USDA Forest Service
   3200 SW Jefferson Way
   Corvallis, OR 97331
   541-750-7293
   abower@fs.fed.us

4. Jaroslaw Burczyk
   Kazimierz Wielki University
   Chodkiewicza 30
   85-064, Bydgoszcz Poland
   4852 3419199
   burczyk@ukw.edu.pl

5. Charlie Cartwright
   BC Ministry of Forests
   Cowichan Lake Research Station
   PO Box 335
   Mesachie Lake, BC V0R 2N0
   250-749-6811
   charlie.cartwright@gov.bc.ca

6. Pei-yu Chen
   University of Alberta
   751 General Services Building
   Edmonton, Alberta T6G 2M1
   peiyu@ualberta.ca

7. John Church
   GHH Engineering
   5841 Rich Hill Dr.
   Orangevale, CA 95662
   916-988-7873
   johnchurch@yahoo.com

8. Tom Conkle
   Institute of Forest Genetics-retired
   2530 Nason Ave.
   El Cervito, CA 94530
   510-235-9994
   tfconkle@pacbell.net

9. Denise Cooper
   OSU Forest Egineering Dept.
   321 Richardson Hall
   Corvallis, OR 97331
   541-737-8450
   denise.cooper@oregonstate.edu

10. Sierra Curtis-McLane
    University of British Columbia - Student
    2424 Main Mall
    Vancouver, BC V6T 1Z4
    604-313-8260
    sierracm@gmail.com

EVENT PARTICIPANT LIST

Western Forest Genetics Association 2009 Meetng
August 9, 2009 - August 13, 2009

11. Joan Dunlap
USDA Forest Service
2375 Fruitridge Rd.
Camino, CA 95709
530-642-5031
jdunlap@fs.fed.us

12. Andrew Eckert
University of CA, Davis
One Shields Ave.
2320 Storer Hall
Davis, CA 95616
530-754-5743
ajeckert@ucdavis.edu

13. Lauren Fins
University of Idaho
Dept. of Forest Resources
Moscow, ID 83844
208-885-7920
lfins@uidaho.edu

14. Laura Gray
Unveristy of Alberta-student
9861 87th Ave.
Edmonton, AB T6E 2N4
780-278-6910
lkgray@ualberta.ca

15. Andreas Hamann
University of Alberta
739 General Services Building
Edmonton, Alberta T6G 2H1
780-492-6429
andreas.hamann@ualberta.ca

16. Jim Hamlin
USDA Forest Service
2900 NW Stewart Parkway
Roseburg, OR 97470
541-957-3374
jhamlin@fs.fed.us

17. Valerie Hipkins
USDA Forest Service
2480 Carson Rd.
Placerville, CA 95667
530-622-1609
vhipkins@fs.fed.us

18. Jason Holliday
Virginia Tech
Dept. of Forest Res. & Environ. Cons.
451 Latham Hall
Blacksburg, VA 24061
540-231-7267
jah1@vt.edu

19. Glenn Howe
Oregon State University
321 Richardson Hall
Corvallis, OR 97331
541-737-9001
glenn.howe@oregonstate.edu

20. Kathleen Jermstad
Institute of Forest Genetics
2480 Carson Rd.
Placerville, CA 95667
530-295-3025
kjermstad@fs.fed.us

EVENT PARTICIPANT LIST

Western Forest Genetics Association 2009 Meetng
August 9, 2009 - August 13, 2009

21. Zeki Kaya
Middle East Technical University
Dept. of Biological Sciences
06531, Ankara Turkey
90 312-210 5177
kayaz@metu.edu.tr

22. Angelia Kegley
USDA Forest Service
34963 Shoreview Dr.
Cottage Grove, OR 97424
541-767-5703
akegley@fs.fed.us

23. Michael Landram
USDA Forest Service
1323 Club Drive
Vallejo, CA 94592
707-562-8737
mlandram@fs.fed.us

24. Ron Lanner
Institute of Forest Genetics
2651 Bedford Ave.
Placerville, CA 95667
530-626-7158
pinetree30@comcast.net

25. Bill Libby
Zobel Forestry Associates
28 Valencia Rd.
Orinda, CA 94563
925-376-5896
wlibby2@aol.com

26. Jeremy Littell
University of Washington
Box 354235
Seattle, WA 98195
206-221-2997
jlttell@u.washington.edu

27. Nina Lobo
University of British Columbia - Student
8-365 E 14th Ave.
Vancouver, BC V5T 2M9
778-558-2647
nllobo@interchange.ubc.ca

28. Carol Loopstra
Texas A&M University
Dept. of Ecosytem Science & Mgmt.
TAMU 2138
College Station, Texas 77843
979-862-2200
c-loopstra@tamu.edu

29. John Major
Canadian Forest Service
1350 Regent St.
Fredericton, NB E3B 5P7
506-452-3262
jmajor@nrcan.gc.ca

30. David Neale
University of CA-Davis
Mail Stop 4
262 C Robbins hall
Davis, CA 95616
530-754-8431
dbneale@ucdavis.edu

EVENT PARTICIPANT LIST

Western Forest Genetics Association 2009 Meetng
August 9, 2009 - August 13, 2009

31. Greg O'Neill
BC Ministry of Forests
3401 Reservoir Rd.
Vernon, BC V1T 2X5
250-260-4776
Greg.ONeill@gov.bc.ca

32. David Roberts
University of Alberta-student
4217-36th Ave.
Edmonton, AB T6L 3R8
780-758-3225
drr3@ualberta.ca

33. Anna Schoettle
USDA Forest Service
Rocky Mountain Research Station
240 W Prospect Rd.
Fort Collins, CO 80526
970-498-1333
aschoettle@fs.fed.us

34. Stefan Schreiber
University of Alberta-student
Dept. of Renewable Resources
815 General Services Bldg.
Edmonton, Alberta T6G 2H1
780-492-2540
stefan.schreiber@ales.ualberta.ca

35. Gancho Slavov
West Virginia University
53 Campus Dr.
Morgantown, WV 26506
304-293-5201
gancho.slavov@mail.wvu.edu

36. Victoria Sork
UCLA
Ecol & Evolutionary Biology
Box 95-1606
Los Angeles, CA 90064
310-825-7755
vlsork@ucla.edu

37. Brad St. Clair
USDA Forest Service
3200 SW Jefferson Way
Corvallis, OR 97331
541-750-7294
bstclair@fs.fed.us

38. Detlev Vogler
USDA Forest Service
2480 Carson Rd.
Placerville, CA 95667
530-621-6881
dvogler@fs.fed.us

39. Hongfang Wang
Beijing Normal University
19 Xinjiekouwai St.
College of Life Sciences
100875, Beijing China
86 10 58805291
wht@ucla.edu

40. Tongli Wang
Univ. of British Columbia
3041-2424 Main Mall
Vancouver, BC V6T 1Z4
604-822-1845
tlwang@interchg.ubc.ca

EVENT PARTICIPANT LIST

Western Forest Genetics Association 2009 Meetng
August 9, 2009 - August 13, 2009

41. Jill Wegrzyn
University of CA, Davis
Dept. of Plant Sciences
One Shields Ave., MC 4
Davis, CA 95616
619-316-8548
jlwegrzyn@ucdavis.edu

42. Robert Westfall
USDA Forest Service
PO Box 245
Berkeley, CA 94701
510-559-6438
bwestfall@fs.fed.us

43. Nick Wheeler
Oregon State University
21040 Flumerfelt Rd
Centralia, WA 98531
360-278-3535
nickwheeler@scattercreek.com

44. Jack Woods
Forest Genetics Council
68 Boundary Rd.
Lake Cowichan, BC V0R 2N0
250-715-6285
jwoods.fgc@shaw.ca

45. Jessica Wright
USDA Forest Service
1731 Research Park Dr.
Davis, CA 95168
530-759-1742
jessicawwright@fs.fed.us