WESTERN FOREST GENETICS ASSOCIATION

GENETICS OF FOREST AND WILDLAND CONSERVATION AND RESTORATION

JULY 25-28, 2011

PORTLAND, OR

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Presentations

Posters

WFGA GOALS_____

The Western Forest Genetics Association is an informal organization that has
been dedicated for 56 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 Portland OR, our theme is on the genetics of forest and wildland
conservation and restoration. www.fsl.orst.edu/wfga/

SPONSOR_____

Pacific Northwest Region, USDA Forest Service.

WFGA 2011 Organizing Committee_____

Andy Bower (Chair), USDA Forest Service, Olympic National Forest
Brad St. Clair (Field trip lead), USDA Forest Service, PNW Research Station
Marilyn Cherry (President – WFGA), Oregon State University
Andreas Hamann (VP – WFGA), University of Alberta
Denise Cooper (Treasurer – WFGA), Oregon State University
Glenn Howe, Oregon State University
RC Johnson, USDA ARS , Pullman WA

WFGA 2011 - Genetics of Forest and Wildland Conservation and Restoration

Agenda

Monday, July 25

1:00   **Welcomes** – Andy Bower, Marilyn Cherry, Bov Eave, Vicky Erickson

1:30   **Invited speaker: Jeremie Fant** – Chicago Botanic Gardens - Restoration genetics and the genetic, demographic and community factors that influence restoration success.

2:10   **Invited Speaker: Elizabeth Leger** – University of Nevada, Reno – Local adaptation and rapid evolution of native and invasive plants.

2:50   **BREAK**

3:20   **Invited Speaker: Erin Espeland** – USDA ARS – Maternal effects and their potential to affect restoration success.

4:00   **Mark Lesser** – University of Wyoming - You aren't from around here, are you? Parentage and long-distance dispersal in long-term expansion of disjunct ponderosa pine populations.

4:20   **Kristen Chadwick** – USDA Forest Service – USFS Monitoring on the Margins.

4:40   **Charlie Cartwright** – B.C. Ministry of Forests and Range – Genetic variation in Pacific Northwest *Abies*.

Tuesday, July 26

8:00   **Invited Speaker: Greg O'Neill** – B.C. Ministry of Forests and Range – Adapting to adaptation: Seed Transfer 2.0.

8:40   **Laura Grey** – University of Alberta - Assisted migration to address climate change: recommendations for western Canada.

9:00   **Pia Smets** – University of British Columbia - Growth Response to Climate for Western larch and Western redcedar.

9:20   **Bob Westfall** – USDA Forest Service - Mortality in Subalpine Forests of the Sierra Nevada, California, USA: Differential Response of Pines (*Pinus albicaulis* and *P. flexilis*) to Climate Variability.

9:40   **Brian Knaus** – USDA Forest Service - Early results from the Douglas-fir transcriptome observatory.

10:00   **BREAK**

10:30   <u>**Invited Speaker:**</u> **Zeki Kaya** – Middle East Technical University - Importance of Genetics and Genetic Resource Conservation Programs in the Mediterranean Oaks: Adaptation to Climatic Changes.

11:10   **Amanda de la Torre** – University of British Columbia - Genetic structure of a broad and complex hybrid zone between *Picea glauca* and *Picea engelmanni* along elevational and latitudinal gradients in western North America

11:30   **Warren Devine** – USDA Forest Service - Climate Change and Forest Biodiversity: A Vulnerability Assessment and Action Plan for National Forests in Western Washington.

11:50   **LUNCH and WFGA BUSINESS MEETING**

1:00-2:40 **POSTER SESSION**

2:40   **Tongli Wang** – University of British Columbia - Converting geographically based seed planning units into a climate-based seed-transfer system for adapting to a changing climate

3:00   **BREAK**

3:20   **Andreas Hamann** – University of Alberta – Methods to develop seed zones and seed transfer guidelines for uncertain future climates

3:40   **Ron Beloin** – Oregon State University – Online Mapping of Climate Based Seed Zones with the Seedlot Selection Tool.

4:00   **Brad St. Clair** – USDA Forest Service – Genetic diversity and genecology of bluebunch wheatgrass (*Pseudoroegneria spicata*).

4:20   **RC Johnson** – USDA ARS – Genecology of indian ricegrass and tapertip onion.

4:40   **Andy Bower** – USDA Forest Service – Provisional seed zones for native plants.

<u>Wednesday, July 27</u>

Bus will leave from the parking lot at <u>8:00</u>.

8:00   Leave hotel in Troutdale

9:00   Arrive at Wind River Experimental Forest – Carson, WA

9:00-10:00   Assisted Migration Adaptation Trial, canopy crane research facility (Greg O'Neill – B.C. MFR, Ken Bible - UW)

10:00   Load bus to training center

10:15-11:00 Presentation on WREF history, intro to Hemlock Dam removal project (Chris Donnermeyer and Andrea Ruchty – USFS Gifford Pinchot NF)

11:00-12:00 Walk to Hemlock Dam and view restoration site

12:00-1:00	Lunch
1:00 - 2:00	Tour Wind River Arboretum (Dean DeBell – PNW Research Station Retired)
2:00-2:30	Walk to 1915 Douglas-Fir heredity study site
2:30-4:00	Presentation/discussion at heredity study (Brad St. Clair – PNW Research Station)
4:00-4:30	Walk back to Training Center
5:00-6:30	BBQ dinner
6:30	Depart
7:30	Arrive back at hotel in Troutdale

Thursday, July 28

8:00   **Invited Speaker – Andrew Eckert** – UC Davis – Landscape genomics: Historical approaches for the detection of loci under divergent selection.

8:40   **Invited Speaker – Bryce Richardson** – USDA Forest Service – Assembling the adaptive genetic and genomic pieces in Intermountain shrub species to provide conservation and restoration guidelines.

9:20   **Nick Wheeler** – Oregon State University – Conifer Translational Genomics Network: bringing genomics based breeding to application.

9:40   **Denise Cooper** – Oregon State University – Center for Forest Provenance Data: Current Status and Future Plans.

10:00   **BREAK**

10:20   **Invited Speaker – George Newcomb** – University of Idaho – Role of endophytes in resistance of trees to pathogens and for control of invasive plants.

11:00   **Bob Westfall** – USDA Forest Service – Slow rust resistance in sugar pine.

11:20   **Richard Sniezko** – USDA Forest Service – Genetic Resistance to Pathogens and Insects in Forest Trees: Past, Present, Future and the Prospects under Climate Change.

11:40   **John Church** - Measurement of Carbon Use Efficiency in Ponderosa Pine, White Fir, Redwood and Giant Sequoia.

12:00   **LUNCH**

1:00   Conference ends

Ecological genetics and the genetic, demographic and community factors that influence restoration success.

Jeremie Fant

Chicago Botanic Garden, Glencoe IL

The outcomes of an ecological restoration will depend on a broad spectrum of factors, some beyond our control. Ecological genetics attempts to understand a species genetic structure in the context of the interactions among and between the organisms and their environment. An understanding of the natural processes which shape the genetic architecture of a species can help us determine the appropriate material for restoration and increase the likelihood of attaining a desired restoration outcome. Over the past decade Chicago Botanic Garden has conducted research for a number of forb species, from the Great Basin to the Tallgrass prairies; this has included microsatellite analysis, to look at provenance, common garden studies, to examine adaptive variation, ecological studies to look at genotype-community interactions and experimental crosses to test for inbreeding and outbreeding depression. Molecular markers can reveal significant genetic diversity and divergence among populations associated with variation in provenance, although the main biological factors driving this divergence varied from pollinator preference to historical events; in *Penstemon spp*, the primary pollinator had a strong influence on provenance, while in a rare endemic, *Cirsium pitcheri*, glaciation history played a larger role in the current distribution of genetic diversity than seed or pollen dispersal. With these different drivers of genetic provenance and absence of selection, it is not surprising that these neutral genetic demarcations did not always translate to patterns for divergence in quantitative traits. When populations of *Eriogonum* and *Penstemon* species were grown at two different common garden sites, for all species examined the characters associated with growth showed a strong environmental component, while characters associated with phenology and plant performance varied more by population and was correlated to ecological variation rather than genetic relationships. When variation in flower morphology in one species of *Penstemon* was examined in the field, it was associated with important shifts in pollinator community, suggesting important genotype by community interactions. Long distance crosses, spanning increasing geographic and genetic distances revealed both inbreeding and outbreeding depression in progeny of the bee-pollinated species of *Lobelia* and *Penstemon,* which had the highest degree of population divergence, but not in the first generation of the hummingbird-pollinated species. While additional research on many forb species is urgently needed, these results provide insight into the development of seed transfer zones, restoration outcomes and can help guide the movement and mixing of seeds for different forb species being used in ecological restoration efforts.

Local adaptation and rapid evolution of native and invasive plants

Elizabeth Leger

Department of Natural Resources and Environemental Science, University of Nevada, Reno, NV

There is abundant evidence that plants adapt to particular environments, and it is presumed that a combination of climatic, soil, and biotic factors contribute to patterns of local adaptation observed in the wild. The introduction of invasive species has the potential to change the selective environment, both by directly changing the nature of intraspecific interactions, and in the case of some invaders, indirectly changing other aspects of the environment by, for example, increasing fire frequencies, altering soil properties, or changing soil biota. In these situations, the traits that confer "local adaptation" may radically change over small scales, not because a species has moved in space, but because an invader is present. My lab studies the effect of a particularly aggressive invader, cheatgrass (*Bromus tectorum*) on patterns of adaptation in native perennial grasses in the Great Basin. We have found that contrasting traits improve survival and increase fitness in areas that are within meters of each other, but differ only in the presence or absence of this invader. For example, in invaded areas, seedlings of the native perennial grass *Elymus multisetus* are larger if plants produce more root tips and fewer coarse roots, while in uninvaded areas, the opposite is true.. We have observed changes in additional traits consistent with natural selection by cheatgrass in invaded areas, indicating that different traits increase fitness when plants experience intense competition with invaders. A challenge for restoration is to continue to match traits of transplanted material with local adaptive optima, recognizing that the degree of contemporary disturbance may affect plant fitness as much as historical evolutionary relationships with local environmental conditions.

Maternal effects and their potential to affect restoration success

Erin Espeland

USDA-ARS NPARL, Pest Management Research Unit, Sidney MT

Maternal growing environments affect the germination and growth of plants. How do these maternal affects either help or hinder the success of these seeds within restoration? Using a common western restoration species, *Poa secunda*, we asked how seed production environment determines germination characteristics. Using a common garden design in the maternal generation, we grew twenty genotypes in three environments: Pullman WA, Bend OR, and Sidney MT. We collected seeds from these genotypes and conducted germination tests in growth chambers reflecting the April temperature conditions of each garden. We also planted seeds with and without competition in pots and grew them in growth chambers reflecting the April temperatures of each garden. Competitors were either a non-native perennial grass (*Agropyron cristatum*, or, crested wheat) or a non-native annual grass (*Bromus tectorum*, or, cheatgrass). We found that total germination of *Poa secunda* was always highest in the "OR" growth chamber. However, early germination (germination at day 4) was higher in the maternal environment chamber for seeds collected from OR and MT. Early germination conferred an advantage to *P. secunda* plants by diminishing the size of their competitors. This indicates that for restoration projects, seeds produced at locations close to the restoration may have earlier germination and thus better competitive ability than seeds produced far away.

You aren't from around here, are you? Parentage and long-distance dispersal in long-term expansion of disjunct ponderosa pine populations

Mark R Lesser and Stephen T Jackson

University of Wyoming, Program in Ecology (Dept. of Botany), Laramie, WY

Climate change can influence vegetation in a variety of ways, including increases and decreases in established populations, extirpation of entire populations, and establishment of populations in new locations. Models of vegetation response to changing climate predict shifts in communities with resulting landscapes radically altered from their present states. Colonization of new sites is predicted to be widespread for many tree species, but the mechanisms by which this happens are poorly understood, because establishment and expansion of tree populations may span decades to centuries. To adequately assess how tree species will respond to changing environmental conditions we need to understand the factors controlling recruitment and expansion patterns. One such factor, that can play a major role in population development, is the relative contribution of long-distance dispersal, versus intrinsic growth, over the course of a newly-founded population's development.

To examine the contribution and timing of long-distance dispersal to population growth, we studied four disjunct populations of ponderosa pine, in the Bighorn Basin of north-central Wyoming. These populations are separated from continuous ponderosa pine forest by distances ranging from 15 to over 100 km. There is strong evidence that the initial colonizers are still present, and that there has been no erasure of past trees at the sites, giving us a complete record of population history. All trees in each of the populations were aged using dendroecological techniques and needle tissue was collected and used for molecular genetic analysis at nine microsatellite loci. Microsatellite data were paired with tree-age data to carry out parentage analysis. We used the software package CERVUS to determine parent pairs based on maximum likelihood analysis. Trees establishing from long-distance seed dispersal events were identified as individuals where no parents were found in the population. If one parent was identified from within the population we interpreted this as long-distance pollen dispersal.

We obtained genotypes and ages for >1100 trees. During the first century following initial colonization almost every individual (>80%) was the product of long-distance seed dispersal. The proportion of each population derived from long-distance dispersal decreased over time. This level of immigration may be vital in the early stages of expansion, if populations are to overcome Allee effects and exceed a threshold size, below which they will not persist over the long-term.

Monitoring on the Margins

Forest Health Protection Forest Service Washington Office Program
Kristen L. Chadwick

Monitoring on the Margins (MoM) is a Forest Health Monitoring program initiative for an integrated, enhanced monitoring program for critical ecosystems in areas threatened by insects, disease, and climate change. The Forest Health Monitoring Management Team is charged to develop a template adaptable to any species across the country and a proposal for monitoring at risk tree species. Data collected under this template will tier to the "National Roadmap for Responding to Climate Change" (http://www.fs.fed.us/climatechange/pdf/roadmap.pdf) which proposes targeted monitoring based on vulnerabilities.

The model has been developed as a template for any species of concern, using high elevation, five needle pines as the initial focus for the program initiative. These pines include whitebark, foxtail, Great Basin and Rocky Mountain bristlecone, limber, and southwestern white pine. For the last century, white pine blister rust (WPBR) has spread from its introduction site in the Pacific Northwest, initially devastating western white pine and sugar pine. However, only in the last 20 years has the spread and impact of WPBR on high elevation, five needle pines caused wide concern for the viability of the species. Recent mountain pine beetle epidemics in these pines in the interior West have expanded the concern. Long-term climate warming projections also raise concerns that the habitats of these pine will greatly decrease. Warmer recent weather has also been implicated in the mountain pine beetle epidemics.

A core team have developed a strategy following the monitoring on the margins approach, as outlined in "A Model for Monitoring and Conserving Forest Trees Threatened by Climate Change and Invasive Species", (Smith and others 2009). This approach lays out an eight step process as follows:
1- Creation of a resource distribution map of trees and ecosystems (document the resource)
2- Creation of a multi-threat disturbance map (document current and imminent threats)
3- Combine the resource and threats maps to determine resource conditions at risk (margins).
4- Map existing spatial genetic knowledge for species of interest.
5- Perform regional level assessments to determine high priority monitoring conditions.
6- Determine existing plot coverage and need for (additional) monitoring (what and how).
7- Install, maintain, and analyze monitoring results.
8- Use threat analysis and ongoing monitoring results to direct genetic conservation management activities.

Implications of Patterns of Provenance Variation in PNW Species of *Abies* for Adaptation, Conservation and Gain

Charlie Cartwright and Cheng Ying (retired)

BC Ministry of Forests, Lands and Natural Resources Operations, Cowichan Lake Research Station, Mesachie Lake, BC

Provenance testing of the 4 species of the genus *Abies* that occur in British Columbia has been undertaken by the provincial Ministry of Forests. Trials were established for grand fir (*Abies grandis)* and noble fir (*A. procera*) in the early 1980's and for Pacific silver fir (*A. amabalis*) and sub-alpine fir (*A. lasiocarpa*) ten years ago. All have in common relatively strong provenance effects for growth across broad ranges, but the degree to which the species are closely adapted to their environments differs. Results from the provenance trials are described in terms of implications for silvicultural deployment, and gene conservation in consideration of likely climate change scenarios.

Adapting to adaptation: Seed Transfer 2.0

Greg O'Neill

Tree Improvement Branch, BC Ministry of Forests, Lands and Natural Resource Operations, Kalamalka Forestry Centre, Vernon BC, Canada

A growing body of provenance test data highlights the importance of seed source selection in reforestation and also suggests that climate change will render many tree populations substantially maladapted in the near future, resulting in significant changes in health, productivity and distributions of tree species. Assisted migration – planting seed sources adapted to current and future climates - is emerging as a key strategy to address anticipated maladaptation in forest trees.

These observations have placed a new urgency on the development of seed source selection systems to ensure selected seed sources are adapted to current and future climates. Availability of geographic information systems, fine scale climate models, stronger provenance data, and new analytical techniques have revolutionized opportunities for the development of new seed transfer systems.

This presentation examines opportunities presented by new seed transfer systems and assisted migration, and discusses the design of seed transfer systems from the perspective of their structure, critical seed transfer distance calculation, and delineation methods. A hybrid fixed/focal point seed transfer system and methods to integrate assisted migration into existing fixed and focal point seed transfer systems will be proposed.

Assisted migration to address climate change: recommendations for aspen reforestation in western Canada

Laura Gray and Andreas Hamann

Department of Renewable Resources, University of Alberta, Edmonton AB

Human-aided movement of species populations in large scale reforestation programs could be a potent and cost effective climate change adaptation strategy. Such large-scale management interventions, however, tend to entail the risks of unintended consequences, and we propose that three conditions should be met before implementing assisted migration in reforestation programs: (1) evidence of a climate-related adaptational lag, (2) observed biological impacts, and (3) robust model projections to target assisted migration efforts. In a case study of aspen (*Populus tremuloides* Michaux.) we use reciprocal transplant experiments to study adaptation of tree populations to local environments. Secondly, we monitor natural aspen populations using the MODIS enhanced vegetation index as a proxy for forest health and productivity. Lastly, we report results from bioclimate envelope models that predict suitable habitat for locally adapted genotypes under observed and predicted climate change. The combined results support assisted migration prescriptions and indicate that the risk of inaction likely exceeds the risk associated with changing established management practices. However, uncertainty in model projections also implies that we are restricted to a relatively short 20-year planning horizon for prescribing seed movement in reforestation programs. We believe that this study exemplifies a safe and realistic climate change adaptation strategy based on multiple sources of information and some understanding of the uncertainty associated with recommendations for assisted migration. Ad hoc migration prescriptions without a similar level of supporting information should be avoided in reforestation programs.

Growth response of western larch and western redcedar populations to climate, as evaluated in controlled climate chambers

Pia Smets

Centre for Forest Conservation Genetics, Department of Forest Sciences, University of British Columbia, Vancouver, BC

Appropriate seed source populations need to be chosen based on both their adaptation to present climates as well as their capacity to respond well to future climates. According to bioclimatic envelope models, western larch (*Larix occidentalis*) and western redcedar (*Thuja plicata*) have the potential to substantially increase their range in British Columbia with climate warming, but population responses to future climates need to be better understood to plan assisted migration. It is difficult, costly and time consuming to plant field experiments on sites with sufficiently warm climates to serve as analogs for predicted future conditions. Growth at warmer than current temperatures can easily be achieved in controlled climate chambers, and the resulting data may provide support for moving these species outside of their current climate envelopes. We grew 20 populations of western redcedar and 26 populations of western larch in short term seedling experiments in controlled climate chambers. Simulated climates included five temperature regimes and two moisture levels. These conditions correspond to interior B.C. climates, with mean annual temperatures ranging from 1 to 13 °C. Phenotypic plasticity among treatments for growth and biomass was large for both species, but genetic differences among sources were also evident. These experiments provide baseline data on relative population performance in warmer climates in the absence of wide-ranging established field trials.

Mortality in Subalpine Forests of the Sierra Nevada, California, USA: Differential Response of Pines (*Pinus albicaulis* and *P. flexilis*) to Climate Variability

Constance Millar, **Robert Westfall**, and Diane Delany

PSW Research Stn, US Forest Service, Albany, CA, USA

Widespread forest mortality in high-elevation forests has been increasing across western North American mountains in recent years, with climate, insects, and disease the primary causes. Subalpine forests in the eastern Sierra Nevada, by contrast, have experienced far less mortality than other ranges, and mortality events have been patchy and episodic. This situation, and lack of significant effect of non-native white-pine blister rust, enable investigation of fine-scale response of two subalpine Sierran species, whitebark pine (*Pinus albicaulis*, PiAl) and limber pine (*P. flexilis*, PiFl), to climate variability. We report similarities and differences between the two major mortality events in these pines in the last 150 years: 1988-1992 for PiFl and 2006-ongoing for PiAl. In both species, the events occurred within monotypic, closed-canopy, relatively young stands (< 200 yrs PiAl, < 300 yrs in PiFl); were localized to central-eastern Sierra Nevada; and occurred at 2740-2840 m along the eastern edge of the escarpment on north/northeast aspects with slopes > 40%. Mortality patches averaged 40-80 ha in both species, with mean stand mortality of trees > 10 cm diameter 75% in PiAl and 60% in PiFl. The ultimate cause of tree death was mountain pine beetle (*Dendroctonus ponderosae*) in both species, with increasing 20th/21st C minimum temperatures combined with drought the pre-conditioning factors. Overall growth in the past 150 years suggests that PiFl is more drought hardy than PiAl but responds sensitively to the combined effects of drought and increasing warmth. Although PIAL is less responsive to temperature and precipitation, it is sensitive to water deficits, particularly precedent conditions. After the 1988-1992 drought, surviving PiFl recovered growth. PiAl trees grew very poorly during that drought, and continued poor growth in the years until 2006 when the mortality event occurred in PiAl. A significant species effect is the apparent difference in levels of within-stand genetic diversity for climate factors. Differential growth between 19th C (cool, wet) and 20th/21st C (warming, drying) of trees that died versus survivors indicates that considerable within-stand genetic diversity for climate existed in PiFl, though somewhat less so in PIAL. For both species, the late 20th C mortality event acted as strong natural selection to improve within-stand fitness for warmer and drier conditions.

Early results from the Douglas-fir transcriptome observatory.

Brian J. Knaus[1], Peter Dolan[2], Dee Denver[3] and Rich Cronn[1]

[1]Pacific Northwest Research Station, USDA Forest Service
[2]Department of Mathematics, University of Minnesota, Morris
[3]Department of Zoology, Oregon State University

Despite rapidly-increasing Angiosperm resources, conifer genomic assets remain relatively rare, due in part due to their exceptionally large genome sizes and 200+ million years of divergence from other well-annotated plant models. These obstacles are less daunting if focus is restricted to the expressed portion of the genome, since the 'transcriptome' is considerably less repetitive than the total genome, and meaningful translations are readily inferred via comparisons to gene models from other organisms. Sequencing efforts have resulted in a Douglas-fir reference transcriptome based on Roche/454 sequencing technology. More recently, we have constructed another using strand specific Illumina sequencing, demonstrating the utility of short read technology and foreshadowing a time when this may be a routine exercise. Transcriptome sequencing has resulted in a first characterization of differential expression among taxonomic varieties. Given the dominance of Douglas-fir in western U.S. ecosystems, we expect this transcriptome reference to have immediate relevance for a wide array of uses, including wood products utilization, evolutionary biology, carbon sequestration, and defining the impact of climate change on key forest species.

Importance of Genetics and Genetic Resource Conservation Programs in the Mediterranean Oaks: Adaptation to Climatic Changes

Zeki Kaya

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

Fossil records indicate that oaks (*Quercus*) were evolved during secondary and tertiary period. Oaks are naturally distributed in the temperate and dry zones of the northern hemisphere. It is generally accepted that most oaks were evolved in places where most diversity resides today, suggesting the primary refuge areas. About 28 of over 400 world-oak species were native to the Mediterranean Region. Oak species of the Mediterranean Region range from rare and endangered to widespread. Natural hybridization is common among oak species that make the systematic studies and priority settings in conservation efforts to be difficult tasks to handle. When certain species (e.g., *Q.cerris*) involved in mixed oak forests, natural hybrids are prevailing with display of mainly hybrid donors vs. receiver species. Many oak species are managed as coppice forests which are physiologically getting older and requiring to be converted to high forests. Genetic information from neutral markers and adaptive traits is incomplete and partial. Genetic studies are concentrated on a few species such as *Quercus petraea, Q.robur, Q.suber*. Especially studies on ecogenetics of species lack. Predicted climate change will increase the frequency and the intensity of droughts in the Mediterranean Region, likely reducing growth and increasing mortality of many oak species, in turn, reduction in natural range of some species (red and white oaks) while increase (sclerophyllous oaks - *Q. coccifera, Q. ilex, Q.suber, Q. aucherii*) in others. Oak forests will play vital role in sustainable agriculture, range management, and forestry in changing climate, but it requires well planned and structured genetic resource conservation programs. Especially, dynamic *in situ* conservation programs for priority species and areas which will be based on genetic information and genetic refugia should be initiated for the Mediterranean countries. The further implication of genetic resource conservation in oaks with respect to climate change and oak forestry will be provided in the presentation.

Genetic structure of a broad and complex hybrid zone between *Picea glauca* and *Picea engelmanni* along elevational and latitudinal gradients in western North America

Amanda De La Torre and Sally Aitken

Centre for Forest Conservation Genetics, Department of Forest Sciences, University of British Columbia, Vancouver, BC

Picea glauca (white spruce) and *Picea engelmanni* (Engelmann spruce) are two closely related species that hybridize extensively in British Columbia and the western part of Alberta. Both species and their hybrids are economically important, with tens of millions of trees planted annually for reforestation. We analyzed 86 single nucleotide loci and 10 microsatellite loci from 800 individuals distributed across the zone. The results of the analyses indicate that seed collected from parents below between 600 and 1800 m elevation are highly introgressed and have a greater contribution on average from Engelmann than from white spruce. Pure white spruce, found below 600 m elevation, is rare. Both hybrid index and quantitative traits show strong elevational clines and moderate latitudinal clines corresponding to climatic gradients in temperature and precipitation. Analysis of survival, height, bud burst and bud set from progeny trials established by the B.C. Ministry of Forests, Lands and Natural Resources Operations indicate that hybrids are fitter than parental species s in their own environments, suggesting the hybrid zone is maintained by selection gradients due to environmental heterogeneity. The high proportion of advanced generation hybrids indicates that introgression is extensive and that the zone is likely old. Introgression appears to be asymmetric with backcrossing disproportionately towards Engelmann spruce, possibly reflecting differences in reproductive phenology or other types of hybrid incompatibility. This bias to reproduction may be a substantial challenge to forest breeders and managers because Engelmann spruce is slower growing than white spruce and as climates change, Engelmann spruce will likely become less adapted to many reforestation environments.

Climate Change and Forest Biodiversity: A Vulnerability Assessment and Action Plan for National Forests in Western Washington

Carol Aubry, **Warren Devine**, Robin Shoal, Andrew Bower, Jeanne Miller, and Nicole Maggiulli

USDA Forest Service, Olympic National Forest, Olympia, WA

Significant changes in climate are projected for the Pacific Northwest during the 21st century, with increasing temperatures and altered seasonal hydrology. However, there is limited information on climatic tolerance for many tree species and even less information on what complex interactions could result from ecosystem-wide exposure to a changing environment. We sought to answer the question: how can the national forests in western Washington conserve biodiversity and increase resiliency given the predicted changes in climate? In this project, we: (1) conducted a climate change vulnerability assessment of forest tree species, (2) assessed the vulnerability of non-forested habitats to climate change, and (3) proposed practical management actions that can be implemented by national forests in cooperation with other land managers. Although our emphasis was on the national forests, our analysis included all public lands and should be useful to a wide range of managers. For each of the area's tree species, we compiled information relevant to climate change and created maps of documented occurrences. After exploring multiple options for assessing relative vulnerability of tree species to climate change, we selected the Forest Tree Genetic Risk Assessment System (GRAS) (Potter and Crane 2010). Our application of GRAS included five climate change risk factors used to rate each species' vulnerability: distribution, reproductive capacity, habitat affinity, adaptive genetic variation, and insect and disease threats. The species with the highest climate change vulnerabilities generally were higher-elevation species, with Pacific silver fir, subalpine fir, and Engelmann spruce scored most vulnerable. The most common tree species of the region, Douglas-fir, western hemlock, and western redcedar, had low vulnerability scores. Based on regional experts' knowledge and the scientific literature, we identified three non-forested habitat types especially vulnerable to climate change: alpine and subalpine ecosystems, native dry grasslands, and wetlands. Overall, our analysis showed that, although climate change impacts may be numerous and complex, the trees and non-forested habitats at high elevations are at greatest risk. We made specific recommendations to managers that fell under three categories: (1) learn about and track changes in plant communities as the climate changes, (2) maintain and increase biodiversity and increase resiliency through vegetation management and gene conservation, and (3) prepare for the future by choosing management activities that will work under a variety of climate scenarios. Our western Washington analysis is published, and we are now analyzing the other forested areas of Washington and Oregon. Region-wide results will be published in 2012.

Converting geographically-based seed planning units into a climate-based seed-transfer system to adapt to a changing climate in British Columbia

Tongli Wang and Sally N. Aitken

Centre for Forest Conservation Genetics, Department of Forest Sciences, University of British Columbia, Vancouver, BC

Current seed transfer guidelines in British Columbia are based on geographically delineated Seed Planning Zones (SPZs) and Units (SPUs). To facilitate seed transfer in consideration of climate change, we have developed a method to convert these SPUs into a climate-based seed transfer system that can be dynamically adjusted according to climate change projections for future periods. This method involves the following steps: 1) modeling the geographically based SPUs with climate variables generated by ClimateWNA using Random Forest; 2) constructing climatically delineated basic units (CDBUs) that cover the entire province and shift in geographical locations with climate change; 3) migrating the predicted SPUs to the CDBUs; and 4) projecting the shifts of the climate-based SPUs in future climates. In modeling the current SPUs, we found that some areas outside of the current SPUs occupy the same bioclimate envelopes as some SPUs, while some current SPUs are redundant and therefore separate units are not necessary. Thus, the bioclimate envelopes of the current SPUs (i.e., the predicted SPUs) were used as the basis to develop the climate-based seed transfer system. For the CDBUs, we used the bioclimate envelopes of biogeoclimatic variants (BGC variants) in the BC biogeoclimatic ecosystem classification, which were predicted in our previous study. The bioclimate envelopes of the SPUs were migrated to the CDBUs through climatic matching. As changes in the CDBUs can be predicted for future time periods, seed transfer guidelines can then be dynamically adjusted over time. In addition, the climate-based feature of the new system will allow us to integrate climatic response functions of populations and species into the new seed transfer system to optimize forest resilience and productivity.

Methods to develop seed zones and seed transfer guidelines for uncertain future climates

Andreas Hamann

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Managing seed movement is an important component of forest resource management to minimize maladaptation of planting stock in forest plantations. I describe a new approach to analyze geographic patterns of adaptive and neutral genetic variation in forest trees, and to link this genetic information to geographic or environmental variables for the delineation of seed zones and the development of seed transfer guidelines. I apply multivariate regression trees to partitioning genetic variation, using a set of environmental or geographic predictor variables as partitioning criteria in a series of dichotomous splits of the genetic dataset. The method can be applied to any type of genetic data (growth, adaptive, or marker traits), and can simultaneously evaluate multiple traits observed over several environments. The predictor variables can be categorical (e.g. ecosystem of seed source), continuous (e.g. geographic or climate variables), or a combination of both. With climate variables as predictors, the approach reveals adaptation of genotypes and how seed zones may shift under anticipated climate change.

Online Mapping of Climate Based Seed Zones with the Seedlot Selection Tool

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The *Seedlot Selection Tool* (SST, http://sst.forestry.oregonstate.edu) is a Web-based decision support tool to help forest managers choose *seedlots* that are well adapted to a chosen planting site, or *planting sites* that are appropriate for a particular seedlot. Geographically defined zones are used commonly to match genetically adapted seed sources to planting sites. However, climate based zones are now possible, and may be especially critical with future changes in climate. The SST leverages recently developed regional climate models, genecological research, and climate change modeling to generate species specific, climate based, focal point seed zones. The tool generates maps of climate based zones that match user-selected climate variables and transfer limits. These maps may be of current (recent historical) climate conditions or future predicted climate conditions under various climate models and emission scenarios. The SST is a planning and educational tool that is particularly suitable for exploring alternative future conditions, assessing risk, and planning potential responses, including assisted migration. We will describe the underlying concepts, demonstrate the basic functions, and show how to use the tool with your own parameters, management practices, climate change assumptions, and integrated risk assessments.

Genetic diversity and genecology of bluebunch wheatgrass (*Pseudoroegneria spicata*)

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Bluebunch wheatgrass (*Pseudoroegneria spicata*) is a cool-season, long-lived, self-incompatible, perennial bunchgrass of semi-arid regions of western North America. It is found in a wide variety of habitats, is a dominant species of many grasslands, and is widely used in restoration after fires. The wide distribution across a diverse range of climates suggests that bluebunch wheatgrass is genetically variable, and much of that variation may be adaptive. We evaluated bluebunch wheatgrass populations from the inland Northwest in three common garden tests in eastern Washington and western Idaho to explore the magnitude and patterns of genetic variation, to relate population variation to the environments of seed sources, and to delineate seed zones based on those results. Considerable variation was found among populations for traits of growth, reproduction, leaf morphology, and floral phenology. Moderate correlations of population means with the climates of seed sources suggest the presence of adaptively significant genetic variation that should be considered when moving populations in restoration projects. Geographic genetic variation was mapped based on the relationships between traits and climate, and seed zones were delineated to help guide the choice of adapted populations for revegetation and restoration projects in grasslands in the interior Pacific Northwest.

Genecology of Indian Ricegrass and Tapertip Onion

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Much of the Western U.S. is dominated by semiarid to arid landscapes essential for wildlife habitat, recreation, and grazing resources. However, urbanization, climate change, frequent fires and increasing pressure from invasive weeds are interacting to cause an unsustainable cycle of environmental degradation to plant communities. Often a single source of germplasm is used for revegetation or restoration across a region without considering its suitability from an adaptive or ecological perspective. Genecology to develop seed transfer zones based on the intersection of genetic diversity and climate may be the best approach to guide restoration and promote conservation of genetic diversity in situ. Although commonly used for conifers, genecology and seed zone development has not been completed for most shrubs, grasses, and forbs. Genecology studies and seed zone mapping was completed for two key North American rangeland species, Tapertip onion (*Allium acuminatum*) in the Great Basin, and Indian ricegrass (*Achnatherum hymenoides*) across the Southwester U.S. Collection of germplasm was completed to represent diverse geographic and climatic areas and evaluated in common gardens for production, phenology, and morphology traits. Analyses of variation were conducted to identify plant traits with genetic variation and of potential adaptive value. Multivariate statistics were used to generate genetically based composite plant traits that accounted for a large fraction of the total variation. And finally, regression of multivariate plant traits was completed to derive models for mapping seed transfer zones across the landscape. Common garden studies showed strong differences in plant traits from diverse seed source locations for both species ($P<0.01$), indicating strong genetic variation. Correlation linked seed source location environmental variables such as temperature and precipitation with production and phenological plant traits, suggesting that genetic variability was associated with adaptation. Regression of multivariate trait scores on location environmental variables resulted in models with R^2 values ranging from 0.52 to 0.72. These models along with GIS methodology were used to map seed zones to guide restoration of tapertip onion and Indian ricegrass. We recommend that genecology studies for additional key restoration species be pursued.

Generalized Provisional Seed Zones for Native Plants

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Deploying vigorous, well adapted, and ecologically appropriate plant materials is a core component of a successful restoration project. The key to identifying appropriate plant materials (e.g. seeds) lies in understanding the genetics of adaptation through common garden studies. However, restoration practitioners often deploy plant species on the landscape for which no seed transfer guidelines have been established through genetic research. So what are practitioners to do when no seed transfer guidelines have been established for a species of interest? We have developed generalized provisional seed zones that can be applied to any plant to help guide seed movement. These seed zones area based on the intersection of high resolution (800m x 800m cell size) observed climatic data. The intersection of winter minimum temperature and annual precipitation delineates zones for trees, shrubs, and woody plants, while the intersection of average maximum termperature and precipitation is used for zones for grasses and herbaceous plants. The resulting seed zones represent areas of relative climatic similarity, and movement of seed within these zones should help to minimize maladaptation. Superimposing Omernick's level III ecoregions over these seed zones helps to distinguish areas that are similar climatically yet different ecologically. These provisional seed zones should be considered a starting point as guidelines for seed transfer, and should be utilized in conjunction with appropriate species specific information as well as local knowledge of microsite differences.

Landscape genomics: Historical approaches for the detection of loci under divergent selection

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Standing patterns of nucleotide diversity within forest tree populations result from the interplay of numerous ecological, genetic and evolutionary processes. Inferences about the processes that produced these patterns can be made under simplifying assumptions, which forms the logical basis of most outlier tests for natural selection. It has been shown repeatedly, however, that incorporation of samples from multiple time points vastly improves inference from standing patterns of nucleotide diversity. Here, I use an analogous framework to address patterns of divergent selection across sampled populations of coastal Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco var. *menziesii*) and loblolly pine (*Pinus taeda* L.) that, while not based directly on samples from multiple time points, encapsulates the same logic. This method first uses large samples of genotyped single nucleotide polymorphisms (SNPs) to make inference about standing levels of population structure. This inferred structure is then leveraged to estimate allele frequencies in the ancestral population of the identified genetic clusters, from which population-specific values of F_{ST} are calculated for each extant population. Finally, these population-specific values of F_{ST} are correlated to various measures of environmental change since the Last Glacial Maximum. Applications of this method to ~300 SNPs for coastal Douglas-fir and ~4,000 SNPs for loblolly pine revealed several striking patterns consistent with diversifying selection across populations for both species. In total, 10 out of 119 candidate genes for Douglas-fir and 351 out of 3,393 unigenes for loblolly pine were identified as overly correlated to environmental change since the Last Glacial Maximum. The implications of these results, as well as the limitations and further developments of this methodology will be discussed.

Assembling the adaptive genetic and genomic pieces in Intermountain shrub species to provide conservation and restoration guidelines

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Shrub species occupy much of the desert and semi-desert ecosystems of the West. In most cases critical genetic information necessary for restoration and mitigation of climate change is lacking. Studies that address both adaptive and neutral genetic variation are required to meet this need. Next-generation sequencing approaches can be advantageous for these non-model species, because they require no prior sequence information. We report on two approaches that utilize next-generation sequencing to elucidate SNPs for inference into the population genetics and phylogeography of big sagebrush (*Artemisia tridentata*) and blackbrush (*Coleogyne ramosissima*). A transcriptome approach was used in big sagebrush. RNA from leaf tissue was sequenced in three subspecies: *vaseyana*, *tridentata*, and *wyomingensis*. Assemblies from these reads were mined for SNPs and validated. Forty-eight genes were selected based on SNP patterns within putative secondary metabolite pathways. These genes were PCR amplified and resequenced in 370 individuals from 54 collection sites. In blackbrush a different approach that sequences fragments directly from DNA was used. This genotype by sequencing approach will be compared with an amplified fragment length polymorphism (AFLP) dataset. These sequencing projects are designed to complement ongoing common garden trials of these species. The merits of these sequencing approaches will be discussed along with preliminary data from common gardens.

Conifer Translational Genomics Network: bringing genomics based breeding to application

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The Conifer Translational Genomics Network (CTGN) consists of researchers from six institutions representing tree improvement cooperatives, genomics laboratories, and USDA Forest Service research projects responsible for developing most of the conifers planted in the United States. The goal of the CTGN project is to provide tree breeders with the genomic based tools to make traditional tree breeding both more effective and efficient. The four year project, funded by the USDA National Institute for Food and Agriculture (formerly CSREES) and the USDA Forest Service, seeks to leverage more than 50 years of traditional population development conducted by the tree improvement cooperatives with the genomic and population genetics skills provided by researchers at those same institutions and UC Davis. Additional activities supported by the project include comprehensive education and outreach programs and the development of genetic stock center for both southern pine and Douglas fir. While each institution has its own research emphasis, all are based on the use of genotyping large numbers of single nucleotide polymorphisms (SNPs) for substantial numbers of individuals. This data is being used to characterize genetic variation in managed populations, seek signatures of natural and artificial selection, and improve selection efficiency through marker-trait association and development of better analytical tools. Just as the CTGN was built on previous research, one of its chief accomplishments has been to provide impetus and tools for future projects, most notably the recently announced Pine Reference Sequence Project and the Southern Pine Climate Change Mitigation and Adaptation Project. A brief overview of significant progress emerging from the CTGN will be presented as well as a summary of findings from the recently completed symposium on genomics based breeding in forest trees held in Davis, CA in late June, 2011.

Center for Forest Provenance Data: Current Status and Future Plans

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The Center for Forest Provenance Data has developed a centralized data and information management system to archive and make available to researchers data from long-term provenance tests and seedling genecology studies. A wide variety of datasets with different test site designs, provenance and parent-tree locations, treatments applied, and response variables are regularly handled. The web program for submitting and accessing the data is in place to make the procedure as straightforward and user-friendly as possible. Data is submitted in five components: general study information, accession information, test site information, response data and associated metadata, and contact information. The data retrieval process uses a search engine to call up the data in Excel 2003 or Excel 2007 formats. Security measures are applied, and data from studies around the world are now available. The end-result of this will be to promote collaboration to improve our understanding of forest genetics and plant adaptation to help guide management decisions to ensure adapted, healthy, and productive forests.

Endophytes influence resistance to pathogens, growth, fecundity, thermotolerance and competitiveness of plants.

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Endophyte influences on resistance to pathogens can be demonstrated with both forest trees and herbaceous plants. With white pine blister rust, poplar leaf diseases, and Centaurea rust, we have shown that endophytes can have significant local and systemic effects. Endophytes can also significantly influence plant growth, fecundity, thermotolerance, and competitiveness, all of which we have investigated with herbaceous plants as models. However, in spite of exciting, new research, endophytes remain more of a potentiality than an actuality in forestry. Of many upcoming challenges to endophyte applications in forestry, four will be discussed: 1) the assay-based, selection problem, 2) the question of replacement dynamics within complex, endophytic communities, 3) the need to complement the objectives of tree improvement programs, and 4) the difficult decisions that will need to be made on deliberate introductions of selected endophytes outside sites where they were initially discovered.

Strong Partial Resistance to White Pine Blister Rust in Sugar Pine

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Sugar pine, one of the most susceptible to the blister rust fungus (*Cronartium ribicola*) of all white pines, has a major gene (*Cr1*) at low frequency in populations that confers immunity to the disease. Sugar pines bearing at least one copy of *Cr1*, however, are vulnerable to specific virulence from a complementary gene (*vcr1*) in the pathogen. Partial resistance (PR; aka, slow-rusting) is a suite of traits that reduces susceptibility to blister rust in pines challenged by either the avirulent (*Avcr1*) or virulent (*vcr1*) forms of the pathogen. Combining the two types of resistance in synthetic lines could be mutually reinforcing by reducing the likelihood of infection in pines challenged by either pathotype.

In 2006, a plantation was established at Happy Camp in northwestern California to assess the degree and inheritance of PR in 135 sugar pine families having diverse pedigrees. Progenies consisted of open-pollinated seedlings from survivors of previous epidemic waves on the same site (all presumed to carry some degree of PR), control-pollinated families from parents with known or suspected PR, and bulk seed lots from wild stands, presumed to be highly susceptible. Since 2006, all progenies have been naturally exposed to blister rust at the test-site, in which alternate host *Ribes* spp. have been interplanted among the rows. Progenies were evaluated in 2010 after successive wave years of *C. ribicola* caused overall infection to reach 70%. Numbers of separate infections were counted on each seedling and characterized as normal susceptible or reactive PR responses. Families varied from 10 to 100% in the percentage of progeny with normal susceptible infections. Mean infections per family ranged from 0.39 to 12.03 infections per tree, a 30-fold difference; normal infections in 2011 ranged from 100% to 12%. The most susceptible families were from open-pollinated parents from wild stands, or parents with a history of yielding susceptible offspring. Families with the least infection tended to come from F1 parent survivors from prior epidemics. As expected, the presence of the *Cr1* gene in a parental genotype had no effect on PR responses of the progeny. PR was demonstrably strong in some crosses and presents opportunities for combining PR with major gene resistance to develop long term, durable resistance. The 2010 and 2011 readings indicate consistency of results among families.

Genetic Resistance to Pathogens and Insects in Forest Trees: Past, Present, Future Utilization and the Prospects under Climate Change

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Forest trees in natural ecosystems, planted forests, and urban plantings are subject to serious damage or mortality, including potential extinction, by an array of biotic organisms or abiotic events. To counter these impacts, many of which are from non-native pests, new and ongoing programs to develop genetic resistance in a number of our native trees are underway and have made good progress. Developing this natural genetic resistance represents a key and sometimes the only method for retaining some trees species as healthy components in our natural or planted forests. It also has the advantage that it is a natural 'green' path to implement with little or no negative 'side-effect' consequences. Knowledge of the pattern of susceptibility and resistance over the landscape provides options for establishing economically viable plantations and urban plantings, as well as restorative plantings; and opens up the option of proactive strategies.

The information learned from current resistance programs can be used to help fast-track the discovery and utilization of resistance in other programs. Recent work in the high-elevation five-needle pine species such as whitebark pine, limber pine, southwestern white pine and Rocky Mountain bristlecone pine has been greatly accelerated from the knowledge gained earlier in the ongoing resistance programs for western white pine and sugar pine. For several of these species, over the last five to 10 years, resistant trees have been verified via seedling screening tests and the first plantings have been established. Seedling screening assays or future molecular tests for genetic resistance can greatly accelerate finding resistance, but these must be complemented by long-term field trials.

Some types of resistance are useable immediately; others may need breeding to increase the overall level and/or combinations of resistance. Resistance levels vary, depending on the tree species, the biotic agent, the site hazard, whether seed or vegetative propagules are used, and the level of improvement. Continued monitoring and research, as well as support for operational programs is needed to evaluate the durability of resistance, its efficacy under a changing climate and varied site conditions, as well as to refine site hazard information, develop other management tools to complement resistant stock, and to fast-track the development and utilization of higher levels (or combinations) of resistance in existing and future programs.

Measurement of Carbon Use Efficiency in Ponderosa Pine, White Fir, Redwood and Giant Sequoia

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Growth rates of plant tissues depend on both the respiration rate and efficiency with which carbon is incorporated into new structural biomass. Calorespirometric measurement of respiratory heat and CO_2 rates, from which both efficiency and growth rate can be calculated, is a well established method for determining the effects of rapid temperature changes on the respiratory and growth properties of plant tissues. Data on the temperature dependence of the substrate carbon conversion efficiency (ε) are tabulated. These data show that ε is maximum and approximately constant through the optimum growth temperature ranges and decrease rapidly as temperatures approach temperature limits to growth. ε measured on ponderosa pine ranged from 0.0 to 1.0 with means at 10°C, 15°C, 20°C, 25°C, 30°C and 35°C of 0.730, 0.726, 0.698, 0.662, 0.696, and 0.620, respectively. This is consistent with the 0.6 to 0.8 range typically reported in literature. Data will be provided for white fir, redwood and giant sequoia.

POSTER PRESENTATIONS

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

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Wood stiffness (modulus of elasticity (MOE) is one of the most important mechanical properties of structural lumber, but generally declines as rotation lengths are shortened. Previous research on Douglas-fir (*Pseudotsuga menziesii*) indicates that log-based and standing-tree acoustic tools can be used to measure and select for improved bending stiffness of 25-year-old Douglas-fir trees. We now want to understand the relationships between these log-based tools and standing-tree tools on younger age classes to determine the most promising standing-tree tools and approaches to use in progeny tests. There is a strong interest in measuring and selecting for wood stiffness at younger ages (e.g., 6-12) but we do not know which approaches are best, or what results to expect. Furthermore, genetic improvement of wood stiffness in western hemlock (*Tsuga heterophylla*) has not been studied. Therefore, our long-term objectives are to (1) evaluate alternative methods for measuring wood stiffness on young trees of Douglas-fir and western hemlock, (2) estimate genetic parameters and potential genetic gains for juvenile wood stiffness in both species, (3) develop optimal measurement and genetic selection scenarios for both species, and (4) estimate phenotypic age-age correlations for Douglas-fir wood properties. Acoustic velocity was measured on 9-12 trees of Douglas-fir and hemlock at each of 5 operational plantations with four standing-tree acoustic tools: Microsecond Timer, TreeSonic, TreeSonic with different sensors (SD02), and Ultrasonic Timer. For each tool, we tested the same-face versus opposite-face methods of placing the acoustic probes, and compared measurements made within interwhorls versus across branch whorls. We calculated correlation coefficients between all combinations of tools and techniques across all 5 sites. Based on these results, we concluded that the same-face method appears to be more reliable than the opposite-face method. We also concluded that measuring across a whorl of branches seems to have little adverse effect in these young trees, and may be superior if one can measure acoustic velocity across a longer distance. Using the same-face method, correlations among interwhorls are about the same in both species. For the next steps, we will compare our standing-tree acoustic measurements to log-based measurements and then use the most promising standing-tree tools and methods in progeny tests of Douglas-fir and western hemlock to estimate heritability and calculate potential genetic gains for each species.

Genome-wide effects of selective breeding on adaptive diversity for future climates

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Trees have a long evolutionary history of adapting to climatic fluctuations, but the effect of anthropogenic climate change on forest productivity in the foreseeable future is uncertain. To address this, AdapTree is a large-scale forest genomics project. The AdapTree project aims to identify adaptive SNPs linked to climatic variables that influence forest productivity, quantify the geographic distribution and levels of variation for them, and produce research outcomes that can inform future re-distribution of forest genetic material in western Canada to mitigate climate change effects on timber production.

As a component of AdapTree, my PhD research will investigate the effects of selective tree breeding on adaptive diversity and divergence through the following four questions: 1) What effects does selective tree breeding have on adaptive genetic diversity? 2) How much do adaptive phenotypic traits differ between natural populations and seed orchard-produced reforestation seedlots? 3) Are there correlated responses to selection height and phenotypic traits that are important to local adaptation to climate? 4) How much genetic divergence is there between natural populations and seed orchard reforestation material?

For each species I plan a common garden experiment with 1000 seedlings from seed orchard seedlots and 1000 seedlings from natural seedlots, sampling the range of lodgepole pine and interior spruce in British Columbia and Alberta. In addition to SNP genotyping for approximately 1500 SNPs, seedlings will be phenotyped for five key types of traits over a three-year period: bud phenology, cold hardiness, heat stress tolerance, drought stress tolerance, and growth.

This study will facilitate evaluation of reforestation standards for genetic diversity and provide a detailed assessment of how the current selective tree breeding process with height as the primary selection trait, affects adaptive genetic diversity and composition for other climate-related phenotypic traits that ultimately influence sustainable timber production.

SEEDZONE MAPPER: A Mapping & Planning Tool for Plant Material Development, Gene Conservation and Restoration

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Deploying vigorous, well adapted, and ecologically appropriate plant materials is a core component of a successful restoration project. To better understand the genetics of adaptation and identify appropriate plant materials (e.g. seeds) for restoration, the USDA Forest Service, BLM, ARS and NRCS have generated considerable data from common garden studies and other research activities relating to seed zone development for key native species. In addition, climate-based provisional seed zones have been developed to assist practitioners in matching seed sources and planting site conditions as closely as possible when empirical genetic data are not yet available. The SEEDZONE MAPPER application allows a broad array of end-users to easily view and acquire available data on seed zones for use in plant material development and gene conservation and restoration activities. Data sources include species-specific seed zones from completed common garden studies as well as climate-based provisional seed zones. Client applications range in functionality from a simple geobrowser (requires only a web browser) to ArcGIS ArcMap, a full-feature GIS software platform that allows the user to integrate their own data and create map layouts. The SEEDZONE MAPPER application is available at: http://www.fs.fed.us/wwetac/threat_map/SeedZones_Intro.html.

SEEDZONE MAPPER is part of a family of Wildland Threat Mapping (WTM) applications developed by WWETAC (USFS Western Wildland Environmental Threat Center, Prineville, OR) to portray the spatial interactions of wildland threats and high value resources that occur in wildlands. In WTM, users can evaluate seed zones in relation to other map services and wildland threats published by WWETAC such as climate change projections or wildfire risk. WTM can be accessed at: http://www.fs.fed.us/wwetac/threat_map/index.html.

Genetic diversity and population structure of golden chinquapin (*Chrysolepsis chrysophylla*).

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Golden chinquapin (*Chrysolepsis chrysophylla*) is a broadleaved evergreen that grows in coniferous forests from coastal central California to the Olympic Peninsula in Washington. Its range is nearly continuous from the Coast Range of northern California to the Columbia River. A peripheral population in Skamania County just north of the Columbia River and a disjunct population on the Olympic peninsula are the only occurrences of the species in Washington. Because of its rarity, it is on the Forest Service Region 6 Regional Forester's Sensitive Species List for National Forests in Washington and is listed as a State of Washington Sensitive species (rank G5S2). *C. chrysophylla* is also the only known host to the golden hairstreak butterfly (*Habrodais grunus herri*), which is listed as sensitive by the U.S. Forest Service and a Candidate species by Washington State Department of Wildlife (proposed State Endangered). Because the Olympic Peninsula population is at the northernmost part of the species range and is reproductively isolated, it likely has developed significant genetic differences and environmental tolerances than the populations in the core of the species range. A range-wide sampling of golden chinquapin populations will be used to determine levels of genetic diversity and population structure which is currently unknown. This information will be crucial in developing a conservation plan for this species in Washington.