Advances in Genetic Resources: Management for an Uncertain Future

2015 Joint Meeting:
Western Forest Genetics Association and
Northwest Seed Orchard Managers Association

June 23-24, 2015
University of Washington, Botanic Gardens
Seattle, Washington

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WFGA/NWSOMA meeting – June 23-24, 2015.

University of Washington, Center for Urban Horticulture
Seattle WA

TUESDAY AM JOINT SESSION

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8:20 – 12:00 APPLIED GENOMICS: SCIENCE AND PUBLIC PERCEPTIONS

Invited Talks

8:20 – 9:00 Ross Whetten – *What are genomic technologies, and are they cost-effective for applied tree breeding?*
9:00 – 9:40 Sally Aitken – *AdapTree survey results of public perception of genetics*

9:40 – 10:00 Break

10:00 – 10:40 Kevin Folta - *Rethinking Communication in Agricultural Biotechnology*
10:40 – 11:20 James Curry and **Cintia Ribeiro** - *Public Policy Challenges in Agricultural Biotechnology and Opportunities in Tree Biotechnology*
11:20 – 12:00 Panel discussion – Mike Warjone, facilitator

12:00 -1:00 Joint Lunch

1:00 – 3:00 CONCURRENT WFGA AND NWSOMA SESSIONS

NWSOMA session

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1:45 – 2:00 *New Orchard Technology – Drone use in orchard management* - **Mike Crawford (BLM)**
2:00 – 2:45 *Efficacy of systemic injections of emamectin benzoate and imidacloprid to control Douglas-fir cone gall midge and fir coneworm in Douglas-fir seed orchards* - **Alex Mangini (USFS)**

2:45 – 3:00 *Succession planning in industrial orchard management and contractor recruitment* - **Mike Warjone**, Port Blakely Tree Farms and **Keith Jayawickrama**, NW Tree Improvement Cooperative

WFGA CONCURRENT SESSIONS

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1:35 – 1:55 **Ian MacLachlan** - *The effects of selective breeding on adaptive phenotypic traits in interior lodgepole pine.* **(Student)**
1:55 – 2:15 **Cheng Ding** - *Genetic parameters of growth and adaptive traits for aspen (Populus tremuloides): implications for tree breeding.* **(Student)**
2:15 – 2:35 **Jon Degner** - *Using genotyping-by-sequencing (GBS) to elucidate population structure in Oregon white oak (Quercus garryana).* **(Student)**
2:35 – 2:55 **Marcus Warwell** - *Phenotypic selection and genecology of growth rhythm in whitebark pine (Pinus albicaulis) grown 12 years under climate warmer and drier than climate of origin.* **(Student)**
2:55 – 3:15 **Andy Bower** – *Population genetics of Baker cypress*

3:15 – 3:45 Break

3:45 – 5:30 Tour of Center for Urban Horticulture/Arboretum/Campus interests

5:30 - 6:30 Poster Session/cocktail hour

6:30 - 9:00 Banquet at CUH – Jack Nesbit speaking

WEDNESDAY AM JOINT SESSION

8:00-10:00 QUANTITATIVE GENETICS AND RESPONSE TO CLIMATE CHANGE

Invited Talks

8:00 – 8:40 Rong-Cai Yang - *Genotype × environment interaction in plant breeding: to avoid it or to exploit it?*
8:40 – 9:20 Connie Harrington - *Rise and Shine! How winter temperatures affect the timing of spring budburst and diameter growth*
9:20 – 10:00 Ingo Ensminger - *Tree responses to environmental cues*

10:00 – 10:30 Break

10:30-12:00 WFGA and NWSOMA CONCURRENT SESSIONS

NWSOMA CONCURRENT SESSION

10:30 – 10:50 **Lisa Worthen** – *Phenology, dichogam, and floral synchronization in a northern red oak (Quercus rubra L.) seed orchard.*
10:50 – 12:00 Panel Discussion: Controlled Mass Pollination (CMP) in Douglas fir.

WFGA CONCURRENT SESSIONS

10:30 – 10:50 **Keith Woeste** - *Estimating heritability of disease resistance and long-term survival in butternut (Juglans cinerea L.) confronting an invasive fungal disease*
10:50 – 11:10 **Charlie Cartwright** - *Whitebark Pine Provenance Trials: Early Results.*
11:10 – 11:30 **Olga Grant** - *Contrasting ecophysiology and growth of genetically diverse Sitka spruce seedlings grown under limited vs. optimal water availability.*
11:30 – 11:50 **Jessica Wright** - *Assessing range-wide natural variation in Valley Oak (Quercus lobata) using a newly established provenance test*

12:00 – 1:00 JOINT LUNCH

1:00 –3:00 WFGA SESSIONS

1:00 – 1:20 **Arnaldo Ferreira** – *Managed Relocation of tree genetic resources under climate change*
1:20 – 1:40 **Valerie Hipkins** - *Project CAPTURE: A National Prioritization Assessment of Tree Species for Conservation, Management, and Restoration*
1:40 – 2:20 **Andy Bower** – *Climate change and forest trees in the Pacific Northwest: a vulnerability assessment and recommended actions for National Forests.*
2:20 – 3:00 **TBA**

3:00 – 3:20 BREAK

3:20 – 5:00 WFGA Business meeting

What are genomic technologies, and are they cost-effective for applied tree breeding?

Ross Whetten

Department of Forestry and Environmental Resources, North Carolina State University

The past ten years have seen phenomenal progress in the development of tools for detecting and analyzing genetic and biochemical variation. These tools have generally been developed and first applied in biomedical research, and have then spread to other fields as diverse as agriculture, ecology, population biology, and forestry. These tools are sometimes referred to as genomic technologies, because they allow analysis of many, if not all, genes or gene products in an organism in parallel. Such methods have been applied in research projects on forest trees over the past decade, and the question naturally arises of when they might find application in practical breeding programs working with either conifer or hardwood tree species. This presentation will provide an overview of genomic technologies, including high-throughput methods for discovery and analysis of genetic variation as well as methods for detection of regulatory interactions among genes or between genes and environmental signals. A key question is how to decide when these technologies are ready to move into application in practical breeding programs, and a reasonable approach is to prioritize the opportunities based on the probability of return on investment and the opportunity cost of failing to apply tools as they become available.

Dr. Whetten received a Bachelor's degree in Microbiology from Arizona State University, followed by a Ph.D. in Molecular Biology from Vanderbilt University, followed by post-doctoral research appointments at Utah State University and North Carolina State University. He has been a faculty member at North Carolina State University since 1992, and is currently Professor in the Department of Forestry and Environmental Resources there.

Genomics is a tool, not an outcome, for developing reforestation strategies for new climates

Sally Aitken

Department of Forest and Conservation Sciences, University of British Columbia

Assisted gene flow (AGF), also known as climate-based seed transfer, is the practice of sourcing of seed for reforestation from non-local populations to facilitate adaptation to new climates (Aitken and Whitlock 2013). A survey of the general public in Alberta and British Columbia shows AGF is acceptable to the majority of people; however, respondents showed a preference for the continued planting of local seed from local species (Hajjar et al. 2013). Professional foresters in British Columbia strongly support AGF as a forest management tool for adapting forests to climate change. However, a great deal of uncertainty arises and acceptability drops when genomics is included as a source of information in management options, suggesting the need for careful attention to how knowledge is translated to stakeholders and end users.

AGF strategies are ideally based on species and region-specific data on genetic differentiation of populations. Genomics has the potential to provide information on the extent of local adaptation to climate and population differences more rapidly than traditional provenance trials. Genome-wide analysis of genetic variation can be used to identify genes and genomic regions that show variation in markers along climatic and geographic gradients. Genomics can also be used to identify genes associated with climate-related phenotypes such as phenology and cold hardiness. We are currently using these approaches to understand local adaptation to climate and inform AGF strategies in lodgepole pine (*Pinus contorta*) and interior spruce (*Picea glauca, P. engelmannii,* and their hybrids)

Genomic patterns of variation, like phenotypic variation from provenance trials and seedling common gardens or climate data, can be used to group similarly adapted populations into seed zones, to understand the amount of adaptive variation within populations, and to develop climate-based seed transfer recommendations. AGF strategies are urgently needed for adapting managed forests to climate change. Whether such strategies come from genomic studies, provenance trials or climatic data should not form the main message when translating results for forest managers or the public. Genomics is simply one of several possible tools, not an outcome in and of itself.

Aitken SN, MC Whitlock. 2013. Assisted Gene Flow to Facilitate Local Adaptation to Climate Change. *Annual Review of Ecology, Evolution, and Systematics* **44**:367-388.

Hajjar R, E McGuigan, M Moshofsky, R Kozak. 2014. Opinions on strategies for forest adaptation to future climate conditions in western Canada: Surveys of the general public and leaders of forest-dependent communities. *Canadian Journal of Forest Research* **44**: 1525-1533.

Rethinking Communication in Agricultural Biotechnology

Kevin M. Folta

Professor and Chair, Horticultural Sciences Department, University of Florida, Gainesville, FL

Transgenic crop technologies have demonstrated a favorable record of safety and efficacy over almost two decades. However, new technologies are slow to emerge, and existing applications suffer from a generally negative public perception despite a strong scientific consensus supporting their use. This disconnection between perception and reality is due to a combination of factors, including active manufacture of risk by anti-corporate activists and those that profit from a message of fear about food. Scientists and companies supporting these technologies have countered the fear message with an evidence-based approach that does not resonate with concerned citizens simply looking for answers. The result is a continued distrust of technology used to produce food. Going forward it is necessary to reframe scientific discussions by starting from a platform of common concerns, and then demonstrating how transgenic technologies can help meet those shared goals. Compelling emotional appeals can be generated from discussion of real opportunities lost. Successful communication in biotechnology will require scientists to earn trust, make personal connections, discuss shared values, and demonstrate how these technologies can benefit farmers, the environment, the needy, and the industrialized-world consumer.

Kevin M. Folta is a Professor and the Chairman of the Horticultural Sciences Department at the University of Florida. His laboratory examines fundamental light signal transduction and its application to control plant growth, metabolism and development, with focus on high-value crop traits. His group also uses state-of-the-art genomics approaches to identify novel genes that control important traits (such as flavor and disease resistance) in small fruits, and led the strawberry genome sequencing project in 2010- producing the 12th plant genome sequenced. He has been recognized with several awards, including the NSF CAREER Award, the University of Florida Research Professorship, and the HHMI Distinguished Mentor Award. A key extension of his program is communicating science to non-scientific audiences, and training scientists how to perform public outreach in scientific or controversial topics. BS/MS Northern Illinois University 1989/1992, Ph.D. University of Illinois at Chicago, 1998.

Public Policy Challenges in Agricultural Biotechnology and Opportunities in Tree Biotechnology

James Curry and Cintia Ribeiro,
Monsanto

Biotechnology in agriculture remains a hot topic right now in state legislatures and in front of voters around the country. Activism on mandatory food labeling and crop production bans have hit close to home in recent years, with several statewide and local ballot measures decided by voters in the Pacific Northwest. Monsanto Company, a leader and pioneer in seed trait technology, has been at the forefront of those political battles and a lightning rod for activists. James Curry, Monsanto's regional government affairs director, will present on the current political landscape, the public perception issues and activism that drive the politics in this area, how the campaigns have been fought and won, and what to expect next at the local, state and federal levels. Cintia Ribeiro, PhD, with Monsanto's Emerging Leaders in Science Program, will speak to opportunities and challenges in tree biotechnology, including future traits of interest and the scientific community's challenges with the public.

Dr. Cintia Ribeiro joined the Emerging Leaders in Science program at Monsanto Company in the fall of 2014. Prior to joining Monsanto, Cintia received a PhD from University of Florida, in Gainesville, researching yield genomics in Forestry species. During the 4 years at University of Florida, Cintia received numerous scientific and academic awards, was an active member of the Alpha Zeta Agricultural Honors Fraternity and a representative of the Graduate Student Body. Born and raised in Brazil, Cintia received bachelor's degrees in Biology and Teaching from Sao Paulo State University. During her undergraduate studies, she researched biotechnology in Eucalyptus trees and worked with forestry breeding in Pulp and Paper companies. She also had research experience with human cancer and fish population genetics. In Brazil, she volunteered teaching adult education classes and workshops at rural schools.

James Curry is the Director of State and Local Government Affairs in the Pacific Northwest Region for Monsanto Company. In this capacity, James manages the company's legislative and political interests in eight states in the northwest portion of the country, based in Portland, Oregon. He joined the company in the spring of 2014, working with an experienced group of individuals that make up Monsanto's state and local government affairs team across the country. Prior to joining Monsanto, he spent two years as the Director of Government Affairs for the Northwest Food Processors Association in Portland, directing the association's legislative programs in Washington, Oregon and Idaho. Before joining the food and agriculture sectors, James worked for eight years with Washington State's largest and longest-standing government affairs practice at Carney Badley Spellman, PS. While with the Seattle-based firm, he represented clients before the legislature on construction, insurance, health care, energy and general business issues. James serves on the board of directors of Oregonians for Food and Shelter and Washington Friends of Farms and Forests. Born and raised in Tacoma, Washington, James received a bachelor's degree in Political Science from the University of Washington in Seattle.

Forest genetic and tree improvement research in the US: past, present and future[1].

Nicholas Wheeler[2], Kim Steiner[3], Scott Schlarbaum[4] and David Neale[5]

[2] Molecular Tree Breeding Services, LLC, [3]Penn State University, [4] University of Tennessee, [5]University of California at Davis

Forest genetics (FG) research in the United States began over 100 years ago with racial (seed source) trials of ponderosa pine (*Pinus ponderosa* Douglas ex C. Lawson) and Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco), and, over the ensuing four decades gradually emerged as a distinct and important discipline of study within the forestry research community. Coupled with the allied field of tree improvement (TI), the discipline enjoyed rapid and expansive growth for over 30 years beginning in the early 1950's. The subsequent 30 years witnessed an equally dramatic contraction and transformation of the FG/TI community. We review the economic, social and policy factors that contributed to the decline of FG/TI and the transformation to a discipline that now includes a strong ecosystem management component. Cautionary lessons are coupled with a call for enhanced funding of traditional and genomic FG/TI efforts in the face of growing forest health and climate change threats that are having profound effects in the nation's forests.

[1] Wheeler, N.C., K.C. Steiner, S.E. Schlarbaum, and D.B. Neale. 2015. The evolution of forest genetics and tree improvement research in the United States. Journal of Forestry (in print).

The effects of selective breeding on adaptive phenotypic traits in interior lodgepole pine

I. R. MacLachlan*, T. Wand*, A. Hamann†, P. Smets*, J. Tuytel*, S. N. Aitken*

*Department of Forest and Conservation Sciences, University of British Columbia, † Department of Renewable Resources, University of Alberta

The AdapTree project is quantifying phenotypic and genomic architectures of local adaptation to climate in lodgepole pine (*Pinus contorta* Doug. *ex* Loud. var. *latifolia* Engelm.) to inform future provincial climate-based seed transfer policies. In Western Canada, reforestation using seedlots from selective breeding programs is increasing rapidly, but the impacts of selective breeding on climate-relevant phenotypic traits in current and predicted future climates remain unclear. To address this knowledge gap, we established a large seedling common garden (n = 2880 individuals) representing 281 natural seedlots and 20 selectively bred seedlots from provenances across British Columbia and Alberta. We have made detailed assessments of growth, phenology and cold hardiness traits. Our analyses compare trait means, climatic clines and trait-trait correlations between natural and corresponding selectively bred seedlots.

Growth traits show large differences between seedlot types within breeding zones resulting from selective breeding. Clines in growth traits along provenance climate gradients are steeper in selectively bred material than natural populations, indicating that selection for timber volume has increased the strength of local adaptation. However, trade-offs between gains in growth due to selection and phenology or cold hardiness traits appear to be weak. At the moment our work suggests that the same assisted gene flow prescriptions will be appropriate for selectively bred and natural reforestation seedlots to pre-adapt planted forests to new climates without compromising local adaptation. All the seedlings in this trial are now being genotyped using the AdapTree 50K SNP array, allowing us to compare adaptive genetic diversity between selectively bred and natural populations.

Genetic parameters of growth and adaptive traits for aspen (*Populus tremuloides*): implications for tree breeding.

Chen Ding[1]*, Andreas Hamann[1], Rong-Cai Yang[2] & Jean S. Brouard[3]

[1] Department of Renewable Resources, University of Alberta, [2] Department of Agricultural, Food & Nutritional Science, University of Alberta,[3] Isabella Point Forestry Ltd

Populus tremuloides is a widespread commercial forest tree of high economic importance in Canada and has been subject to tree improvement efforts over the past two decades to increase productivity of the forested land base. Successful selection and breeding programs rely on accurate estimate of genetic gain for commercial traits and correlated responses of other traits linked to fitness. Here, we estimate genetic parameters of growth and adaptive traits in 10 progeny trials (i.e., alpha design) containing more than 30,000 trees with known pedigree structure based on a partial factorial mating design, including 60 half-sib families, 100 full-sib families and 1,400 clones. Narrow-sense and broad-sense heritabilities were generally low with values around 0.2 and standard errors of approximately 0.1. Phenology traits, bud break and leaf abscission, had moderate broad- and narrow-sense heritabilities around 0.4 with standard errors of 0.1. For all measured traits, additive genetic variation was most important and dominance and epistatic variance components were small or zero. Moderate to strong genetic correlations were found between growth and phenology (r=-0.3 and 0.7) with tall trees being associated with early budbreak and late leaf abscission. Survival was not compromised, but facilitated by early bud break or late leaf abscission, indicating that utilization of the growing season was more important than avoidance of spring and fall frosts across all test sites in this experiment. We conclude that selection for juvenile growth in aspen trees only promises small genetic gains, but higher heritabilities are expected at a date when trees are older based on the trend in elder trials. Strong additive genetic correlations between growth and phenology indicates that much of the genetic gain at the early stage of stand development will be due to expanding the growing season, which may increase the risk of frost damage in spring and fall.

Using genotyping-by-sequencing (GBS) to elucidate population structure in Oregon white oak (*Quercus garryana*)

Jonathan Degner and Sally Aitken

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

A pilot study was performed to obtain basic information on population differentiation across the species range of Oregon white oak (*Quercus garryana*), assess the validity of the three currently accepted taxonomic varieties, and to test the applicability of genotyping-by-sequencing (GBS) for obtaining genetic data for this species. Eighty-seven individuals representing 11 populations were sequenced in a single multiplexed GBS library, generating 20 megabases of unique sequence data with high coverage, estimated to represent ~2% of the genome. 20,751 high-quality single nucleotide polymorphisms (SNPs) were discovered, which were used to determine population differentiation and genetic structure. Ordination-based and Bayesian clustering analyses revealed two distinct genetic clusters, one corresponding to *Q. garryana* var. *garryana* and the other to both vars. *semota* and *breweri*. Some evidence supports the presence of additional hierarchical structure within both of these genetic clusters, although no evidence could be found to support the taxonomic division between vars. *semota* and *breweri*. F_{ST} averaged 0.091, and was strongly correlated with physical distance (multiple R^2=0.93, p<0.0001). Population pair-wise F_{ST} was significantly higher between populations of different genetic clusters than among them. Heterozygosity was negatively correlated with latitude (R^2=0.72, p=0.001), and was higher in vars. *semota* and *breweri* than in var. *garryana* (p<0.0001). The success of sequencing and analyses using GBS merited expansion of this pilot project into a larger-scale study with higher representation within and among populations. Collections have been made for this expansion and further genetic data is pending.

Phenotypic selection and genecology of growth rhythm in whitebark pine (*Pinus albicaulis*) grown 12 years under climate warmer and drier than climate of origin.

Marcus Warwell

Rapid, ongoing climate change threatens to desynchronize growth rhythm for many forest tree populations, which will result in maladaptation. In response, forest tree populations may persist with reduced productivity, migrate, genetically adapt, and/or become extirpated. Information about all these factors is required to predict the response of forest tree populations. However, we have only limited understanding about selection on growth rhythm and its impact on the evolution of forest tree populations. As a first step toward assessing genetic adaption of forest trees under changing climate, the form of phenotypic selection on measures of growth rhythm was evaluated over a 12-year period for young whitebark pine (*Pinus albicaulis* Engelm.) trees grown in two, low-elevation, common-garden field experiments over a 12-year period under climates that approximated projected climate change in the present century (+ 4.4°C to 9.1°C mean annual temperature). The whitebark pine originated from 49 populations representing interior northwestern USA. In addition, variation in growth rhythm among populations and its relation to climate of seed source were evaluated to assess how growth rhythm varies in relation to climate across the region. Timing of apical shoot elongation was used as a proxy for growth rhythm. Height at the end of the study was used as the best available measure of fitness. Results showed that survival and the unconditional expected value for height were dependent on timing of apical shoot elongation within and among growing seasons. Directional and stabilizing selection was detected and associated with differential survival. Individuals that exhibited intermediate apical shoot elongation rates in the earliest years were inferred to have the highest fitness in 2012. Differences among seed sources for growth rhythm were mild and were modestly associated ($r^2 = 0.08 - 0.28$) with climatic clines. Such information can directly inform forest management decisions regarding gene conservation and reforestation, and preliminary results provide estimates of selection that can be combined with information on trait inheritance to estimate evolutionary trajectory in the short term.

Genetic diversity and population structure in the rare, endemic Baker cypress (*Cupressus bakeri*)

Andrew D. Bower[1] and Valerie Hipkins[2]

[1]USDA Forest Service, Olympic National Forest, [2]USDA Forest Service, National Forest Genetics Laboratory, Placerville, CA

Baker cypress (*Cupressus bakerii*) is one of ten species of cypress found on the west coast of North America. It is restricted to a small number of highly disjunct, isolated populations, making it particularly vulnerable to the influences of genetic drift, inbreeding, and reduced gene flow. Baker cypress is fire adapted and its serotinous cones require the heat of a fire to open and release their seeds. Altered fire regimes in some areas have negatively impacted the health and vigor of some populations and lower levels of genetic diversity may make this species more susceptible to the impacts of predicted future climate change. Previously, no information on Baker cypress genetics was available. We used 12 polymorphic allozyme loci to assess genetic diversity and population structure for eight of the 11 known populations of Baker cypress. Overall mean observed heterozygosity (H_o) was 0.178 and expected heterozygosity (H_e) was 0.204, values higher than for other cypress species and other fire-adapted conifers. Despite the relatively high levels of genetic diversity, in many populations $F>0$ indicating a deficiency of heterozygotes, most likely due to inbreeding and possibly a Wahlund effect. Population differentiation among seven of the eight populations (the northernmost population excluded) was 9%, considerably lower than for other conifers with disjunct populations. Our results indicate that the current population structure of the species is likely a fairly recent reduction from a formerly widespread distribution. Implications of genetic diversity and population structure for potential restoration work is discussed.

Genotype × environment interaction in plant breeding: to avoid it or to exploit it?

Dr. Rong-Cai Yang

Research Scientist, Alberta Agriculture and Rural Development (ARD) & ARD professor,
University of Alberta

The usual approach to dealing with genotype × environment interaction (GxE) in crop plants and forest trees is to select for the best genotype across all environments. This conventional approach ignores GxE by focusing on genotypic stability across all environments. In this presentation, I will discuss some new approaches that enable plant breeders to exploit GxE by identifying genotypes best suited to specific environments through the use of genomic and geo-ecological information.

Rong-Cai Yang obtained his PhD degree in quantitative genetics/plant breeding from the University of Saskatchewan. He is currently a Research Scientist with Alberta Agriculture and Rural Development (ARD) and ARD Professor with the University of Alberta. Dr. Yang has maintained a very active research program in statistical genomics related to plant and animal improvement. His current research interests and activities include: (i) Barley breeding platform; (ii) genomics of lodgepole pine resistance to western gall rust; (iii) statistical and genetic analyses of large-scale genomic data; and (iv) geostatistics and its applications to precision agriculture.

Rise and Shine! How winter temperatures affect the timing of spring budburst and diameter growth

Connie Harrington

USDA Forest Service, Pacific Northwest Research Station, Olympia, WA

Most northwest tree species have a chilling requirement which needs to be fulfilled for rapid budburst to occur in the spring. The more hours of cool but not freezing temperatures they experience in the spring, the fewer hours of forcing (warm temperatures) are needed. The tradeoff between chilling and forcing has been determined for several northwestern tree species. Re-initiation of diameter growth in the spring also has a chilling requirement but fewer hours of chilling are required, resulting in diameter growth initiation occurring a month or more ahead of budburst. Quantifying these relationships helps explain what we observe in the field and can allow us to make predictions of how climate change or moving seed lots to new areas will affect these elements of spring phenology.

Connie Harrington is a research forester with the USFS Pacific Northwest Research Station in Olympia, WA. Her research focuses on plant responses to the environment and management actions.

Tree responses to environmental cues

Ingo Ensminger

Department of Biology, University of Toronto Mississauga, Mississauga, ON, L5L 1C6, Canada

Trees use environmental cues such as water availability, temperature and light to synchronize growth and development with seasonal changes, and to compete for resources with other plants. The ability of trees to effectively sense and respond to these signals requires programs to enable them to track change rapidly and adapt accordingly. This presentation will review some of our recent work on understanding tree responses to episodes of drought, elevated temperature, low temperature, and photoperiod. These cues are amongst the most important environmental factors affecting tree performance over the course of the season and in a changing climate. Examples will include recent studies on conifers using controlled environments (phytotrons) and field experiments to illustrate the significance of the interaction of multiple cues and dynamic natural environments. I will conclude with a brief overview of transcriptomic approaches used in our group to understand adaptation and plasticity in different conifers.

Estimating heritability of disease resistance and long-term survival in butternut *(Juglans cinerea* L.) confronting an invasive fungal disease

Nicholas LaBonte[1], Keith Woeste[2]

[1]Department of Forestry and Natural Resources, Purdue University
[2]USDA Forest Service Hardwood Tree Improvement and Regeneration Center at Purdue University

For most wild species affected by exotic pests or pathogens, the relative importance of heritable genetic differences in determining apparent variation in disease resistance is unknown. This is true in particular for butternut, a North American hardwood affected by butternut canker disease and undergoing demographic contraction. Little is known about site effects on butternut decline, in part because long-term monitoring data are lacking. We collected detailed disease phenotypes and multilocus microsatellite genotypes for all surviving individuals in a large natural population of butternut in 2003 (n=302) and 2012 (n=113). We then applied two analytical methods, correlations between pairwise phenotypic similarity and pairwise relatedness, and estimation of among-family variance, both indicated weak heritability of disease-related traits and no heritability for overall tree health in the population. Additionally, an analysis of spatial data collected in 2001 (n=341) and 2012 (n=113) demonstrated that drier, upland sites contribute to increased likelihood of survival. We conclude that genetic differences among wild butternut individuals contributed little to observed variance in survival over ten years but fine-scale site differences were useful predictors of butternut mortality.

Whitebark Pine Provenance Trials: Early Results.

Charlie Cartwright

Cowichan Lake Research Stn, Tree Improvement Branch, Min. of Forests, Lands and NRO
Mesachie Lake, BC

Whitebark pine is currently undergoing catastrophic population declines largely due to white pine blister rust and to a lesser extent both mountain pine beetle and wild fires. As part of supporting restoration efforts, field trials are underway to eventually allow for developing climate based seed transfer guidelines and identifying rust resistant trees and seed sources. 500 whitebark parent trees from 80 populations were collected from throughout the range of whitebark pine, and are to be tested in long term field trials. 2 series of 4 test sites, each with half the families, are to be deployed across the range in BC with the first series to be established in 2015 and the second 2 years later. Survival and effects of rust will be scored on the seedlings periodically, along with measuring growth. As well as resistance, it is anticipated that eventually trait durability will be determined, facets of genetic architecture, and impacts of climate change. Nursery data reported provide insights concerning nursery practices as well as quantifying provenance differences detected so far. Implications of the listing of the species as endangered under the Federal Species at Risk Act will also be touched upon, as well as how these trials and other activities on the part of the Province of British Columbia will assist in recovery on provincial lands.

Contrasting ecophysiology and growth of genetically diverse Sitka spruce seedlings grown under limited *vs.* optimal water availability.

Olga M. Grant[1], David Thompson[2], Conor O'Reilly[1]

[1]UCD Forestry, School of Agriculture & Food Science, University College Dublin, Belfield, Dublin 4, Ireland, [2]Coillte Tree Improvement Centre, Kilmacurra, Co. Wicklow, Ireland

Sitka spruce is the predominant species used in afforestation in Ireland, with material of Washington provenance considered appropriate for Irish growing conditions. Increasing the vigour of Sitka spruce will improve timber yields. In some areas where afforestation is planned, water availability is expected to decline in future. Therefore material selected now must maintain vigour in relatively dry conditions. Seedlings from a range of full-sibling families produced by crossing different elite trees were compared under optimal and water-limited conditions in a greenhouse experiment, established when seedlings were one year old, and maintained until age four. Seedlings of unimproved Washington provenance were included as a control. Families contrasted markedly in annual height and root collar diameter increments. Limited water availability resulted in a reduction in branch water potential, leaf stomatal conductance, and whole plant transpiration. Increased carbon isotope composition in all material, except for the control and the least vigorous family, suggested increased photosynthetic water use efficiency as a result of water-limitation. This was reflected in a 50% increase in the ratio of biomass gained to water transpired over a growing season – but this measure of whole plant water use efficiency did not differ between families. Bud flush was delayed by water limitation and in some families growth ceased earlier. Specific leaf area increased and the number of first-order branches and the area and mass of leaves per unit stem length increased. Height increments were reduced, with the greatest reductions occurring in the most vigorous families. These very vigorous families, when water-limited, were nonetheless taller and had wider root collar diameters at the end of the experiment than well-watered seedlings of the least vigorous material. Therefore selection under optimal conditions may be an appropriate approach to select the best material, even for sub-optimal environments. This should be validated with older material.

Assessing range-wide natural variation in Valley Oak (*Quercus lobata*) using a newly established provenance test

Jessica W. Wright[1] and Victoria L. Sork[2]

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Valley oak is a majestic California native oak found throughout California's foothills, valleys and flood plains, and is under threat due to habitat loss, low recruitment in remnant stands and climate change. Valley oak is considered a foundational species that shapes the ecosystem and its biodiversity where it is found. To better understand the ecological genetics of this species, we established a range-wide provenance test. We sampled 674 maternal trees from 95 different collecting sites from across the entire species range. The acorns were germinated in a greenhouse and out-planted into the field two years later. There are two field planting sites- one at the USDA-FS PSW Institute of Forest Genetics, the other at the USDA- FS Genetic Resource and Conservation Center, Chico. The study has multiple goals, with a primary focus on understanding tree responses to climate change. First we hope to define seed transfer guidelines for Valley oaks in California, as well as identify populations of conservation concern- particularly in light of climate change. We are measuring traits associated with growth and fitness, as well as response to a changing climate- including phenology. Here we report early findings from the trees in their first 2 years of growth in the greenhouse and field. We have found that there are significant genetic correlations among traits, and significant variation when trees started to leaf out in the spring.

Managed relocation of tree genetic resources under climate change

Arnaldo Ferreira

USDA Forest Service, Placerville CA

Identification of potential areas sensitive to shifts of major forest types under climate change would be critical to restore resilience to our forest ecosystem. GIS-based models for climate change and vegetation distribution can be used to identify these shifts. In combination with local knowledge from foresters and ecologists, better understanding of how climate change could alter species distribution/composition would be of foremost importance on the design of Managed Relocation strategies of forest populations across the landscape. In this presentation, I'm proposing an operational procedure to implement a population-level Managed Relocation to the Forest Service Pacific Southwest Region ecological restoration practices. We believe this is a proactive and moderate approach to promote resilience of our forests to the effects of climate change on long-term forest health.

Project CAPTURE: A National Prioritization Assessment of Tree Species for Conservation, Management, and Restoration

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A variety of threats, most importantly climate change and insect and disease infestation, will increase the likelihood that forest tree species could experience population-level extirpation or species-level extinction during the next century. Project CAPTURE (Conservation Assessment and Prioritization of Forest Trees Under Risk of Extirpation) is a cooperative effort across the three USDA Forest Service deputy areas to establish a framework for conservation priority-setting assessments of forest tree species across the entire United States. Project CAPTURE uses extensive lists of life history trait data, as well as climate change and pest and pathogen threat information, to categorize and prioritize nearly 400 tree species for conservation, monitoring, management and restoration across all forested lands in the contiguous United States and Alaska. The Project CAPTURE framework was developed with input from a 2014 workshop that included resource managers and scientists across the country and from the three Forest Service deputy areas. The Project CAPTURE framework allows for the quantitative grouping of species into vulnerability classes that may require different management and conservation strategies for maintaining the adaptive genetic variation of the species contained within each class. This assessment tool should be valuable for scientists and managers attempting to determine which species and populations to target for monitoring efforts and for pro-active gene conservation and management activities.

Climate Change and Forest Trees in the Pacific Northwest: A vulnerability assessment and recommended actions for National Forests.

Andrew Bower[1, 4], Warren Devine[2], Carol Aubry[3]

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Climate change presents new challenges to land managers. At stake is our ability to make thoughtful, science-based decisions and to add climate change considerations to our project and management plans. We also must prioritize among the opportunities that can be included in adaptation strategies because funding and time are limited, now more than ever. We conducted a vulnerability assessment of common overstory forest tree species for the Pacific Northwest and provided recommended actions based on the results of this assessment. These recommendations will sharpen the focus of activities on the most vulnerable species while simultaneously conserving biodiversity and building resiliency. Our analytical approach did not include spatially explicit predictions of future tree species habitats. Rather, it uses life history traits, distribution, and pest and pathogen data for individual tree species, combined with consensus regional climate projections to rate each species' relative vulnerability to a changing climate. The analytic method we employed here with forest trees is transparent, flexible, and simple to apply and could be adapted to apply to other native plants including forbs and grasses. Vulnerability scores varied by species and geographic area, but there was a consistent positive relationship between vulnerability to climate change and mean elevation with many of the most vulnerable tree species occurring at the highest elevations. There were three overall recommendations for land managers that came out of this assessment: 1) learn about and track changes in plant communities as the climate changes, 2) maintain and increase biodiversity and increase resiliency, and 3) prepare for an uncertain future. Specific action items were proposed to address these recommendations based on the results of the vulnerability assessment.

NWSOMA ABSTRACTS

Efficacy of Systemic Injections of Emamectin Benzoate and Imidacloprid to Control Douglas-fir Cone Gall Midge and Fir Coneworm in Douglas-fir Seed Orchards

Alex C. Mangini[1]*, Candace J. Cahill[2], Daniel W. Cress[3], Jeffrey D. DeBell[4], Lawrence K. Miller[5]

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Two systemic insecticides, emamectin benzoate and imidacloprid were tested for efficacy against the Douglas-fir cone gall midge, *C. oregonensis* (Foote), and the fir coneworm, *D. abietivorella* (Groté), major cone pests of Douglas-fir, *Pseudotsuga menziesii* (Mirb.) Franco. The study was conducted in four Douglas-fir seed orchards, three in Washington and one in Oregon in 2012. Three treatments: emamectin benzoate as TREE-äge®, imidacloprid as Imajet® (both products of Arborjet, Inc.) and an untreated control were applied to 15 ramets each at the three Washington orchards and to 8 ramets each at the Oregon orchard. The study design in all orchards was a randomized complete block with clone as the blocking variable. Applications were made in October 2012 after stimulation for cone production. A Quik-Jet® injector and Arborplugs® (Arborjet, Inc.) were used to inject the systemics at labeled rates. In 2013, Douglas-fir cone gall midge damage was estimated by cut-cone counts in mid-summer. Coneworm damage was evaluated at harvest. Green cones were collected at three orchards for chemical residue analyses. Cone samples from each treatment at each orchard were collected for seed extraction and radiography to estimate damage from seed bug, *Leptoglossus occidentalis* Heidemann, and Douglas-fir seed chalcid, *Megastigmus spermotrophus* Wachtl. Results and implications for Douglas-fir seed orchard IPM programs will be discussed.

Phenology, dichogamy, and floral synchronization in a northern red oak (*Quercus rubra* L.) seed orchard

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We developed a novel scoring system to assess spring phenology in a northern red oak clonal seed orchard. The system was used to score between 304 and 364 ramets for three reproductive seasons and place clones into early, middle, and late phenology groups. While the absolute number of clones in each phenological class changed from year to year, the overall order of clonal flowering was highly stable ($r_s = 0.67$, $p < 0.001$). The average length of pollen shed for a clone was 10 days; the average length of a clone's female flower receptivity was 9.5 days. Temperature had a clear effect on the duration of flowering in the seed orchard, where early clones flowered significantly longer than later flowering clones in all three years. Dichogamy was present in the orchard with male flowers of a clone emerging between 1.4 and 3.0 days sooner than its female flowers. Mean dichogamy values for individual clones ranged between 0.0 and 4.9±1.3 days. Year strongly influenced a clone's dichogamy value (F=12.8, p<0.001) while genotype had no influence. The mean overall phenological synchronicity for the three years of observation was 0.30±0.01, or about 30% overlap between all receptive females while males were shedding pollen. In all years, late flowering males had the highest phenological overlap (*PO*) values, followed by intermediate males. Early flowering males had the lowest *PO*. Female flowers had the opposite pattern – early flowering females had the highest *PO* values while late flowering females had the lowest *PO*. This represents the first effort to quantify phenology in an artificial population of northern red oak and provides a snapshot of the current relationship between temperature, phenology, and floral synchronization.

Western Forest Genetics Association and
Northwest Seed Orchard Managers Association Joint Annual Meeting

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